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AUJUS EDITORIAL TEAM

Editor in Chief

Lorenzo Cremaschi is a Professor in the Department of Mechanical Engineering and Director of Undergraduate Research at Auburn University (Auburn, AL, U.S.). He received his Ph.D. from the University of Maryland (College Park, MD, U.S.) in 2004. In 2001, he was awarded his M.S. and B.S. diploma degrees from the University of Modena (Italy). Before joining Auburn University, Dr. Cremaschi was a post-doctoral research associate at Purdue University's Herrick laboratories, followed by assistant and associate professor in the School of Aerospace and Mechanical Engineering at Oklahoma State University (Stillwater, OK).

Dr. Cremaschi's interests focus on buildings' energy efficiency and sustainability, scalable thermal energy systems, water desalination and purification, and the water-energy-food nexus. His current research includes thermodynamics and heat transfer of low Global Warming Potential refrigerants, air dehumidification processes, frost and defrost, and moisture transport in thermal insulation systems. He is the principal investigator of several research projects and the author of over 105 papers. He revised three book chapters and gave several presentations at conferences, meetings, and university seminars. Dr. Cremaschi is the inventor of two international patents.

Dr. Cremaschi served as an associate editor for the Science and Technology for the Built Environment Journal. He has several honors and awards, including the 2022 Research Award for Excellence in the College of Engineering and the 2020 Exceptional Service Award from the American Society of Heating, Refrigerating and Air-Conditioning Engineers (ASHRAE).

Dr. Cremaschi teaches Thermodynamics, Refrigeration, Renewable Energy Systems, and Cryogenics courses. These courses are offered at the undergraduate mechanical engineering curriculum's second, third, and fourth years and the graduate level. Dr. Cremaschi advised 35 graduate students (14 Ph.D. and 21 M.S. students) and over 50 undergraduate students in academic curriculum and career choice. He also mentored 23 undergraduate students and 9 international visiting exchange scholars during research and scholarly activities. Dr. Cremaschi is the faculty advisor of the Auburn University ASHRAE student organization. He fostered several scholarships and awards for undergraduate students involved with research, including the 2023 Matthews fellowship program, which promotes engagement in undergraduate research by Pell-eligible students.

Dr. Cremaschi is the chair of the American Society of Thermal and Fluids Engineers (ASTFE) Executive Committee and served on the ASHRAE Research and Administration Committee. He is chair of the International Institute of Refrigeration (IIR) U.S. National Committee and the International Energy Agency (IEA) U.S. Heat Pump National team member. He has served on several technical and standard committees for 20 years. Dr. Cremaschi was the technical program chair for two ASTFE conferences in 2019 and 2021. He organized numerous technical sessions, panel forums, and seminars within ASHRAE, ASTFE, IIR, and the American Society of Mechanical Engineers (ASME).

Production Editor

Lexy Barraza is a second-year graduate student pursuing her Doctorate in Audiology. Lexy graduated from the University of South Florida with a Bachelor of Science degree in Health Science. She is a Graduate Assistant for the Office of Undergraduate Research. She is in charge of processing and editing AUJUS highlights and articles. Her research studies the effects of hearing loss on Hispanic cultures in Alabama. Lexy's other on-campus involvements include being a Student Academy of Audiology member and an Auburn University Rural Health Fellow. In her spare time, she volunteers at the Chambers County Community Health & Wellness Center and spends quality time with her family in Florida.

Production Editor

Hannah Sellers is a third-year graduate student pursuing her Doctorate in Audiology. She is currently working at an off cite ENT clinic for her program. She is a Graduate Assistant for the Office of Undergraduate Research. She is in charge of the mentor matching program, newsletter and editing for the AUJUS journal. Her past research was studying motivation behind volunteer work and presenting at a state wide research convention. Involvement now includes working on research related Auditory Processing Disorders and being a member of the Student Academy of Audiology. She loves to travel whenever she can and in her spare time, she enjoys reading, spending time with her pets, family and friends.

Associate Editor

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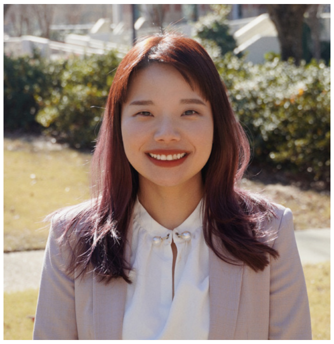
Associate Editor

Maliha Yel Mahi is in her third year of pursuing a Ph.D. in Mechanical Engineering, specializing in Computational Fluid Dynamics (CFD) and Multiphase Fluid Flow. She has achieved her Master's degree in Mechanical engineering from the University of North Dakota. She enjoys reading books, spending time with family and friends, and traveling in her spare time.

Associate Editor

Jeremiah Pfitzer is a fifth-year graduate student pursuing his Ph.D. in Pharmacology at the Harrison College of Pharmacy at Auburn University. He received his Bachelor of Science in Biology and Genetics in 2019. Jeremiah's research investigates novel secondary therapeutics in multiple myeloma with an emphasis on Ras driver mutations. He previously worked in targeting glutamate dysregulation in Alzheimer's disease and in discovering mechanisms driving tauopathies. He is also an assistant conference developer for the annual Innovations in SoTL Medical Education conference.



Associate Editor

Ying Yan is a Ph.D. candidate in the Consumer and Design Sciences. She has rich work and research experience in multiple fields, including industrial design, interior design, consumer behavior, and business. She previously graduated from Nanjing Agriculture University with a Bachelor of Industrial Design in Mechanical Engineering, as well as a Master of Industrial Design at Auburn University. Throughout her research, she has been continuously fascinated by the intersection of design and well-being. Recognizing the profound influence environments have on our mental and physical health, she was drawn to explore how design can positively impact human well-being. Currently, Ying's research focuses on increasing college students' learning motivation through game-based learning to enhance learning experiences in design education.

Associate Editor

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Associate Editor

Claudia Ann Rutland is a PhD student and a graduate research assistant in the Department of Crop, Soil, and Environmental Sciences, studying weed science under Dr. Scott McElroy. She graduated from Auburn University in 2020 with a Bachelor of Science in Microbiology. Her current research focuses on target-site resistance in herbicide resistant weed species, more specifically understanding the mechanisms of resistance in auxin-mimic herbicides. In her free time, she enjoys reading, painting, and playing with her dog Obi.

Associate Editor

Ifeoluwa Odeniyi is a PhD candidate and graduate research assistant in the Department of Nutritional Sciences. He obtained both his bachelor's and master's degrees from Nigeria in Biochemistry. He has rich work and research experience in patient tumor xenograft model and tumor dissociation, mouse breeding, genotyping and metabolic cage assessment and adipocyte differentiation. Currently, his PhD research in Dr. Greene's lab focuses on the link between obesity and its role in the development and progression of colorectal cancer through integrating molecular biology, genetics, and nutrition. Outside his academic undertakings, Ifeoluwa's leadership acumen shines through his role as the President of the African Students Association during the academic year of 2022/2023. His exceptional dedication was meritoriously acknowledged with the title of student leader of the year, accompanied by an array of additional awards. He has published 8 peer-reviewed journal articles and numerous conference presentations. During moments of respite, he finds solace and joy in strumming the guitar, a pursuit that harmoniously balances his multifaceted life

Associate Editor

Olumide Falana is a second-year Ph.D. student in Biosystems Engineering Department and a researcher at National Poultry Technology Center. Olumide's academic journey commenced with a Bachelor of Science in Agricultural and Environmental Engineering from Obafemi Awolowo University in Nigeria. He further expanded his horizons with a Master of Science in Agricultural Engineering from the same institution. Olumide is conducting research in the poultry industry, contributing to animal welfare and food security research. Presently, he is studying the thermal environment in commercial poultry houses in Alabama. Beyond his academic pursuits, he finds joy in volunteerism, cultural integration, and strategic social media engagement. Olumide Falana's journey is one of continuous learning, proactive research, and a commitment to driving positive change within Biosystems Engineering and its application in agriculture.

Associate Editor

Gabrielle Brown is a PhD student in the Counseling Psychology program and a graduate research assistant for the department of Special Education, Rehabilitation, and Counseling. She earned her Master of Public Health in Health Policy and Management from Emory University and Bachelor of Arts in Psychology from Vanderbilt University. Her research interest include teletherapy utilization, mental health service accessibility, dismantling health disparities and the connection between applied psychology and health policy. In her spare time, she enjoys drinking tea, reading and spending time with friends and family.

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Associate Editor

Pooja Zen Santhamoorthy is a fourth-year Ph.D. student and a graduate research assistant in the Department of Chemical Engineering, working on developing optimization tools under Dr. Selen Cremaschi. She graduated from Anna University in 2019 with a Bachelor of Technology in Chemical Engineering. Her current research focuses on developing portfolio optimization models for planning carbon capture and utilization and solution approaches to solve the developed mathematical model. She enjoys reading fiction, playing DOTA, and caring for her sweet pets, Valerie and Rocket.

Associate Editor

Olamide Isaac Durodola is a graduate student of Biosystem Engineering. He had his undergraduate in Agricultural and Environmental Engineering at Obafemi Awolowo University in Nigeria. His research efforts have been dedicated to conducting spatial analysis within incubators, with the goal of achieving optimal performance and increased productivity by refining air velocity, temperature, and humidity conditions. In his spare time, he dedicates moments to staying updated on technological advancements, learning new skills, and enjoying valuable moments with his family and friends.

Associate Editor

Chhabi Raj is a second-year MS student and graduate research assistant in the Department of Crop, Soil, and Environmental Sciences, doing research to improve agricultural sustainability while enhancing water quality. He obtained his BSc (HONORS) in Agriculture from India. Raj loves hiking, running, and volunteering at different events.

Associate Editor

Olivia Brahms is a Ph.D. candidate and graduate teaching assistant in the Department of Biological Sciences under the guidance of Dr. Jason Upton. She is also pursuing a graduate certificate in Health Equity Science. In addition to being associate editor for AUJUS, she currently serves as a Biological Sciences Graduate Student Association Senator and the Social Media chair for Graduate Women in Science. She graduated from Auburn University in 2019 with a Bachelor of Science in Animal Sciences. Currently, her research investigates the role of interactions between an uncharacterized herpesvirus gene and a host protein complex in cytomegalovirus pathogenesis. In her spare time, Olivia enjoys walking her dog, Milo, playing with her guinea pig, Winston, and painting.

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Associate Editor

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Associate Editor

Mason Parkes is a PhD student in the Physics Department. He graduated from BYU in 2019 with a Bachelor of Science degree in Physics. His research focuses on the physics of resource sharing in hippocampal presynapses. He's particularly interested in why synaptic vesicles are shared between presynapses, what cytoskeletal elements support that sharing, and what that means for wider brain function. In his free time he enjoys spending time with his wife and two daughters, and playing Dungeons and Dragons with his friends.

Auburn University Journal of Undergraduate Scholarship

Validation of a Fast Solvent Evaluation and Selection Model for Extractive Distillation

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Abstract

Extractive distillation is a solvent-based separation used to separate mixtures containing azeotropes or close boiling components. An external component (solvent) is added to the process to overcome the separation barrier. Selecting the optimal solvent for extractive distillation using solvents' physical properties has been studied, but process parameters, such as the number of stages and reflux ratio, must also be considered when selecting a solvent. A fast solvent evaluation and selection (FSES) model using solvent properties and process parameters has been proposed for designing an optimal extractive distillation process. The FSES model evaluates and ranks potential solvents to identify the solvent with the minimum total annualized cost (TAC) for the separation. This paper presents a validation study of the FSES model results for separating two mixtures: acetone-methanol and benzene-cyclohexane. The study employed rigorous process simulation and optimization of extractive distillation for both separations, considering five candidate solvents for each. A derivative-free optimization (DFO) approach was used to identify the optimal process design and operating conditions that minimize the TAC for each solvent. Solvent rankings based on minimum TAC by optimization and predictions by the FSES model were compared. The FSES model and TAC-based optimization ranked the potential solvents for the acetone-methanol separation from best to worst as dimethylsulfoxide, water, ethylene glycol, ethanol, and 2-propanol. For the benzene-cyclohexane separation, the solvents were ranked sulfolane, furfural, dimethyl phthalate, N-methyl-2-pyrrolidine, and aniline from best to worst. The TAC-based rankings yielded the same order, except it ranked N-methyl-2-pyrrolidine better than dimethyl phthalate.

Key Words: extractive distillation, derivative-free optimization, process design, solvent selection

Introduction

Extractive distillation (Gerbaud et al., 2019) is a widely applied process for separating azeotrope or close boiling mixtures. In extractive distillation, a third component, solvent or entrainer, is added to overcome the separation barrier. Extractive distillation can perform high-purity separation for azeotrope or close boiling mixtures. An effective solvent facilitates the separation of azeotropic or close boiling mixtures by shifting the composition of the azeotrope. The solvent must also not form any new azeotropes with either mixture component. Since adding the solvent creates a three-component mixture, the process uses two distillation columns to separate the three components.

Fig. 1 gives the vapor-liquid equilibrium curves for the acetone-methanol mixture with and without solvents. In Fig. 1, the x-axis is the acetone liquid mole fraction in the mixture, and the y-axis is the acetone vapor mole fraction. The acetone-methanol mixture contains an azeotrope around liquid and vapor mole fractions of 0.8, as seen by the intersections of the dotted orange curve with the parity line (dashed black line). Adding water or dimethylsulfoxide (DMSO) to the mixture shifts the azeotropic composition (intersection of dashed-dotted blue or solid purple lines with the parity line in Fig. 1). This shift enables the separation of acetone and methanol at high purities.

Water or DMSO can be used as solvents in extractive distillation to separate the acetone-methanol mixture; however, the separation cost or performance would differ for each solvent. For example, adding DMSO so that its mole fraction is 0.2 in the mixture (i.e., $x_{DMSO}=0.2$)

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shifts the acetone-methanol azeotrope to a higher composition than adding water with the same mole fraction (i.e., xwater=0.2), which indicates that DMSO can facilitate a higher purity separation than water.

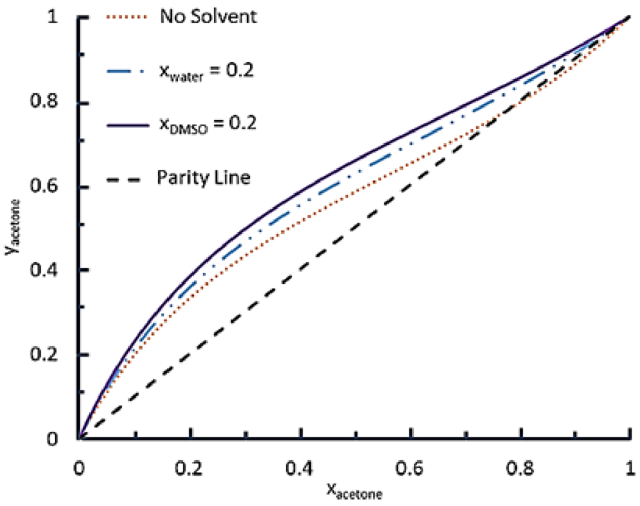

Fig. 1 Vapor-liquid equilibrium plot of acetone-methanol mixture with different solvents. The x and y axes represent acetone liquid and vapor mole fractions. The mole fraction of the solvent, either water or DMSO, in the mixture is 0.2. The acetone mole fractions for the mixture containing a solvent have been adjusted to [0, 1] range for generating the corresponding lines.

Fig. 2 shows the process flow diagram for extractive distillation. A two-component mixture (A, B) and solvent are fed separately to the first distillation column. The distillate of the first column contains pure product A, and the bottoms of the column contains component B and the solvent. This mixture is then separated in the second column to recover the solvent. The regenerated solvent is recycled back to the first column with makeup solvent added to replace the small amount of solvent lost in the distillate streams.

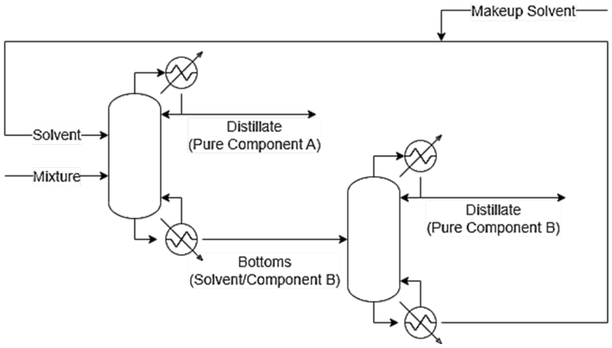

Fig. 2 General extractive distillation process flow diagram.

The extractive distillation process depends on the effectiveness of the solvent used, and different solvents can lead to vastly different designs, operating conditions, and process costs (Shen et al., 2015). Methods for selecting suitable solvents for extractive distillation and other solvent-based separation processes have been proposed. Kossack et al. (2008) proposed a rectification body method that can calculate process properties such as minimum solvent flowrate and minimum energy demand for selecting the optimal solvent. But, the method is computationally expensive. Cignitti et al. (2019) proposed an optimization model to design and identify suitable solvents by maximizing the separation driving force based on the group contribution method. The optimum solvent was validated by rigorous process simulation/optimization. Shen et al. (2015) proposed a solvent screening method based on five solvent physical properties, such as boiling point and selectivity. After adding weighted attributes to these properties, the solvents were ranked based on their 'total score,' and the ranking results were validated by process simulation. However, these methods only use physical properties as their design/screening criteria without considering the effects of process properties. For example, a higher boiling point solvent is often preferred in solvent screening due to its ease of regeneration, but this may result in the use of a higher grade of utility, which has a higher utility cost.

A fast solvent evaluation and selection (FSES) model (Xu et al., 2022) was developed to evaluate solvent performance quickly and efficiently. The FSES model uses both physical properties, such as boiling point, solvent flowrate, and process properties, such as reboiler duty, column stages, and reflux ratio, to predict solvent performance for extractive distillation. This study aims to assess the accuracy of the FSES model solvent recommendations by studying the separation of two mixtures, acetone-methanol, and benzene-cyclohexane, using extractive distillation with multiple solvents. It includes the simulation and derivative-free optimization of the extractive distillation process, which were applied to the acetone-methanol and benzene-cyclohexane separation tasks. The optimization studies minimized the total annualized cost (TAC) of the separation process using each solvent. The solvents were ranked based on their TAC, and the rankings were compared to the FSES model rankings. The results revealed that the

FSES model closely matched the rankings based on minimum TAC.

Methods

Extractive Distillation Process Simulation. Fig. 3 the extractive distillation flowsheet modeled and simulated using Aspen Plus (Aspen Technology, Inc., 2017). As seen in Fig. 3, the process includes two distillation columns and a recycle loop for the solvent. The azeotropic mixture A-B and recycled solvent, SOLVFEED, are fed to the first distillation column, D1. The distillate of D1 contains component A, and the bottoms stream S1 contains the solvent and component B. The bottoms stream S1 is fed to the second distillation column, D2. The distillate of D2 contains component B, and the bottoms stream SOLVOUT contains the recovered solvent. MAKEUP solvent is added to the recovered solvent and recycled back to D1 in stream SOLVFEED.

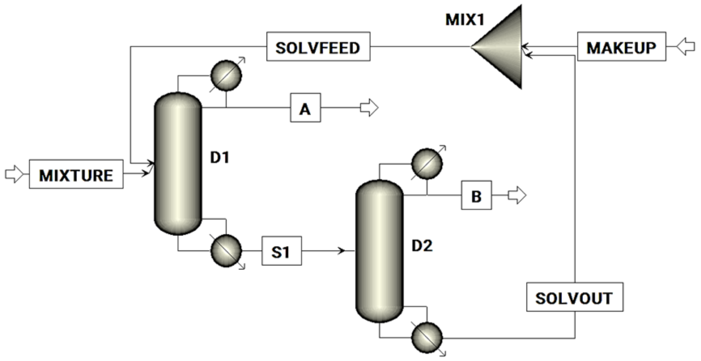

Fig. 3 Aspen Plus simulation flowsheet for extractive distillation for separating a mixture containing components A and B.

The inputs required for the simulation, as described in Fig. 3, were the SOLVFEED, and MIXTURE flowrates and temperatures into column D1, the MIXTURE component concentration, stream and column pressures, the total number of stages for D1 and D2, the feed stages for D1 and D2, the SOLVEFEED feed stage for D1, and the MAKEUP flowrate. The values for these inputs were initially set using literature results and a systematic trial-and-error approach.

Distillation columns (D1 and D2 in Fig. 3) were modeled using the RadFrac block in Aspen Plus. An appropriate thermodynamic model was selected to adequately model the behavior of the components in each separation case. Purity and recovery specifications were defined. Only the results of simulation runs that met these specifications were used to calculate TAC. These specifications were achieved utilizing the Design Spec and Vary features within Aspen Plus. The Design Spec feature allows for process parameters to be set to a certain value, while the Vary feature is utilized to automatically adjust process parameters over a set range to achieve the design specifications. The design specifications in Design Spec must be met with adjusted process parameters from Vary within the set boundaries for a simulation to converge without errors.

Each process simulation was converged without errors using inputs from literature and trial-and-error before it could be used for optimization.

Fast Solvent Evaluation and Selection (FSES) Model. The FSES model (Xu et al., 2022) uses both physical properties and process parameters to predict solvent performance. The physical properties used include solvent boiling point and flowrate (SOLVFEED in Fig. 3). The process parameters are the minimum number of stages, reboiler duty, and column reflux ratio of D1 and D2 (Fig. 3). The extractive distillation column D1 is divided into stripping, extractive, and rectifying sections for calculating the minimum number of stages because the two-component mixture and solvent are fed separately to D1. The stripping section is below MIXTURE feed of D1, the rectifying section is above SOLVENT feed of D1, and the extractive section occurs between the two feeds (Fig. 3). The Fenske equation is applied separately to calculate each section's minimum number of stages, assuming constant relative volatility within each section. The sum of the resulting minimum number of stages is used as the minimum number of stages required for D1. The minimum reflux ratio is calculated by the intersection of the operating line and vapor-liquid equilibrium curve. Each physical or process property contributes to the overall score for a solvent, and a simple summation method is used to rank the solvents, as shown in Table 1. The best solvent has the lowest overall score and is predicted to yield the lowest TAC for separating A-B mixture using extractive distillation.

In Table 1, Sp is the solvent, $V_{p,r}$ is the value of property r for solvent p, $Score_{p,r}$ is the ranking score of property r for solvent p, and N is the total number of solvents evaluated.

Table 1 Fast Solvent Evaluation and Selection Model Ranking Method for Extractive Distillation.

Solvent, p		S_1		S_p		S_N
Properties, r	Reflux Ratio	$V_{1,1}$	…	$V_{p,1,min}$	…	$V_{N,1}$
		$Score_{1,1}$		1		$Score_{N,1}$
	Stages	$V_{1,2}$		$V_{p,2,max}$		$V_{N,2}$
		$Score_{1,2}$		N		$Score_{N,2}$
	Heat Duty	$V_{1,3}$		$V_{p,3}$		$V_{N,3}$
		$Score_{1,3}$		$Score_{p,3}$		$Score_{N,3}$
Total score of solvent, p		$Score_p = \sum_r Score_{p,r}$				

Derivative-Free Optimization (DFO) of Extractive Distillation Process. The optimization problem was solved using a DFO solver to identify the optimal process design and operating parameters for each separation. The optimum was defined as the parameter values that minimize the TAC of the system, shown in Equations 1-3.

$$min: TAC = \frac{i(i+1)^n}{(i+1)^n - 1} \times IC + AUC \tag{1}$$

$$st. IC = \sum_j Cost_j(q_{s,j}) \tag{2}$$

$$AUC = 24 \times 300 \times \sum_j Utility_j(q_{o,j}) \tag{3}$$

In Eq. (1), *TAC* is the total annualized cost, *IC* is the investment cost, *AUC* is the annualized utility cost, *i* is interest, and *n* is the plant life (*n*=5 was used in this model). In Eq. (2), $Cost_j$ is the investment cost of equipment *j*, and $q_{s,j}$ is the sizing variable for equipment *j*. In Eq. (3), $Utility_j$ is the utility cost of equipment *j*, and $q_{o,j}$ is the operating variable for equipment *j*. The full cost model was developed following the method in Peters et al. (2003, Appendix A).

Equations 4-7 define the variable bounds on flowrates and column stages used in the DFO.

$$F_{S,L} \leq F_S \leq F_{S,U} \tag{4}$$

$$N_{k,feed,L} \leq N_{k,feed} \leq N_{k,feed,U} \tag{5}$$

$$N_{k,L} \leq N_k \leq N_{k,U} \tag{6}$$

$$N_{1,S,L} \leq N_{1,S} \leq N_{1,S,U} \tag{7}$$

F_s is the solvent flowrate, N_k is the number of stages in column *k*, $N_{k,feed}$ is the materials feed stage of column *k*, $N_{1,S}$ is the solvent feed stage of the first column, and *L* and *U* represent the lower and upper bounds.

Python was used to link the Aspen Plus simulations with the DFO solver and find the optimum process conditions, i.e., decision variables, that yielded the lowest TAC. The DFO solver RBFOpt (Costa & Nannicini, 2018; Nannicini, 2021) was used to adjust the decision variables, which were the solvent ratio, total stages for both distillation columns, the mixture feed stage for both columns, and the solvent stage in the first column. To aid in simulation convergence and determine the appropriate upper/lower bounds for the decision variables, an optimization structure consisting of an inner and outer loop (Fig. 4) was used to solve this optimization problem.

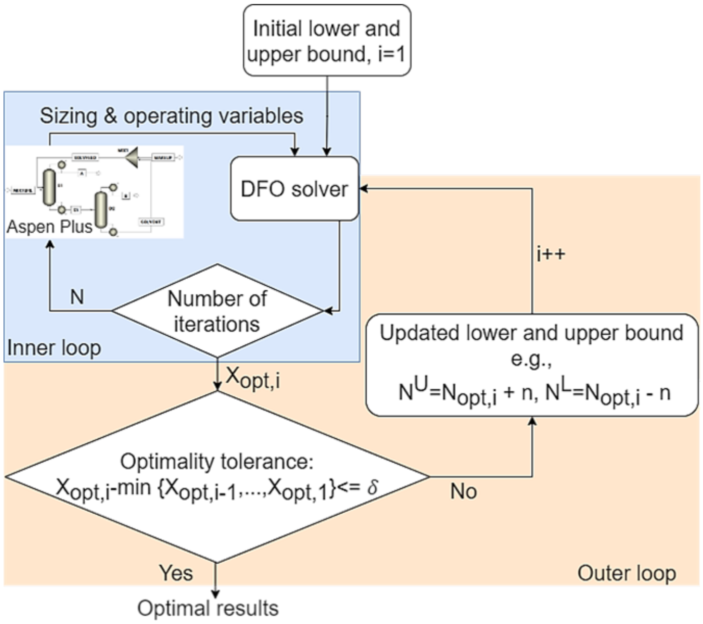

Fig. 4 Derivative free optimization structure.

The inner loop loops between the DFO solver and the process simulation model for 1000 iterations. During these iterations, the solver searches the decision-variable space defined by the bounds for the optimum. The inner loop output, the operating conditions that yield the lowest TAC, is passed to the outer loop, which compares the current lowest TAC to the TAC of the previous inner loop results and updates the bounds if necessary. The bounds are updated using the decision variable values of the lowest TAC of the completed inner loop iterations. The bounds are set so that the solvent ratio is within ±0.5 of the previous best value, and all stage values (total number and feed locations) are within ±10 of the previous best values. If the TAC does not change from one iteration to the next, e.g., Fig. 5, the outer loop terminates and provides the solution with the lowest TAC as the optimum.

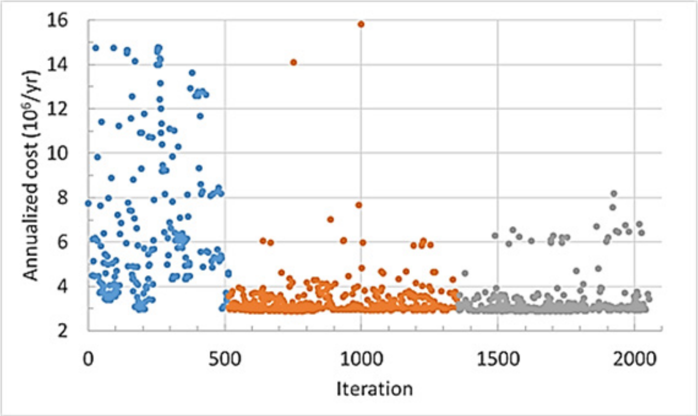

Fig. 5 Total annualized cost for acetone-methanol separation with DMSO as solvent generated using DFO solver using the structure shown in Fig. 4. *Note.* Each color represents a complete inner loop.

Case Studies

Acetone-Methanol Separation. The acetone-methanol mixture contains a minimum-boiling azeotrope. This mixture can be separated using a heavy entrainer with acetone and methanol as the first and second columns' distillate streams. The solvents (Gerbaud et al., 2019) considered were water, DMSO, ethanol, ethylene glycol, and 2-propanol. The thermodynamic package UNIQUAC was selected for each solvent based on the vapor-liquid equilibrium data. A converged process simulation model in Aspen Plus was the first simulation model of the inner loop iterations (Fig. 4) for the DFO structure for each solvent. The solvents were ranked from lowest to highest using their minimum TAC (identified by the DFO). This ranking was compared to the results of the FSES model.

Benzene-Cyclohexane Separation. The benzene-cyclohexane mixture also contains a minimum-boiling azeotrope and can be separated using a heavy entrainer. Cyclohexane is the product of the first column and benzene the second column. The potential solvents for the acetone-methanol case study were sulfolane, N-methyl-2-pyrrolidone (NMP), furfural, aniline, and dimethyl phthalate. The thermodynamic package NRTL was used for sulfolane and furfural, and UNIFAC was used for NMP, dimethyl phthalate, and aniline.

Results and Discussion

Acetone-Methanol Separation. The rankings based on the minimum TAC were DMSO, water, ethylene glycol, ethanol, and 2-propanol from first to last. The process using the DMSO as the solvent yielded the lowest TAC, and 2-propanol yielded the highest. The details of the optimum process with the DMSO solvent are shown in Fig. 6.

The TAC results of the optimization problem solution and FSES model scores for each solvent are listed in Table 2. The FSES model resulted in the same solvent rankings.

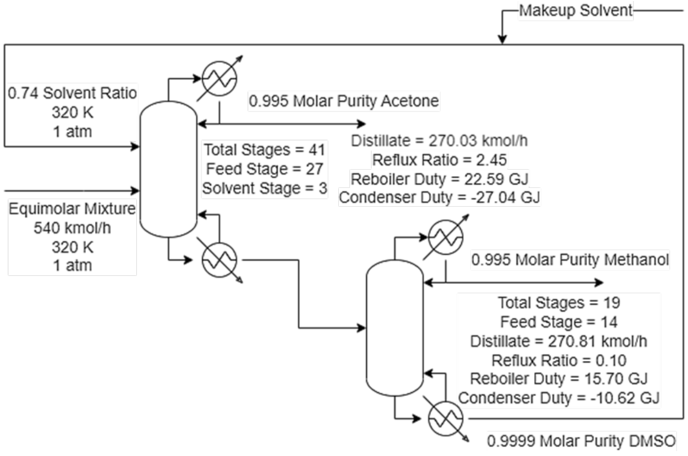

Fig. 6 Optimum acetone-methanol separation process flowsheet with DMSO as solvent.

Table 2 Comparison of optimization and FSES model results for acetone-methanol separation.

Solvent	TAC ($\times10^6$\$/yr)	FSES Model Score
DMSO	2.87	15
Water	3.32	19
Ethylene glycol	4.63	24
Ethanol	6.64	27
2-propanol	7.60	35

Benzene-Cyclohexane Separation. The minimum

TACs for the benzene-cyclohexane separation process resulted in a solvent ranking as sulfolane, furfural, NMP, dimethyl phthalate, and aniline from first to last. Sulfolane yielded the process with the lowest TAC and aniline the highest. The optimum separation process with sulfolane solvent is shown in Fig. 7.

The TAC from optimization and FSES model scores for each solvent are given in Table 3. The FSES model yielded a similar solvent ranking but ranked dimethyl phthalate as a better solvent than NMP. The FSES model correctly predicts column stages of dimethyl phthalate and NMP to be similar, but the high boiling point of dimethyl phthalate causes the discrepancy between the optimization and FSES model results. The high boiling point of dimethyl phthalate results in higher column temperatures, requiring a furnace. This causes the capital cost of the dimethyl phthalate system to be higher than the NMP system. While boiling point contributes to the FSES model ranking results, the method in the FSES model does not account for the significant cost effect of the high boiling point of dimethyl phthalate.

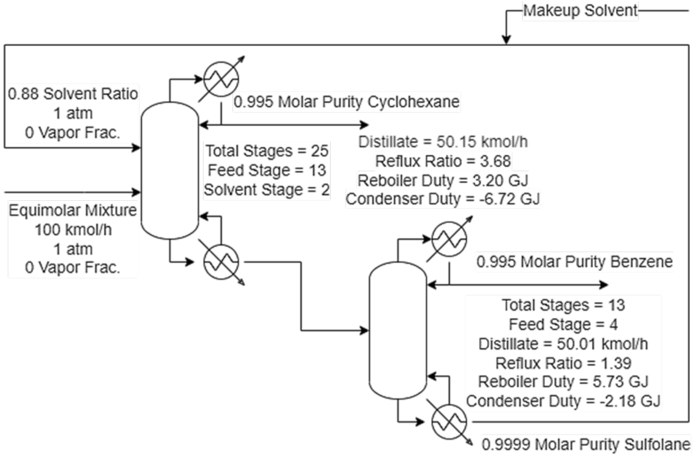

Fig. 7 Optimum benzene-cyclohexane separation process flowsheet with sulfolane as solvent.

Table 3 Comparison of optimization and FSES Model results for benzene-cyclohexane separation.

Solvent	TAC ($x10^{6}\$/yr$)	FSES Model Score
Sulfolane	0.63	19
Furfural	0.72	21
NMP	0.74	24
Dimethyl phthalate	0.95	22
Aniline	0.96	34

Conclusions and Future Direction

Due to the importance of solvent selection, the FSES model was proposed to quickly and accurately predict solvent performance. This model uses both physical and process properties to rank solvents based on their potential performance. This work validates the proposed FSES model predictions by completing rigorous process simulation and derivative-free optimization of multiple extractive distillation separation processes. After completing process simulation and optimization for the acetone-methanol and benzene-cyclohexane separations with five solvents each, the optimum process design and operating parameters were identified for both separations. The optimum process designs for the acetone-methanol and benzene-cyclohexane separations utilize DMSO and sulfolane as solvents.

The FSES model correctly predicted solvent performance for extractive distillation based on total annualized cost. The optimization and FSES model yielded the same results for the acetone-methanol separation. For the benzene-cyclohexane separation, a similar solvent ranking was obtained between the optimization and FSES models, but the FSES model ranked dimethyl phthalate as a better solvent than NMP. This was due to the high boiling point of dimethyl phthalate. While the solvent ranking for the benzene-cyclohexane separation was imperfect, the FSES model ranked the two best solvents correctly.

Future work will consider integrating the presented FSES model into extractive-distillation process synthesis for either solvent selection or solvent design.

Acknowledgments

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- Toby Crump, Undergraduate Student, Department of Chemical Engineering

Nomenclature

$FSES$ – Fast solvent evaluation and selection model
TAC – Total annualized cost
DFO – Derivative-free optimization
$DMSO$ – Dimethyl sulfoxide
S_p – Solvent p
$V_{p,r}$ – Value of property r for solvent p
$Score_{p,r}$ – Ranking score of property r for solvent p
N – Total number of solvents evaluated
IC – Investment cost
AUC – Annualized utility cost
i – Interest
n – Plant life
$Cost_j$ – Investment cost of equipment j
$q_{s,j}$ – Sizing variable for equipment j
$Utility_j$ – Utility cost of equipment j
$q_{o,j}$ – Operating variable for equipment j
F_S – Solvent flowrate
N_k – Number of stages in column k
$N_{k,feed}$ – Materials feed stage of column k
$N_{1,S}$ – Solvent feed stage of the first column
L – Lower bound
U – Upper bound

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Authors Biography

Toby Crump is a 2023 graduate from Auburn University with a B.S. degree in Chemical Engineering. He has played key research roles in process simulation and optimization. Toby is originally from Nashville, Tennessee and participated in the Auburn University Marching Band playing trumpet. He also served as service chair for the Alabama Alpha chapter of Tau Beta Pi for the 2022-23 academic year.

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Chromobacterium RiPP-like Biosynthetic Gene Clusters May Influence Inhibition of Globisporagium ultimum

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Abstract

Globisporangium ultimum is a fungal-like organism called an oomycete that attacks germinating seedlings and causes pre- and post-emergence damping-off in many hosts. Synthetic fungicides are primarily used to control this disease, but since oomycetes are not fungi, they do not share many of the same targets that would inhibit true fungi. Therefore, there are a limited number of oomycete-active chemicals used in seed treatments, posing the need for alternative options. The soil is a natural source of bacteria that produces bioactive metabolites. A survey of soybean spermosphere microbiomes at the Old Rotation revealed that historically irrigated soil has a significantly higher concentration of purple-pigmented bacterium than non-irrigated soil. Sequencing 16S rRNA from these cultures revealed them to be *Janthinobacterium*, a close relative of *Chromobacterium*, two genera of Gram-negative bacteria known for producing purple pigment violacein, a known antifungal agent. When co-cultured with *C. violaceum*, the aerial hyphae of *G. ultimum* collapsed, and violacein was observed to travel along the oomycete hyphae over time. When subcultured to fresh agar Petri dishes, *G. ultimum* died, leading to the hypothesis that contact-independent and dependent interactions were lethal to *G. ultimum*. To test the hypothesis of contact-independent antibiosis and its potential to protect soybean seeds from infection, sixteen *Chromobacterium* and *Janthinobacterium* isolates from at least five species were tested for their ability to protect soybean. Soybeans were co-cultured with and without both *G. ultimum* and each bacterial isolate, then disease severity was rated for each seed. Isolates that significantly reduced disease severity were identified. Violacein production did not correlate with disease inhibition, leading to the hypothesis that other secondary metabolites are responsible for *G. ultimum* inhibition. Five strains of *Chromobacterium* had their genomes sequenced to compare differences in biosynthetic gene clusters between inhibitory and non-inhibitory strains.

Future experiments will involve testing bioactive *Chromobacterium* and *Janthinobacterium* strains in the growth chamber to test their inhibitory abilities in soil.

Key Words: co-culture; biosynthetic gene cluster; ribosomally synthesized and post-translationally modified peptide (RiPP)

Introduction

Globisporangium Background

Globisporangium ultimum, formerly *Pythium ultimum* (Nguyen et al. 2022), is an oomycete and ubiquitous plant pathogen with a wide host range (Beckerman, 2011) that causes root rot as well as pre-and post-emergence damping off. It can produce oospores that can survive in the soil for many years, making them difficult to irradicate. Damping-off occurs when *G. ultimum* colonizes seeds during or soon after germination, causing seed disintegration and seedling collapse. In older plants, infection can lead to root rot ("Diseases Caused by Pythium"). *G. ultimum* can produce zoospores that move through the water toward their host. Therefore, moist environments, such as those created by heavy rainfall or overwatering, create ideal infection conditions, especially at lower temperatures, which slows seed germination and increases exposure to pathogens. Re-planting crops in a field once infected with the pathogen can result in the re-occurrence of stand failure, even if preventive fungicide treatment is used (Groves and Smith, 2013). Crop rotation has limited effectiveness due to the wide host range of *G. ultimum*. Current *G. ultimum* control measures include using fungicides, but *G. ultimum* has many key

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differences in molecular targets commonly attacked by fungicides. For example, ergosterol biosynthesis inhibitors are a major class of agricultural fungicides, but this synthesis pathway is not observed in oomycetes, rendering these compounds ineffective against oomycetes (Alcazar-Fuoli and Mellado, 2013). Additionally, there is concern about overreliance on the few chemical fungicides used to control oomycetes since, in some cases, they may contribute to the rise of fungicide-resistant plant pathogen populations. As such, bioactive microorganisms and their metabolites are alternatives for *G. ultimum* control. Several Trichoderma species have been investigated as *G. ultimum* biocontrol agents (Sanchez-Montesinos et al. 2019). In addition, *Bacillus* species have been shown to inhibit plant disease and promote plant growth by secreting secondary metabolites and phytohormones (Miljaković 2020). Understudied and unexplored bacterial species may also produce novel anti-oomycete secondary metabolites.

Chromobacterium

Chromobacterium is an eleven-species genus of motile Gram-negative proteobacteria known for producing violacein, a purple-pigmented secondary metabolite with exhibited in vitro inhibition of bacteria, viruses, protozoa, and even tumors (De Souza 1999; Andrighetti-Fröhner, 2003; Leon, 2001; Melo, 2016). Violacein helps protect the bacterium from oxidative stress (Konzen et. al. 2006). The outer membrane of *Chromobacterium* exhibits greater endotoxicity and enhanced resistance to phagocytosis than other Gram-negative species (Bennett, 2020). *Janthinobacterium*, like *Chromobacterium*, is Gram-negative, motile, and produces violacein. One species, *J. lividum*, suppresses fungal growth on amphibian skin (Becker et al. 2009). The author also describes significant in vitro inhibition of *Fusarium graminearum* when co-cultured with violacein-producing *Janthinobacterium*.

Existing Bacterial Genomes

Both *Chromobacterium* and *Janthinobacterium* lack comprehensive genomic analysis in the literature as neither genus has complete genomes, and available gene cluster analyses widely focus on the violacein operon. Complete bacterial genomes are realistic with long-read third-generation sequencing like Oxford Nanopore combined with short-read and accurate Illumina sequencing. When biosynthetic gene clusters can be hundreds of thousands of base pairs long, adding long-read sequencing helps discover new and complete biosynthetic gene clusters that may encode novel antifungals. Therefore, complete genomes for other species that may contain novel biosynthetic gene clusters have yet to be explored.

Ribosomally Synthesized and Post-Translationally Modified Peptide (RiPP) Biosynthetic Gene Clusters

RiPPs have been recently discovered via genome sequencing to be a fifth class of natural biosynthesized products, in addition to the previously known classes of terpenoids, alkaloids, polyketides, and non-ribosomal peptides (Arnison, et. al. 2013). RiPPs have been identified among Bacteria, Archaea, and Eukarya. Since the discovery of RiPPs and the characterization of their nomenclature and properties, further research into the gene clusters that synthesize these peptides has been ongoing.

Preliminary Experiments

Preliminary experiments characterizing the soybean spermosphere microbiome from the Auburn University Old Rotation (Auburn, AL, USA) in irrigated versus non-irrigated soil were done (Harrison et. al., 2022). Twelve isolates of *Chromobacterium* were transferred from cryotubes stored at -80°C with a sterile loop to 10mL of tryptic soy broth and grown in the shaker at 28 degrees Celsius at 250 rpm for 72 hours. After three days of growth, 10 microliters of isolate broth were pipetted at the points of a concentric pentagon on quarter-strength potato dextrose agar plates (Figure 1). Soybeans were sterilized in a 10% bleach solution, rinsed with sterile water, and allowed to air dry in a biosafety cabinet. Sterilized soybeans were then placed on top of each of the isolates, and equally sized plugs of *G. ultimum* were placed at the center of each plate. Each treatment had three replicates. Positive controls contained no bacteria, only *G. ultimum*. Negative controls contained neither bacteria nor *G. ultimum*. Co-cultures were incubated at room temperature 72 hours, and the disease ratings of each seed per treatment and replicate were taken according to Noel et al. 2019 (Table 1).

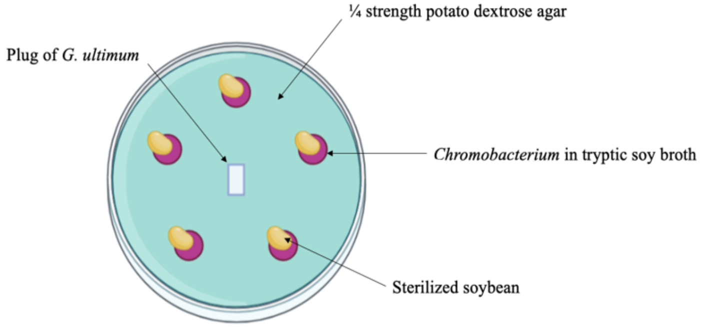
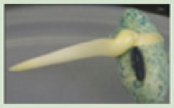
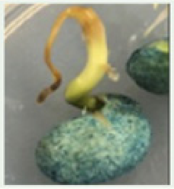


Fig. 1. Rendering of co-culture setup with *G. ultimum*, bacterial sample, and sterilized soybean. Created with BioRender.

Table 1: Disease severity chart for seed ratings adapted from Noel et al. 2019.

Disease Severity Rating	Description
	0 germinated healthy seedling
	1 germinated, limited to no discoloration
	2 germinated, non-coalesced lesions present
	3 germinated, coalesced lesions present
	4 not germinated and/or seed fully colonized

Preliminary findings indicated *C. sphagnii* and *C. vacinni* had a statistically significant amount of disease inhibition against *G. ultimum*, and *C. subtsugae* showed significant disease inhibition to a lesser degree.

In this experiment, we observed an increased concentration of purple-pigmented bacteria in irrigated soil. Sequencing the 16S rRNA gene revealed these bacteria to be *Janthinobacterium*. To test potential disease inhibition, *Janthinobacterium* isolated from irrigated soil was co-cultured with *G. ultimum* and monitored. At four days post-inoculation, *G. ultimum* aerial hyphae collapse was observed. At seven days post-inoculation, further hyphae collapse was noted, and violacein was observed traveling across the hyphae of *G. ultimum*.

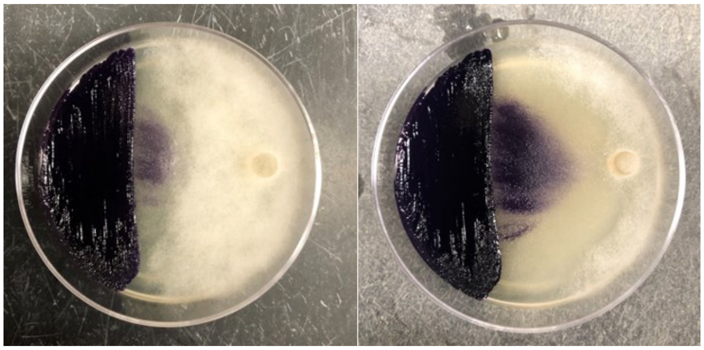


Fig. 2. Left- *Janthinobacterium* and *Globisporangium ultimum* at four days post-inoculation. Right- *Janthinobacterium* and *G. ultimum* at seven days post-inoculation.

At seven days post-inoculation, *G. ultimum* was subcultured from close, mid, and far distances from the *Janthinobacterium*. In each subculture, *G. ultimum* did not grow, indicating the oomycete had died in the presence of *Janthinobacterium*.

Hypothesis

We hypothesized that other violacein-producing species, like *Chromobacterium*, produce metabolites that may be inhibitory toward *G. ultimum* and that there are differences in biosynthetic gene clusters encoding these metabolites between inhibitory and non-inhibitory strains. Therefore, the objectives of this paper were to identify inhibitory and non-inhibitory strains of *Chromobacterium*, sequence their genomes, and analyze the differences in biosynthetic gene clusters across strains. We analyzed in vitro relationships between *Chromobacterium* species and *G. ultimum* and describe the genomic relationships of the observed inhibitory effects described.

Methods

Differential Time to Production of Violacein

Over incubation, *Chromobacterium* colonies start clear or opaque yellow, then will develop violacein as the colonies grow in broth. Complete violacein development was experimentally defined as the entire broth tube having deep purple pigment. We incubated strains of *Chromobacterium* in TSB for five weeks and identified when violacein production was generated.

Genome Sequencing of *Chromobacterium*

Complete genomes of five *Chromobacterium* strains with differential inhibition toward *G. ultimum* were sequenced with a combination of short-read Illumina and long-read Oxford Nanopore sequencing. Tryptic soy agar plates of *Chromobacterium* were sent to SeqCenter (Pittsburgh, PA), the genomic DNA was extracted, and the DNA sequenced. Genome sequence assembly was conducted by SeqCenter staff. Prediction of biosynthetic gene clusters was performed with AntiSmash v.6.1.1 (Blin et. al. 2021). Taxonomic identity based on genomic data was confirmed using the MiGa pipeline (Rodriguez-R et. al. 2018, 2020).

Results

Differential Inhibition Based on *Chromobacterium* Species and Violacein Production

Each species represented had varying degrees of inhibition within and between themselves. Figure 5 shows two inhibitory strains, CHV and CHB-4, and one non-inhibitory strain, CHA-B. CHV shows clear inhibition zones surrounding the seeds, while CHB-4 did not have a clear zone of inhibition (ZOI) but had healthy seeds. CHA-B is a non-inhibitory strain that did not show clear ZOIs or healthy seed germination.

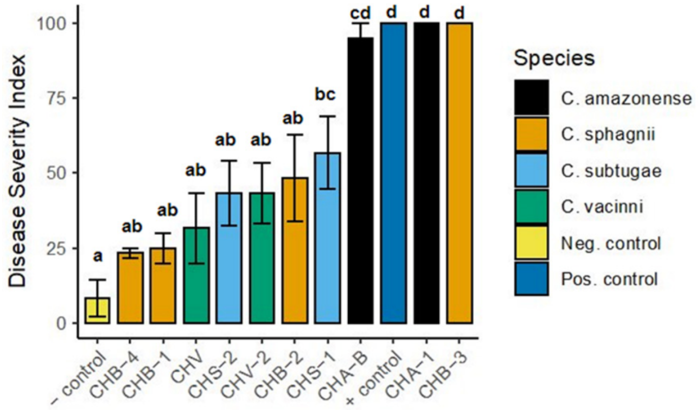


Fig. 3. DSI averages across isolates for co-culture experiments.

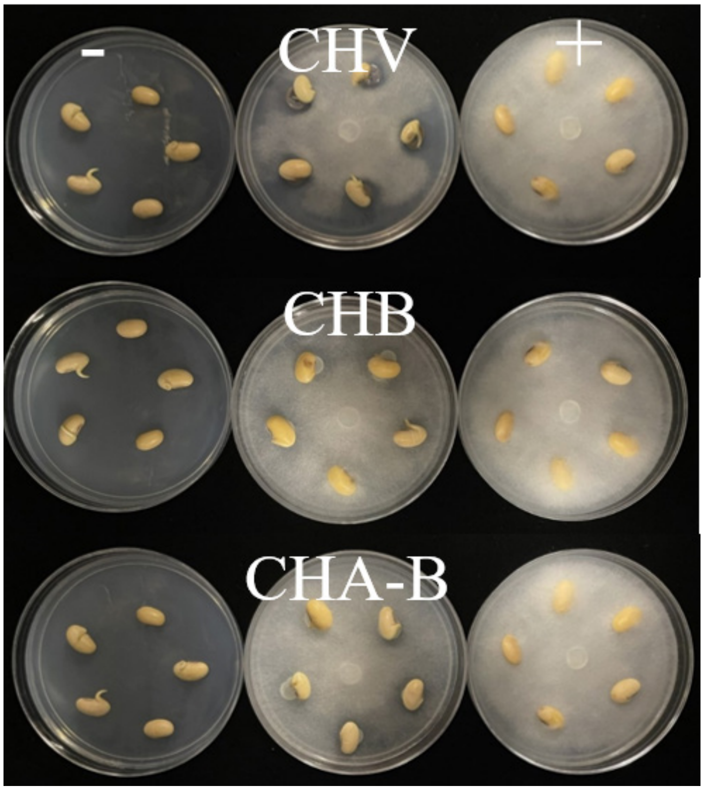


Fig. 4. Co-culturing plates of CHV and CHB (inhibitory strains) and CHA-B (non-inhibitory strain) alongside positive (right) and negative (left) controls

Means were separated based on a one-way ANOVA with Tukey HSD.

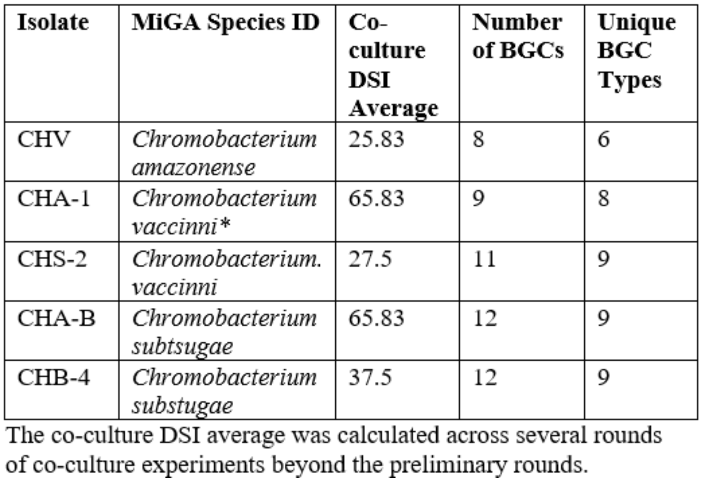
Analysis of the disease severity indexes in preliminary experiments (Figure 3) shows that *Chromobacterium amazonense* and one *Chromobacterium sphagnii* isolate had no significant difference in DSI against the positive control. On the other hand, two other *Chromobacterium sphagnii* isolates, alongside Chromobacterium vacinni and one *Chromobacterium substugae* isolate, did not have any significant difference in DSI against the negative control. One *Chromobacterium substugae* had no statistically significant difference in DSI between the positive and negative control.

It was thought at the beginning of the experiment that violacein would be responsible for disease inhibition against *G. ultimum*, but some of the most inhibitory strains, including CHB-4, did not produce violacein under laboratory conditions. Some of the least inhibitory strains also vigorously produced violacein. This led to the hypothesis that other secondary metabolites were responsible for *G. ultimum* inhibition. Significant variation in the time from incubation to complete violacein development across isolates was also observed.

Genome Sequencing of Chromobacterium

CHV, CHA-1, CHS-2, CHB-4, and CHA-B were sent for genome sequencing. To examine biosynthetic gene clusters encoding for secondary metabolites, each genome was analyzed in antiSMASH. Of the 52 gene clusters identified across the five strains, only six were returned with 75% or greater similarity to a known gene cluster. 18 returned with no identifiable similar biosynthetic gene cluster, indicating they are novel (Table 2).

Table 2: Overview of biosynthetic gene clusters by isolate.



Isolate	MiGA Species ID	Co-culture DSI Average	Number of BGCs	Unique BGC Types
CHV	*Chromobacterium amazonense*	25.83	8	6
CHA-1	*Chromobacterium vaccinni**	65.83	9	8
CHS-2	*Chromobacterium. vaccinni*	27.5	11	9
CHA-B	*Chromobacterium subtsugae*	65.83	12	9
CHB-4	*Chromobacterium substugae*	37.5	12	9

The co-culture DSI average was calculated across several rounds of co-culture experiments beyond the preliminary rounds.

The co-culture DSI average was calculated across several rounds of co-culture experiments beyond the preliminary rounds.

There was a total of 18 different BGCs between the five strains. Comparison of BGC types between strains indicated that neither the number of unique BGC types nor overall BGCs correlated to disease inhibition.

RiPP-like BGCs are Twice as abundant in Inhibitory Strains

The three most inhibitory by DSI average had 31 BGCs, while the two least inhibitory had 19 BGCs. In particular, the inhibitory strains had double the number of ribosomally synthesized and post-translationally modified peptides (RiPP)-like BGCs. Each of these clusters returned with 0% similarity to clusters described in antiSMASH, indicating they were novel.

Discussion

In this study, we investigated the inhibitory effect of violacein-producing bacteria in the genus Chromobacterium against the plant pathogen *G. ultimum*. The most important results indicated that violacein production did not necessarily correlate with the inhibition of *G. ultimum* as initially hypothesized, meaning that other metabolites may be responsible for the inhibitory responses observed. The genomes of the *Chromobacterium* strains indicated a diverse set of novel BGCs that may be responsible or partially responsible for the inhibition observed. Inhibitory strains had twice the number of RiPP-like BGCs than non-inhibitory strains. The metabolites that these BGCs produce may be exploited for further characterization and use as alternative compounds against *G. ultimum*.

There are a few options for delivering these metabolites into the soil for seed protection, one being alginate beads. When bacteria or metabolites are mixed with alginate and pipetted dropwise into sterile 2.0% calcium chloride on a stir plate, uniform spherical beads are created, in which the bacteria and metabolites can survive for months, improving their shelf life. Future testing of different formulations for inclusion in the soil or as a seed dressing is needed.

The phylogenies of the RiPP-like BGCs were studied using NCBI BLAST. They were largely similar between isolates with similar DSIs, but the RiPP-like BGCs from non-inhibitory isolates with larger DSIs did not appear to be as closely related. Given that most of the BGCs found in the isolates studied were novel, further examination into characterizing the chemical structure and effect on *G. ultimum* growth is needed. Ideally, the metabolites encoded by these BGCs will be isolated, extracted, and tested for disease inhibition individually. Isolation of these metabolites and mass production into a seed treatment is ideal, but methods for the storage and delivery of *Chromobacterium* into the soil or as seed dressings are needed. Further research into the environmental determinants of metabolite production is needed to understand differences in disease inhibition within Chromobacterium species. The long-term goals of this research are to produce a biological control method that is commercially available for farmers to use.

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Authors Biography

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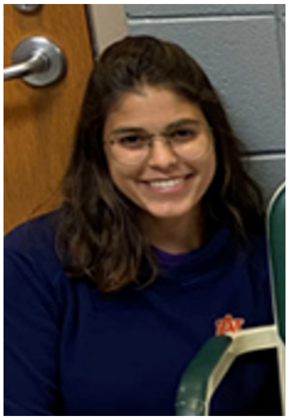

Laura Rodriguez obtained a bachelor's degree in Environmental Microbiology from the University of Puerto Rico Arecibo. Interested in learning more about plant-fungal interaction decided to pursue a Master's in the Plant Pathology Department at Auburn University. Here, she mainly works with the detection of fungi that can alleviate water stress in peanut plants and the identification of changes in peanut soil microbial communities under different water gradients.

Oluwakemisola Olofintila is a scientist focused on plant microbiology and plant biotechnology. As a research assistant in plant pathology, she conducted research on the assembly of the crop microbiome and biocontrol of fungal/oomycete pathogens using molecular biology techniques and bioinformatic tools. She currently works on the development of transgenic crops as a research associate at the Donald Danforth Plant Science Center.

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Auburn University Journal of Undergraduate Scholarship

A Kinematics-based Approach To Future Joint Angle Prediction

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Abstract

Machine learning models and neural networks are powerful algorithms that can be used for predicting future joint angles in biomechanical applications. However, their high computational demand makes near-future prediction difficult or even impossible. As such, the purpose of this study was to establish a non-machine-learning baseline to future joint angle prediction for more complex model performance comparison. It was hypothesized that the use of simplistic, kinematics-based models would be beneficial for predicting joint angles in a near-future application due to lower computational demand, as long as their prediction accuracies could rival that of machine learning models. Six kinematically-informed prediction algorithms were developed to understand this tradeoff between runtime and prediction error. The prediction models were tested on the ankle flexion angle kinematic curves of nine individual subjects who each performed three distinct stair ascent trials (27 total trials). Each model's runtime and prediction error was recorded and compared with each other and to a baseline Random Forest machine learning model that was trained and tested solely on ankle flexion angles. The results of the study indicated that kinematically-informed models had runtimes ~50x faster than commonly used machine learning models (runtimes: Damped Angular Acc. model = 0.30 ms; Linear Extrapolation model = 0.31) while simultaneously rivaling the prediction error of the Random Forest model (prediction errors, reported in ° RMSE: Damped Angular Acc. model = 7.49; Linear Extrapolation model = 8.45; Random Forest model = 5.00). Such results provide the basis for inclusion of kinematically-informed algorithms in near-future joint angle prediction applications.

Key Words: kinematics; prediction; runtime; joint angles

Introduction

Predicted joint angle control methodology has been used in a wide range of biomechanical applications, including prosthetic (Antfolk et al., 2010), robotic (Bingul and Ertunc, 2005), and exoskeleton control (Coker et al., 2021). In an exoskeleton application, such a control scheme allows for actuation of a wearable robotic along a predicted curve that seeks to track the user's desired kinematics in order to increase machine-man agreement and reduce metabolic cost (Agarwal and Deshpande, 2018). As such, machine learning and neural networks are powerful algorithms that have been commonly used in this attempt to map data recorded from the body (e.g., accelerations, EMG-activity, pressure gradients) to a desired output kinematic curve (Tack, 2019). While previous studies have reported minimal prediction errors for machine-learning-based models used in future joint angle prediction (Chen et al., 2017; Huang et al., 2019; and Gautam et al., 2020), many fail to report the necessary runtime required to make such a prediction. For studies that do report computational demand, the runtimes are elevated such that real-time, near-future (~100ms) joint angle prediction becomes difficult or impossible with such machine learning algorithms (Luo et al., 2018; Xiao et al., 2018; Hua et al., 2019).

As such, alternative prediction methods and algorithms need to be considered for this application. Several studies have successfully predicted joint kinematic profiles using non-machine learning methods. Moissenet et al. (2019) developed a multiple-regression model for predicting lower-limb joint kinematics as a function of walking speed, BMI, gender and age. Rabani et al.

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(2022) used an empirical mathematical model and Fourier series expansions to predict lower-limb joint kinematics on varying surface gradients. While these models are beneficial for clinical or offline use, they are not designed to make real-time predictions for exoskeleton control. For near-future kinematic prediction, it may be beneficial to prioritize the current kinematic quantities of a joint over its kinetic and neuromuscular quantities. To our knowledge, a near-future joint angle prediction algorithm that is solely a function of current joint kinematics has not yet been developed for the sake of real-time exoskeleton control. Such kinematically informed models would seek to use simple kinematic equations of motion and historical trendline extrapolation to predict future joint kinematics. Due to their simplicity, these kinematic models would likely have a decreased computational demand when compared to machine learning performance on similar data.

However, decreased computational demand cannot often be achieved without an increase in prediction error (Yao et al., 2018; Hua et al., 2019). Therefore, the purpose of this study is to characterize the performance (prediction error and runtime) of various kinematically-informed algorithms in a near-future joint angle prediction application. Such an analysis will allow for the characterization of the trade-off between prediction error and runtime for such models. Additionally, the kinematically-informed models will be able to function as a baseline to which machine learning and neural network models will be compared to justify their use in time-restricted applications. The primary hypothesis of this study is that the kinematically-informed models will rival the prediction accuracy of the machine learning models while simultaneously having significantly lower computational demand for a near-future prediction application.

Methodology

Participants. Nine healthy subjects (5 male, 4 female, age = 21.1 ± 1.6 years, height = 172.2 ± 8.3 cm, weight = 72.3 ± 11.1 kg) participated in the study. Each participant was a nonpathological ambulator who reported no lower extremity pain or surgery in the six months prior to the study. The study protocol was approved by the Auburn University Institutional Review Board (IRB), and each participant provided informed consent prior to the study.

Experimental setup and procedure. A ten camera Vicon motion-capture system was used to record lower-limb kinematics. Retroreflective markers were placed on each of the subjects according to the in vivo point-cluster method developed by Andriacchi et al. (1998). Subjects were asked to perform three stair climb trials, consisting of the ascent of two consecutive seven-inch steps, and three level-walking trials. Musculoskeletal models for each trial were developed within Visual 3D from marker positional data filtered with a 15Hz low-pass Butterworth filter. From this model, joint angles in the sagittal, frontal, and transverse planes at the ankle, knee, and hip were calculated. However, only ankle angles in the sagittal plane (the ankle flexion angles) were used through the remainder of this study.

Model Architecture

Six kinematically-informed algorithms and one machine learning algorithm were developed as joint angle prediction models. Each of the models were developed from trendline extrapolation, kinematic forecasting techniques, or from an existing Python (v3.9.12, Python Software Foundation; https://www.python.org/) library, as follows.

Naïve forecasting. Naïve forecasting is the simplest of the extrapolation methods. This method uses the current joint angle, $\hat{\theta}(t + t_{pred})$, at a given time, t_{pred}, in the future. Therefore, the naïve approach is a function of only one recorded joint angle. The naïve approach is governed by Eq. (1) below:

$$\hat{\theta}\left(t + t_{pred}\right) = \theta_i \qquad (1)$$

Although a naïve prediction is merely a responsive replication of a previous data point, and therefore may not be supremely beneficial in a predictive exoskeleton control scheme, such a model was included in the analysis to serve as a baseline comparison for the other kinematically-informed models.

Linear extrapolation. The linear extrapolation method is a function of two consecutive joint angle data points, seeking to define a linear curve through the historical data. Future joint angles are computed by evaluating this linear curve at a desired future time as defined by Eq. (2).

$$\hat{\theta}\left(t + t_{pred}\right) = \theta_i + \left(\frac{\theta_i - \theta_{i-1}}{t_i - t_{i-1}}\right) * t_{pred} \qquad (2)$$

Deriving the slope of the linear curve effectively yields an angular velocity, $\omega i,avg$, of the joint. As such, the linear extrapolation method is identical to a kinematic approach assuming an average angular velocity and constant angular acceleration, as is outlined by Eq. (3) and (4).

$$\hat{\theta}(t + t_{pred}) = \theta_i + \omega_{i,avg} * t_{pred} \tag{3}$$

...where:

$$\omega_{i,avg} = \left(\frac{\theta_i - \theta_{i-1}}{t_i - t_{i-1}}\right) \tag{4}$$

Quadratic extrapolation. The quadratic extrapolation method seeks to fit a quadratic curve, $f_{quad}(x)$ (governed by coefficients *a*, *b*, and *c*), to the previous three recorded angular data points by. Predicted joint angles are computed by evaluating this quadratic-fit curve at the desired future time, as demonstrated by Eq. (5) below.

$$\hat{\theta}(t + t_{pred}) = a(t + t_{pred})^2 + b(t + t_{pred}) + c \tag{5}$$

Cubic extrapolation. The cubic extrapolation method is the final extrapolation method deployed in this study. The cubic extrapolation method uses the four previously recorded joint angle data points to develop a polynomial cubic curve, f_{cubic} (x) (governed by coefficients *a*, *b*, *c*, and *d*). By evaluating this resulting cubic-fit curve at a future time, a joint angle prediction can be reported, as is indicated by Eq. (6).

$$\hat{\theta}(t + t_{pred}) = a(t + t_{pred})^3 + b(t + t_{pred})^2 + c(t + t_{pred}) + d \tag{6}$$

Angular acceleration informed. The angular acceleration approach seeks to expand upon the linear extrapolation method, additionally including the effects of angular acceleration on the prediction. Eq. (7) below indicates the development of an average angular acceleration value, α_(i,avg), of three joint angles, similar to how Eq. (4) outlines the calculation of an average angular velocity from current and past joint angles.

$$\alpha_{i,avg} = \left(\frac{\omega_{i,avg} - \omega_{i-1,avg}}{t_i - t_{i-1}}\right) \tag{7}$$

The calculation of this average angular acceleration allows for the use of a kinematic relationship to predict future joint angles, as is defined by Eq. (8).

$$\hat{\theta}(t + t_{pred}) = \theta_i + (\omega_{i,avg} * t_{pred}) + \cdots$$
$$\cdots + (\alpha_{i,avg} * t_{pred}{}^2) \tag{8}$$

Damped angular acceleration effect. The damped angular acceleration approach seeks to minimize the effect of potential noise in the system, as angular accelerations are not reported directly but are rather twice-derived from marker positional data. In the hope of still including some effect of the joint's angular acceleration on the predicted value, a scaling factor, β, was included on the acceleration term of the kinematic relationship. This scaling factor alters the effect of the acceleration in the equation and is constrained such that $0<\beta<1$. Therefore, this approach is a function of three historical kinematic data points and a variable damping coefficient. The damped angular acceleration approach is defined by Eq. (9) below.

$$\hat{\theta}(t + t_{pred}) = \theta_i + (\omega_i * t_{pred}) + \cdots$$
$$\cdots + \beta * (\alpha_i * t_{pred}{}^2) \tag{9}$$

Were $\beta=0$, the resulting equation would mirror that of the linear extrapolation method and Eq. (3). Were $\beta=1$, the resulting representation would be identical to the general angular acceleration approach outlined in Eq. (8). This damped approach allows for the exploration of effective β values that provide the benefit of including acceleration data for prediction during changes of direction while neglecting the effects of positional data noise. The effect of the scaling factor on model performance was explored by indexing β on the range $0 < \beta < 1$ at an interval of 0.001. Model performance was then compared to the varied values of β to understand the optimal sizing of the scaling factor for this dataset.

Random Forest. Finally, a Random Forest (RF) model was developed to serve as the baseline machine learning model for comparison. An RF algorithm is a supervised machine learning algorithm that consists of several branches of decision trees and can be used for both classification and regression applications. The RF regression model developed for this study was tested and trained on the ankle flexion angle curves for level-walking that were collected prior to this study. The RF model was developed using the *Scikit-learn* Python module, using the default hyperparameters (for example, n_estimators = 100, max_depth = None). Although the RF model used in this study was trained and tested on a different dataset than the kinematically-informed models, it is expected that the difference in performance of the RF model from level-walking to stair-ascent would be minimal for an initial comparison. Ensemble RF regression model source code and documentation is accessible via https://scikit-learn.org/.

Model Performance Evaluation

Each of the six kinematically-informed models was used for joint angle prediction for each stair ascent trial. Model performance was evaluated on all three trials for each subject, a total of 27 stair ascent trials. For each trial, each model predicted the sagittal ankle angles for a single gait cycle of the leading limb at t_{pred}=100ms into the future. The leading limb was defined as the limb that was in stance phase on the initial step, and a single gait cycle was defined from heel strike of the leading limb on the initial step to heel strike of the leading limb on the top step. The models incorporated varying sliding window sizes, depending on the number of frames required by each model to make a prediction. Sliding window sizes are documented below in Table 1. Predictions were computed for every measured angle.

Table 1 Sliding window sizes for each kinematically-informed prediction model. Data collected at 120 Hz (8.33 ms per frame).

Model	t_{window} [ms]
Naïve forecasting	8.333
Linear extrapolation	16.667
Quadratic extrapolation	25
Cubic extrapolation	33.333
Angular acceleration informed	25
Damped angular acceleration effect	25

Each model was developed within the Python programming language on a Lenovo ThinkPad x270 (Lenovo Group Limited; Hong Kong) with an Intel Core i5-7200U CPU (Intel Corporation; Santa Clara, CA). Models were tested on each subject's stair climb ankle angle kinematics in an offline analysis. Model performance was evaluated by comparing the predicted joint angles to the ankle angles measured by the motion-capture system using a root-mean-square error (RMSE) metric. Additionally, the computational runtime for each of the models was recorded. RF prediction accuracies and runtimes discussed in this paper are indicative of testing performance only and not training time or training error. A repeated measures ANOVA followed by post-hoc paired t-tests were performed to compare the differences between each of the models' prediction errors and runtimes.

Results

ANOVA results indicated strong statistically significant differences between each of the models' prediction errors. Prediction errors are plotted by model type in comparison with the RF model in Figure 1, while prediction errors are presented numerically in Table 2 below for each of the models. The top performing kinematically-informed models demonstrated comparable prediction errors to that of the RF model (Damped Angular Acceleration = 7.49° RMSE; Linear Extrapolation = 8.45° RMSE; RF model = 5.0° RMSE).

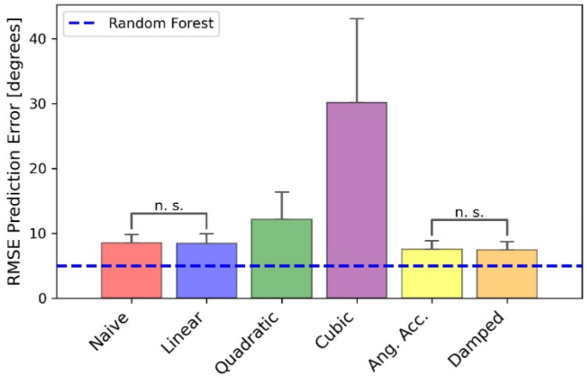

Figure 1 Average prediction errors (reported in °RMSE) of individual models over all stair ascent trials. Error bars denote one standard deviation from the average. The dashed-horizontal line denotes RF model prediction error. Unless indicated with n.s. (no statistical difference), all models exhibited statistically significant differences in their prediction errors.

Table 2 Prediction errors and standard deviations for each kinematically-informed model.

Model	Average RMSE (°)	Std. Deviation $(\pm 1\sigma, °)$
Naïve forecasting	8.55	1.28
Linear extrapolation	8.45	1.48
Quadratic extrapolation	12.19	4.19
Cubic extrapolation	30.20	12.91
Angular acceleration informed	7.56	1.31
Damped angular acceleration effect	7.49	1.23

Additionally, the computational demand of each prediction model is presented in Figure 2.

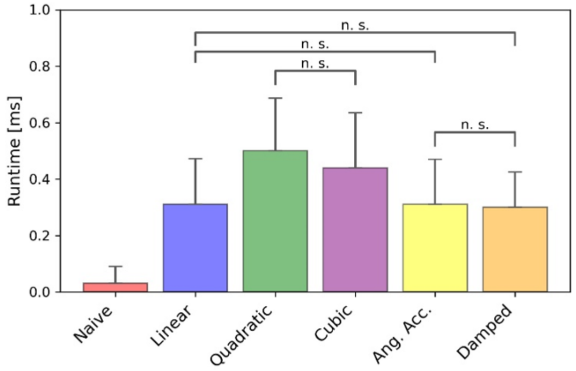

Figure 2 Average runtimes (reported in milliseconds) of each prediction model. Machine learning models trained and tested on similar datasets reported runtimes of ~30ms. Unless indicated with n.s. (no statistical difference), all models exhibited statistically significant differences in their computational demand.

Finally, the effect of scaling factor β on the prediction accuracy of the damped angular acceleration model is shown below in Fig. 3. For this analysis, a $\beta=0.802$ was determined to be the most effective value for minimizing prediction error – unless otherwise stated, this value for β has been used throughout this analysis to represent the maximum performance that the damped angular acceleration model (Eq. 9) could attain for this dataset.

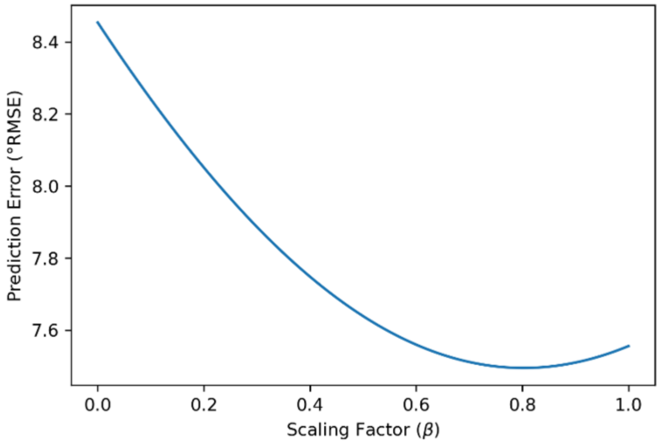

Fig. 3 Prediction error as a function of the scaling factor (β) for the damped angular acceleration prediction model. A $\beta=0$ yields the linear extrapolation model, while a $\beta=1$ yields the angular acceleration informed model.

Discussions and Conclusions

The primary hypothesis of this study was confirmed the kinematically-informed models had significantly decreased computational demand with comparable prediction errors to a machine learning approach. The root-mean-squared errors (RMSEs) of the kinematic models ranged from 7.49° - 30.20°, depending on the model architecture. The RMSEs of the most accurate kinematic models (Damped Angular Acc. model = 7.49°; Linear Extrapolation model = 8.45°) were comparable to the prediction error of 5.0° reported by the RF machine learning model. It is expected that the prediction error for this RF model (which was trained and tested on level-walking trials) would be comparable to a RF model trained and tested on stair ascent trials subsequent studies that seek to expand upon this work should ensure that the datasets being used by both the kinematically-informed models and RF model are identical. Additionally, the runtime of the slowest prediction model was reported as <0.5ms, which is ~50x faster than common machine learning models trained and tested on similar datasets.

Such results may provide the basis for inclusion of kinematically-informed prediction models in real-time ankle exoskeleton applications. Because of the decreased computational demand of these models, additional time can be allocated towards exoskeleton actuation to the desired joint angle without significantly compromising prediction accuracy. Additionally, because kinematically-informed models are not “trained” on specific datasets like machine learning models, they can be considered task agnostic. As such, kinematics-based models can be used in future joint angle prediction for varying actions without significant loss of accuracy, which may be beneficial for free-exploration exoskeleton applications that are not restricted to a single action in a laboratory setting.

The primary limitation of this study involves the noise associated with marker positional data. Developing a method that seeks to report acceleration more accurately is critical to mitigate the effects of noise in joint angle prediction. Potential solutions to such a problem may include expanding the sliding window size of models that rely on acceleration as an input, such as the Angular Acceleration Informed model. Expanding the sliding window would allow for the development of an effective acceleration that incorporates a larger set of datapoints, thus reducing the effects of noise in between consecutive points. In practice, a potentiometric goniometer or an encoder would likely be used to measure joint angles rather than retroreflective markers. In addition to a goniometer, aligning IMUs with respect to a local joint axis, as outlined by Seel et al. (2014), would provide a more robust value of acceleration that does not rely on the derivation of angular position and velocity.

Additionally, studies that seek to expand upon this study and understand the performance of kinematically-informed models in a real-time application should be performed. While an offline analysis of near-future joint angle prediction provides a fundamental understanding of the relative performances of each model, the true performance and ability of each model will only come during an online test that requires each model to make joint angle predictions in real-time. Such a study will further provide justification for such kinematically-informed models in a near-future exoskeleton control application.

Acknowledgments

The authors would like to acknowledge and thank Sarah Bass, Sierra Eady, and Ethan Koenig for their assistance and feedback throughout this study.

Nomenclature

α = *angular acceleration [deg/sec/sec]*
β = *acceleration scaling factor [dimensionless]*
i = *timestep*
ω = *angular velocity [deg/sec]*
t = *time [sec]*
t_{pred} = *prediction time [sec]*
t_{window} = *sliding window length [sec]*
θ = *measured angle [deg]*
$\hat{\theta}$ = *predicted angle [deg]*

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Authors Biography

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Auburn University Journal of Undergraduate Scholarship

Predicting College Football Commitments Using Statistical and Machine Learning

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Abstract

One of the keys to success when building a college football team is skilled talent. Such talent is in high demand, with finite resources existing with which to sway it. Predicting recruits' decisions before they occur is, accordingly, important for recruiting staff. This knowledge allows them to optimally distribute their resources among players, filling gaps before they occur and recruiting the best players available to the team.

Making this prediction on the individual scale is difficult, however. College applications shape the rest of a player's life, so the pressure on them rises and makes predicting individual decisions a challenge. This study uses statistical analysis enhanced with machine learning techniques such as random forest traversals, nearest prototype classifications, and support vector machines.

This model is validated using a dataset with 30+ features on the 1,200 students Auburn University made an offer to from 2017 to 2021. In this snapshot of high school recruits, we find significant success using a support vector machine for predicting the college a recruit will attend, and using an ensemble of a perceptron, decision tree, nearest neighbor classifier, and quadratic discriminant analysis for predicting if a recruit will attend a specific university.

Key Words: Machine Learning, Statistical Learning, Support Vector Machine, College Football

Introduction

In the United States, the national pastime has shifted. No longer does baseball rule, football has supplanted it. In 2019-2020, Auburn University earned $97M from football. All other sports combined earned $15M over the same period. These sports earn a sixth of what football generates but cost Auburn the same [1].

Winning plays a leading role in this earning. High-value teams – such as Auburn, playing in the Southeastern Conference – earn roughly 3% more money for each win [2]. Success in college football can also increase the quantity of a school's applications by as much as 8% [3]. In highly competitive conferences such as the Big Ten, Big Twelve, and Auburn's own SEC, successful recruiting strategies account for 63% to 80% of a team's overall success and winning [4]. Successfully recruiting high-talent players becomes an important task.

This paper details the creation of predictive models designed to provide football staff with knowledge on how likely a recruit is to say yes to an offer before giving it. These findings are based in algorithms from the scikit-learn Python package [5]. Through this information, staff will be able to better allocate resources when recruiting players. It is not the place of this paper to replace staff, as they will know best what players they want to recruit and what talent can fill gaps on the team. Instead, the data this study provides is meant to serve as a potential aid to staff so that they can divide their recruitment resources more optimally.

Data

These algorithms were trained and tested on the 1,200 recruits Auburn has made an offer to within the last 5 years, utilizing over thirty factors in their decision making process. The study required a list of all students in this category. 247Sports online database filled this niche but did not have an easy method for access [6].

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As such, a web scraper was built using the Python package Beautiful Soup [7] to gather these players' names, their talent scores on a scale of 0 to 1, their position, their hometown, and what school they eventually ended up enrolling at seen in Table 1. Factors such as height and weight were gathered but were determined to be unhelpful. Also gathered were all the events involving Auburn and other teams a recruit had been involved with, but this data was not used in the process due to being gathered after an offer is made, not before.

Table 1.1 Subsection of the first half of the athlete database. Each athlete is assigned a unique ID and listed by a score to 4 degrees of precision between 0 and 1, the position they play, and where their listed hometown is.

ID	Score	Position	Hometown
46040471	.9059	DT	Lawrenceville, GA
46040514	.9621	WR	Saint Louis, MO
46040540	.8593	RB	Stone Mountain, GA
46040571	.9186	WR	Memphis, TN
46040672	.9928	RB	Tucson, AZ
46040685	.8548	OT	Memphis, TN
46040691	.8851	WR	Centerton, AR
…	…	…	…
46041185	.9420	S	Griffin, GA

Table 1.2 Subsection of the second half of the athlete database. Each athlete is listed by a set of coordinates, height and weight, and where they officially enrolled at.

ID	Coord.	Meas.	Enrollment
46040471	84W 34N	75" 303lbs	Florida
46040514	90W 39N	74" 169lbs	Ohio State
46040540	84W 34N	71" 211lbs	A&M
46040571	89W 35N	75" 206lbs	Arkansas
46040672	111W 32N	72" 200lbs	Ole Miss
46040685	90W 36N	78" 315lbs	LSU
46040691	94W 27N	74" 180lbs	Baylor
…	…	…	…
46041185	84W 33N	72" 200lbs	Auburn

This study identified Auburn's greatest recruiting rivals using this information. The enrollments of each student Auburn sent an offer to were tallied, and the 25 largest were taken as Auburn's recruiting rivals.

From here, the hometown of each student was converted to longitude and latitude through the Geopy Python package [8]. The haversine distance between this longitude and latitude and the longitude and latitude of Auburn and the rivals were taken and stored as a factor. The longitude and latitude of each student was compared to a list of every county in the United States provided by SimpleMaps [9], with the county with the smallest haversine distance to the player being assigned.

Using information from the 2015 US Census, the median household income, population below poverty, population above poverty, population above 25, and population above 25 with education above the high school level were gathered for each student's county [10] seen in Table 2. This was converted into the county's median household income as a fraction of the United States' median household income, the percentage of the county below poverty, and the percentage of the population in the county over twenty-five with education above the high school level, which were taken as the final factors for the machine learning algorithms.

Table 2 Example table from the 2015 US Census data detailing those above and below poverty. Contains the number of people and the margin of error.

Label	Estimate	MoE
Total	308,619,550	±10,903
Income in the past year below poverty level	47,749,043	±280,598
Income in the past year at or above poverty level	260,870,507	±287,381

Methods and Analysis

Taking the athletes and factors defined above, the data was split, randomly selecting one-fifth of the data to serve as tests for the algorithms while the remaining data was used for training. Eighteen algorithms were chosen for testing, with the thought process that even failed algorithms would give added information. Some of these failures did in fact provide interesting results, and are included below, but other algorithms produced such similar results as other algorithms already tested that they have been overlooked for conciseness. Each algorithm was trained on the training set, where they learned the relationships between each feature and corrected themselves based on the official enrollment.

Each algorithm was used for two experiments: predicting which college among the chosen university – Auburn – and its 25 rivals a recruit will attend, and predicting whether a recruit will attend the chosen university. These were measured by two metrics: accuracy, and recall. Accuracy measures the percentage of the time the algorithm predicts a recruit successfully on the testing set. Recall does the same, but only looks at the algorithm's accuracy on recruits who attend the chosen university, as opposed to the pool of all recruits sent an offer by the university in the time frame.

The algorithms we continued with were split into four categories. The first was for those which create a tree of decisions through which the algorithm descended to make decisions Fig. 1. Decision Trees are the most simple of these, doing exactly that. Extra Tree makes a group of Decision Trees, taking information from the entire training set but deciding optimizations randomly in order to fill out multiple different trees. Random Forests also make a group of Decision Trees, but instead each of their Trees looks at a random subset of the data, then optimizes based on that subset. The consensus is that ensemble methods such as Extra Trees and Random Forests will produce better results than Decision Trees but have a tradeoff between one another as Extra Trees have less bias and Random Forests have less variance.

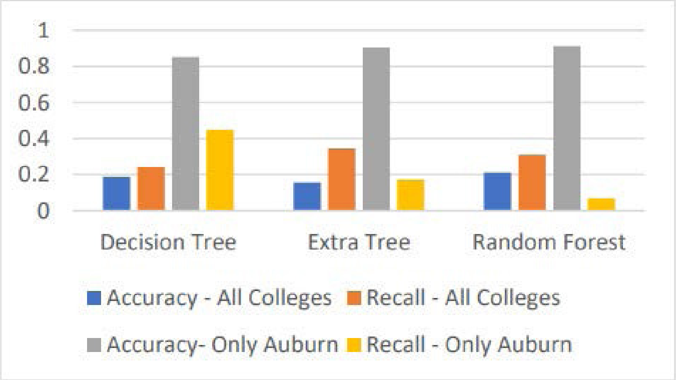

Fig. 1. Tree-based algorithms

The second was for those which plot each training point on n-dimensional space, then determine a prediction based on distance Fig. 2. A Nearest Centroid model does this most explicitly, taking the mean of the coordinates for each point then assigning the point being tested to the prediction of the point with the most similar mean. K-Nearest Neighbors is similar, but instead of looking at means it instead takes the distance between the point being tested and each training point, then takes a vote on the prediction from between the K closest points. We used K=1 and K=3 for this data. Other Ks were tested but ultimately discarded. Some algorithms have a recall of 0, as the algorithm never predicts that a student will attend the chosen university

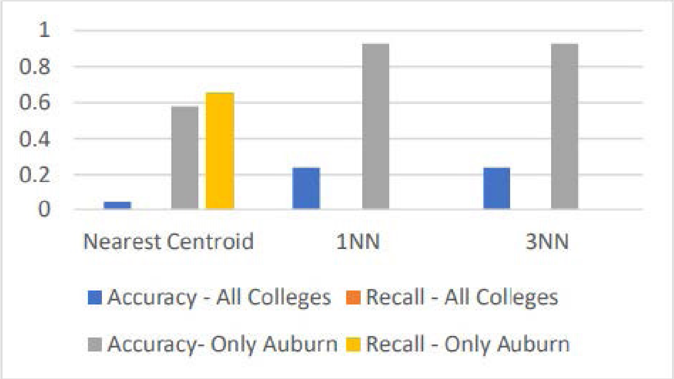

Fig. 2. Nearest-neighbor algorithms

The third was for algorithms which develop linear combinations of variables which discriminate between categories Fig. 3. Linear Discriminant Analysis separates classes by creating a linear combination of the training features optimized so that inputs from a specific class group with similar inputs. Quadratic Discriminant Analysis is similar but creates a quadratic combination. Both require assumptions about the data that our dataset does not match, but they are being included as useful baselines on what to expect in our other models. A Ridge Classifier takes various inputs and converts them all into either -1 or 1 before minimizing the sums of the square of the difference between prediction and target.

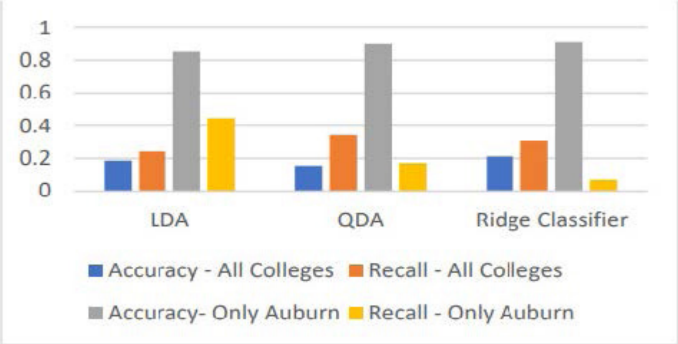

Fig. 3. Statistical learning algorithms.

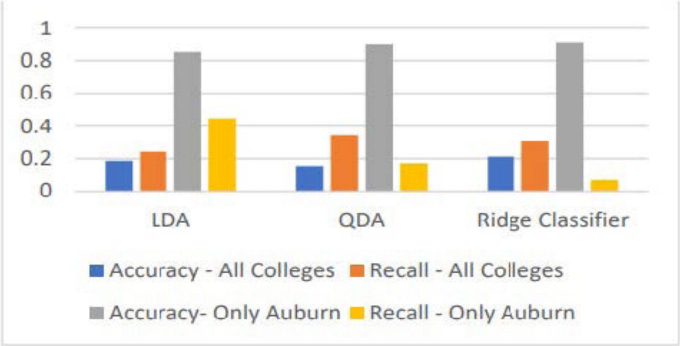

Fig. 3. Statistical learning algorithms.

The final was for algorithms which weigh each factor by an amount the training data calculated, then make a prediction based on that weight Fig. 4. The first of these methods is a Perceptron. A Perceptron is like Linear Discriminant Analysis in that it attempts to separate classes by creating a linear combination of features, but unlike LDA, it is robust and does not require data to be entirely linearly separable to work. A Multi-Layer Perceptron is similar but captures a better idea of the data. Multiple perceptrons are generated and work together to produce an output. This allows for relationships that are not linear to be captured. Support Vector Machines plot each training point in n dimensional space, then form a hyperplane that separates points in one class from another class. In multi-class problems this becomes impossible, so we use One-Versus-Rest methodology as a work around. The SVM will iterate through each class, then create a hyperplane that separates that class from every other class. Predictions are made by looking at this collection.

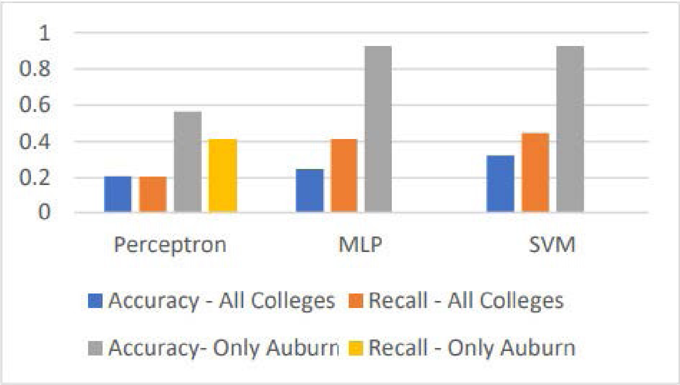

Fig. 4. Perceptron-based algorithms.

Looking only at accuracy and recall when guessing on all colleges, the Ridge Classifier and Support Vector Classifier (SVC) give the best results at 28.7% and 32.3% accuracy respectively. The Ridge Classifier has only a moderate recall at 27.6%, which means that when only looking at the subsection of students who committed to Auburn, it doesn't perform nearly as well. This implies that its prediction strategy leans towards guessing the biggest category rather than the best. The Multi-Layer Perceptron (MLP) and the SVC, meanwhile, have the highest recall when guessing every college at 41.4% and 44.8% recall respectively. This means that rather than just guessing a specific single category repeatedly, they are actually engaging with the material and making an informed estimation on each recruit.

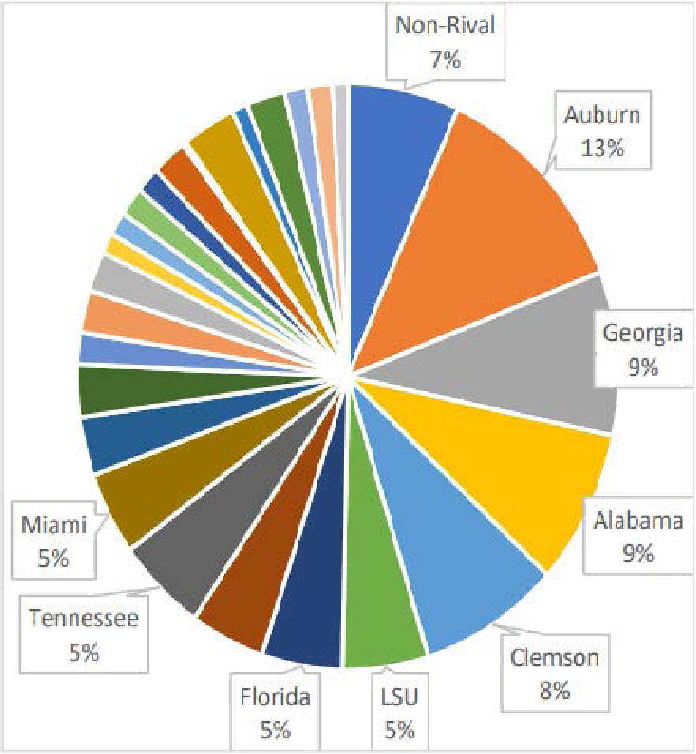

Fig. 5. Example probability map generated by the SVM for making a prediction on which college a specific recruit will attend.

If we instead look at accuracy when guessing Auburn attendance, the results are quite different. This data is lopsided, and many algorithms guess the larger category nearly every time. Quadratic Discriminant Analysis (QDA) performs interestingly on this dataset, almost always guessing a student is attending Auburn instead. The best performer for recall is the Nearest Centroid Classifier (NCC) at 62% accuracy, though the Decision Tree Classifier and Perceptron Classifier have decent results at

45% and 41% respectively.

Looking only at these algorithms as they successfully guess Auburn students, Decision Tree has by far the best accuracy at 85%, while NCC and Perceptron top out at 57%. As seen in Fig. 1-4 various other algorithms have higher accuracy, but all algorithms with recall below 25% were deemed unsuitable to our purposes. The goal of these algorithms is to guess where students will go successfully, rather than just achieve the highest number. If an algorithm tells a coach no on every single student, then even if that no is generally very accurate, it is useless. Taking the successful Decision Tree, NCC, and Perceptron, we'll make an ensemble algorithm which votes between the results of the component algorithms to produce a result.

Voting between Tree, NCC, and Perceptron gives the highest overall result of these votes at 79%, with 55% recall. Voting between Tree, NCC, and QDA meanwhile gives the best recall at 76% and gets 58% accuracy on the entire set. Voting between all four of Tree, NCC, Perceptron, and QDA gives what this study believes to be the most useful result, at 78% overall accuracy with 62% recall. A sample vote is shown in Table 3.

Table 3 Example results for the same recruit as in Fig. 5. Rather than predicting which college the recruit will attend, the algorithms are instead predicting if a recruit will go to the chosen university. Here, even though two of the models in the vote got the answer wrong, the ensemble predicted the result successfully.

Model	Result
Decision Tree	Auburn
Nearest Centroid	Not Auburn
Perceptron	Not Auburn
Quadratic Discriminant Analysis	Auburn
Vote	Auburn
Ground Truth	Auburn

Conclusions

The most impressive of our results was in predicting where a given recruit will attend college. At roughly 33%, this is a very useful metric primarily due to how few sources it uses. Most predictors rely on getting to know a candidate, look at where they visit, and only make a guess after all the offer letters have been given. Our predictor can instead be run at any point in an athlete's decision making process, as the only time reliant feature that might throw off a prediction is an athlete moving, moving position, or having a sharp increase or decrease in skill – all things that are very rare for the 4 and 5 star recruits top schools are looking at.

The goal of this study, however, is to decrease uncertainty for coaches in the early days of recruitment when they are trying to decide who they want to invest time and resources in, which has been accomplished. At nearly 80% accuracy on if a given athlete will attend Auburn, coaches will have a good idea on if their efforts are worth it long before any effort is actually put in.

With the creation of the transfer portal, athletes have more agency in their college sports career than ever before. As such, it is the hope of this study to begin shifting the research narrative away from decisions based on teams and towards decisions based on players. At the end of the day people should be and are the most important part of any endeavor, sports included, and shaping our research around what those people want to do as opposed to what others want to do with them is vital.

Moving to the future, this model should be validated on freshmen, with the database receiving updates every season. More factors from the census can also be gathered, further refining the algorithms as they have more information to input. With that said, the model will likely never be perfect. Choosing what school to attend is a deeply personal decision, and one which no one can fully predict other than the athletes themselves.

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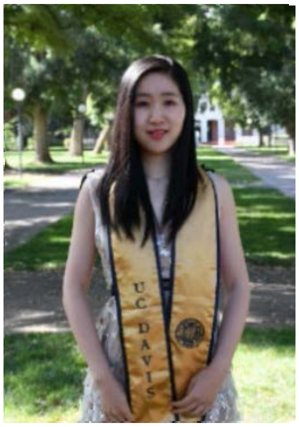
Authors Biography

Davy Walker is a senior-year student pursuing a B.S. in Applied Discrete Mathematics and a B.S. in Computer Science concurrently at Auburn University. They have played a key role in problem conception, code generation, and statistical analysis. Upon graduation they intend to pursue their M.S. in Data Science/ Data Engineering from Auburn University.



Dr. Jingyi Zheng is an Assistant Professor in the Department of Mathematics and Statistics at Auburn University. Her research interests are in areas of Data Science, Machine Learning, and Data-driven computing.

Dr. Nedret Billor is a Professor of Statistics in the Department of Mathematics and Statistics at Auburn University. Her primary interests include robust multivariate data analysis, robust functional data analysis, outlier detection

A Fundamental Study on the Influence of Biomass Source and Operation Conditions on the Self-Assembly of Cellulose-Based Hydrogel Beads

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The research behind potential functionality and utilization of cellulose-derived products has expanded drastically over the years, gaining traction with the desire for more environmentally conservative products and procedures to replace those derived from petroleum as well as the characteristic versatility and modifiability of cellulose in application. The study of regenerated cellulose and its production with environmentally conscious methods paves the way for a sustainable alternative to petroleum-based products. Moreover, these products would benefit by the extensive ability of cellulose to be easily functionalized and chemically modified to fit a variety of applications and shapes. (Trygg et al., 2013).

Cellulose beads have been prepared using a variety of starting materials including various feedstocks and regeneration baths. One of the notable differences in determining which cellulose to use is the variation in solubility which determines characteristics that present after formation such as density and porosity (Gomez-Maldonado et al., 2021) (Akalin & Pulat, 2018) (Nie et al., 2021) (Gericke et al., 2013). Solubility is important in the determination of dissolution bath components. The variation in properties available due to the use of different materials has been understudied. Thus, this is an opportunity to better understand the potential when considering the use of various starting materials depending on the desired properties for the final beads.

The primary focus of this research was to understand the functional properties of cellulose in the formation and shaping of hydrogel beads that may be used in applications like drug delivery, water remediation, and molecule separation, as a substitute of plastic beads present in cosmetics, etc. (Gericke et al., 2013) (Niinivaara & Cranston, 2020). This was done by comparing the morphological characteristics between the resultant beads composed of the different cellulose feedstocks and acid regeneration baths.

The cellulose starting materials chosen for comparison in this work were cellulose nanofibrils (CNF) from soybean hulls, wood, and the more traditionally used dissolving pulp. The beads were regenerated in three different acid baths: sulfuric acid, nitric acid, and citric acid.

These hydrogel beads are formed through the dissolution and regeneration of cellulose. A solution composed of a cellulose starting material, sodium hydroxide, urea, and ultrapure water is mixed at low temperatures (-11°C) and then administered dropwise into an acid bath in which the solution coagulates to form small hydrogel beads (Gericke et al., 2013). The beads are then washed using ultrapure water until neutral pH to prevent further degradation during storage (Gomez-Maldonado et al., 2021).

Characterization using scanning electron microscopy (SEM) (Figure 1-8) showed an apparent difference in porosity between beads. This indicates a difference that may be studied further to better understand possible functionalization due to the given properties.

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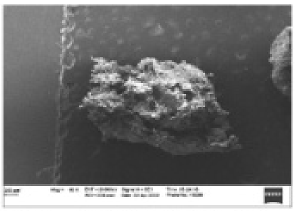

Fig. 1. SEM Dissolving Pulp Nitric Acid

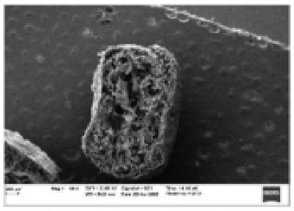

Fig. 2. SEM Dissolving in Pulp in Sulfuric Acid

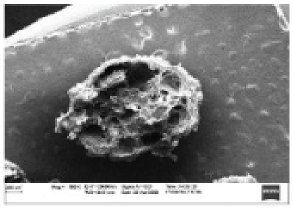

Fig. 3. SEM Dissolving Citric Acid

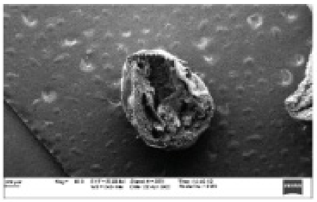

Fig. 4. SEM Wood CNF in Nitric Acid

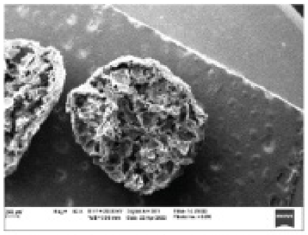

Fig. 5. SEM Wood CNF in Sulfuric Acid

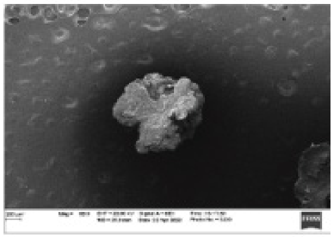

Fig. 6. SEM Wood CNF in Citric Acid

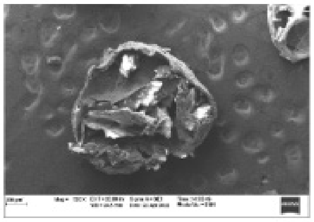

Fig. 7. SEM Soybean CNF in Nitric Acid

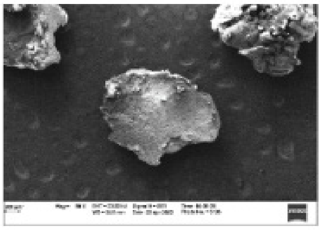

Fig. 8. SEM Soybean CNF in Citric Acid

Fig. 1-8. Depicts the solid content and diameter of each bead produced. Differences can be observed, especially in solid content. The beads produced in the sulfuric acid bath had a higher solid content than the ones in nitric or citric. Despite the differences in porosity and solid content, the diameter of the beads was relatively similar.

Further research needs to be conducted to determine what role these differences could play in the functionalization and utilization of cellulose-based hydrogels formed from various starting materials and regeneration baths.

In future work, we plan to continue to examine the findings presented and explore other properties of the beads such as thermal behavior and surface area. There will also be more in-depth investigations into the potential of these hydrogels in practical applications.

Table 1 Solid content and diameter measurements for each starting material regenerated in each acid bath.

	Nitric Acid	**Sulfuric Acid**	**Citric Acid**
Dissolving Pulp	Solid Content (%)- 8.48 Diameter (mm)- 2.88	Solid Content (%)- 15.62 Diameter (mm)- 3.22	Solid Content (%)- 9.45 Diameter (mm)- 3.07
Wood CNF	Solid Content (%)- 6.01 Diameter (mm)- 2.89	Solid Content (%)- 14.26 Diameter (mm)- 2.94	Solid Content (%)- 11.03 Diameter (mm)- 2.71
Soy-bean CNF	Solid Content (%)- 3.86 Diameter (mm)- 2.60	Solid Content (%)- 21.15 Diameter (mm)- 2.63	Solid Content (%)- 9.56 Diameter (mm)- 2.27

Statement of Research Advisor

Florrie's work is part of a larger effort in my group to understand the structure-properties relationship between sources of biomass and supramolecular structure of cellulose assemblies. In this work, Florrie has developed a strategic experimental design to advance our understanding of pore structure on regenerated cellulose beads, to be evaluated as adsorbents for water contaminants. Florrie has developed a great deal of skills during this period, including time management, data acquisition and analysis.

-Maria Soledad Peresin, College of Forestry, Wildlife and Environment.

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Authors Biography

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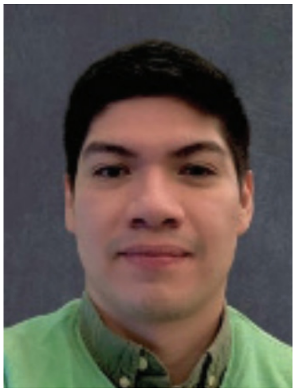

Diego Gomez-Maldonado is a Post-Doctoral Research Fellow in the Sustainable Bio-based Materials Laboratory. He is very active in helping undergraduate student expand their knowledge.

Maria Soledad Peresin is an Associate Professor in the College of Forestry, Wildlife, and Environment at Auburn University. She is the principal investigator for the Sustainable Bio-based Materials Laboratory.

Lower Body Power is Related to Hitting Performance in Youth Baseball Athletes

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Baseball hitting is a linear and rotational motion requiring force generated at the lower extremities to be transferred through the pelvis, trunk, upper extremities, and finally the bat to maximize hitting performance [2,3]. Therefore, strength and conditioning coaches seek to improve lower body power in baseball athletes [5]. They implement a battery of lower body power tests to monitor training progress. Prior research suggests that broad and vertical jumps are associated with hitting performance [1,4]; however, it is unknown if a more sport-specific single leg jump with a rotational component is more closely related to hitting performance.

The purpose of the study was to determine the relationship between a battery of lower body power tests (vertical jump, broad jump, and single leg lateral rotational jump) with youth hitting performance.

Fifty-one youth (9-17 yrs) baseball athletes [right-handed (n = 48); 11.5 ± 1.7 yrs, 152.4 ± 13.2 cm, 50.5 ± 15.5 kg] who were active on a team roster and injury free for the past six months participated. Prior to data collection, participants signed consent forms, and their anthropometric measurements (age, height, weight) were recorded. Each participant rotated at random through a battery of tests, including two trials each of a maximal effort standing broad jump (SBJ), triple broad jump (TBJ), and single leg lateral rotational jump (LRJ) (bilaterally), and three maximal effort swings off a stationary tee positioned in the center of the strike zone.

For the SBJ and TBJ, participants aligned their toes with a starting line and then jumped as far as possible consecutive times for the SBJ and TBJ, respectively. For the single leg LRJ, the jump was initiated with a countermovement followed by an explosive rotational jump off one leg landing on both feet simultaneously. Hitting performance (exit velocity) was measured using a Rapsodo® Hitting 2.0 (Figure 1) unit positioned 4.3 meters from home plate. Peak values for the SBJ, TBJ, single leg LRJ, and exit velocity were used for analysis.

Pearson-product moment correlations were used to determine bivariate associations between jump distances (cm) and exit velocity (mph). A forward multiple linear regression, including height (cm) and jump distances, was performed to determine the best predictor of exit velocity. Height was entered initially to estimate the proportion of variance accounted for by the anthropometric measure. The additional predictive value of each jump distance, above and beyond the predictive effects of height, was also estimated (ΔR2). Statistical significance was set a priori to $p < .05$.

The mean peak exit velocity was 56.1 ± 8.0 mph. Descriptive statistics are reported in Table 1. Bivariate correlations determined SBJ, TBJ, and single-leg LRJ distances were all significantly and positively related to exit velocity (all p-values < .001) (Table 2).

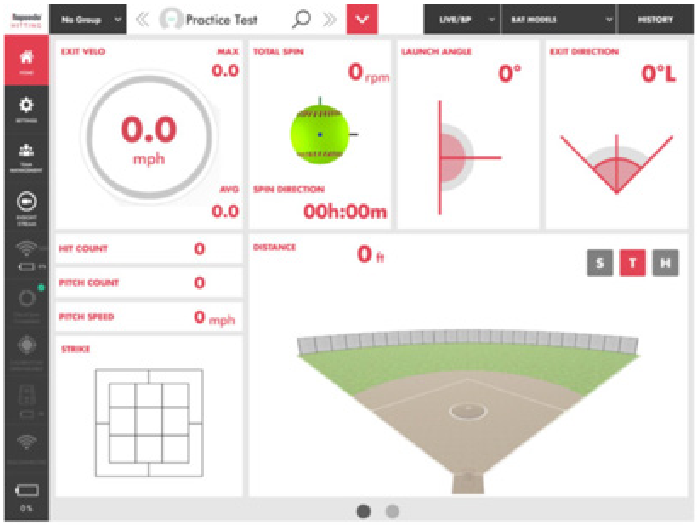

Fig. 1. Rapsodo® Hitting 2.0-Unit Screen

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Table 1. Descriptive statistics

Variable	Value (Mean ± SD)
Height, cm	**152.4 ± 13.2**
Exit Velocity, mph	**56.1 ± 8.0**
Jumps	
SBJ, cm	**161.4 ± 27.9**
TBJ, cm	**495.4 ± 83.7**
D SLLRJ, cm	**129.2 ± 22.5**
ND SLLRJ, cm	**130.6 ± 23.0**

Note: Bold = p < .05; Standing Broad Jump = SBJ; Triple Broad Jump = TBJ, SLLRJ = Single Leg Lateral Rotational Jump, D = Dominant, ND = Non-Dominant

Table 2. Bivariate correlations

Variable	Correlation Value	p-Value
Height, cm	**.812**	**<.001**
Jumps		
SBJ, cm	**.728**	**<.001**
TBJ, cm	**.697**	**<.001**
D SLLRJ, cm	**.580**	**<.001**
ND SLLRJ, cm	**.626**	**<.001**

Note: Bold = p < .05; Standing Broad Jump = SBJ; Triple Broad Jump = TBJ, SLLRJ = Single Leg Lateral Rotational Jump, D = Dominant, ND = Non-Dominant

The regression analysis indicated that body height accounted for 65.9% of the variance in exit velocity alone. The predictive model was improved by adding peak SBJ [$\Delta R2 = .090$; $R2 = 0.749$, $F(2, 48) = 71.7$, $p < .001$]. On average, the model predicted a 1.1 mph increase in exit velocity for every 10 cm increase in peak SBJ ($\beta = .376$, $p = < .001$).

The finding from this study indicates most of the variance above and beyond that of the athletes' anthropometric measurements was the SBJ. These findings agree with previous examinations relating SBJ performance to hit ball kinetic energy in youth baseball athletes [4]. The SBJ is the most common jump test strength and conditioning coaches use. Compared to the other jump tests used in this study, it is the easiest to perform, leading to a potential bias towards more experienced, skilled athletes over novice athletes. Future studies should examine higher-skilled athletes performing all of the tests utilized in the current study and determine whether the same relationship exists.

Although all lower body power tests were related to hitting performance, the SBJ best predicted exit velocity. This finding may be due to the simplicity of the standing broad jump, whereas the TBJ and single leg LRJ required a lot more coordination from novice athletes. Therefore, when strength and conditioning coaches design time-efficient testing protocols, the standing broad jump may be the best lower body power test to monitor training progress related to improved hitting performance in youth baseball athletes.

Statement of Research Advisor

Trent contributed to the understanding of how frequently utilized lower body tests are related to youth hitting performance. The findings from this study indicates that most of the variance above and beyond that of the athletes' anthropometric measurements was in the SBJ. These results will aid strength and conditioning coaches in selecting the most effective test for monitor training progression. Trent strengthened his research skills by assisting in all aspects of the study, including research design, data collection, statistical analysis, results interpretation, and abstract writing.

- Gretchen Oliver, Department of Nutritional Sciences, School of Kinesiology

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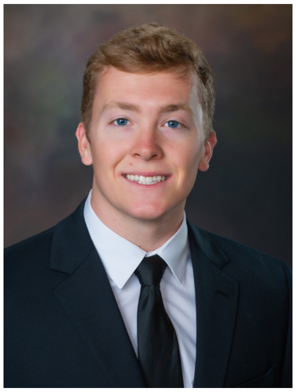
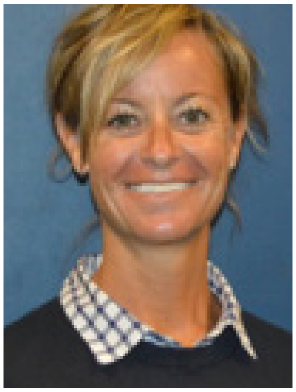


Trent Agee is a senior-year student pursuing a B.S. in Nutrition Science at Auburn University. He has been a research assistant for the past 2 years and is currently a research fellow in the Sports Medicine & Movement Laboratory, focusing on jump and hitting performance. He will start medical school next fall.

Nicole Bordelon is a post-doctoral researcher in Auburn University's Sports Medicine and Movement Laboratory and a Sports Science Consultant for the University of Maryland Softball. One of her primary research interests is in baseball and softball hitting performance.



Dr. Oliver is a full professor in the School of Kinesiology and Director of the Sports Medicine & Movement Laboratory at Auburn University. She is the President of the American Baseball Biomechanics Society, Executive Board Member of the International Shoulder Group, and Executive Board Member of the International Society of Biomechanics in Sports. Her primary research focuses on injury prevention and performance enhancement in youth baseball and softball athletes. Among her peers, she is the expert in youth baseball and softball injury prevention and is world-renowned for her research expertise in windmill softball pitching.

Ultrasensitive Electrochemical Biosensor Based on Zn/S Graphene Hybrids for SARS-CoC-2 Antigen Rapid Detection

Carolina Amezaga[1,], Mao-Chia Lin[2], Shatila Sarwar[3] and Xinyu Zhang[3]*

[1] Undergraduate Student, Department of Material Engineering, Auburn University
[2] Graduate Student, Department of Chemical Engineering, Auburn University
[3]Associate Professor, Department of Chemical Engineering, Auburn University

The Coronavirus disease, commonly referred as COVID-19, is an infectious disease cause by the SARS-CoV-2 virus. Presently, the Quantitative Reverse Polymerase Chain Reaction (qRT-PCR) Method has been implemented as the primary technique used to detect COVID-19 due its capability of providing an early and prompt diagnostic. The following method, however, imposes issues in time effectiveness and selective usage. This leads to the development of an ultra-sensitive electrochemical biosensor based on Zinc Sulfide and Graphene (ZnS/ Graphene) nano composites that would rapidly detected COVID-19 antigens.

The nano composites used within this experiment are developed from a one-step procedure that implements a microwave-based heating approach. The COVID-19 antigens are detected from electrochemical probes designed to find hybridized SARS-CoV-2 Deoxyribonucleic Acid (DNA) samples. In this study, both clinically and laboratory synthesized DNA samples were studied and thoroughly examined. Furthermore, the technique used to perform the following studies was additionally experimented in hopes to determine the most efficient method.

Experimental results revealed that the following biosensor could detect primarily low concentrations of SARS-CoV-2 antigens, specifically the S, N, ORF 1a, and ORF 1b genes, when using a Graphene-based nanocomposite. Similarly, it was determined that the one-step hybridization technique was presented to be the most time efficient. This ultra-sensitive electrochemical biosensor based on ZnS/Graphene, has the potential to lead inspiration for innovating applications within COVID-19 research and future infectious diseases. More details of the research can be found in the authors' published work. More details on the work presented in this Highlight can be found in authors' publication [1].

Statement of Research Advisor

The results from this project promoted significant advance in biosensor fabrications, fundamental understanding of interactions between paired DNA molecules and the electrochemical biosensor surfaces. This approach resulted in high sensitivity and selectivity detection of the COVID-19 viruses. It will lead to fast, inexpensive, and facile detection for large biological molecules and biomarkers in the future.

-Xinyu Zhang, Sammuel Ginn College Chemical Engineering

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Authors Biography

Carolina Amezaga is a senior-year student pursuing a B.S. degree in Materials Engineering at Auburn University. She has conducted research under her mentor, Dr. Xinyu Zhang, for two years and has research interests in electrochemistry, plasma-synthesized nanomaterials, and nanobiotechnology

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Mao-Chia Lin is a graduate student in the Department of Chemical Engineering at Auburn University. He received B.S. and M.S. degrees in Chemical Engineering at Feng Chia University. He previously served as a Research and Development Engineer at YI-PU TECHNOLOGY CO.,LTD. His research interests include nanobiotechnology and thin film coatings

Shatila Sarwar is a postdoctoral student at the University of California San Diego. She received a graduate degree in in Chemical Engineering at Auburn University and a B.S. in Chemical Engineering at Bangladesh University of Engineering and Technology. Her research interests include nanomaterial synthesis, supercapacitors, and thin film coatings

Xinyu Zhang is a Professor in Department of Chemical Engineering at Auburn University. His work focuses on interfacial science and surface engineering of sustainable, multifunctional nanocomposites, and their applications in electrochemical energy and biosensor related areas. Before Joining Auburn University in 2008, he studied in the Chemistry Department at the University of

Gust Interaction of Red- Tailed Hawks

Colin Bamford[1], Jack Nix[2], Paul Swiney[3], Tyson Hedrick[4], Vrishank Raghav[5,]*

[1]Undergraduate Student, Department of Aerospace Engineering, Auburn University
[2]Graduate Student, Department of Aerospace Engineering, Auburn University
[3]Aerospace Engineer, U.S. Army Aviation & Missile Center
[4]Professor, Department of Biology, University of North Carolina at Chapel Hill
[5]Associate Professor, Department of Aerospace Engineering, Auburn University

In recent years, unmanned aerial vehicles, or UAVs, have exploded in popularity. Governments and companies have utilized UAVs in military, commercial, and entertainment roles. Unfortunately, all UAVs possess a major drawback in the form of flight stability. Unmanned vehicles lose stability in the presence of sudden vertical gusts. To solve this issue, engineers have looked towards bio-inspired designs to resist gust instability. A leading design for this is a flapping-wing drone, modelling the flight of birds. To further advance bio- inspired design, research has been conducted to understand how flying birds respond to sudden gusts (Cheney et al. 2020) (Quinn et al. 2017). By better understanding both the response and the stimuli prompting the response, a robust, gust-resistant drone can be built.

In this project, our group observed the flight of a red-tailed hawk (Buteo jamaicensis) through an indoor flight arena, seen in Figure 1. Two Phantom VEO 640L and two Phantom VEO 4k 990L cameras were set up around the arena to obtain high speed footage of the flight. Six industrial fans of diameter twelve inches were placed in the middle of the flight path. The fans would be turned to a low or high setting depending on the desired gust to forward velocity ratio. The hawk would be flown through the tunnel, and the effect of gusts would be observed.

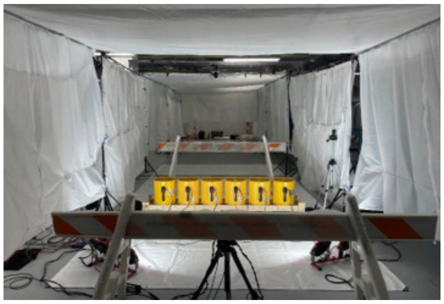

Fig. 1 Fully assembled indoor flight arena.

Before any set of flights, the cameras would be calibrated for tracking using a checkerboard calibration technique (Theriault et al. 2014). After completion of a series of flights, the camera videos would be imported the DLTdv8 MATLAB application created by Dr. Hedrick (Hedrick 2008). Accurate 3-D point data was gathered for the wings, tail, and hawk body, as shown in Figure 2. The data was exported and manipulated using computer scripts to produce geometric variables such as roll angle, pitch angle, and yaw angle. A lower-order unsteady aerodynamic model was applied to these variables to produce lift coefficient values (Ignacio et al. 2022). Together with drag coefficient estimations, a linear dynamic model was created to estimate the expected change in height due to gust interaction. This model would provide information on the gust response effectiveness, and what aerodynamic forces would cause the observed response.

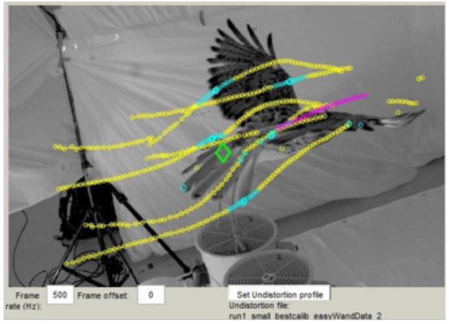

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Fig. 2 Bird flight tracking using DLTdv8.

A general path track for wing and tail points can be seen in Figure 3. We observed a downwards pitch in both wings after crossing the fans. High gust ratio runs, where the gust speed to forward velocity ratio was greater than one, saw only slightly greater downward pitch than low gust ratio runs. After leaving the gust column, both run regimes saw a slight pitch back upwards.

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Lift coefficient values were found for high gust ratio and low gust ratio runs. Due to the equation used, the lift coefficient starts at zero, when the wing first encounters the gust. The high gust regime sees a rapid increase in lift coefficient initially, before levelling out and increasing at a constant rate. After leaving the gust, the lift coefficient decreases rapidly.

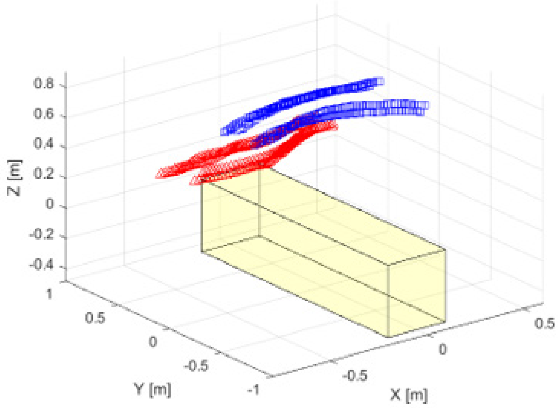

Fig. 3 Three-dimensional tracks of wing points and tail points over fans.

A linear model was created using the equations below (Josselson 1997). Together with the lift coefficients found previously and estimations of the drag coefficient of a bird's wing, expected height changes were calculated (Withers 1981).

$$\dot{u} = \frac{F_x}{m} + (rv - qu) \tag{1}$$

$$v = \frac{F_y}{m} + (pw - ur) \tag{2}$$

$$\dot{w} = \frac{F_z}{m} + (rv - qu) \tag{3}$$

The model assumed that only the aerodynamic forces over the wing were significant. The low gust ratio estimates possess somewhat large errors, but are still within realm of error given the lift and drag estimates used. The high gust ratio estimates are very far off, with relative errors greater than two hundred percent. Attempts were made to decrease error by assuming stall conditions; however, no manipulations of the aerodynamic forces decreased error significantly. A review of lift and drag force calculations was conducted to ensure the observed model response was not due to sub-par lift and drag estimations. Past investigations showed that the lift estimation scheme is sufficiently accurate for sine-squared gust patterns (Ignacio 2020). The fans used in this research produce a sine-squared gust pattern, making such substantial error unlikely (Swiney et al 2020).

The high gust ratio results suggests that there is some outside phenomenon the model is not taking into account. One possibility is tail response effects, which are not accounted for in this model. Future research will have to account for coupled wing and tail effects when examining gust responses.

Statement of Research Advisor

With the increasing rate of adoption of drones in civilian and military applications there is a need to design drones that are robust to aerodynamic perturbations such as gusts. In this study, a bio-inspired approach is adopted to investigate how a bird adapts to an adverse aerodynamic environment in a controlled manner. In the future, the plans are to design aerodynamic vehicles to include such bio-inspired gust mitigation techniques.
- Vrishank Raghav, Department of Aerospace Engineering, Samuel Ginn College of Engineering.

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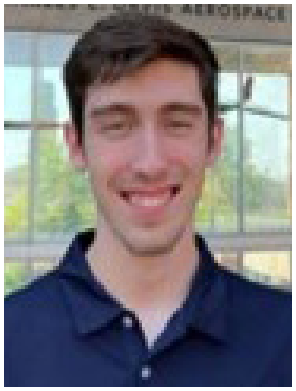
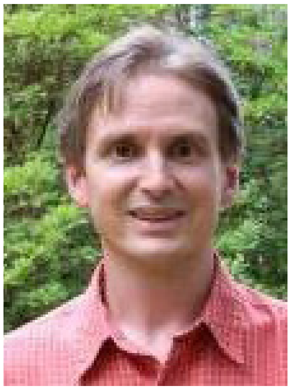


Colin Bamford is a senior-year student pursuing a B.S. degree in Aerospace Engineering. He assisted a research group with collecting data on a hawk's response to vertical gusts, and conducted a detailed analysis of the unsteady aerodynamics observed.

Jack Nix is a graduate student in aerospace engineering at Auburn University. He received a B.S. in Mechanical Engineering and Aerospace Engineering from the University of Florida. Jack is current working on developing a dynamic simulation platform for simulation of novel flight models under normal flight and gust perturbations.

Paul Swiney is an aerospace engineer for the U.S. Army Aviation & Missile Center. He received a Bachelor of Mechanical Engineering in 2018 and a Master of Science in Aerospace Engineering in 2020 at Auburn University. His research at Auburn University was on unsteady flows in fluid dynamics and the biomechanics of avian adaptations to gust perturbations in the Applied Fluids Research Group.



Dr. Tyson Hedrick is a Professor of Biology at the University of North Carolina at Chapel Hill. Dr. Hedrick received a B.S. in Biology from Brown University and a Ph.D. in Biology from Harvard University. His research focus is on the physiology and biomechanics of animal locomotion, especially animal flight.

Dr. Vrishank Raghav is an Associate Professor of Aerospace Engineering at the Auburn University. Dr. Raghav received a BTech in Mechanical Engineering from NITW and a Ph.D. in Aerospace Engineering from Georgia Tech. His research focus is on experimental fluid dynamics and its application across multiple disciplines.

The Lemonade Man: A Children's Storybook About James Echols

Kalandra L. Blake[1], Aaliyah Lantigua[2], and Robert Bubb[3,]*

[1] Undergraduate Student, Department of Human Sciences, Auburn University
[2] Undergraduate Student, Department of Human Sciences, Auburn University
[3] Lecturer, Department of Human Sciences, Auburn University

Auburn, Alabama, was shaped and influenced by the inspirational experiences of African Americans, yet these stories are not openly shared or available. The contribution of James Echols is one such story. Everyone in Auburn knows about Toomer's Drugs famous lemonade. However, few know an African American man was responsible for making the lemonade world famous. The objective of the project was to increase the accessibility of stories like Mr. Echols'. Change starts with our youth, so the project focused on authoring and publishing a children's book.

James Echols was known as "The Lemonade Man." He worked at Toomer's Drugs for over 40 years—beginning his employment as a delivery driver before Civil Rights and retiring in 1991. As a delivery driver, he refused to deliver to the back door of residences as was required of African Americans in the Jim Crow South. Eventually, he would work the counter at Toomer's Drugs, where he would serve fountain drinks and his famous lemonade and coffee. Mr. Echols squeezed up to 200 lemons a day, tinkering with each glass to make it "perfect" for each customer who purchased a cup.

Fig 1. James Echols behind the counter at Toomer's Drugs mixing his famous lemonade.

In 2001, the lemonade was listed as the first reason it was good to be an American by Esquire Magazine (Pierce, 2001).

The project continued the work of Kira Kingston and the research group rPAAST (Research to Preserve African American Stories and Traditions) under the mentorship of Human Sciences Lecturer Dr. Robert Bubb. Kingston interviewed James Echols and his children and wrote a manuscript for publication in an academic journal (Echols, 2018; Moore, 2018). The children's book project uses the manuscript as a starting point.

After receiving the summer research fellowship, we reached out to James Echols only to be met by one of his children, who informed us that Mr. Echols had passed away two days earlier. We were deeply saddened by the news and timing, but the children of Mr. Echols felt that a children's book about their father would be an excellent way to honor his legacy.

Fig. 2. James Echols's children pictured (L – R) seated: Mary L. Bryant, Barbara A Moore; standing/back: Janie Echols-Brown, Johnny Echols, Johnnie E. Dowdell.

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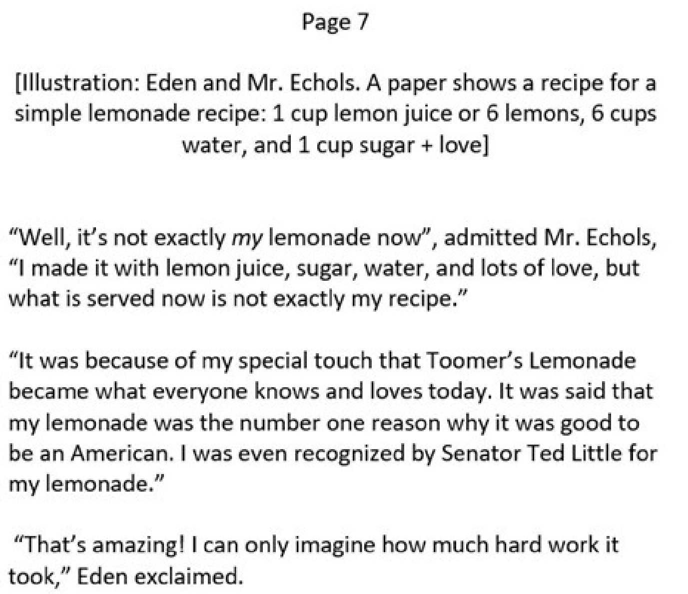
Kalandra Blake coordinated with the Echols family to write the manuscript for the children's book. After several revisions and edits, the manuscript was finalized in March of 2023. The finalized manuscript is 21 pages, including the cover and back page.



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[Illustration: Eden and Mr. Echols. A paper shows a recipe for a simple lemonade recipe: 1 cup lemon juice or 6 lemons, 6 cups water, and 1 cup sugar + love]

"Well, it's not exactly *my* lemonade now", admitted Mr. Echols, "I made it with lemon juice, sugar, water, and lots of love, but what is served now is not exactly my recipe."

"It was because of my special touch that Toomer's Lemonade became what everyone knows and loves today. It was said that my lemonade was the number one reason why it was good to be an American. I was even recognized by Senator Ted Little for my lemonade."

"That's amazing! I can only imagine how much hard work it took," Eden exclaimed.

Fig. 3. Page 7 of children's book manuscript.

Kalandra Blake and Aaliyah Lantigua coordinated efforts to identify an illustrator who used the manuscript to produce sample sketches. The Echols family reviewed four sets of sketches and selected Shonette Pierce as the illustrator. Coordination among us, the Echols family, and the illustrator is currently ongoing.

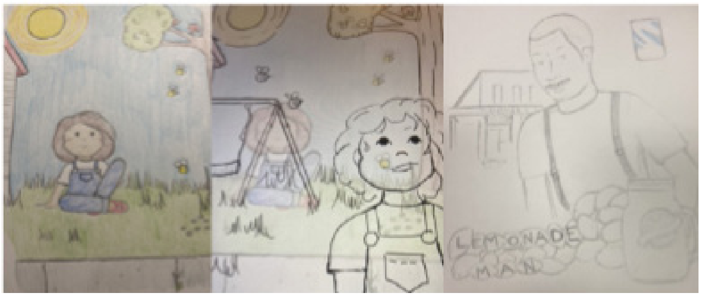

Fig. 4. Page sketches from Shonette Pierce.

The children's book will continue to develop over the summer 2023 semester. Once complete, several copies of the book are planned to be donated to local area libraries, schools, and community centers. The proceeds from sales of the book will go toward a memorial educational scholarship in honor of Mr. James Echols. The James Echols Memorial Scholarship is awarded annually to a talented young adult in the local community who has similar interests in skilled trades as Mr. Echols. Skilled labor fields include carpentry, electrical, plumbing, truck driving, welding, cosmetology, nursing, the arts, and more. With a huge shortage in these types of jobs, the family thought this would be an awesome opportunity for a career that is both rewarding and pays well. In addition to the scholarship, the Echols Family Social Club offers mentorship and an extended family to the recipient.

Readers should contact the corresponding author of this Highlight at the email listed on the bottom of the first page if they are interested in making Donations for the Memorial Educational Scholarship.

Statement of Research Advisor

Kalandra Blake demonstrated initiative, leadership, and collaborative skills throughout the project. The publication of a children's book will not only honor the life and legacy of James Echols but will give credit and acknowledgment for his contribution to Auburn and the lore that surrounds Toomer's Corner and the famous lemonade sold at Toomer's Drugs. The book will also inspire and educate the next generation of children to the rich African American history that is seldom discussed outside of close community circles, but to which we all owe a great debt of gratitude.

- Robert Bubb, Department of Human Sciences, College of Human Sciences

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Authors Biography

Kalandra Blake graduated with a B.S. degree in 2022 in Human Development and Family Science at Auburn University. She is the primary researcher and recipient of the Undergraduate Research Fellowship.

Aaliyah Lantgua is a senior undergraduate student pursuing a B.S. degree in Human Development and Family Science at Auburn University. She selected the illustrator and coordinated communication with the Echols family. She will finalize the details of the project.

Robert Bubb is a lecturer for the Human Development and Family Science Department at Auburn University.

Sensory Spaces: Inclusive Design for All

William Bozeman[1] and Kelly Homan[2,]*

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Abstract

Surrounding yourself with nature activates the parasympathetic nervous system and the sympathetic nervous system, which promotes mental health as described in the "Green Mind Theory". Green Mind Theory connects the body with natural and social elements [1]. Surrounding one's environment with natural elements is proven to be beneficial to the brain and body as a whole. The brain is split up into two main categories when examining its interaction with nature, the top and bottom brain, and is a product of the activated parasympathetic nervous system (top brain) along with the sympathetic nervous system (bottom brain). The benefits vary in quantity depending on the user's focus, attention, awareness, and immersion. Benefits can also include longer-lasting memories, which occur when neurons are created by the hippocampus as a reaction to an enriched environment. [1] While natural spaces are beneficial to everyone, they can be designed in a way that is especially beneficial to those with sensory disabilities. This article and project proposal investigates sensory gardens design in Auburn, Alabama and explores land design as a way to provide a wide range of sensory experiences to children with unique sensory capabilities. The design includes different features, surfaces, objects, and plants to stimulate the multitude of senses. Results show how design can respond to the needs of people groups who process the world around them in different ways.

Introduction

While typical gardens utilize senses in everyone, specific types of sensory spaces can be designed to meet the needs of children who struggle with different types of sensory processing disorders. Research shows that sensory spaces are most successful when structured with "stations" allowing children to be more social and interactive. [2] Sensory spaces are more beneficial than spaces designed for a single sense or without consideration of atypical sensory needs. [3]

Children with unique sensory needs often experience the world differently. Some may find certain sounds, textures, or movements overwhelming, while others might seek additional sensory input. A child with hypersensitivity to noise might cover their ears in loud environments, while a child with hyposensitivity might seek intense sensory stimuli by spinning or jumping. Sensory-friendly designed environments can provide new types of spaces and experiences for an underserved population grappling with managing sensory challenges.

Sensory Garden Case Study

This project generated a design based on existing research for children who hear, see, smell, and feel in unique ways. By acknowledging and accommodating through design diverse sensory needs, children can be empowered to navigate the landscape comfortably. When researching sensory gardens, Hazreena Hussein, examines how these spaces are beneficial to children with mental disabilities [2]. Hussein's article "*The Influence of Sensory Gardens on the Behavior of Children with Special Educational Needs.*" provides data that backs up the importance of sensory gardens. As a start to Hussein's article, she introduces the idea of sensory gardens and their history. Hussein interviewed and collected data from landscape architects, teachers, therapists, and students. She also looked at the behavioral traits of the Lyndale Special School and how groups of students interact in sensory gardens, analyzing how the park was split into four zones with twenty-seven individual behavioral settings.

Autism Spectrum Disorder

The rate of autism spectrum disorder is increasing across the world. According to the CDC, one out of every thirty-six children have autism [4]. This rate has

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increased from one out of every one hundred and ten in 2006. One main reason this number has increased significantly over the twenty-first century is due to evaluation availability. [4] With no formal "autism test," clinicians have gotten better at spotting what is present and diagnosing Autism. This led to an eye-opening rate of increase since 2006. Since more children are being diagnosed, the problem is still growing. Having an increased rate of diagnoses will correlate to cause of concern for these parents. The brain is wired differently for children with autism. Research shows that the somatosensory cortex of children with autism is more sensitive to touch sensory such as a brush on the palm or feeling different textures. [5] The brain works like this for each of the senses, providing sensory sensitivity.

Park Design + Methods

When selecting a project site in Auburn, Alabama, location, accessibility, and practicality were a priority. A site was chosen next to East Samford Middle School, which currently is the Kiwanis Fitness Trail. After several site investigations, current conditions were documented, and an iterative design process began. This process includes sketching, prototyping through plan iterations, and investigations through the act of creating sections and perspectives. This type of process, termed research through design, is exploratory and cyclical. Inclusive design was the focus to support those with sensory challenges. The new design is made to function as a park for everyone, but certain areas are tailored to benefit those with Autism. The five main human senses each have their own set "area" along with other features that are more associated with traditional part design (Figure 2).

Park Elements

Implementing an herb bed section engages with the smell sensory. Adding Rosemary (Salva Rosmarinus), Gardenia (Gardenia jasminoide), Honeysuckle (Lonicera periclymenum), and Lavender (Lavandula spp.) evoke strong, sweet smells and are found throughout sensory spaces. Children are allowed to freely pick, smell, and taste the plants. For sight, raised beds (Figure 1) are added throughout the park for visual sensory. These beds have 2-foot levels, so visual sensory is engaged vertically. Seasons were also thought about in this design with evergreen plants, along with other plants that show vibrant colors outside of summer.

Figure 1. Raised Beds Section Cut

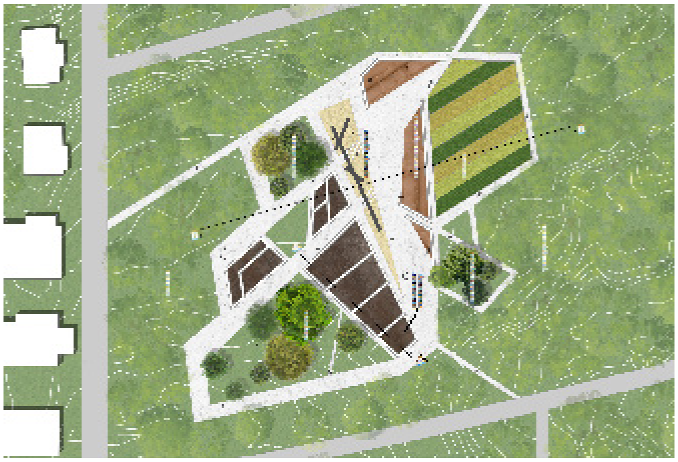

Figure 2. Park Plan View

Colorful chimes move with the wind and children are in control while they push and pull tubes, imagining their own musical symphonies in the Sound Sensory Grove. These chimes engage sound sensory with natural wind, but also with human manipulation. Texture is something that is cohesively used throughout the park. Textured walls are installed throughout the sensory park including rough, uneven surfaces that induce tactile sensations. Sand is also used in the center section to provide touch sensory.

Sensory design is heavily emphasized in the plans, but there are several areas that target the needs of autism that don't pertain to one specific sensory. Raised arches are designed to accommodate children with unique auditory processing capabilities. The sound of the water falling, and the act of splashing generates sound experiences and unique forms of play. The Archway playground (Figure 3) curves through the land interwoven with cascading sheets of water. Children splash, jump, kick; interacting with the water in various ways. This allows many different senses to simultaneously interact with the brain. The swing grove also adds to the play experience. Circular seats suspended and tethered by ropes are designed to engage in the act of pushing and pulling, moving in circles, and the feeling of air moving quickly.

Figure 3. Archway Perspective Rendering

Conclusion

Sensory Spaces shows that it can be beneficial for certain people groups to use design to facilitate sensory disorders and the researcher believes more outdoor spaces should be designed with multiple sets of values. Whether it is designed for Autism, ADA Accessibility, or other disabilities, spaces have a more complex level of impact on society. Sensory gardens are becoming more common across the world, but still need to grow. This project brings awareness and a sensory garden to Auburn, Alabama.

Statement of Research Advisor

"Through his research fellowship, Will Bozeman investigated ways designed landscapes can facilitate the health and well-being of underserved populations. This type of design, termed inclusive design, can enhance the lives of people living with unique sensory challenges. Bozeman's proposal shows a great sensitivity to ways of designing structural elements, engaging with seasonal change, and creating safe and enticing spatial conditions that allow for a multitude of sensory explorations."

- Kelly Homan, School of Architecture, Planning, and Landscape Architecture, College of Architecture, Design, and Construction

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Authors Biography

William Bozeman is a Senior in Environmental Design. He plans on getting his master's in landscape architecture post-graduation.

Mentor Kelly Homan is an assistant professor in Auburn University's College of Architecture, Design, and Construction's Environmental Design program. Kelly's research includes documenting Alabama grassland communities, ecologically focused urbanism, and landscape-scale conservation design.

Auburn University Journal of Undergraduate Scholarship

Disparities of Food Insecure Communities in Montgomery, Alabama

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Food deserts, high rates of poverty, and spatial mismatch–the geographical distance between potential suitable job opportunities and communities that are low-income–are contributors to the overwhelming rates of food related health issues, generational challenges, and urban crime within Montgomery, Alabama. The social and health-related inequalities of food desert communities, as well as the many crippling effects of limited food accessibility and affordability in Montgomery, reflect many regions across the nation. To address these concerns, Montgomery city officials and community leaders are compelled to incentivize grocery retailers, create community-based initiatives, and form an improvement prevention program which addresses both future food-related health risks and economic development.

For many urban and west Montgomery residents, the connection between food desert communities and the lack of economic opportunities and growth is quite evident. As low- income community members attempt to find various forms of transportation and live without appropriate grocery food retailers within their neighborhood (or less than a mile away), the city of Montgomery will also continue to experience a higher rate of morbidity and mortality–when compared to the state and national averages–which are results of food related health issues (e.g., diabetes, cancer, etc.). To further prevent this, community-based initiatives such as community gardens and food pantries have been a welcoming solution for many communities and urban regions across the nation that similarly face food insecurity.

Providing potential grocery retailers with tax incentives to locate to urban, food insecure communities has also been a positive attribute to practicing cities facing the challenges of food deserts in the United States. This return on investment– providing tax incentives to grocery retailers in food desert regions and communities– assists communities beyond the increased accessibility to healthy foods.

Grocery stores are largely recognized as vehicles for economic growth as they also increase property value in surrounding communities and commercial real estate. For cities such as Philadelphia, Pennsylvania, newly placed supermarkets in food insecure communities increased home equity for homeowners in surrounding communities from one-quarter to one-half of a mile. For the city of Montgomery, various opportunities (such as the recruitment of grocery retailers, the implementation of community-based gardens, and the promotion of food education, etc.) will not only decrease the rate of food insecurity but also invest in the lives and generational outcomes for community members.

In this project, I analyzed the population data of Montgomery County, in which Montgomery city residents represent eighty- seven percent, and the rate of individuals experiencing food insecurity. Food insecurity–a household-level economic and social condition of limited access to adequate food–currently impacts nearly 40,000 individuals in Montgomery County, Alabama.

When compared to the nation, Montgomery County has consecutively for the past four years maintained a higher percentage of food insecurity (Figure 1). As inner-city and west Montgomery residents combat the inaccessibility to grocery stores, the effects of minimal employment opportunities due to the lack of economic development contribute to the rise and frequent occurrence of poverty amongst urban communities within the city. Although the city of Montgomery is finding

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strategies to enhance economic opportunities by way of the Retail Development subsection of the city's Development Division, the rate of poverty amongst those within the city are 9.6% higher than the national average. Contributions to this extreme poverty are linked to the direct disadvantage of minimal job opportunities and low economic opportunity.

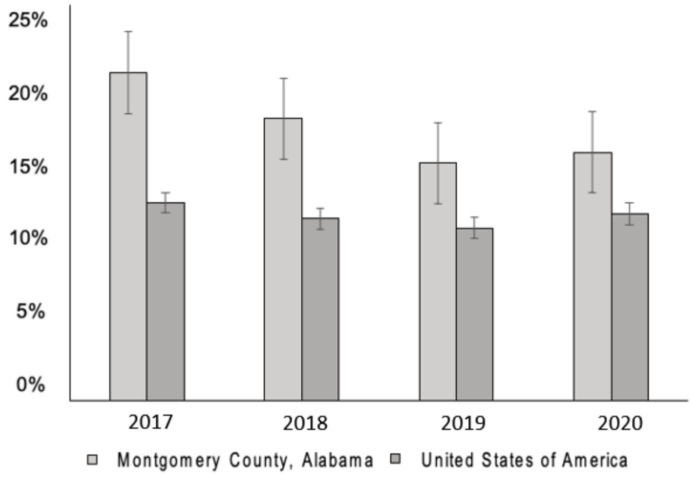

Fig. 1 Rate of food insecurity in Montgomery, AL.

Furthermore, the United States Census Bureau indicates that in 2021 twenty-one percent of individuals in the city of Montgomery were impoverished. As most impoverished communities in Montgomery also experience the hardships of food deserts–communities that meet the thresholds of being both low-income and have low accessibility to a grocery retailer (a mile or less away), it is no coincidence that these communities are also isolated from potential suitable job opportunities due to low vehicle accessibility and limited forms of transportation in these areas of the city (Figure 2).

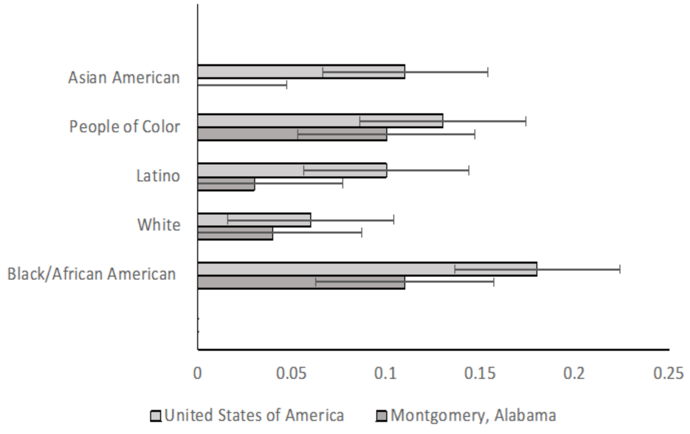

Fig. 2 Vehicle inaccessibility for Montgomery, AL residents.

As established, minimal food and vehicle accessibility amongst these regions guarantee food insecurity; however, in combination with these inequalities, poverty and low economic opportunities create additional stressors for Montgomery residents. Like the rate of food insecurity, Montgomery's rate of reported crime and low social capitol exceed the national average in a consecutive four-to-five-year period. Although the reported crime in Montgomery decreased in the year 2020, the percentage of food insecure individuals increased. Due to the COVID-19 pandemic, food deserts are of great concern for many city officials and local nonprofit organizations, but so is the expected high rate of crime now that city-implemented health restrictions have now lessened.

Researchers have determined that crime with the intent of monetary gain (e.g., robbery and burglary) typically align more with food insecure communities. Utilizing the city of Montgomery's Crime Mapping System, out of 316 crime related incidents within the past observed 180 days, 146 criminal incidents are related to larceny, burglary, robbery, or some form of theft in inner-city and west Montgomery. Although nonviolent crimes are more associated with food insecure communities than reported violent crimes, the city of Montgomery has a violent crime rate that consecutively surpasses the national average of violent crimes in the nation (Figure 3).

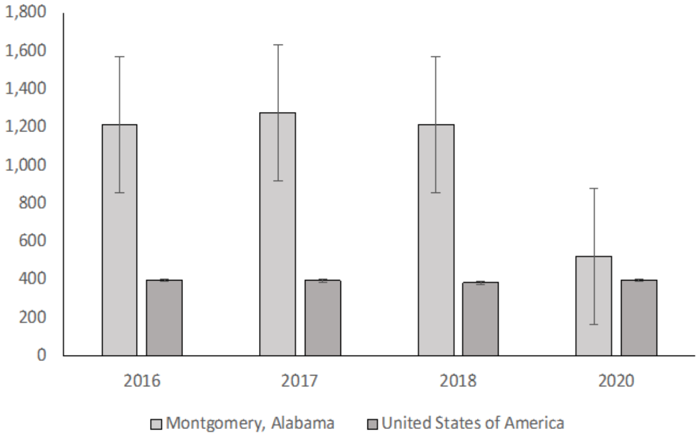

Fig. 3 Rate of violent crimes in Montgomery, AL.

Although there is an established correlation and connection between food insecurity, poverty, and spatial mismatch–and the effects of these variables–within inner-city and west Montgomery communities, unobserved variables (such as primary and secondary education rates amongst community members) may also present pertinent data that further explains the relationship between food insecurity, poverty, and spatial mismatch.

Nevertheless, I determined from my research that vehicle inaccessibility, crime, and the rates of morbidity and mortality seen in food insecure communities within Montgomery, Alabama are related and can be explain by the high rates of food insecurity experienced by community members. As citizens in food insecure communities are likely to not have vehicle accessibility, they are also more likely to experience spatial mismatch and the inaccessibility to economic opportunity beyond their communities. Additionally, the crime rates relating to food insecure communities can be explained by the increased rates of poverty and minimal economic opportunities.

To address food insecurity and the correlating issues, city leaders of Montgomery should be more inclined to attract grocery retailers in urban, food insecure regions of Montgomery. To promote more economic growth, recruiting grocery retailers will likely create a positive impact on the high rate of poverty and limited vehicle accessibility, as well as decreasing the high rates of morbidity and mortality seen in inner-city and west Montgomery.

Statement of Research Advisor

This project analyzes various socioeconomic and communal issues that impact food insecure communities in Montgomery, Alabama. Jordan has successfully identified potential areas of opportunity for city officials and local community members to increase food security and economic growth for impoverished, food desert communities in Montgomery, AL.
- Rebecca Retzlaff, Department of Political Sciences, College of Liberal Arts

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Authors Biography

Jordan Branchman, a native of Montgomery, Alabama, is an undergraduate student at Auburn University pursuing a B.A. degree in Political Science. Jordan has a strong interest in food justice and equity in urban centers and impoverished communities.

Rebecca Retzlaff, PhD, AICP, is a professor in the Master of Community Planning Program and director of the interdisciplinary Academic Sustainability Program. Her research interests are planning law and planning history.

Impact of Fire History and Seed Depredation on Seedling Emergence of Four Southeastern Tree Species

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[3] Research Forester, Southern Research Station, U.S. Forest Service
[4] Instructor, College of Forestry, Wildlife and Environment, Auburn University

Across the southeast region of the U.S., decades of intentional fire exclusion have contributed to substantial decreases in cover of fire-dependent longleaf pine (Pinus palustris) forests, with consequent declines in biodiversity of associated flora and fauna, including endangered species such as the gopher tortoise (Gopherus polyphemus) and red-cockaded woodpecker (Leuconotopicus borealis) (Jose et al. 2006). In response, there has been considerable research investigating factors that impact natural regeneration of longleaf pine, especially in fire-restored forests. However, one especially important, yet understudied, process that could impact longleaf regeneration relative to hardwood competitors is seed depredation. A seed is depredated if it damaged and no longer viable or removed from the system by an animal. Thus, the objective of this research is to quantify how fire history and seed depredation impact early seedling emergence of longleaf pine seeds in comparison to three common competitors, tulip poplar (Liriodendron tulipifera), sweetgum (Liquidambar styraciflua), and blackgum (Nyssa sylvatica).

In January 2023, we deployed several types of predator exclosures, which differentially restrict access of vertebrate and invertebrate predators, at two study sites near Auburn, AL, USA: the Mary Olive-Thomas Demonstration Forest and the Tuskegee National Forest. Within each site, three stands with no burn history and three stands that are on two-year burn intervals were selected to study. Ten seeds were placed in petri dishes within each exclosure type: invertebrate only access, full access by small vertebrates, or complete exclosure (Figure 1). During each trial, the exclosures were monitored for seed removal rates after two weeks. Three trials have been conducted in the months of February, March, and April 2023.

Fig. 1. Longleaf pine seeds placed in an exclosure that restricts vertebrate access and allows invertebrate access.

In February 2023 Trial 1, we observed no significant difference in depredation rate between tree species ($p = 0.3$). We also observed no significant difference in depredation rate between burned and unburned stands ($p = 0.4$) (Table 1).

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Table 1 The average number of seeds remaining after two week trial in February 2023 in burned and unburned stands

Burn	Yes	No
Tree Species		
blackgum	9.28 (2.05)	9.82 (0.53)
longleaf pine	9.83 (0.71)	9.44 (2.12)
sweetgum	9.56 (0.92)	8.67 (2.66)
tulip poplar	9.83 (0.51)	9.72 (0.75)

Overall, the data collected from this research will alleviate a deficit in research on the early seedling establishment and seed depredation rates of four southeastern species in unburned and burned stands. Further awareness of the early life stages of longleaf pine in relation to competing hardwood species will aid forest managers in understanding the interacting influences of fire frequency and seed predators on community assembly.

Statement of Research Advisor

Payton contributed ideas to project experimental design, built seed predation exclosures, implemented seed predation field trials at Mary Olive Thomas Demonstration Forest, assisted with those at Tuskegee National Forest, and performed preliminary data entry and analysis. She did a great job with her research project!
-Heather D. Alexander, College of Forestry, Wildlife and Environment

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Authors Biography

Payton Brewer is a senior-year student pursuing a B.S. degree in Wildlife Ecology and Management at Auburn University. She has played key roles in the research through implementing the experimental design at Mary Olive Thomas Demonstration Forest.

Dr. Heather D. Alexander is an associate professor of forest and fire ecology at Auburn University. She has served as the designated mentor and research facilitator for this study.

John L. Willis is a research forester at the Southern Research Station of the U.S. Forest Service. He served as an experimental designer and aided in the implantation of the study at Tuskegee National Forest.

Kathleen Gabler is an instructor and research technician at the College of Forestry, Wildlife and Environment at Auburn University. She has conducted three trials of this study at Tuskegee National Forest.

A Study of Climate Change Impact on Alabama Crops

Gracen M. Bridges[1,] and Ruiqing Miao [2]*

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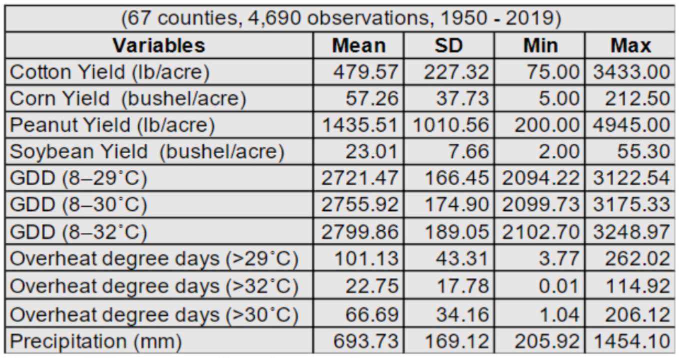
[2] Associate Professor, Department of Agricultural Economics and Rural Sociology, Auburn University

The purpose of this research is to investigate the impact of climate change on yields of corn, cotton, peanuts, and soybeans in Alabama using a large panel data set over 1950–2019. Many studies have focused on the negative impact of climate change overall (e.g., Schlenker and Roberts, 2009), but not specifically for the state of Alabama. This researched aims to fill the research gap.

We collect the county-level data for corn, cotton, peanuts, and soybeans from the National Agricultural Statistics Service (NASS) of the U.S. Department of Agriculture (USDA). Historical climate data are obtained from Schlenker and Roberts (2009). The future climate data are obtained from the Multivariate Adaptive Constructed Analogs under Global Climate Model HadGEM2 under and representative concentration pathways 8.5. The summary statistics of our data are presented in Table 1.

Table 1. Summary Statistics of Dataset for Corn, Cotton, Peanut, and Soybean Yields and Climate Analyses from 1950 - 2019.



(67 counties, 4,690 observations, 1950 - 2019)				
Variables	**Mean**	**SD**	**Min**	**Max**
Cotton Yield (lb/acre)	479.57	227.32	75.00	3433.00
Corn Yield (bushel/acre)	57.26	37.73	5.00	212.50
Peanut Yield (lb/acre)	1435.51	1010.56	200.00	4945.00
Soybean Yield (bushel/acre)	23.01	7.66	2.00	55.30
GDD (8–29˚C)	2721.47	166.45	2094.22	3122.54
GDD (8–30˚C)	2755.92	174.90	2099.73	3175.33
GDD (8–32˚C)	2799.86	189.05	2102.70	3248.97
Overheat degree days (>29˚C)	101.13	43.31	3.77	262.02
Overheat degree days (>32˚C)	22.75	17.78	0.01	114.92
Overheat degree days (>30˚C)	66.69	34.16	1.04	206.12
Precipitation (mm)	693.73	169.12	205.92	1454.10

Note: GDD = growing degree days.

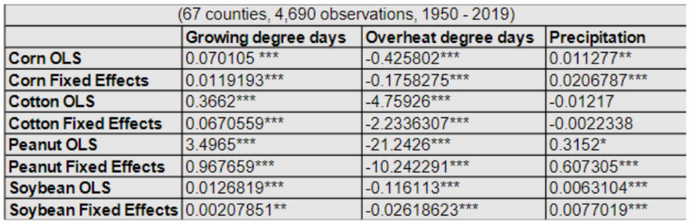
We performed two sets of regression analyses: the Ordinary Least Squares (OLS) and the Fixed Effects Model. Equation (1) represents the OLS regression and equation (2) represents the Fixed Effects Model.

$$y_{it} = \beta_0 + \beta_1 * \text{GDD} + \beta_2 * \text{OverheatGDD} + \beta_3 * \text{Precipitation} + \beta_4 * \text{TimeTrend\_t} + e_{it} \qquad (1)$$

$$y_{it} = \beta_0 + \beta_1 * \text{GDD} + \beta_2 * \text{OverheatGDD} + \beta_3 * \text{Precipitation} + \beta_4 * \text{TimeTrend\_t} + u_i + e_{it}\,, \qquad (2)$$

where the β's are coefficients to be estimated, u_i is the county fixed effects, and e_{it} is the error term.

Table 2. Determinants of Corn, Cotton, Peanut, and Soybean Yields from 1950 - 2019



(67 counties, 4,690 observations, 1950 - 2019)			
	Growing degree days	**Overheat degree days**	**Precipitation**
Corn OLS	0.070105 ***	-0.425802***	0.011277**
Corn Fixed Effects	0.0119193***	-0.1758275***	0.0206787***
Cotton OLS	0.3662***	-4.75926***	-0.01217
Cotton Fixed Effects	0.0670559***	-2.2336307***	-0.0022338
Peanut OLS	3.4965***	-21.2426***	0.3152*
Peanut Fixed Effects	0.967659***	-10.242291***	0.607305***
Soybean OLS	0.0126819***	-0.116113***	0.0063104***
Soybean Fixed Effects	0.00207851**	-0.02618623***	0.0077019***

Note: Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05

From Table 2 we can see that the coefficients of GDD for the crops are positive numbers which mean the yield will increase as the GDD increases. The overheat GDD coefficients being negative means it will have an adverse effect on yield, by decreasing yields. The coefficients of precipitation are positive for all crop analyses except cotton. The coefficients of precipitation are positive, it will increase yields. Cotton fixed effects model show a negative precipitation coefficient, which will decrease the yield. The precipitation values for the corn fixed effects and OLS models are insignificant.

After performing the two methods of analyses, the coefficients are then used to predict yields under future climate scenarios. The yields were determined by using four variables: GDD, overheat GDD, precipitation, and year. We predicted the yields for 2050. After predicting the yields, we then calculate the percentage of yield changes based on the 2000-2019 average crop yields.

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The historical yields from Figures 1 and 2 were calculated by taking the average crop yield between 2000 – 2019. The future climate yields were calculated using Equation (2). Figure 1 includes the historical and future yields for corn and soybeans, measured in bushels per acre. Figure 2 includes the historical and future yields for cotton and peanuts, measured in pounds per acre. We find that if there were no technology improvement, climate change by 2050 will decrease corn yield by 54% when compared with the average corn yield over 2000-2019, will decrease soybean by 76%, will decrease cotton by 74%, and increase peanut yield by 10%.

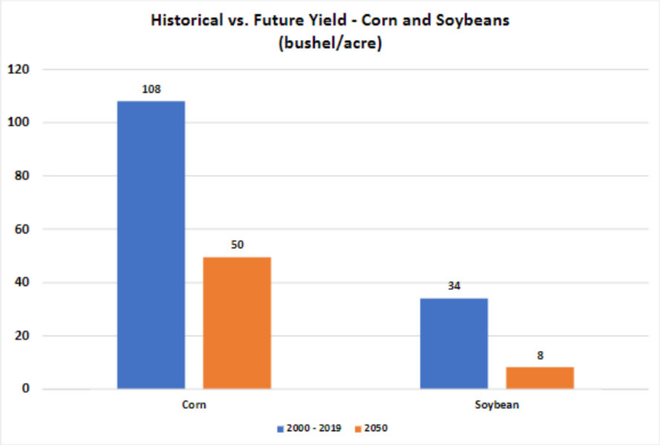

Fig. 1. Historical vs. Future Yield for Cotton and Peanuts measured in bushels per acre.

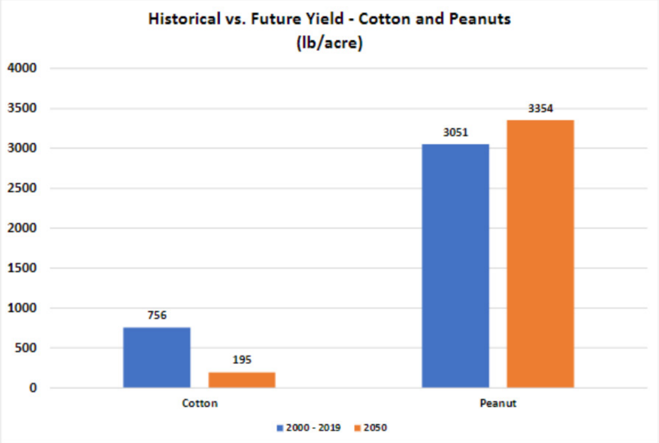

Fig. 2. Historical vs. Future Yield for Cotton and Peanuts measured in pounds per acre.

Statement of Research Advisor

Gracen Bridges showed immense initiatives when working on this project. She collected the county-level crop yield data and merged the yield data with weather data. She also conducted the statistical analysis and prepared the final report and this highlight. Under this project Gracen showed outstanding work ethic and skills associated with data processing, statistical analysis, and technical writing.

- Ruiqing Miao, Agriculture Economics and Rural Sociology, College of Agriculture

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Authors Biography

Gracen Bridges is a senior-year student pursing a B.S. degree in Agricultural Business and Economics at Auburn University. She has played a key research role on how climate change affects four Alabama Crops.

Ruiqing Miao is an associate professor in the Department of Agricultural Economics and Rural Sociology of the College of Agriculture. His research focuses on the interaction between agricultural production and its environment, aiming to understand and quantify 1) agriculture's impact on land use, water use, water quality, and biodiversity, and 2) how agricultural production is affected by farmers' behaviors, public policies, agricultural innovation, technology adoption, and climate change.

Addition of Self-assembling Small Molecules to Cellulose Hydrogels to Enhance Gelation and Tune Microstructure

Jordan N. Clemmons[1,*], *Symone Alexander*[2]

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Chronic kidney disease (CKD) affects 1 in 7 U.S. adults (CDC). 71% of those with CKD are treated with dialysis (NIDDK), which lowers the quality of life for patients due to the long treatment times and the stress it puts on the patient's body. In this work, orally administered sorbent microgels synthesized from cellulose are being explored as an alternative treatment to NIDDK. These dual-functioning microgels mimic dietary fiber by absorbing uremic toxins while releasing probiotics.

Cellulose is an abundant organic compound found in plants [1]. Due to cellulose being natural and biodegradable, it is the perfect matrix material for gels and microgels. Cellulose microgels have many advantages including tunable pore size for diffusion, large surface area, and an adaptive shape. These characteristics make cellulose microgels useful for absorbing materials and carrying active substances through the body [7].

However, a few challenges with these gels include a lengthy gelation time and variable microstructures, which affects the diffusion of materials into and out of the microgels [6,8]. Self-assembling small molecules can be added to cellulose gels to tune the microstructure of the gel and ensure the correct pore size and geometry [2,3]. The addition of these small molecules can also decrease the gelation time due to rapid self-assembly. In this study, we investigate the gelation characteristics of an Fmoc-derivative that is a pH-responsive small molecule and its effect on cellulose-based microgel structure.

Cellulose is soluble at low temperatures in high pH sodium hydroxide (NaOH) solutions, while the small molecule used in this study self-assembles to form a gel at high pH; by mixing these solutions, we form a sacrificial template (small-molecule gel) for cellulose gel formation at high pH. The small molecule used is mono-Fmoc ethylene diamine hydrochloride, which contains the Fmoc protecting group. The Fmoc protecting group is widely used to synthesize small molecule gels and helps with self-assembly due to π-π stacking and structural packing arrangements [4]. Additionally, the Fmoc group is connected to a hydrophobic peptide chain that leads to gelation at high pH.

To fabricate the most effective gel, the stability of Fmoc at different pH levels was investigated. The pH level also corresponds to NaOH concentration and, for a strong base, significant changes in concentration are needed to decrease the pH. Fmoc gels synthesized in pH ranging from 12.5 to 12.9 were fabricated by dissolving 0.5 mg of mono-Fmoc ethylene hydrochloride in 1 mL of DI water. Different concentrations of NaOH solutions were calculated using equations (1) - (3), then mixed with the Fmoc solution to create the gels at different pH levels. The vial inversion test was then used to determine whether a gel was formed [2,5].

$$M_1V_1 = M_2V_2 \tag{1}$$

$$pOH = -\log[OH^-] \tag{2}$$

$$pH = 14 - pOH \tag{3}$$

The gel at the lowest pH, 12.5, did not fully gel and flowed during the vial inversion test. The gels at a higher pH were noticeably more opaque and maintained stability and position when inverted (Figure 1). This leads to the conclusion that Fmoc forms a more uniform gel as you increase the pH.

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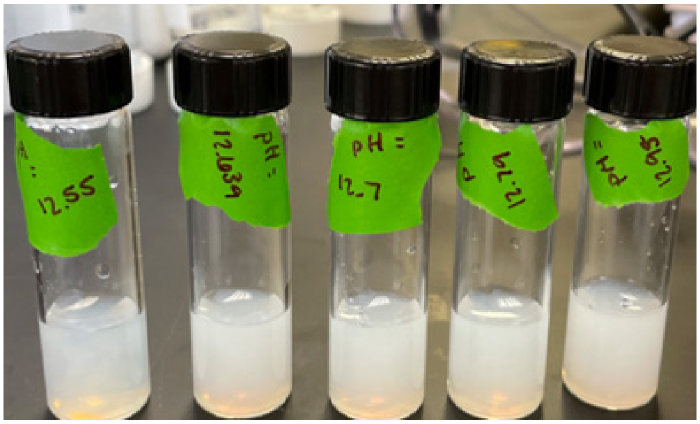

Fig 1. NaOH and Fmoc gels immediately after gelation.

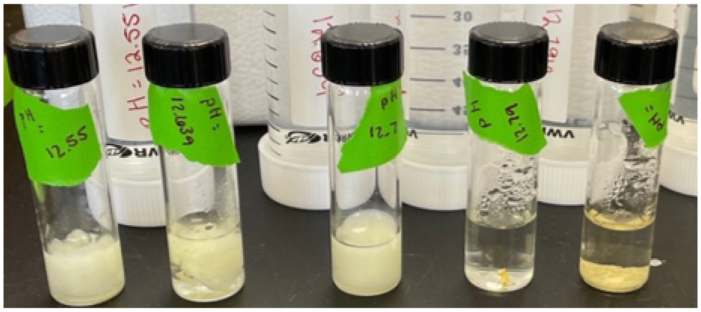

Fig 2. NaOH and Fmoc gels after a month

Following the effects of the pH on gelation, the stability of the gel over time was investigated (Figure 2). The gel at the highest pH broke down the fastest with the gel showing decomposition after 3 weeks. The gel at the lower pH also broke down quickly with decomposition present at 3 weeks, but with more gel present than in the higher pH. In contrast, the gels at a pH of 12.7 remained the most stable with the gel still uniform after 1 month, and the gel even remained after 2 months. From this, it can be determined that the Fmoc also destabilizes at a certain high pH, leading to the breakdown of the gel [10]. On the other hand, the lower pH gel behavior can be explained by the Fmoc not fully forming a gel when the pH is lowered to a certain pH.

Light microscopy was used to determine the effect of pH on the gel structure. The microscopy images showed an increase in the density and connectivity of fiber networks that was proportional to an increase in pH, as shown in Figure 3. In Figure 3, (A) showed a uniform interconnected network with Light microscopy was used to determine the effect of pH on the gel structure. The microscopy images showed an increase in the density and connectivity of fiber networks that was proportional to an increase in pH, as shown in Figure 3. In Figure 3, (A) showed a uniform interconnected network with a concentration of 10 x 10-3 M NaOH (pH ~12.7). Image (B) in Figure 3 used a concentration of 7.5 x 10-3 M NaOH (pH ~12.5) and (C) in Figure 3 had a concentration of 5 x 10-3 M NaOH (pH ~12.3); these images show a jump between where the gel is still able to form a fiber network. From (B) to (C), a loss of stability occurs due to the fibers having less of an interconnected network. Image (D) has a sparser formation with a concentration of 2.5 x 10-3 M NaOH (pH ~12.1). In image (D) a gel was not fully able to form. This is consistent with the hypothesis that the lower concentration of NaOH was unable to create enough fiber networks to make a stable gel.

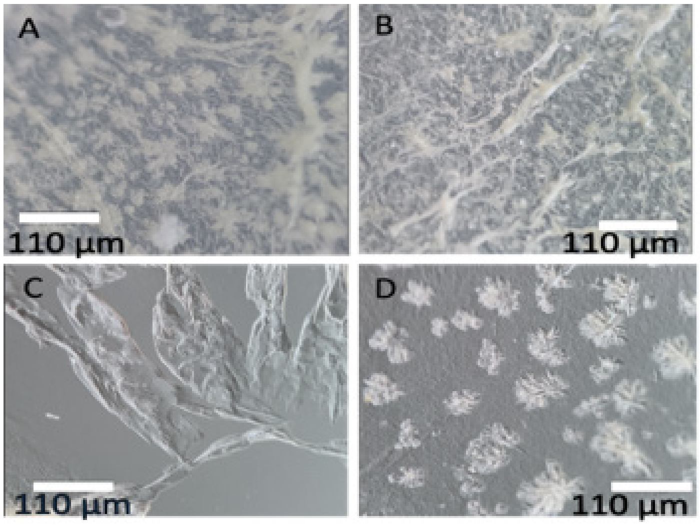

Fig 3. Microscopy images on Fmoc solutions.

Proton nuclear magnetic resonance spectroscopy (H-NMR) was used to better understand the non-covalent interactions in the gel. Along with NaOH, urea is used to help dissolve cellulose in aqueous solutions; therefore, the interactions between urea and Fmoc also need to be considered. H-NMR shows the chemical shifts and hydrogen bonding that occur when the different compounds are mixed together. The H-NMR spectra in Figure 4 indicate that there are interactions between the Fmoc and NaOH, but not Fmoc and urea. Specifically, comparing peaks (a) and (b) for native Fmoc with respect to the other mixtures, it can be seen that these peaks are only suppressed with the addition of NaOH – indicating interactions via hydrogen bonding between the two compounds. Furthermore, it can be seen that a urea peak is present in the Fmoc and urea sample, while it is missing in the Fmoc, NaOH, and urea sample; this indicates that there are hydrogen bonding interactions between the urea and NaOH compounds, but not between urea and Fmoc.

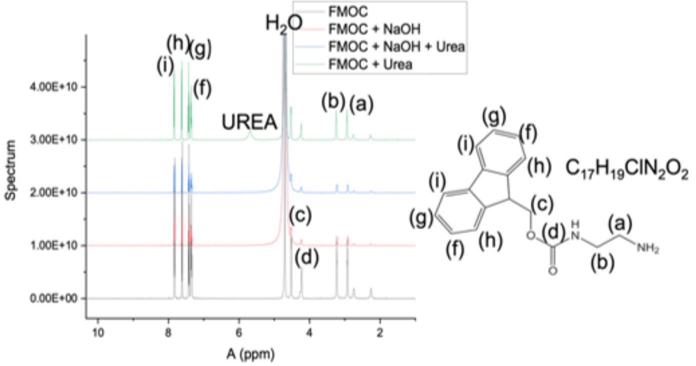

Fig. 4 HNMR Microscopy images on Fmoc solutions.

In summary, there is an optimal range for pH during gelation of Fmoc-based gels that influences the formation of the fiber network needed for gel stability. Additionally, there are time dependent effects on gel stability that relate to gel composition. Lastly, H-NMR spectroscopy indicates hydrogen bonding and physical interconnections between NaOH and Fmoc that can be used during gelation with cellulose solution to tune gel properties. Future work includes characterizations of these Fmoc gels coassembled with cellulose gels as well as mechanical testing to quantify gel stability.

Statement of Research Advisor

Jordan is an excellent researcher and her leadership, enthusiasm, and productivity has helped answer key fundamental research questions about co-assembly of small-molecules with biopolymers like cellulose. She is independently leading this project and her work is critical to solving materials and manufacturing design problems related to cellulose gels and microgels. I am proud of the expertise she has gained in nontrivial analytical techniques like NMR and microscopy and look forward to witnessing her very promising research career.

- Symone Alexander, Department of Chemical Engineering, Samuel Ginn College of Engineering

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Authors Biography

Jordan N. Clemmons is a sophomore-year student pursuing a B.S. degree in Chemical Engineering. She is an undergraduate researcher for the Alexander Research Team.

Dr. Symone Alexander is an Assistant Professor in the Department of Chemical Engineering at Auburn University. During her time as an Eckert Postdoctoral Research Fellow at Georgia Institute of Technology in the Department of Chemical and Biomolecular Engineering, she led investigations on extreme organismic biophysics with a focus on ultra-fast motion in nature in Prof. Saad Bhamla's research group. She earned her Ph.D. in Macromolecular Science and Engineering as an NSF Graduate Research Fellow at Case Western Reserve University, advised by Prof. LaShanda Korley. During her graduate career, she led research on the influence of high molecular weight polymers on self-assembling small molecules and how those networks can be utilized to generate bioinspired, responsive polymer composites. She obtained a B.S. in Chemical Engineering from Howard University in 2013, where she investigated DNA-polymer assemblies utilizing Atomic Force Microscopy under the advisement of Dr. Preethi Chandran and Dr. Joseph Cannon. Dr. Alexander recently served as the elected chair of the 2019 Polymers Gordon Research Seminar (GRS) and actively participates in science communication through via Twitter. She is a recipient of numerous awards and honors, including grad and postdoc fellowships, selection as a 2020 Emerging Leader by Georgia Tech Dept. of Mechanical Engineering, selection as a 2019 American Chemical Society Future Faculty Scholar (ACS PMSE), and being selected as a 2018 Rising Star in Chemical Engineering by the Massachusetts Institute of Technology (MIT).

A Global Analysis of the Impacts of Free-ranging Dogs on Native Wildlife

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[2]Applied Quantitative Ecologist, Cornell Lab of Ornithology
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Humans knowingly and unknowingly disperse species around the world, resulting in some becoming invasive and impacting native ecosystems(1). Invasive species can cause decreases in native biodiversity as well as threaten the economic, social, and political values of local people(2). Among the most notorious of these invasive species is the domestic cat (Felis catus). These small carnivorous mammals have been the cause or a notable factor in the extinction of many species worldwide, resulting in an increasing amount of management attention, particularly in Australia. The most devastating impacts recorded are the predation of threatened and endangered vertebrates, but they also threaten biodiversity through resource competition and disease transmission (3).

Because of the problems with cats, there have been numerous articles published on the urgency of cat management in order to prevent further biodiversity loss, but among these we have found a gap in the literature. Specifically, another introduced carnivore might be producing similar ecological effects, but has not been researched, published, or managed nearly as much: feral dogs (*Canis lupus familiaris, Canis dingo*). Among the comparatively fewer publications on their impacts (Fig. 1), we have discovered considerable evidence that dogs might pose a similar ecological threat to biodiversity that cats do. The relationship between humans and dogs is extensive and complex, with dogs holding a role in society as our companions, pets, and workers. Humans have brought dogs with them as they have expanded around the world, allowing dogs to thrive under the care and protection of humans. With this advantage and their opportunistic eating habits, dogs have been reported to eat many of the same species as cats, which suggests that they could be having similar ecological effects (3,4) .

To address the gap in our knowledge about dogs, we propose to quantify the ecological effects of free ranging dogs by evaluating the prey species they consume. There have been hundreds of articles published documenting the species that free-ranging dogs kill and eat, but there has not been a thorough compilation and analysis of these data, meaning that we could be overlooking a major environmental crisis. As such, we hypothesize that free-ranging dogs are a major contributor to native species predation and are environmentally as damaging as free-ranging cats. The diets of free-ranging cats have been documented more frequently, and the result of a synthesis of that data, performed in the Fantle-Lepczyk/-Lepczyk lab, showed reason for concern. Dogs are eating hundreds (perhaps thousands) of species and may be threatening the conservation status of many. With this research, we are seeking to quantify these impacts to increase public awareness and provide needed information to practitioners and policymakers.

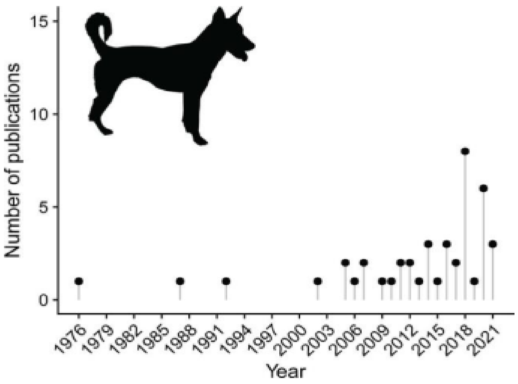

Fig. 1. Timeline of research studies published directly pertaining to a dog predation event. The first event

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on record is in 1976, the most recent in 2021, and the highest volume in 2018.

This research project is a work in progress, meaning that we have already completed some aspects of the methods. Beginning in January of 2022 we worked with our college's science librarian to collect all available articles from the primary literature regarding free-ranging dog diet using structured literature reviews via Web of Science, Google Scholar, BIOSIS, BioOne, JSTOR, and library records. Using the search terms (dog* OR "canis familiaris" OR dingo* OR "canis lupus dingo" OR "canis dingo" OR "canis lupus familiaris" OR "canis familiaris dingo" OR "community dog*") AND (feral OR wild OR stray OR "free-ranging" OR "free ranging" OR unowned), we gathered 2,000+ articles from this search, which were then uploaded to Zotero where each paper was scanned to remove duplicates and any papers that did not pertain to our research. This process left us with approximately 250 articles, which we are currently collecting data from. This search provided us with global studies dating back to 1927. We considered a study for inclusion if the dog, either feral or a free- ranging pet, killed any animal, whether on purpose or accidentally. We are including accidental depredation because we have data suggesting that many animals are put at risk due to dogs stepping or running over them/their nests. We define free-ranging dogs as being either unowned, off-leash, or truly feral. We are also including dingoes in the study as they are invasive dogs that have invaded Australia, which is where a significant amount of the feral dog and cat studies originate.

We are completing the data extraction and entry this semester, Spring of 2023. The work will be continued in Fall of 2024, and we will then analyze the complete dataset. The data analysis will evaluate what species are being depredated and where, the time and location of the predation event was recorded, as well as the dog type (free-ranging pet, feral, or dingo) and the sampling method (scat analysis, gut content analysis, observed predation, or inferred predation). We will also evaluate the prey species' taxonomic classification as well as its listing on the International Union for Conservation (IUCN) Red List. The IUCN quantifies the risk of this species of endangerment or extinction and assigns a status: least concern, near threatened, vulnerable, endangered, and critically endangered. While there are several species that had not yet been assessed by the IUCN or were domestic and thus not applicable, many of the species are included in this assessment.
At the time of this analysis the partial database contains 638 incidents of depredation, and at this rate we expect a total of approximately 1,500 when the work is completed. The analysis of the studies shows a concerning number of depredated species having a status of Near Threatened, Vulnerable, Endangered, or Critically Endangered (Fig. 2). The results of this study thus far support the hypothesis that dogs are a much larger threat than they are represented as - they exist globally and in abundance, form bonds with humans that protect and feed them, and are pack animals, which offers them more protection and allows them to kill larger prey. If management for these carnivores is not implemented soon, we can only expect to see this downward trend continue. Social awareness of their impact needs to be made more public so that locals understand their threat and do not act in ways to aid free-ranging dogs, as well as keeping their own dogs leashed or enclosed.

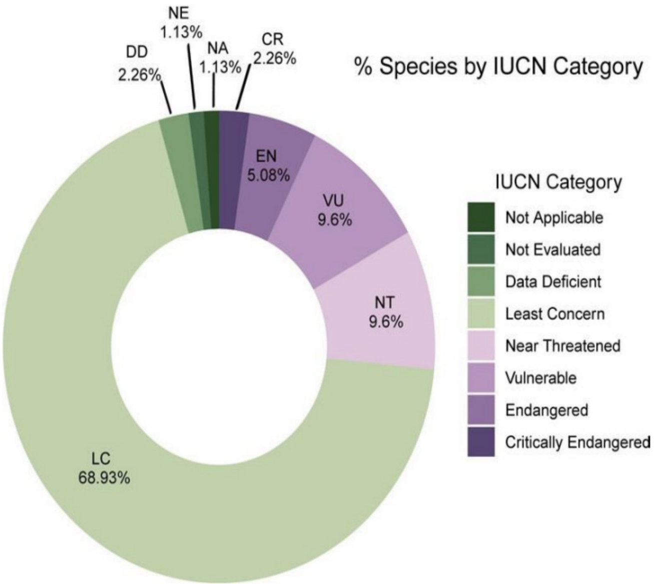

Fig. 2. Distribution of species depredated by dogs classified by IUCN Red List Category: Not Applicable (NA), Not Evaluated (NE), Data Deficient (DD), Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), and Critically Endangered (CR).

As aforementioned this research is ongoing, meaning that we do not have all the information needed to construct a complete PRISMA Flow Diagram, but a partial chart is included to document progress (Fig.3).

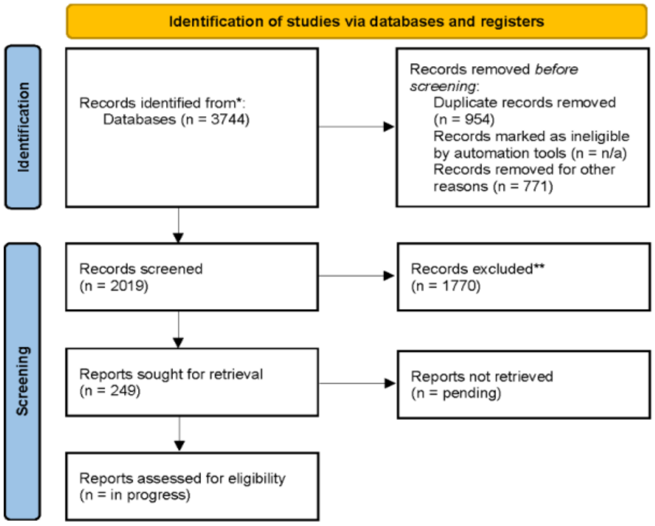

Fig. 3. PRISMA Flow Diagram detailing the number of articles at different stages through the study.

Statement of Research Advisor

Invasive species are a global problem causing both ecological and economical harm. Ally's resesearch exploring one invaseive species, free-ranging dogs, comes at a time when we are starting to fully understand the negative impacts that pets have on the environment.

- Dr. Chrisopher Lepczyk, Professor, College of Forestry, Wildlife and Environment

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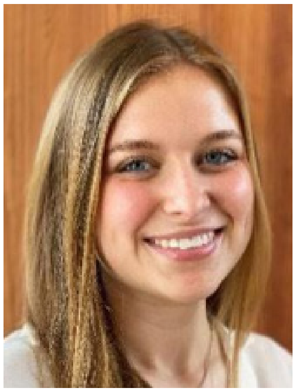
Authors Biography



Ally Cobern is a junior pursuing a B.S. degree in Wildlife Ecology and Management at Auburn University. As an under graduate research fellow, she has played key research roles in invasive species data refinement, collection, and analysis.

Garrett Ake is a recent Auburn graduate with a B.S. degree in Wildlife Ecology and Management. He played a role in data refinement.

Patricia Hartman is an Associate Professor of Research and Instruction. She is the departmental librarian for Biology, Forestry and Wildlife Sciences, and Math.

Kylee Dunham is an Applied Quantitative Eco logist at the Cornell Lab of Ornithology. She played a key role in data analysis and graphics.

Dr. Jean Fantle-Lepczyk is an Assistant Research Professor in the College of Forestry, Wildlife and Environment at Auburn University. Her research involves the conservation of wildlife, especially species that are under- studied and of conservation concern, using a variety of non-invasive tools.

Dr. Christopher Lepczyk is an Alumni Professor in the College of Forestry, Wildlife and Environment at Auburn University. He is ecologist and conservation biologist who focuses on wildlife, landscapes, citizen science, bio-diversity, urban ecosystems, and both endangered and invasive species.

Functionalizing Cellulose Nanocrystals for Targeted and Sustainable Applications of Agriculture Agents

Elise G. Collins[1], Delaney E. Clouse[2], and Virginia A. Davis[3,]*

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The United Nations released a report that agricultural production needs to double by 2050 in order to keep up with population growth (United Nations, 2009). The most common method of increasing agricultural yield is the use of agricultural agents such as pesticides, herbicides, and fertilizers. Unfortunately, as little as 10 % of pesticides actually make it into plants; instead, these chemicals enter the ecosystem through run-off or air, where they can harm wildlife, plant life, and people (Zhang et al., 2020). New methods of delivering these agricultural agents are needed to meet agricultural demands while reducing the risks to environmental and public health. Several studies have focused on the use of lignocellulosic nanomaterials as carriers for agrochemicals (Lima et al., 2021). The purpose of this research is to successfully attach and detect agricultural agents on the surface of cellulose nanocrystals (CNCs) for utilization as a targeted-delivery system into plant cells.

CNCs are derived from cellulose, which is an organic, non toxic, and abundant biopolymer that can be extracted from sources like trees, cotton, and biomass wastes. Cellulose is mechanically extracted from the hemicellulose and lignin portions of the polymer and hydrolyzed using acid or enzymes to create CNCs. CNCs have a readily tunable surface chemistry as well as nanoscale dimensions that allow them to be taken up easily by plants through roots or stomata (Puppala et al., 2023). Sequence alignment comparing CLRDV-AL to the previously isolated strains from South American countries indeed showed some mutations within the domain known for VSR function (Agrofoglio et al., 2019).

The herbicide chosen for this research was 2,4- dichlorophenoxyacetic acid (2,4D), which is widely used across the world to kill broadleaf weeds in lawncare or agricultural settings. Microbes in the soil break down 2,4D, but the high concentrations released into the environment by broadcast spraying can still cause issues because of its toxicity to plant and animal life ("2,4D," 2023). More efficient delivery of 2,4D to weeds promises to reduce the amount needed and the risk to the environment.

A novel reaction scheme, depicted in Figure 1, was developed using some common organic chemistry pathways and biochemical reagentsto produce 2,4D-CNC. Both the 2,4D and CNC used in this reaction were obtained from a commercial supplier. The sulfuric acid hydrolysis used to create the CNCs leaves some sulfate half-ester groups on the surface along with the expected hydroxyl groups seen in Figure 1, but there has been no evidence that they substantially impact the reaction process. The CNC was diluted to an initial dispersion concentration that would prevent gelling and allow even mixing during the reaction. The reagents were added in excess to maximize attachment, so purification of the conjugated CNC in the form of centrifugation or dialysis had to occur after each step. First, an epoxy ring is added to the surface using epichlorohydrin. Then, ammonia opens the ring and adds a primary amine that can react with 2,4D in the presence of EDC (1-Ethyl-3-(3-dimethylaminopropyl)carbodiimide) and sulfo NHS (sulfo-(N-hydroxysulfosuccinimide)).

Because of CNCs' structure and tendency to aggregate, it has been difficult to achieve a high reaction conversion. The synthesis scheme was carried out with varying initial dispersion concentrations of 1 wt.% and 2 wt.% CNC to determine if reagents' side reactions with water were negatively impacting substitution.

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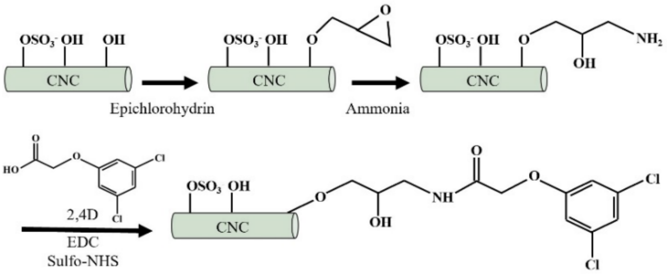

Fig. 1. 2,4D-CNC reaction scheme.

Various characterization techniques—including thermogravimetric analysis (TGA), Ultraviolet-visible spectroscopy (UV-vis), attenuated total reflectance infrared spectroscopy (ATR-IR), and a couple elemental analysis methods—were used to identify 2,4D after forming the conjugated CNC product in order to determine a method that could be used to quantify the degree of attachment. Many methods could identify the presence of 2,4D because nitrogen and chlorine are present in the added functional groups but not in the original CNC material. Unfortunately, the complexity of the conjugated material prevented most methods from being able to determine the quantity of 2,4D added. As chlorine was the only element solely present in 2,4D, an elemental analysis technique, energy dispersive X-ray spectroscopy (EDS), was ultimately used to quantify the degree of substitution of 2,4D through chlorine content. EDS gives the weight percentage concentration of the elements present in a sample. The degree of substitution could be determined for each reaction through chlorine weight percent using Equation 1 (Akhlaghi et al., 2015).

$$DS = \frac{162 \times \%Cl}{3545 - 221.04 \times \%Cl} \qquad (1)$$

Where DS is degree of substitution and %Cl is weight percent of chlorine. The results of this method are listed in Table 1.

Table 1 Chlorine weight percent and degree of substitution for the different 2,4D-CNC products.

Initial Dispersion Concentration (wt. %)	Cl (wt. %)	DS (%)
1	0.027 ± 0.007	0.12
2	0.050 ± 0.01	0.23

The increase in degree of substitution with increasing initial dispersion concentration indicates that the hypothesis of water side reactions may be correct. In the future, initial dispersion concentration will be increased further to find the reaction or substitution limits.

Samples of 2,4D-CNC have been sent to collaborators for testing on plants. After receiving results from them, there will be opportunities to improve the materials and draw conclusions that could influence future agrochemical nanocarrier work. These findings could be applied to other pesticides as well as fertilizers and other growth agents. By utilizing organic nanomaterials, plants can be used to enhance agricultural production and minimize the amounts of toxic chemicals in the environment.

Statement of Research Advisor

Elise Collins is an excellent researcher who has been an integral part of this project. She has an outstanding ability to synthesize knowledge from the literature and develop an efficient research plan. Her synthesis and analytical chemistry skills enabled us to progress the research more quickly. In particular, her research into the effects of CNC concentration on the degree of 2,4D substitution was a key contribution to the work.

-Virginia A. Davis, Samuel Ginn College of Engineering

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Authors Biography

Elise G. Collins is a senior-year student pursuing a B.S. degree in Chemical Engineering at Auburn University. She has played key research roles in optimizing reaction conditions and exploring characterization methods.

Delaney E. Clouse is a graduate student in the Department of Chemical Engineering at Auburn University. She received a B.S degree in chemistry at the University of Southern Mississippi. Her work focuses on the use of cellulose nanocrystals in agricultural applications.

Dr. Virginia A. Davis is the Daniel F. and Josephine Breeden Professor in Chemical Engineering. Her research interests include sustainable nanomaterials, polymers, additive manufacturing, and STEM education.

Auburn University Journal of Undergraduate Scholarship

Hybrid- Exoskeleton Construction

Joseph Crapet[1,], Ellis Spieler[1], and Brendon Allen[2]*

[1] Undergraduate Student, Department of Mechanical Engineering, Auburn University
[2] Assistant Professor, Department of Mechanical Engineering, Auburn University

Neurological conditions (NC) affect millions of Americans and often reduce the quality of life for those afflicted by causing decreased muscular strength and limb control. These can then lead to secondary health conditions such as obesity, muscle atrophy, and other chronic conditions (Bellman et al., 2014). Although Common recreational activities could help them grow, they may lack the strength to repetitively perform the necessary actions for growth. However, performing these actions with neuromuscular electrical stimulation (NES) can provide sensory afferent feedback for those with NCs. This can then promote enhanced bone density, muscle development, and motor control; however, the individual's endurance limits the benefits. A limitation rehabilitation robots can and have overcome (Anaya et al., 2018).

Hybrid exoskeletons combine the advantages of NES with rehabilitation robots to effectively help those with NC. The project at hand is to design and construct a hybrid exoskeleton device that will act as a test bed for future studies. The design has two degrees of freedom which allows movement about the patient's elbow and shoulder joints. The NES of the device will eventually be controlled using simple control principles (Anaya et al., 2018). Participants can utilize the constructed device to perform various actions such as arm flexion and extension.

Once the project was defined to be a device that allows motion parallel to the transvers plane and rotation about the elbow and shoulder joints, a prototype was made. The first prototype is shown in Fig. 1, and it was meant to help get a simple idea of the device.

Once the basic design was modeled, we focused on improving the elbow joint and adding a sensor and motor. The sensor was to measure the torque experienced at the joint, and the motor helps with movement. Moreover, the design was changed such that aluminum extrusions will provide support instead of aluminum rods. This is because the aluminum extrusions will experience less bending and twisting than the rods. Lastly, a capstan was added to the design to offset the motor, and it is considered to have negligible torque loss due to friction. This is due to a wire tightly wrapped around the driving motor. With both wire ends connected to a wheel. The tension in the wheels causes a torque which will spin the wheel and the part connected to the wheel. This design is shown in Fig. 2.

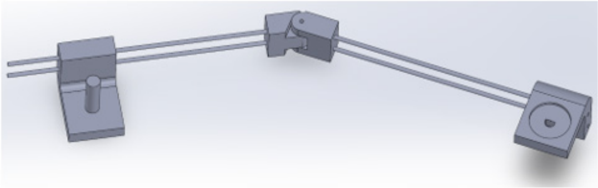

Fig. 1. Basic Design

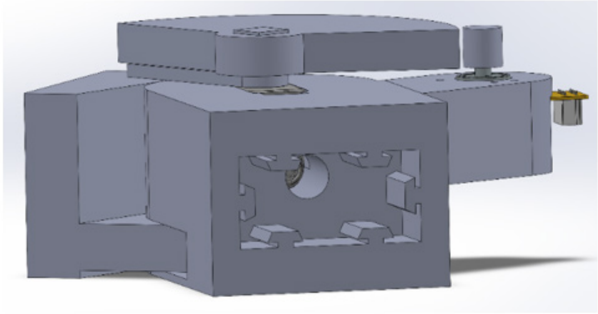

Fig. 2. Joint with Added Sensor and Motor

The elbow design with the torque sensor was then determined to be bulky and complex due to the sensors design and the way it measures torque. As a result, the next design was constructed without the sensor, and this design required less material. Moreover, the capstan was moved to be under the joint, so the joint would be more comfortable for the user. Lastly, grooves were added to the capstan and motor cap so the wire would not slip off the parts. Fig. 3 shows the updated design.

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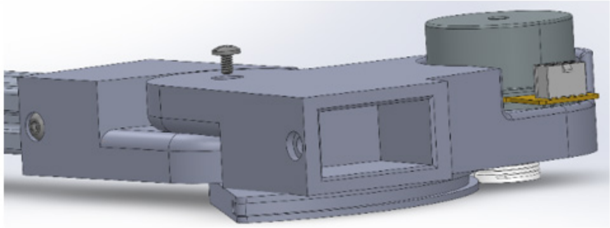

Fig. 3. Capstan Design

Once a design for the capstan was decided, we split up to work on other aspects of the design. One of us made a shoulder design with two spur gears to explore another option, and the other worked on a design for the shoulder. Fig. 4 shows the gear design, and Fig. 5 shows the shoulder design.

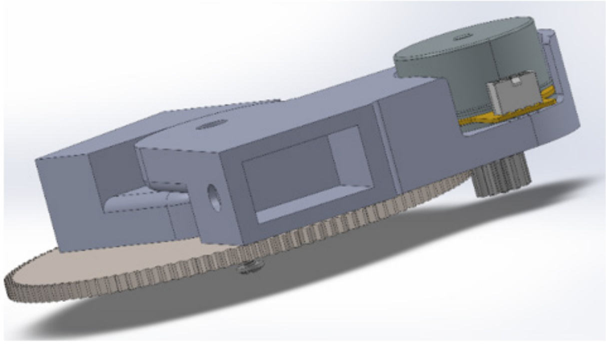

Fig. 4. Considered Gear Design

Once the gear design was modeled, it was realized that the custom gears with the desired setup would be hard to make. Moreover, the gears could wear out overtime, or something could get stuck in the teeth. This means the capstan is the preferred design.

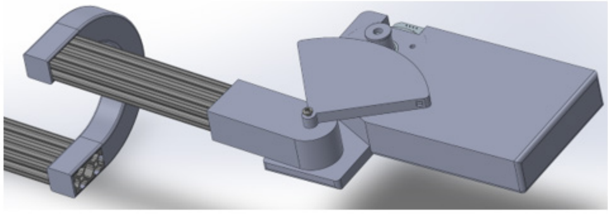

Fig. 5. Shoulder Design

As Fig. 5 shows, the shoulder was designed in a similar fashion to the elbow. Also, there is a U-shaped part in the design. This part is to allow for the elbow joint to rest below the elbow while the shoulder is above the shoulder. It also allows for the length to be adjusted to comfortably fit the user's upper arm. Lastly, a large block can be seen extruding out from the joint. This extrusion will allow for a mount to be constructed to support the device.

The design in SolidWorks was then finalized and the construction began. Figure 6 shows the SolidWorks assembly of the total system.

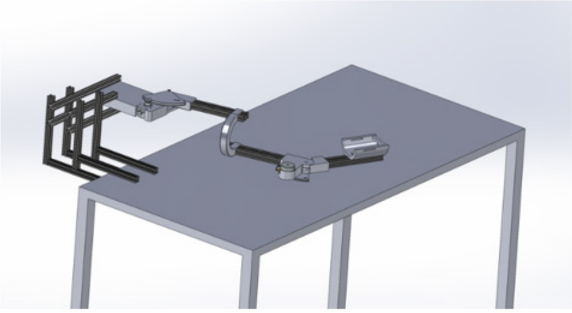

Fig. 6. Complete SolidWorks design with table

Each joint features a motor and a torque transition method called a capstan. This feature allows the motor to be offset from the axis of rotation so that the user does not have the motor directly above or below their joint. The forearm of the exoskeleton will slide on the surface of a table so that the structure is supported throughout the movement. The shoulder joint is suspended over the user's shoulder to allow easier control of the upper arm when in use. A frame made from aluminum extrusions that attach to the table supports the shoulder joint. Figure 7 shows the physical model of the exoskeleton in its current state.

Fig. 7. Current state of physical model

The construction will require further attention in a few areas before testing can take place. For example, the wire needs to be added to the motor caps and capstans. Also, the frame that supports the shoulder needs to be built, and there are a few parts that still need to be 3D printed. Although the construction is not complete, the mobility and general functionality of the system has proven sufficient. The exoskeleton's current state allows manual rotation about each of the joints. This means when the motors are up and running, the assembly will run smoothly.

Once the build is complete, a PID controller will be implemented to control the motors and move the exoskeleton on its own. To make this a hybrid exoskeleton, functional electrical stimulation (FES) needs to be implemented into the system. This will stimulate muscle contraction in the participant wearing the exoskeleton causing it to move. Once this exoskeleton is paired with FES, it will act as a test bed to gather data on how effective hybrid exoskeletons can be in rehabilitating people who suffer from NCs (Anaya et al., 2018).

Statement of Research Advisor

The Controls, Autonomy, and rehabilitative Engineering (CARE) lab in the Auburn University Department of Mechanical Engineering is focused on the design of controllers for nonlinear dynamical systems. In this work, Joseph and Ellis led the design and construction of a hybrid exoskeleton to assist in the rehabilitation of individuals with movement disorders. The exoskeleton incorporates capstans to reduce friction in the joints and is capable of being adjusted to properly fit individuals with ranging arm sizes. The exoskeleton will be used during experiments in the CARE lab for years to come.

-Brendon Allen, Department of Mechanical Engineering, Samuel Ginn College of Engineering

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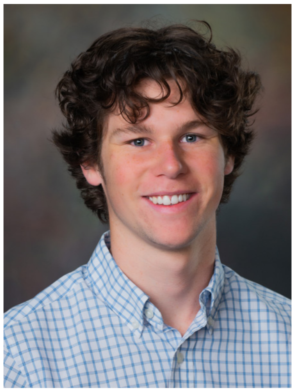
Authors Biography

Joseph Crapet is a junior-year student pursuing a B.S. degree in Mechanical Engineering at Auburn University. He has primarily worked on the elbow joint design for the hybrid-exoskeleton.



Ellis Spieler is a senior-year student pursuing a B.S. degree in Mechanical Engineering at Auburn University. He has designed the working mechanism for the shoulder joint of the hybrid-exoskeleton.

Brendon Allen received his Ph.D. in 2021 from the Department of Mechanical and Aerospace Engineering from the University of Florida. He joined the Department of Mechanical Engineering at Auburn University in 2021. His main research interests include the development of robust, adaptive, or learning Lyapunov-based control techniques for uncertain nonlinear systems such as: rehabilitation robotics, and autonomous systems.

Fusarium solani Species Complex Isolation Act as Transkingdom Pathogens in Clinical and Agricultural Environments

Harrison P. Estes[1,*], *Jeffrey J. Coleman*[2]

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The *Fusarium solani* species complex (FSSC) are a ubiquitous pathogenic filamentous fungal species complex with isolates impacting crops and humans. Previously, a single clade within the FSSC was found to contain the species most frequently responsible for human infections[1]. Over the past several years the same species within the FSSC have been isolated from cotton and soybean fields in Alabama. This project sought to examine the host range of these pathogens and analyze whether clinical isolates are virulent in agricultural environments, and vice versa.

A variety of assays were conducted using fifty-eight FSSC isolates. The phylogeny of these isolates can be seen in Figure 1.

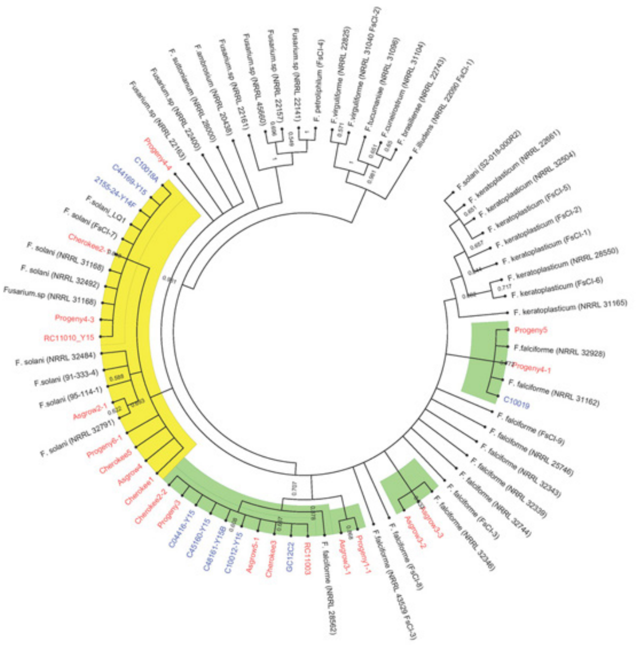

Fig. 1. Phylogeny of the FSSC isolates utilized.

These highlighted in green represent *F. falciforme* and those in yellow are *F. solani.* Black text represents clinical isolates, blue text are cotton-sourced isolates, and red text are soybean isolates.

One of the main limiting characteristics of a pathogen is its thermotolerance and its ability to grow at mammalian body temperatures. Isolates were plated on Petri dishes containing Martin's medium and were allowed to grow for ten days at 28°C and 37°C. After ten days, the distance from the original plug to the hyphal tip was measured and calculated to find its percent inhibition, as seen in the equation below[2].

$$\text{percent inhibition} = \frac{(distance\ at\ 28°\ C) - (distance\ at\ 37°C)}{distance\ at\ 28°C} \times 100\%$$

This assay revealed that the greatest inhibition was less than 50%, indicating all clinical and agricultural FSSC isolates were able to grow prolifically.

The next set of assays is meant to analyze whether the clinical FSSC isolates can be virulent in an agricultural environment. This was completed through inoculating carrots and cucumbers with a small plug of each isolate, and allowing them to incubate at room temperature for seven days. These assays showed a consistent ability of isolates to be capable of infecting these models.

In the future, the virulence of the isolates will be analyzed in a potato model. Additionally, the isolates will be used to infect hydroponic cotton and soybean models. This will be particularly notable with the agricultural isolates, to show yet another example of their wide-ranging virulence. Finally, the isolates will be used to infect Galleria, a heterologous insect model. This will

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*Corresponding author:hpe0004@auburn.edu evaluate whether the agricultural isolates are capable of the level of infection as clinical isolates in this scenario [2].

Statement of Research Advisor

Members of the FSSC have been well established as pathogens of agriculturally important crops, animals, and humans. Harrison's research has begun to evaluate the pathogenicity of environmental and clinical isolates on a broad range of potential hosts. Interestingly, his initial studies have indicated that FSSC isolates collected from the environment may have the potential to cause human infections, while those from a medical setting can infect some crops.
- Jeff Coleman, Entomology and Plant Pathology, College of Agriculture

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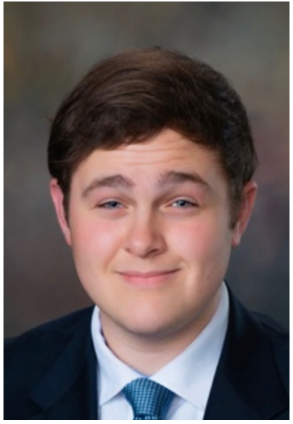

Harrison P. Estes is a fourth-year student pursuing a B.S. in Applied Biotechnology and minoring in Public Health at Auburn University. Since 2020, he has played key roles in the analysis of various FSSC isolates as transkingdom pathogens. Following his graduation in May 2023, he will pursue a Ph.D. in Genetics as a National Science Foundation Graduate Research Fellow from the University of Wisconsin-Madison, where he will focus on fungal genetics, microbial interactions, biopharmaceuticals, and biofuels.

Jeffrey J. Coleman is an Associate Professor in the Department of Entomology and Plant Pathology at Auburn University. After obtaining his Ph.D. in Plant Pathology at the University of Arizona, Dr. Coleman conducted postdoctoral research in medical mycology at Harvard Medical School. Since joining the faculty at Auburn University in 2014, he has developed a laboratory focused on investigating fungal pathogenesis using advanced molecular techniques.

Testing Interoceptive Dysfunction as a Mediator between Sleep Disturbances and Suicidal Ideation among Military Service Members

Walton G. Ferguson[1,], William Grunewald[2], April R. Smith[3]*

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Suicide among military service members (MSM) is a major public health problem. Veterans are at increased risk for suicide compared to non-veterans (Kaplan et al., 2012; McCarthy et al., 2009). Additionally, the suicide rate for active-duty service members has become comparable to that of the general population following sharp increases in recent years (Pruitt et al., 2019). Public health entities such as the Veterans Health Administration have taken steps to reduce the burden of suicide among MSM, but the need to identify factors that confer risks for suicidality among MSM is still significant. Thus, the current study attempted to identify two potential risk factors/mechanisms for suicidality among MSM: insomnia severity and interoceptive dysfunction. Interoception is defined as the central nervous system's ability to monitor and notice signals coming from the body. Likewise, dysfunctional interoception can occur whenever external factors hinder one's ability to accurately assess such signals. Interoceptive dysfunction influences various psychopathologies, and insomnia is a known risk factor for suicidality among MSM (Forrest et al., 2015; Troxel et al., 2015). These constructs may work conjointly to predict suicidality among MSM. Specifically, interoceptive dysfunction may underlie the relationship between insomnia severity and suicidal ideation. Individuals with sleep difficulties may have difficulty perceiving their internal sensations, as a result of poor sleep quality. This interoceptive dysfunction may culminate in suicidal thoughts, given the well-established link between decreased interoception and suicidality. Therefore, we investigated longitudinal relationships between interoceptive dysfunction, insomnia severity, and suicidality among a sample of MSM. We hypothesized interoceptive dysfunction to act as a mediator between insomnia severity and suicidal ideation. For this study, archival data were collected from 195 MSM enrolled in a randomized control trial meant to reduce suicidality among MSM. Participants completed self-report surveys at three timepoints separated by one month each that measured suicidal ideation, insomnia severity and interoceptive awareness (4 subscales included). Analyses focused on a 3-timepoint longitudinal autoregressive cross lagged mediation model using MPlus. Longitudinal paths from insomnia severity to interoceptive dysfunction, interoceptive dysfunction to suicidal ideation, and insomnia severity to suicidal ideation were estimated, each separated by one timepoint. In addition, formal tests of mediation of insomnia severity to suicidal ideation by interoceptive dysfunction were conducted.

Results of this model are presented in Figure 1. Insomnia severity significantly predicted interoceptive dysfunction over time, while interceptive dysfunction predicted increased suicidal ideation over time. Interoceptive dysfunction did not mediate relationships between insomnia severity and suicidal ideation. Significant relationships between insomnia severity and interoceptive dysfunction suggest that insomnia severity may be a risk factor for interoceptive dysfunction in that poor sleep quality may lead to reduced ability to recognize bodily sensations. Furthermore, our results replicate previous research (Forrest et al., 2015) by highlighting that disconnection from one's bodily sensations increases suicide risk.

Given our results, we recommend assessing for both interoceptive dysfunction and insomnia severity as potential risk factors for suicidal ideation among MSM. Furthermore, results suggest that interoceptive dys-

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function may be a promising intervention target to reduce suicidality among MSM. Clinicians may consider improving interoceptive abilities by utilizing mindfulness, exposure, and cognitive-behavioral techniques.

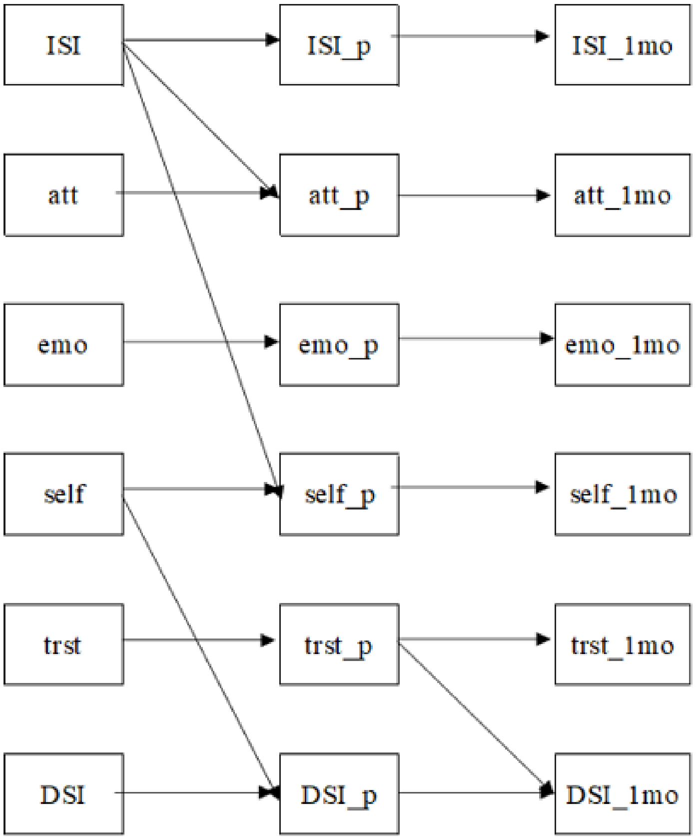

Fig. 1 Significant effects observed from the model. ‘p’ = post, ‘1mo’ = 1 month timepoint. ‘ISI’ = Insomnia Severity Index Scores, ‘att’ = MAIA “attention” subscale, ‘emo’ = MAIA “emotional regulation” subscale, ‘self’ = MAIA “self-regulation” subscale, ‘trst’ = MAIA “trusting” subscale, ‘DSI’ = Depressive Symptom Index suicidality subscale scores.

Statement of Research Advisor

Walton Ferguson led the development of this project testing the relations between sleep disturbances, interoception, and suicidality among military service members (MSM). Under the supervision of graduate student, Will Grunewald, Walton learned how to conduct and interpret the longitudinal path analyses for this study. These results can inform clinical assessments and interventions for MSM.
- April R. Smith, Department of Psychological Sciences, College of Liberal Arts

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Authors Biography

Walton Ferguson is studying Psychology and Statistics at Auburn University. He intends to pursue graduate studies in Psychology. His research interests include learning, neuroplasticity, and interoception and currently has one publication with the REDS lab.

Will Grunewald is a third-year clinical Psychology PhD student at Auburn University. His research interests include identifying risk factors for disordered eating, body image disturbance, and suicidality, with a particular emphasis on these risk factors among vulnerable populations. He also studies the overlap between conformity to masculine norms and Muscle Dysmorphia.

Dr. Smith is currently an Assistant Professor of Psychology at Auburn University and the director of the Research on Eating Disorders and Suicidality (REDS) Laboratory. She received her B.A. in Psychology and Plan II from the University of Texas at Austin in 2004. She received her Ph.D. from Florida State University's Clinical Psychology Program in 2012, and completed her clinical residency at the University of California, San Diego.

Auburn University Journal of Undergraduate Scholarship

Evaluation of Assessment Data Collected by Nursing Staff and Assistive Personnel in a Simulation Environment

Melissa Freeman[1,*] *and Dr. Pao-Feng Tsai*[2]

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[2]Associate Dean for Research, College of Nursing, Auburn University

A complete vital sign assessment includes the measurement of blood pressure, temperature, heart rate, respiratory rate (RR), and oxygen saturation. Vital sign assessment is one of the foundational skills taught in nursing programs in the United States. Obtaining accurate RR data and implementing clinical protocols for intervention requires knowledge, clinical experience, and nursing judgment.

Licensed nurses complete training and clinical practicum hours then sit for state board exams to ensure competency before they can practice nursing. Unlicensed assistive personnel (UAP) are not required to complete such training and are often trained on the job, with no state regulation of competency[1].

Automated technology used currently in clinics and hospitals provides accurate and timely measurements for all except the RR and temperature. UAP delegated the task of collecting and documenting vital signs, including RR data potentially lack the education and clinical judgment necessary to recognize abnormal findings.

The purposes of this pilot study were to determine: if collected, is RR data accurate; if data collected by licensed nursing staff have a higher accuracy rate than data collected by UAP; and if a correlation exists between attitude and accuracy of RR data.

Participants included three licensed registered nurses (RN) and three UAP, one being a current nursing student employed in a UAP capacity at a local hospital.
Utilizing the simulation lab at the Auburn University College of Nursing, four high-fidelity mannequins were programmed with vital sign control data. High-fidelity mannequins allow data to be controlled and simulate human patients as chest rise and fall can be observed, heartbeat and respirations can be auscultated, and pulse points can be palpated.

The two-part study began by instructing participants to assess each mannequin as they would in their employed clinical setting. Research staff, positioned behind two-way glass in the control booth, observed participants' assessment technique and time in seconds that the RR was assessed.

Part two utilized the V-Scale to assess participants' knowledge of, and attitude toward, vital sign collection. This scale consists of sixteen items, scored by a five-point Likert rating scale. It consists of the following subscales: key indicators, knowledge, communication, workload, and technology[2]. Four of the sixteen questions were analyzed for this study as they utilize the psychometric testing of the V Scale to examine participants' knowledge of and attitude specifically toward the RR measurement in clinical settings.

The four questions analyzed included two from each of the knowledge and workload subscales. The responses were recorded as positive or negative based on the Likert scale rating of each participant. If a score of 1-3 was chosen, a negative response was recorded and for scores of 4 & 5, a positive response was recorded.

Findings of part one, illustrated in Fig. 1, show that when RR data is assessed, the RN group has a higher accuracy rate than the UAP group. Using the control as the mean RR data of the RN group achieved higher accuracy than the UAP group across three of the four

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simulators. The control data refers to the vital sign data pre-programmed to each mannequin (M). Research staff could then compare the control data to the RR data recorded by participants. If no RR was assessed, a rate of zero was assigned. This is evident in the M1 results, as only one UAP provided data for RR assessment. In M4, one RN assessed for 15 seconds but failed to multiply by 4 to obtain the 60 second rate, altering the mean.

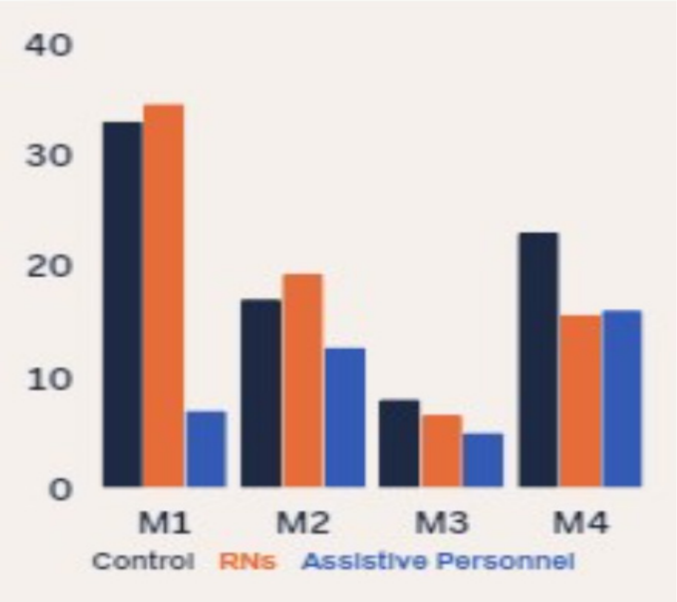

Fig. 1. Mean of participant groups compared to control data.

Findings from part two indicate that a potential correlation existed between attitude and accuracy of the RR measurements, as illustrated in Fig. 2. Overall, half of the participants indicated negative feelings toward RR assessment.

Key findings include 100% of UAP felt RR assessment is a "boring" task and admitted to estimating the rate. None of the licensed staff reported RR as a boring task, but 66% admitted to estimating the rate. Only one of the UAP, the nursing student, felt confident in the pathophysiology and importance of accurate RR data.

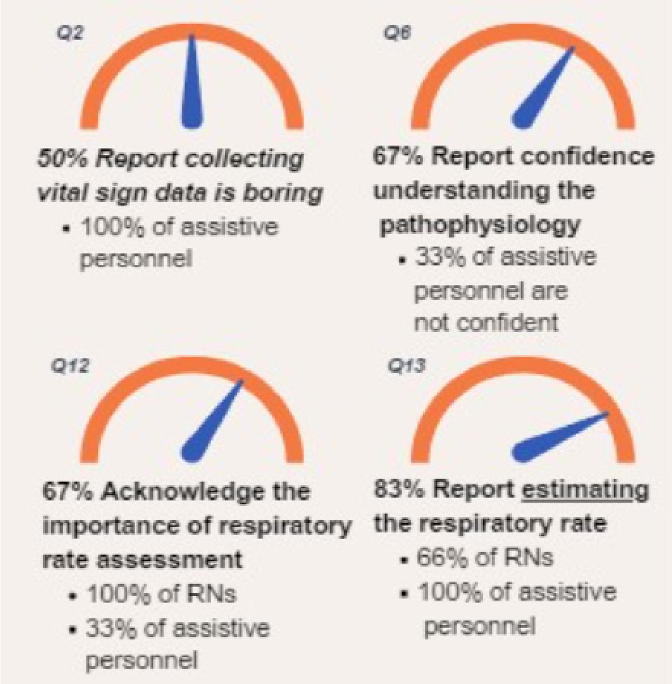

Fig. 2. V-Scale data analyzed.

In the clinical setting, UAP are tasked with assessing and documenting vital signs. The results of this pilot study raise concerns, as RR data is vital in the efficacy of sepsis early warning systems[3]. UAP delegated the task of collecting and documenting vital sign data potentially lack the nursing education and clinical judgment necessary to recognize abnormal findings on a per patient basis. The efficacy of early warning systems is reliant on nurses' assessments and clinical judgment; therefore, delegating nursing tasks to unlicensed personnel may place at-risk patients in unsafe and life threatening scenarios.

More research is needed with a larger sample size to confirm the correlation between education achieved, attitude toward, and accuracy of RR data.

Statement of Research Advisor

Vital signs are measurements of patients' basic functions and are routinely monitored by health care providers. Unlicensed assistive personnel are often delegated the task of collecting and documenting vital sign data. This pilot study highlighted the need for educating unlicensed assistive personnel about the importance and procedure for collecting vital signs accurately. Future work should be done to verify these pilot results.

- Dr. Pao-Feng Tsai, Associate Dean for Research, College of Nursing

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Authors Biography

Melissa F. Freeman is a senior pursuing a B.S. degree in Nursing at Auburn University. She initiated this research idea and played key research roles in this project. Melissa is a Registered Nurse practicing in the fields of pediatrics and emergency medicine. Upon graduation, Melissa intends to further her academic career with a master's degree in nursing – Family Nurse Practitioner, as well as a PhD in Nursing education, aspiring to teach and research at the university level.

Dr. Pao-Feng Tsai is the Associate Dean for Research and Professor in Auburn University's College of Nursing. Her research areas of expertise are chronic pain assessment and intervention, geriatric care, and development of nursing theories. Dr. Tsai is a fellow of the American Academy of Nursing and the recipient of the Betty McClendon Fuller Endowed Professorship.

Internalizing Problems and Declines in Academic Achievement: Mechanisms and Protective Factors

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2 Professor, College of Human Sciences, Auburn University

Internalizing problems and disorders, characterized by depressive, withdrawn, and anxious symptoms, can have a marked effect on students' academic performance (Pedersen et al., 2019). Although this has been attributed to a myriad of causes (e.g., difficulty concentrating, poor memory), internalizing problems are often accompanied by low school involvement and reduced classroom participation (Loukas et al., 2016). Thus, lack of school engagement may be an important factor in explaining the relation between internalizing problems and declines in academic achievement.

Despite this, some students who exhibit internalizing symptoms continue to excel academically (Deighton et al., 2018; Masten et al., 2005). Previous literature has highlighted the protective effect of close student-teacher relationships for students struggling with emotional problems (Baker et al., 2008, Pakarinen et al., 2018; Shi & Ettekal, 2021). For children with internalizing problems, a relationship with the teacher high in warmth and low in conflict may help them remain engaged in the classroom and, in turn, academically successful. Accordingly, to better understand both how and when internalizing problems lead to poor school performance, this study investigated whether: a) classroom engagement mediates the association between internalizing problems (i.e., depression and anxiety) and academic development, and b) closeness or conflict with the classroom teacher moderate the association between internalizing symptoms and classroom engagement.

Data from a 17-year longitudinal study of the academic, interpersonal, and psychological development of 457 children were utilized. This study used data collected when the children were in the 4th through 7th grades. Each year, students completed the Wide Range Achievement Test (WRAT; Wilkenson, 1993) which measures reading, spelling, and math abilities, and teachers completed the Teacher Rating Scale of School Adjustment (TRSSA; Birch & Ladd, 1997), an assessment of classroom engagement. When children were in the 4th grade, teacher-reported closeness and conflict were measured using the Student-Teacher Relationship Scale (STRS; Pianta, 2001), and self-reports of internalizing problems were measured using the Child Behavior Scale (CBS; Ladd & Profilet, 1996).

Four Latent Curve Models with Structured Residuals were estimated. A depiction of the conceptual framework behind this research can be seen in Figure 1. Across the four years studied, a within-person increase in engagement predicted a subsequent increase in achievement, and a within-person increase in achievement predicted a subsequent increase in school engagement. Unexpectedly, internalizing problems in 4th grade were not associated with a concurrent change in engagement scores. Rather, depression and anxiety were associated with a decrease in children's academic achievement, but only for those who had low closeness or high conflict with their teacher. Moreover, for children with a poor relationship with their teacher, internalizing problems were indirectly associated with a decrease in school engagement through reduced academic achievement.

These findings help us better understand the inconsistent results from previous studies investigating associations between internalizing problems and academic achievement. The results suggest that internalizing problems can have effects on achievement but only when they co-occur with a relationship with the teacher characterized by low warmth and frequent conflict. Reduced academic achievement may then lead to a cycle of increasing school disengagement and worsening academic development over time. The findings, however,

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did not explain why internalizing problems are associated with decreases in academic achievement. Thus, further research should be conducted to examine other factors that may be mediating the effects of internizing problems on children's academic development in order to better shed light on the intricate pathways affecting school adjustment and achievement.

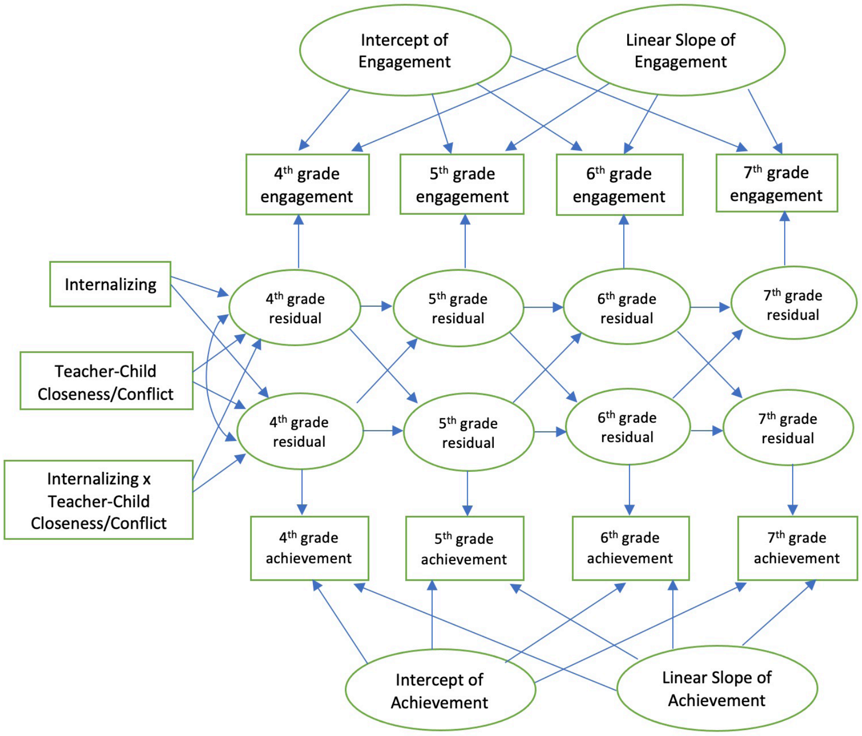

Fig. 1. Conceptual framework for Latent Curve Models with Structured Residuals.

Statement of Research Advisor

Elena identified an important risk factor for poor academic achievement, internalizing problems, and through a careful literature search, realized that little is known as to what accounts for why internalizing problems jeopardizes youth's achievement or what factors protect students with internalizing problems from academic losses. She utilized a highly sophisticated statistical analysis, latent growth curve modeling with structured residuals, to analyze data from a large longitudinal study. Her findings demonstrate that only when youth with internalizing problems have poor relationships with their teacher are they at risk for worsening academic achievement, prompting a cycle of school disengagement and further academic decline.

- Wendy Troop-Gordon, Department of Human Development, College of Human Sciences

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Authors Biography

Elena Gagliano is a junior-year student pursuing a B.A. degree in Psychology and a B.S. degree in Human Development and Family Science at Auburn University. She is a 2022-2023 Auburn Undergraduate Research Fellow.

Wendy Troop-Gordon is a professor in the Department of Human Development and Family Science in the College of Human Sciences. Her research in Auburn's Social Development Lab focuses on child and adolescent peer relationships and how those relationships influence socioemotional health and school adjustment.

Learning Molecular and Cell Biology Methods Using Human Cancer Models

Melissa A. Gathman[1,*], *Razan S.Waliagha*[2], *Amit Kumar Mitra* [3,4]

[1] Undergraduate Student, Department of Biological Sciences, Auburn University
[2] MS Graduate Student, Department of Drug Discovery and Development, Harrison College of Pharmacy, Auburn University
[3] Assistant Professor, Department of Drug Discovery and Development, Harrison College of Pharmacy
[4] Director of the Center for Pharmacogenomics and Single-Cell Omics Initiative (AUPharmGx), Auburn University

Prostate cancer is the most common non-skin cancer in men in the United States (Zhao, 2021). One form of treatment for prostate cancer is drugs that inhibit cell division (Zhao, 2021). Multiple myeloma is a cancer of the plasma cells (Padala, 2021). Proteosome inhibitors (PIs) are the main form of treatment for MM and often have resistance built against it over time in cancer patients, making these genes an effective target to look at (Padala, 2021).

Many cancers can often develop drug resistance to various treatments to primary therapies such as Docetaxel (Prostate Cancer) and PIs (Multiple Myeloma) and are, therefore, viable subjects to look at specific genetic influences on reactions to certain drugs and to study new therapies (Padala, 2021; Mitra, 2020).

My research goal was to learn and practice techniques in order to validate new therapies against drug-resistant and aggressive forms of cancers. This was split into different sections, including Primer Design, Cell Culture, and Assays/Gels.

For primer design, we selected the genes (PSMB4 and PSMB5) that code for proteasomes that break down proteins and cell waste that naturally builds up were first investigated (Padala, 2021; Mitra, 2020). As proteasome inhibitor drugs are used as treatments against Multiple Myeloma, naturally, we focused on genes that code for proteasomes in order to explore potential targets for genetic therapies or identify any impacts on PI treatment as a result of genetic variation.

Genes were queried on the NCBI database (https://www.ncbi.nlm.nih.gov/gene) to obtain an annotated version in order to determine what is a coding exon in comparison to a non-coding intron. After this, a list of common single nucleotide polymorphisms (SNPs) was compiled from the NCBI's dbSNP database (https://www.ncbi.nlm.gov/gene). We focused on those SNPs that are in an exon using the UCSC Genome Browser (https://genome.ucsc.edu/cgi-bin/hgGateway). Representative examples are provided in Figure 1 and Table 1.

Primers were designed via Primer3 (https://primer3.ut.ee/) to generate amplicons between 250-450bp in length to target the selected SNPs' loci. Primer lengths were between 18-24bp. Additional characteristics of the primers included GC content of ~40%-80% and a melting temperature Max of 63.0°C (Mitra, 2011).

Cell culture was practiced with PC3M, an aggressive prostate cancer cell line, in T-25 and T-75 flasks with F12K media. Media was changed every ~2-3 days until 90% confluent and then split by adding trypsin (4 mL in T-25 and 6-7 mL in T-75), spinning them down via a centrifuge, and placing half in a new flask and freezing, and the other half in another flask to keep incubating. PC3M cells are adherent to the flask. Therefore, in order to split cells, trypsin is used to remove them from the bottom. By being able to do this, cell lines were able to be maintained, which is the first step to doing DNA/RNA extraction, and the various assays and gels needed for drug treatment experiments.

MTT assays are used to assess cytotoxicity assays. First, cells must be around 75%-95% confluent. They are then centrifuged down to a pellet, and 10 µL cells are placed into a microtube and counted using a cell counter. This is used to determine cells to be added in each well to add up to 80 µL per well. After cells are plated, they are incubated for 24 hours, and drug is added. Following 48 hours of incubation with the drug, MTT is added, and an absorbance assay was performed for drug sen-

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sitivity studies.

Additionally, SDS-PAGE and Western Blot were learned. These are used in tandem in order to analyze protein(s). SDS-PAGE is a gel run that separates proteins by mass, and a Western Blot transfers that gel to the membrane and uses the antibody-binding principle to target a specific protein.

Additionally, SDS-PAGE and Western Blot were learned. These are used in tandem in order to analyze protein(s). SDS-PAGE is a gel run that separates pro teins by mass, and a Western Blot transfers that gel to the membrane and uses the antibody-binding principle to target a specific protein.

This fellowship supported undergraduate research involved learning many vital techniques and protocols in a lab setting and will hopefully lend to future uses in the experiments mentioned above. Being well-versed in these techniques and protocols is an essential pre-requisite to research on i) developing targeted approaches for cancer treatment, ii) identifying if there are any genetic variations that influence response to these drugs, and iii) predicting which molecular pathways are activated or inhibited following treatment with novel drugs.

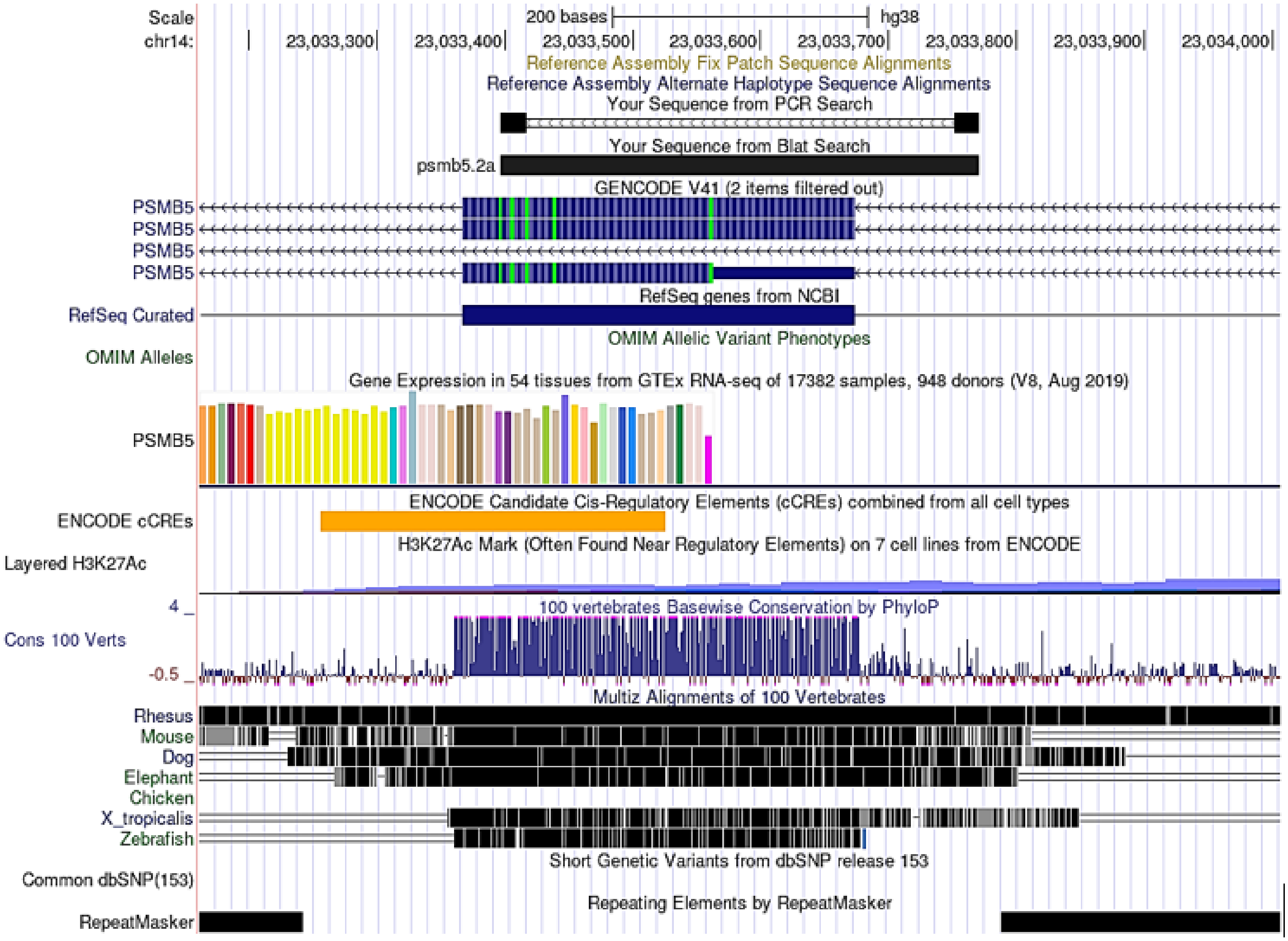

Fig. 1. UCSC Genome Browser image showing PCR primers for the Gene PSMB5 (Exon 2)

Table 1 Primers created using Primer3 for SNP identification using PCR-Sanger Sequencing method.

Gene	Exon	Product Length	Amplicon sequence
PSMD4	1	250bp	AAATGGTCTTTCGCATCTGGACCGCAAACTCCGGTCAGAAATGGTTTCGCATGGCtcttcttttggaggcgtgcttgccagcagtcaaaatggctccattccggaatagatttataggaagtgaagctgtgacggcgaggcgttgcccggcctatctttgctaggcgttctcagaattagttctttctgcccacactagacatggcgcttgccagcgtgttggagagaccgctaccggtgaaccagcgcgggtttttcggacttgggggtcgtgcagatctgctggatctaggtccagggagtctcagtgatggtctgagcctggccgcgccaggctggggtgtcccaaagagccaggaatcgaaatgcttcatggaacaaccaccctggccttcaaggtgtggagccagccccccttgccaggctgagtactgaacgcccgcgacttgcctggcctccagcCTGACCGGAGTTTGCGGT
PSMD4	2	422bp	GAGATGTGCTGGGTTTGGATATGGTGCCCATGGACAGCCCCGAGATGTGCTGGGTTTGGATtgatgcaaaaagaagtatGtaggagtgtttttgtggtcttatgtggcctgttttgtgttttcctctgatcttaacagttccgccatggagtcatagttgcagctgactccagggctacagcgggtgcttacattgcctcccagacggtgaagaaggtgatagagatcaacccatacctgctaggcaccatggctgggggcgcagcggattgcagcttctgggaacggctgttggctcggcaatgtcgaatctatgagcttcgaaataaggaacgcatctctgtagcagctgcctccaaactgcttgccaacatggtgtatcagtacaaaggcatGGGGCTGTCCATGGGCACCAT
PSMB5	2	375bp	GAGATGTGCTGGGTTTGGATATGGTGCCCATGGACAGCCCCGAGATGTGCTGGGTTTGGATtgatgcaaaaagaagtatgtaggagtgtttttgtggtcttatgtggcctgttttgtgttttcctctgatcttaacagttccgccatggagtcatagttgcagctgactccagggctacagcgggtgcttacattgcctcccagacggtgaagaaggtgatagagatcaacccatacctgctaggcaccatggctgggggcgcagcggattgcagcttctgggaacggctgttggctcggcaatgtcgaatctatgagcttcgaaataaggaacgcatctctgtagcagctgcctccaaactgcttgccaacatggtgtatcagtacaaaggcatGGGGCTGTCCATGGGCACCAT

Statement of Research Advisor

Ms. Gathman's research in the lab as an undergraduate research fellow involved extensive orientation to standard cell and molecular biology techniques. She has shown gradual progress over the past year. We are confident that she will be able to contribute to genomics, pharmacogenomics and translational research in industry or academia, whichever career path she chooses to pursue.

-Amit Kumar Mitra, Department of Drug Discovery, Harrison College of Pharmacy

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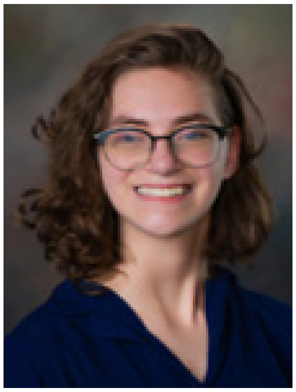
Authors Biography



Melissa A. Gathman is a senior-year student pursuing a B.S. degree in Genetics at the College of Science and Mathematics at Auburn University. She has spent time learning a variety of important techniques necessary to succeed as a lab researcher.

Razan S. Waliagha, MS is a Student Pharmacist and Pharmacogenomics Oncology Graduate at Harrison College of Pharmacy at Auburn University. She is skilled in Good Laboratory Practice (GLP), Medical Terminology, Molecular and Cell Biology techniques, Pharmacology, and Clinical Pharmacology.

Dr. Amit K. Mitra is an Assistant Professor at the Harrison College of Pharmacy at Auburn University, and Director of the AU Center for Pharmacogenomics and Single-Cell Omics Initiative (AU-PharmGx). His research focuses on investigating genomic and pharmacogenomic factors underlying variations in drug sensitivity, as well as predicting secondary drug candidates in aggressive human cancers such as relapsed/refractory multiple myeloma and lethal forms of prostate cancer.

Homopolymer Compression: Multiple Alignment in the Face of Homopolymer Errors

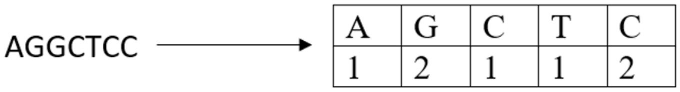
Saksham Goel[1,], Drew Beckwith[2], and Dr. Haynes[3]*

[1] Undergraduate Student, Department of Computer Science and Software Engineering, Auburn University
[2] Undergraduate Student, Department of Computer Science and Software Engineering, Auburn University
[3] Assistant Professor, Department of Computer Science and Software Engineering, Auburn University

All organisms on this Earth have some kind of genetic material, with advanced ones having it in the form of 'DNA'. A DNA sequence is made of four chemical compounds, namely Adenine(A), Guanine(G), Cytosine(C), and Thymine(T) that form a double helix of a chain of base pairs.[3] Adenine only pairs up with Thymine, while Cytosine only pairs with Guanine, and vice versa. DNA sequences are important because not only they can help us solve the mysteries of evolution, but also understand and potentially fix various genetic disorders that may be caused due to random mutations, inheritance, or environmental causes such as UV rays.

Single molecule DNA sequencing is often erroneous due to the challenges of measuring DNA bases that are smaller than the wavelength of light. To get around this, PacBio circular consensus sequencing reads the same piece of DNA multiple times. From these multiple reads, a consensus sequence is determined, which gives us a close determination of what the actual sequence is--close, but not exact. These reads are most erroneous in determining how many of a particular base there is in a stretch of the same base (a homopolymer). A homopolymer stretch of a DNA sequence has only one type of base for a long period. For example, in an incredibly short DNA sequence AGGGGCTC, the GGGG part is a homopolymer. The technique that we implemented for our research aims to provide better results for DNA sequences with error-prone homopolymers. exist to enhance the educational experience, quality of the degree program, and the value to the student.

In our algorithm, we first start by compressing each DNA read into unique base pairs and the frequency of occurrence of each base pair. This can be seen in Fig. 1. Then, for these compressed DNA sequences, we generate a consensus sequence using partial order alignment. A partial order alignment is a method of multiple sequence alignment by incrementally aligning sequences onto a growing sequence graph and using a dynamic programming backtrace to find the consensus sequence.



A	G	C	T	C
1	2	1	1	2

Fig. 1 DNA Sequence compressed into unique base pairs and frequency of occurrence.

After this, we globally align the compressed consensus sequence to every read. A global alignment consists of the two sequences aligned, and the alignment score which reflects how well the two sequences correlate to each other. Fig. 2 showcases what a global alignment looks like.

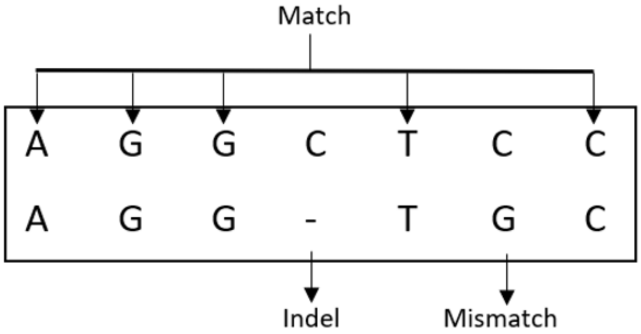


Fig. 2 Global Alignment of two sequences

Once we have all of this, it is time to expand our compressed consensus sequence using the information we have from every read (the unique base pairs and their frequencies). We iterate over every global alignment and

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try to find the frequency of a base at that specific location (starting from index 0) and construct the expanded version of the consensus sequence piece by piece. A question that arises here is out of the different number of frequencies that we have for every read, which one do we choose? We can choose either the mean, the median, or the mode of the list of frequencies. For research purposes, we do all three and compare the results of each of them. Once the expanded sequence is ready, we can globally align it to the original sequences and find the average score of our Homopolymer Compressed consensus sequence. A higher average alignment score means that the consensus sequence better represents the raw reads.

After obtaining our expanded consensus sequences and finding the average score of each of these consensus sequences, we align all our sequences to the consensus sequence that is obtained simply by their partial order alignment (POA).[1] The final step is comparing the scores of our expanded consensus sequences to that obtained by simple POA.

For data, we started by simulating DNA sequences out of A, G, T, and C by randomly picking each of them 'n' times, where n is the sequence length. From this, we generated 'k' mutated sequences. These mutations were generated using a 0.1 probability of single nucleotide polymorphism (SNP) which are mismatches in simpler understanding and a 0.1 probability of insertions or deletions. Using 25 iterations of random sequence generations with 10 mutated DNA reads for each iteration, we took the average score for each iteration for all the consensus sequences and plotted that on the chart. As we can see in Fig. 3, the regular POA performs slightly better on average than all our expanded sequences.

Fig. 3 Results from Randomly Generated Base Pairs

Since we want to target homopolymer sequences, we changed our data simulation such that it would create mutations based on the Poisson distribution of the length of individual homopolymers in the original sequence to better simulate fact that errors are higher in homopolymer sequences. The results are shown in Fig. 4, and we can see that our algorithm with median or mean as the average metric tends to perform much better than the regular POA

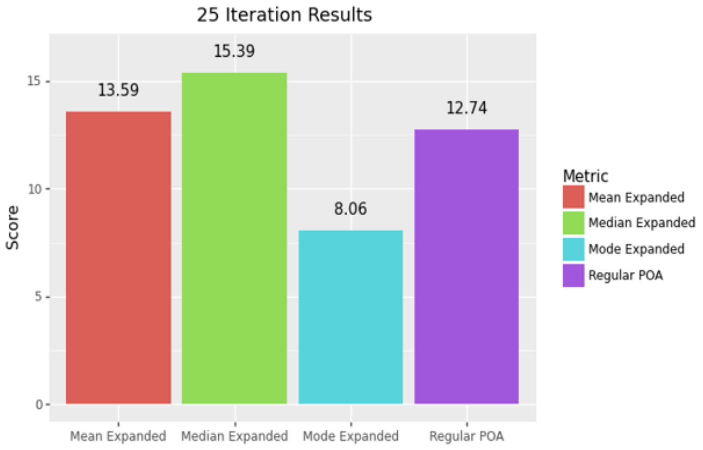

Fig. 4 Results from Data Generated using Poisson distribution of Homopolymers.

Statement of Research Advisor

This work demonstrates a proof of concept that iterative multiple sequence alignment (MSA) done in homopolymer compressed space can improve the consensus sequence quality in sequences that have higher error rates in homopolymer sequences, such as the circular consensus sequencing data from Pacbio. We are now applying this to more sophisticated Pacbio simulated data as well as real sequencing data for which we have high quality ground truth. This work may contribute to single molecule somatic variant calling to improve cancer detection and research. This work was done predominantly by Saksham and Drew.

- Dr. Haynes Heaton, Computer Science, Samuel Ginn College of Engineering

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Authors Biography

Saksham Goel is a senior-year student pursuing a B.S. degree in Computer Science with a minor in Statistics at Auburn University. In this project, he is responsible for the development of data generation, as well as global and partial order alignment. He is planning to move to Redmond, WA to begin his professional career as a Software Engineer upon gradua-

Drew Beckwith is a senior-year student pursuing a B.S. degree in Computer Science with a minor in Statistics at Auburn University. In this project, he is responsible for the implementation of expansion of Homopolymer consensus sequence using various metrics. Through various classes, internships, and self-study, he has found his passion in the areas of Web Development and Data Science. He is planning to move to Birmingham, AL to begin his professional career as a Software Developer upon graduation.

Dr. Haynes Heaton is an Assistant Professor in Computer Science and Software Engineering. He is responsible for the design of the project, along with mentoring the students in the development of code used in the project. He is a Computational Biologist working on methods development on emerging genomics technologies to enable the next generation of biological research. He holds a B.S. in CS and an MD from Brown University and a Ph.D. from Cambridge University.

Who to Turn to When I Need Someone to Turn to? Exploring the Help-Seeking Behaviors of Military Service Members.

Brianna S. Gordon[1,], Allison L. Tidwell[2], and Mallory Lucier-Greer[3]*

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[2] Doctoral Student, Department of Human Development and Family Science, Auburn University
[3] Professor, Department of Human Development and Family Science, Auburn University

The military provides its Service members with many forms of mental health care to ensure their readiness to perform their duties. This care may come from mental health professionals, self-help groups, military Chaplains, and/or medical providers, both within and outside of the military context. Despite these many options, help-seeking within the military has been stigmatized and mental health care remains underutilized (Kazman et al., 2020). Help-seeking behaviors may also vary based on individual perspectives, such as one's belief system. More specifically, help-seeking behaviors of religious and/or spiritual (henceforth R/S) Service members may differ from nonreligious and nonspiritual (henceforth non-R/S) Service members. Religious or spiritual affiliation may influence the frequency of mental health help-seeking and the type of provider the Service member seeks help from. This study investigated the intersections of help-seeking behaviors with religiosity and spirituality and highlights the importance of multidisciplinary practice in addressing Service members' mental health concerns by addressing the following research questions:

Research Question 1: Among soldiers experiencing stress, from which type of providers do they seek help?

Research Question 2: Do patterns of help-seeking differ based on whether soldiers consider themselves to be R/S or non-R/S?

More specifically, are Soldiers more likely to seek out certain types of providers (i.e., Mental Health Professional, Self-Help Group, Medical Professional, or Chaplain or Clergy) based on whether they identify as R/S?

This study utilized data from the Army Study to Assess Risk and Resilience in Servicemembers (STARRS) All Army Study (AAS) dataset (Ursano et al., 2017). All analyses were conducted in SPSS version 29.0.

To address the Research Question 1, descriptive statistics were examined from a sample of Soldiers who reported experiencing overall life stress in the past year and who reported whether they sought help from a provider to address their stress (n = 9,236). Provider types included Mental Health (i.e., military mental health professional, civilian mental health professional, and VA mental health professional), Self-Help Groups (i.e., military self-help group and civilian self-help group), Medical (i.e., military medical doctor, military medic, civilian medical doctor, and VA medical doctor), and Chaplain or Clergy (i.e., military Chaplain and civilian clergy).

To address Research Question 2, the analytic sample consisted of Service members who reported whether they identified as R/S or non-R/S (n = 8,550). Using the same grouping of providers, chi-square tests were conducted to examine differences in help-seeking based on whether Soldiers identified as R/S or non-R/S. Chi-square test results were interpreted with the chi-square likelihood ratio and effect size (Cohen's V).

Most (n = 6,300; 68.2%) Soldiers did not seek help from any type of professional (see Table 1) even though they reported life stress in the last year. Among Soldiers who did seek help (n = 2,936), 66.2% sought help from a mental health professional, 19.1% sought help from a self-help group, 51.6 % sought help from a medical professional, and 36.2% sought help from a Chaplain or clergy member.

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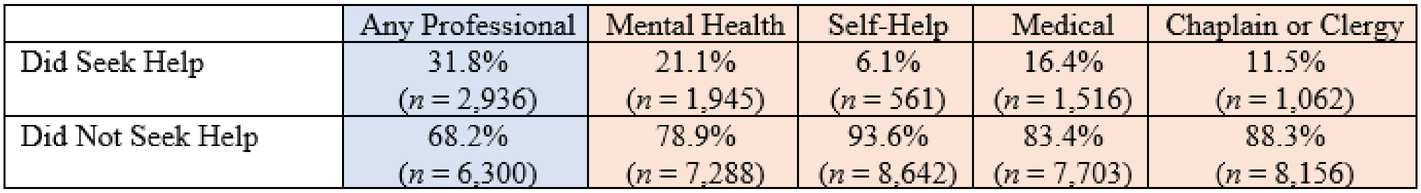
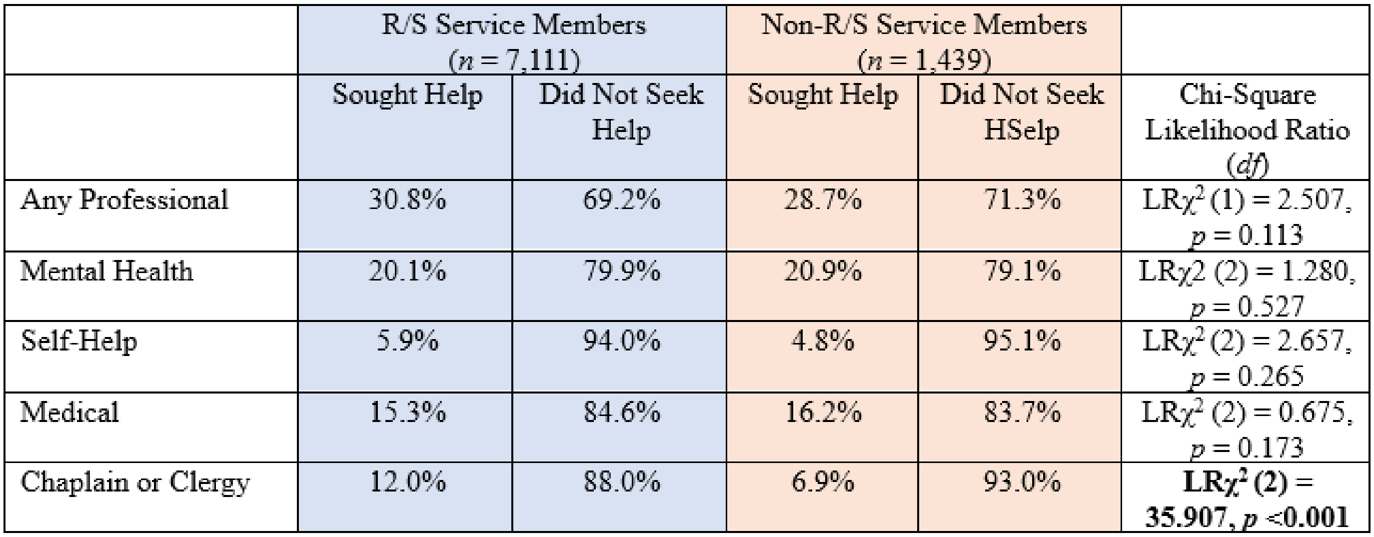
Table 1. Help-seeking by provider type (N = 9,236)



	Any Professional	Mental Health	Self-Help	Medical	Chaplain or Clergy
Did Seek Help	31.8% (*n* = 2,936)	21.1% (*n* = 1,945)	6.1% (*n* = 561)	16.4% (*n* = 1,516)	11.5% (*n* = 1,062)
Did Not Seek Help	68.2% (*n* = 6,300)	78.9% (*n* = 7,288)	93.6% (*n* = 8,642)	83.4% (*n* = 7,703)	88.3% (*n* = 8,156)

Table 2. Help-seeking by provider type and religious or spiritual affiliation (n = 8,550). Note. Not all percentages total to 100% due to some instances of missing data.



	R/S Service Members (*n* = 7,111)		Non-R/S Service Members (*n* = 1,439)		
	Sought Help	Did Not Seek Help	Sought Help	Did Not Seek HSelp	Chi-Square Likelihood Ratio (*df*)
Any Professional	30.8%	69.2%	28.7%	71.3%	$LR\chi^2$ (1) = 2.507, p = 0.113
Mental Health	20.1%	79.9%	20.9%	79.1%	$LR\chi2$ (2) = 1.280, p = 0.527
Self-Help	5.9%	94.0%	4.8%	95.1%	$LR\chi^2$ (2) = 2.657, p = 0.265
Medical	15.3%	84.6%	16.2%	83.7%	$LR\chi^2$ (2) = 0.675, p = 0.173
Chaplain or Clergy	12.0%	88.0%	6.9%	93.0%	**$LR\chi^2$ (2) = 35.907, p <0.001**

Among Soldiers who reported on help-seeking behaviors and their religious and spiritual beliefs, 83.2% (n = 7,111) identified as being R/S. There was no significant difference whether Soldiers sought help generally based on if they identified as R/S or non-R/S (LRχ2 (1) = 2.507, p = 0.113; see Table 2). There were no significant differences in whether Soldiers sought help from a mental health professional (LRχ2 (2) = 1.280, p = 0.527), self-help group (LRχ2 (2) = 2.657, p = 0.265), or medical professional (LRχ2 (2) = 0.675, p = 0.173) based on whether they identified as R/S or non-R/S. However, there was a significant difference whether Soldiers sought help from a Chaplain or clergy member based on whether they identified as R/S or non-R/S (LRχ2 (2) = 35.907, p <0.001). This was a small but meaningful effect (V=0.062,df=2), such that those identifying as R/S were more likely to seek help from a Chaplain or clergy member than Soldiers identifying as non-R/S. More specifically, 12.0% of Soldiers who identified as being R/S sought help from a Chaplain or clergy member. However, only 6.9% of Soldiers who identified as being non-R/S sought help from a Chaplain or clergy member.

It appears there is a gap between the need for help in Soldiers experiencing stress and Soldiers actually seeking help from providers for their stress. This gap may be a result of mental health stigma in the military system which has the potential to impact help seeking, negative attitudes towards treatment, and organizational barriers in seeking help (Kim, 2016). Military leadership, such as unit leaders, can encourage their unit members to seek support for their stress and access resources when they need it. Although R/S Soldiers tended to turn to Chaplain or clergy to manage their stress more than non-R/S Soldiers, some non-R/S did seek help from religious-affiliated providers. This may be because there is typically a Chaplain assigned to every unit, so Chaplains can build a relationship with their unit members more easily (Kim, 2016). Chaplains and clergy members can still be resources to learn coping strategies about stress regardless of a Service members' religious affiliation, though they may be more appealing to R/S Service members as they can provide counseling tailored to religious or spiritual beliefs.

Statement of Research Advisor

Brianna's research is an important contribution in addressing the mental health needs of our military by first understanding service utilization among Service members who report being in distress. By examining a large sample of Soldiers, she has explored trends in help-seeking behaviors and provides a unique lens of how a Soldiers religion and/or spirituality may impact help-seeking behaviors. These results will be beneficial for military leadership and mental health professionals in encouraging Service members to seek help for their stress from diverse providers, regardless of their religious affiliation.

- Mallory Lucier-Greer, Department of Human Development and Family Science, College of Human Sciences

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Authors Biography

Brianna S. Gordon is an undergraduate student pursuing her B.A. in Psychology at Auburn University. Growing up in a military family led to a lifelong passion for contributing back to the military community in profound ways. She is also an undergraduate research assistant at Military REACH, striving to merge the gap between research and practice for military families.

Allison L. Tidwell, M.S., is a doctoral student in the Department of Human Development and Family Science at Auburn University. Her research aims to identify factors which promote resilience among military families.

Dr. Mallory Lucier-Greer is a Professor in Human Development and Family Science at Auburn University. Her research is focused on understanding stress and resilience processes in families with a focus on the wellbeing of military families.

Auburn University Journal of Undergraduate Scholarship

IBS Symptom Management and Depressive Symptoms in the U.S. Adults

Jane H. Greene[1],[*] Sarah Lennon[2], and Andrew D. Frugé[3]

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[2] Graduate Student, College of Human Sciences, Auburn University
[3] Associate Professor, College of Nursing, Auburn University

Irritable Bowel Syndrome (IBS) is a condition that is characterized by broad symptoms consisting of abdominal pain, bloating, irregular bowel movements, and other intestinal issues. IBS is currently estimated to affect 1015% of individuals around the world, with the majority of sufferers being women.[1] This condition is chronic in nature and is typically managed through conservative or therapeutic methods. As with many chronic diseases, individuals rarely seek medical care for IBS, which is not surprising given the personal nature of symptom presentation. Although up to 80% of diagnosed IBS patients attain a degree of symptom relief through conventional medication strategies, many are left without symptom resolution and a decreased quality of life (QOL).[2] The co-occurrence of decreased mental and physical QOL can be devastating, with 40-60% of IBS patients having at least one co-existing mood disorder, including anxiety and depression. Similarly, it has been observed that the severity of IBS is directly associated with the severity of various mood disorders.[3] Often, the patients who suffer the most mentally and physically are unable to benefit from traditional treatment.

Non-pharmacological alternatives such as cognitive behavioral therapy, dietary modifications, lifestyle changes, probiotics, and other dietary supplements show promise.[4] These treatments target the underlying mechanisms responsible for IBS, most notably inflammatory pathways that trigger dysfunction in the gut-brain axis.[5] With increased interest in integrative and alternative approaches to symptom management, and the growing knowledge base regarding manipulation of the gut-brain axis, we developed and distributed a nation-wide survey to determine the incidence and efficacy of symptom management approaches and their association with depression severity, measured by the nine-item Patient Health Questionnaire (PHQ-9). [6]

Survey questions were developed using previously validated instruments and a combination of question batteries utilized in previous IBS studies [7-9] that were modified to include additional therapeutic approaches[10] as well as their efficacy as measured by a 7-point Likert scale. Notably, we framed these questions in the context of the previous three months in order to report the most recent period of symptom management approaches.

Respondents were either formally diagnosed with IBS or met Rome IV criteria for IBS[11] per the screening questions. The survey was distributed by Qualtrics Panels from July 24 to August 9, 2023. Between sex differences were obtained with chi-squared and independent sample t-tests. Backward stepwise linear regression determined the predictive value of independent variables on PHQ-9 scores.

Of 2,063 attempted responses, 1,663 were excluded for having comorbid gastrointestinal diagnoses, non-current symptoms, or failed attention check questions. Of the 400 valid responses analyzed, 63% were medically diagnosed with IBS, 86% were female, 93% were non-Hispanic, with an average age of 34±9 years and a body mass index (BMI) of 29.2±7.9 kg/m2 (Table 1). The average PHQ-9 score was 11.6±6.1 (range 0-27). The most frequently avoided dietary items (>15% of respondents) were dairy, artificial sweeteners, high fructose corn syrup, gluten, and processed meats. Among pharmaceutical and integrative therapeutic approaches, >25% of respondents reported over-the-counter drugs, probiotic supplements, therapy (to reduce stress), and meditation.

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Severity of regular symptoms (β=.281, p<.001) but not flare-ups, age (β=-.191, p<.001), but not years experiencing symptoms, and BMI (β=.117, p=.015) were predictive of depression severity (Table 2).

Table 1 Characteristics of study participants

	All	Female	Male
	N (%)	N (%)	N (%)
Diagnosed Irritable Bowel Syndrome	252 (63)	222 (64.3)	30 (54.5)
Autoimmune Disease	50 (12.5)	47 (13.6)	3 (5.5)
Diagnosed Food Allergy	113 (28.2)	100 (29)	13 (23.6)
Spoken to a healthcare provider	323 (80.8)	281 (81.4)	42 (76.4)
PHQ-9 Score, Mean (Standard Deviation)	11.6 (6.1)	11.6 (6.1)	11.4 (6.1)
Approaches taken within last 3 months to manage symptoms			
Diet	292 (73)	247 (71.6)	45 (81.8)
Supplements or herbal therapies	125 (31.3)	108 (31.3)	17 (30.9)
Over the counter treatments	212 (53)	185 (53.6)	27 (49.1)
Lifestyle change to reduce stress	182 (45.5)	153 (44.3)	29 (52.7)
Altered exercise routine	79 (19.8)	66 (19.1)	13 (23.6)
Prescription medications	81 (20.3)	69 (20)	12 (21.8)
Duration of symptoms			
<6 months	16 (4)	14 (4.1)	2 (3.6)
6 months – 1 year	16 (4)	14 (4.1)	2 (3.6)
1-3 years	70 (17.5)	55 (15.9)	15 (27.3)
3-5 years	70 (17.5)	62 (18)	8 (14.5)
5-10 years	90 (22.5)	79 (22.9)	11 (20)
>10 years	138 (34.5)	121 (35.1)	17 (30.9)

Table 2. Backward stepwise regression of factors affecting depression severity

Model		Beta	p-value
1	(Constant)		<.001
	BMI	0.116	0.016
	Formal Diagnosis	-0.071	0.152
	Age	-0.182	<.001
	Diagnosed food allergies	-0.012	0.801
	Daily symptom severity	0.239	<.001
	Flare-up symptom severity	0.091	0.105
	Symptom duration	-0.043	0.398
5	(Constant)		<.001
	BMI	0.117	0.015
	Age	-0.191	<.001
	Daily symptom severity	0.281	<.001

A limited number of respondents reported taking prescription medications within the past three months. When comparing individuals with no or low depression (PHQ-9 scores less than 10) to those with moderate or severe depression, a greater proportion of patients with greater depressive symptoms reported taking several drug types, including antidepressants (Figure 1).

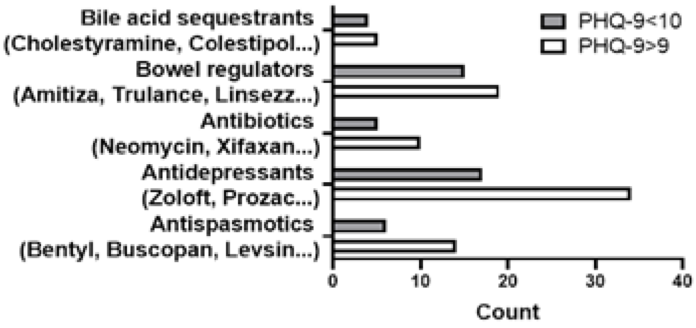

Figure 1. Medications taken by patients with IBS by depression severity.

Over 80% of the individuals had spoken to a healthcare provider about their symptoms. Many tried a variety of different treatment options, with the most popular being diet changes. 73% of individuals made some sort of alteration to their diet by removing certain foods, making it the leading treatment option in the last three months. Following behind that were over-the-counter treatments and lifestyle adjustments to reduce stress, without about half of the sample size trying each, respectively. Supplements and herbal therapies were tried by about a third of the sample size, while prescription medications were only tried by ⅕ of the individuals in the last 3 months.

Among respondents, 35.5% had experienced IBS symptoms for more than ten years, which aligns with the chronic nature of the disease. Given the greater update of dietary and lifestyle modifications compared to pharmaceutical treatment, it appears integrative and holistic approaches are most often sought after and/or retained as approaches.

Contrary to our hypothesis, we found that the most effective and common foods to remove were not entirely consistent with the most commonly prescribed IBS diet, which omits fermentable oligosaccharides, disaccharides, monosaccharides, and polyols (FODMAPs). The most commonly avoided foods were primarily dairy, wheat, artificial sweeteners, and legumes. Another common group emerged of red meats, including lamb, sausage, and beef. Although not commonly listed as a problematic food group, red meats do seem to contribute to IBS symptom presentation. Another unexpected finding was that many found success with removing fermented vegetables. Although fermented foods contain live probiotics, they seem to be aggravating for the majority of respondents.

Among this large and potentially representative sample of US adults with IBS, depression was highly prevalent, and numerous approaches were reported for symptom management. Improving access to medical care for referral to mental health and nutrition professionals is important for reducing symptom burden and improving QOL in IBS patients. It is unknown whether long-term use of over-the-counter products, which were commonly used among the majority of patients, can exacerbate symptoms, so lifestyle and dietary approaches are tools that can improve several domains of health. Multidisciplinary management of IBS is essential for improved QOL and symptom management in this population. [12]

Statement of Research Advisor

This has been an exciting project that was conceptualized by Ms. Greene, and was developed methodically over several months. The journal articles resulting from this research will be highly cited, but more importantly, will help provide guidance and answers for individuals suffering from a highly undertreated medical condition. Excellent work, Janie!

- Drew Frugé, Department of Nursing, College of Nursing

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Authors Biography

Jane Greene is a junior-year student studying Nutrition and Dietetics. While completing her undergraduate degree, she has worked with several dietitians who specialize in holistic healthcare. Her area of interest includes the gut microbiome and its impact on mental health, immune function, and overall prevention of future disease.

Sarah Lennon is a second year PhD student in Nutritional Sciences in the College of Human Sciences. She earned her Master of Science Degree from the University of Memphis where she investigated the effects of aerobic exercise on the gut microbiome.

Drew Frugé is an Associate Professor and Registered Dietitian in the Auburn University College of Nursing. His research spans many domains of health including disease prevention, improving quality of life, and improving physical performance.

Determination of Dissolution Profile of Açaí in Simulated Fed and Fasted Intestinal States

Zalaya Haynes[1,*], *Zarna Raichura*[2], *Angela I. Calderón*[3]

[1]Undergraduate Student, Department of Biomedical Sciences, Auburn University
[2]Graduate student, Department of Drug Discovery and Development, Auburn University
[3]Associate Professor, Department of Drug Discovery and Development, Auburn University

In recent years, there has been an increase in the use of botanical dietary supplements (BDS) along with other medications, specifically cancer treatments. Açaí (*Euterpe oleracea* Mart.) BDS is one such supplement that is seen to have health benefits, such as antioxidant and anti-inflammatory properties. Because BDS are not considered drugs by the Food and Drug Administration (FDA), dissolution profiles are not required and are less available in the literature. Therefore, the purpose of this research was to focus on determining the dissolution profile for two different formulations of açaí capsules. The Fed and Fasted State Simulated Intestinal Fluid (FeSSIF and FaSSIF), simulating physiological conditions of the GI tract, was used to evaluate two different açaí BDS.

For this experiment, the USP dissolution apparatus I (basket) was considered for the dissolution experiment. In order to measure the quality and accuracy of the possible data, the Performance Verification Test was performed using 10 mg prednisone tablets. These tablets were placed in the apparatus with filtered 37 °C water at a speed of 75 rpm for 30 minutes. This experiment was done twice, and the amount of drug released was measured and the absorbance using a UV spectrophotometer was measured. A calibration curve using seven different concentrations of prednisone powder was the reference standard. The geometric mean (GM) and percent coefficient of variation (%CV) calculated were 76.73 and 66.54% when the acceptance criteria were 47-76 and 15%, respectively. The GM was slightly greater than the range given, while the %CV was significantly larger. This shows a high variance between the cells of the apparatus which could be caused by low mechanical calibration. Because of the high variation in the instrument, a shaker was considered for the actual experiment. Shakers have been used for dissolution as well.

The actual dissolution experiment was conducted similarly. Both formulations of açaí capsules were placed in the Fed and Fasted State simulated intestinal fluid media with a pH of 5 and 6.5 and set at the same speed and temperature. The mixtures were on the shaker for 24 hours before samples were taken and analyzed using Liquid ChromatographyMass Spectrometry (LC-MS). They were then cleaned with the different solid phase extraction (SPE) columns to try and find the best method for cleaning out the buffer salts and biomolecules that come from the media.

Fig. 1. Natrol and Nature's Way açaí capsules in the FeSSIF and FaSSIF after being on the shaker for 24 hours.

The samples were the cleanest with the HILIC Tips. Only the anthocyanin, peonidin glucoside, found in açaí was recovered. The chromatograms were still convoluted with proteins, peptides, and salts from the media. The next step for this experiment would be to optimize the cleaning step to better detect other constituents in the capsules. Subsequently, the solubility of the capsules at different intervals will be measured.

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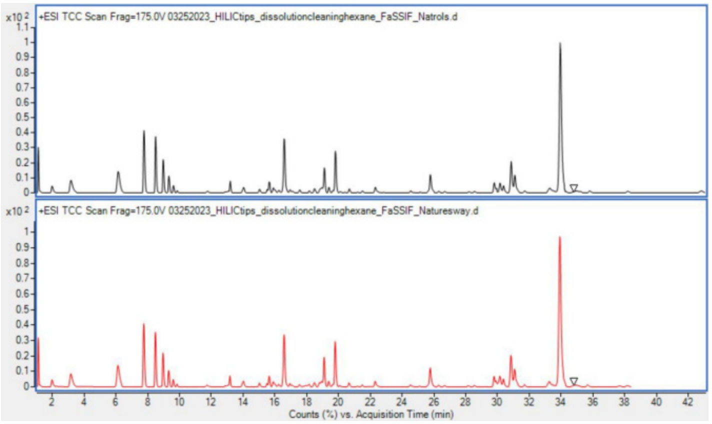

Fig. 2. The chromatograms of Natrol and Nature's Way açaí capsules in the FaSSIF media.

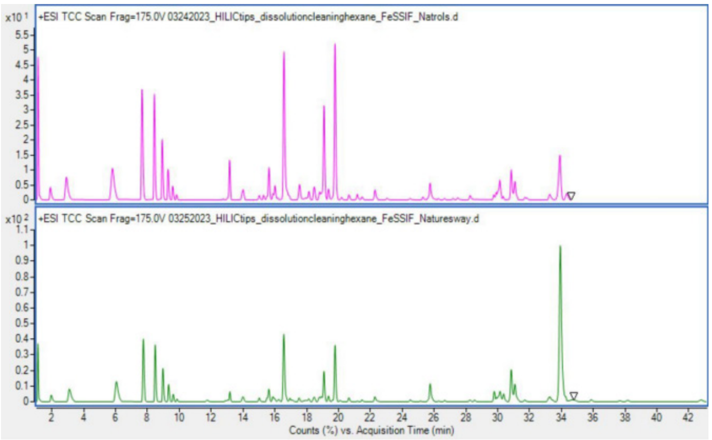

Fig. 3. The chromatograms of Natrol and Nature's Way açaí capsules in the FeSSIF media.

Statement of Research Advisor

Zalaya has contributed to developing an in vitro approach to determine what açaí constituents are dissolved in the gastrointestinal tract and further absorbed. This important approach will help to identify compounds that are responsible for botanical drug interactions.

-Angela I. Calderón, Department of Drug Discovery and Development, Harrison College of Pharmacy

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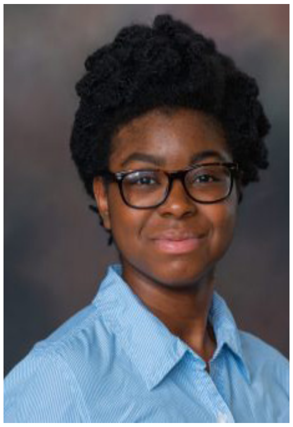
Authors Biography



Zalaya Haynes is a junior-year student pursuing a B.S. degree in Biomedical Sciences with a Minor in Africana Studies at Auburn University. She has played key research roles in researching and developing the protocol for the dissolution experiment. She plans to get into the Harrison College of Pharmacy's Pharm. D. program.

Zarna Raichura is a graduate student pursuing her Ph.D. in Medicinal Chemistry at Auburn University's Harrison College of Pharmacy. She got her bachelor's in pharmacy from Bhanuben Nanavati College of Pharmacy in Mumbai, India. Her research focuses on the possible inhibition of ashwagandha extract on CYP enzymes.

Angela Calderón is an associate professor at Auburn University's Harrison College of Pharmacy. She works in the Drug Discovery and Development Department and her current research deals with evaluating the potential of Ashwagandha extracts to produce CYP-mediated drug interactions and the mechanism of açaí BDS-anticancer drug interaction.

2-Year Student Food Security Module: Cognitive Interviews

Mae Howell[1,], Rita Fiagbor[2], and Onikia Brown[3]*

[1] Undergraduate Student, Department of Nutrition, Dietetics, and Hospitality Management, Auburn University
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[3] Associate Professor, Department of Nutritional Sciences, Auburn University

Food insecurity is the state of being without reliable access to enough affordable and nutritious food to live a healthy and active life (USDA, 2019). The rate of college student food insecurity (<50%), is much higher than the rate of US household food insecurity (11%; GAO, 2018; Coleman-Jensen et al., 2019). Most recently, 35% of surveyed college students were classified as food insecure during the COVID-19 pandemic (Owens,et al. 2020). More research has been reported about college students experiencing food insecurity at 4-year institutions. Thus, the importance of determining and addressing food insecurity at 2-year institutions will add to the body of literature and impact health and societal outcomes.

The project objective is to determine changes that need to be made to the 10-item Food Security Survey Module (FSSM) to be more accurate to college students through cognitive interviews.

Participants were 18-24 years old, enrolled as students at a partnering Alabama Campus Coalition for Basic Needs Junior College/University, and spoke English. Participants completed a demographic survey in which they were to choose a pseudonym and complete the USDA 10-item FSSM module. Students were asked to supply an email address for communication with the student researcher. At the end of the survey, participants were redirected to a calendar system in which they can select a time for the virtual, semi-structured interview. Participants were able to choose their pseudonym to complete the poll. Based on responses from the 10-item FSSM, students will be placed into two categories: food secure and food insecure, before their interview. During the recorded semi-structured, virtual interview, participants were asked questions about the 10-item FSSM. The interviewer read each FSSM questionnaire item out loud and asked the participant to respond using think-aloud, comprehension, retrieval, confidence judgment, and response probes as outlined in Collins (2003). Additional questions were asked for more detailed responses, clarification, or ask what could be modified to capture their experience. Each participant was offered an e-gift card of $25 at the end of their completed interview.

Cognitive interviews were coded via Atlas ti. Themes being coded for included definitions of terms such as “household”, “balanced diet”, and “hungry”. Themes were also coded for the difficulty of each question. The themes picked out through Atlas ti allow for identification of changes that need to be made to the Food Security Survey Module.

Statement of Research Advisor

Mae’s research is focused on determining the appropriateness of food insecurity questions within 2-year college students. This work advances our knowledge of food insecurity in this population and her findings are preliminary to developing a more appropriate and accurate assessment tool. Mae has a sound understanding of community-based participatory research and she presented her research at the Student Research Symposium at Auburn University.
- Dr. Onikia Brown, Department of Nutritional Sciences, College of Human Sciences

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Authors Biography

Mae Howell is a junior-year pursuing a B.S. degree in nutrition- dietetics. She completed cognitive interviews and coded interviews.

Rita Fiagbor is a graduate student pursuing a Ph D. in nutrition. She helped with conducting interviews.

Dr. Onikia Brown is an associate professor in the Department of Nutritional Sciences. She served as a mentor and helped create the study design.

Auburn University Journal of Undergraduate Scholarship

Using Drawing and Representation to Design Nature-Based Infastructure in Coastal Environments

Chase A. Hoytink[1,], Rob Holmes[2]*

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In the face of rising climate change concerns, the use of nature-based infrastructure becomes a promising solution to slow the process of rising sea levels through coastal resilience design [2]. This research explores the transformative role that drawing takes in expressing these solutions. Using softwares such as Photoshop, Illustrator, and Rhino, these drawings help conceptualize infrastructure that focuses on integrating nature-based design into coastal design. The coast is especially vulnerable to climate change. Rising sea levels and infrastructure development cause damage in many coastal communities. Through NOAA ESLR (Effects of Sea Level Rise Program), engineers and landscape architects work together to address sea level rise through a series of nature-based solutions to mitigate those effects [3]. Drawing and digital representation offer a way to visualize what is happening to the coast and develop design concepts effectively [1]. As nature-based infrastructure gains traction as a solution to rising sea levels, focus on drawing and digital representation in the field remains notably underexplored. The objective of this research is to explore digital software, test various ways to set up a drawing, and learn new representational strategies. Four methods are being tested for when it comes to the setup of a drawing. Collages prove effective in representing spatial sequencing and capturing the region's landscape through a series of altered photographs. Ecological Transects cut across various regions across the Fort Morgan Peninsula, displaying landscape elevation, plant communities, and significant site points drawn through technical line work. Typology analysis categorizes the infrastructure of the peninsula, organizing parcels of land from dynamic to fixed, showing the quality of land through a series of technical, yet illustrative drawings. Lastly, perspectives showcase the overall character of the region through a more illustrative lens. Research shows that nature-based drawing plays a crucial role in collaboration, enabling a deeper understanding of the designs.

Statement of Research Advisor

Chase's research into landscape drawing methods has helped our lab get a better understanding of both existing landscapes and nature-based infrastructure concepts for a range of coastal sites in Florida, Alabama, and Mississippi. Landscape architects are increasingly involved in design nature-based infrastructure, and drawing methods are crucial for evaluating the aesthetic dimensions of these new infrastructures, which have the potential to simultaneously support social, ecological, and economic dimensions of coastal resilience. Chase's work engaged multidisciplinary collaborations both within Auburn University and externally with other universities and private consultants – much as all work on nature-based infrastructure is inherently multidisciplinary.

- Rob Holmes, School of Architecture, Planning and Landscape Architecture, College of Architecture, Design, and Construction.

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Authors Biography

Chase A. Hoytink is a junior-year student pursuing a B.S. degree in Landscape Architecture at Auburn University. She has played key research roles in representing nature-based infrastructure

Rob Holmes is an Associate Professor and Undergraduate Landscape Architecture Chair. His research and creative work is primarily concerned with infrastructure design, urbanization, and landscape change. He is a co-founder of the Dredge Research Collaborative, an independent nonprofit organization which aims to improve the design and management of sediment through publications, the DredgeFest event series, and design research.

Auburn University Student's Knowledge about Groundwater

Charlotte A. Jannach [1,] and Ann S. Ojeda [2]*

[1] Undergraduate Student, College of Science and Mathematics, Auburn University
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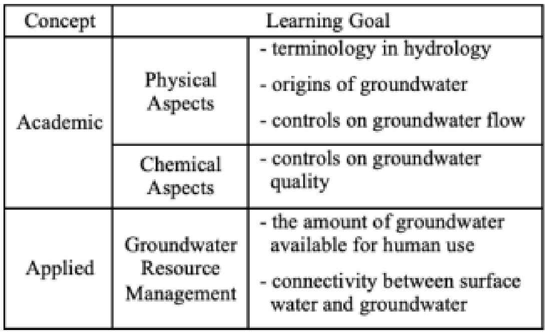
Groundwater is the main source of freshwater consumption for approximately 40% of the United States' population and closer to 50% worldwide (Mandler, 2017). As the demand for freshwater increases, so does the need for protection and management of groundwater resources. Despite its importance, there are many misconceptions and inaccuracies about groundwater in the classroom (Dickerson, 2017) and in the general public (Roche, 2013). A critical aspect to improve groundwater management is to quantify groundwater knowledge and to identify what factors may be affecting this knowledge.

The purpose of this research was to understand the relationship between groundwater knowledge and various factors such as a student's classification, a student's educational experience related to earth science courses, and a student's field of study. To do this, we first designed and implemented a groundwater concept inventory (GWCI) to quantify student's groundwater knowledge. This groundwater concept inventory contained 14 questions that tested concepts related to academic and applied aspects of groundwater knowledge as shown in Table 1.

Table 1. Concepts and learning goals associated with each concept included in the groundwater concept inventory that was used to measure groundwater knowledge.



Concept	Learning Goal	
Academic	Physical Aspects	- terminology in hydrology - origins of groundwater - controls on groundwater flow
	Chemical Aspects	- controls on groundwater quality
Applied	Groundwater Resource Management	- the amount of groundwater available for human use - connectivity between surface water and groundwater

A survey was then created on Qualtrics that included four sections: the groundwater concept inventory, perceptions of water quality, personal experiences, and demographics. The survey was then submitted to IRB for approval (Protocol 22-509). After approval, the survey was deployed by email to presidents of 127 student organizations at Auburn University. The survey was closed after two weeks with 196 total respondents. This sample size was then edited to 156 after removing entries that did not complete all questions.

Rasch analysis was used to validate the GWCI. Briefly, Rasch analysis is a psychometric model that follows item-response theory (IRT). IRT proposes a link between a person's performance on individual items and their performance on the test overall (Hambleton, 1991). Figure 1 illustrates the person ability-item difficulty histogram which is an output of the Rasch analysis. The mean item difficulty (bottom) generally matches the person ability (top) and is one line of evidence that supported an acceptable Rasch model. It is important to note that the mean person ability is set to zero, and the range of the Rasch-adjusted GWCI scores ranges from -4.05 to 4.03.

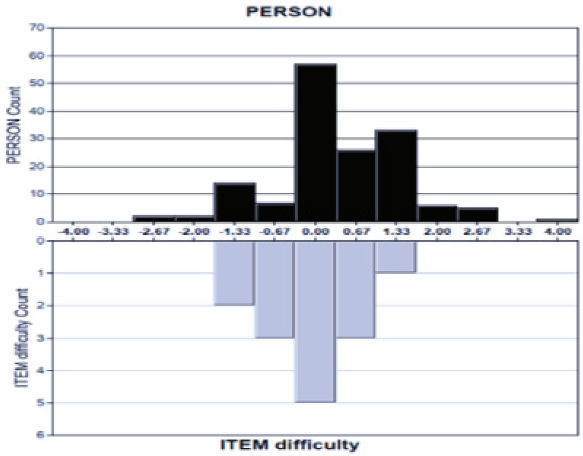


Fig. 1. Person ability-item map for GWCI from Rasch model.

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Here, we focused on four specific factors that we hypothesized would correlate to groundwater knowledge: student classification, field of study, high school Earth Science class experience, and college Earth Science class experience. We hypothesized that 1) upperclassmen will have higher groundwater knowledge scores compared to underclassmen because of more advanced coursework, 2) students from the College of Science and Mathematics will have higher groundwater knowledge scores compared to other colleges because it contains the Department of Geosciences, 3) students who took an Earth Science in college will have higher groundwater knowledge scores compared to those who did not, and 4) students who took an Earth Science class in high school will have higher groundwater knowledge scores compared to those who did not. For each hypothesis, the GWCI scores were extracted for each group and statistically compared as described below.

For hypothesis 1, the effect of student classification on GWCI, the Rasch-adjusted GWCI scores were averaged for freshman, sophomore, junior, and senior student classifications. Analysis of variance and least squares means were used to compare GWCIs as a function of student classification. Our analysis showed there was no statistical difference across the groups proven by a p-value of 0.937. This implies there is no statistical difference in groundwater knowledge as measured by the GWCI across student classifications for this population.

For hypothesis 2, the effect of different colleges on GWCI, the GWCI scores were averaged for each college. If a college did not have a sample size of n>20 it was excluded because of an insufficient number of respondents for the statistical test. The colleges that were included in the analysis were the College of Agriculture, Samuel Ginn College of Engineering, the College of Pharmacy, and the College of Science and Mathematics. Analysis of variance and least squares means were utilized to compare GWCIs as a function of college. Figure 2 illustrates the comparison of the average groundwater knowledge scores between the four different colleges. The College of Pharmacy had significantly lower groundwater knowledge scores compared to the College of Agriculture (p-value of <0.001), compared to Samuel Ginn College of Engineering (p-value of <0.001), and compared to College of Science and Mathematics (p-value of 0.0026). We interpret these differences being related to the curriculum taught in each college. For example, on the College of Agriculture's website a main objective of curriculum listed states, "natural resource conservation and utilization, environmental stewardship, and anticipation of changing climate needs" (Mission Statement, 2023). This focus drives the curriculum to teach concepts related to groundwater like, management and water quality. On the other hand, curriculum from the College of Pharmacy does not contain these concepts that are relevant to groundwater knowledge.

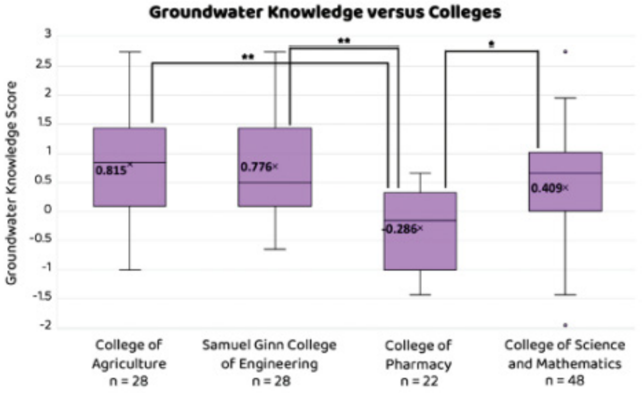

Fig. 2. Comparison of average groundwater knowledge scores between four different colleges at Auburn University. (*p<0.05, **p<0.01)

For hypothesis 3, the effect of an Earth Science course in college on GWCI, the GWCI scores were averaged for either if an individual had taken an Earth Science class in college (Yes) or had not (No). Student's t-test was utilized to compare GWCIs as a function of taking an Earth Science course in college. As shown in Figure 3, students who did take an Earth Science course had a statistically higher GWCI score (0.147 ± 1.023) compared to those who did not (0.395 ± 1.048), proven by a p-value of 0.025. This suggests that taking an Earth Science course in college has a positive effect on groundwater knowledge.

For hypothesis 4, the effect of an Earth Science class in high school on GWCI, the GWCI scores were averaged for individuals had either taken an Earth Science class in high school (Yes) or had not (No). Student's t-test was utilized to evaluate the effect of a high school Earth Science class. It was found there was no statistical difference (p-value of 0.818) between the scores of students who had taken an Earth Science class in high school and those who did not. Potentially, this lack of difference may be due to a deficiency of teaching concepts relevant to groundwater knowledge in high school. In fact, groundwater is not even mentioned in the National Science Education Standards, despite direction to teach the water cycle (Dickerson, 2017).

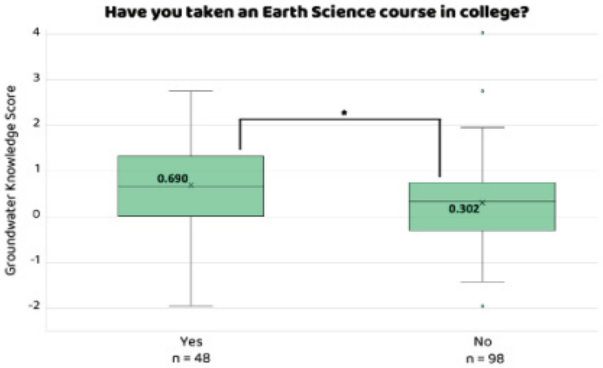

Fig. 3. Comparison of average groundwater knowledge scores between students who did take an Earth Science course in college (Yes) compared to those who did not take an Earth Science course in college (No). (*p<0.05, **p<0.01).

The purpose of this project was to understand the relationship between groundwater knowledge and various factors such as a student's classification, a student's educational experience related to earth science courses, and a student's field of study. A limitation of this project relates to the low sample size from other colleges at Auburn University, and so our current understanding is limited by the population of this survey. Still, our results suggest that other colleges that do not teach curriculum related to groundwater would score similar to students from the College of Pharmacy. Our results support that the GWCI does constitute a valid measurement of groundwater knowledge. Moving forward, the GWCI can be applied to different stakeholder groups (water resource managers, private well users, legislators) that are involved in groundwater decisions and management. Comparing the GWCI scores across these groups can help tailor resources to address misconceptions and ensure decisions are made based on solid foundations of hydrogeology.

Statement of Research Advisor

Charlotte's work has helped to create the first large-scale instrument to measure groundwater knowledge. Constructing and validating the survey involved many iterations and discussions with students, faculty, and professionals both within the world of water resources and outside of it. Ultimately, the GWCI will be a valuable tool as we better quantify groundwater knowledge across stakeholder groups and develop resources to empower sound water management decisions.

- Ann S. Ojeda, Department of Geosciences, Auburn University

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Authors Biography

Charlotte A. Jannach is a senior-year student pursuing a B.S degree in Biomedical Sciences with a Pre-medical concentration. She has worked in the AU Contaminants lab since her freshman year. As a 2022-2023 Undergraduate Research Fellow, she created a survey to quantify groundwater knowledge of Auburn University students dependent on varying factors.

Dr. Ann Ojeda is an Assistant Professor in the Department of Geosciences. Her research is focused in geohealth, primarily in stressors on groundwater quality.

Elucidating the Effect of Reactive Oxygen Species on Confined Cell Motility

WC. Keith [1],*, F. Hemmati[2], F. Amiri[2], P. Mistriotis[3]

[1] Undergraduate Student, Department of Chemical Engineering, Auburn University
[2] Graduate Student, Department of Chemical Engineering, Auburn University
[3] Assistant Professor, Department of Chemical Engineering, Auburn University

Migration is an essential function of many cells for the proper execution of differing physiological processes, including wound healing, proper immune response, and tissue homeostasis[1]. In addition, migration also contributes in the pathologies of diseases; in the typical progression of cancer, metastasis, the process that characterizes the dissemination of cancerous cells from a primary tumor site to the establishment of secondary tumorigenic locations, is defined by the capacity of migratory cells to effectively migrate through differing physiological environments[2].

As the complex nature of tumors makes broad treatment nearly impossible, the prevention of metastasis could provide a way to drastically improve patient prognosis.[3, 4] To be accurately studied, the 3D microenvironment that these migratory cells move through must be replicated in vitro. The channel-like tracks that migratory cells move through range between 3 µm to 30 µm in width and height to 100 µm to 600 µm in length[5]. However, as cells move through these confining spaces, they are subject to differing levels of physical restraint and internal stresses. It has been demonstrated that confinement compromises the nuclear envelope integrity, resulting in DNA double-stranded breaks; studies have suggested that the cause of these DNA double-stranded breaks may be attributed to the diffusion of Reactive Oxygen Species (ROS) across damaged nuclear lamina during NER, but the role of ROS in confined migration remains unclear[6-8].

Using a high-throughput PDMS-based microfluidic model which allows for live-cell imaging during migration, HT-1080 fibrosarcoma cells (cancerous) and fibroblasts (noncancerous) were cultured and seeded into these devices. Cell lines were subjected to both partially(100 μm^2) and fully (30 μm^2) confined channels, and N-acetyl cysteine (NAC), a ROS scavenger, was added to cell culture media at the commencement of each experiment to inhibit the presence of ROS. With HT-1080 cells, we observed that overall migratory speeds increased markedly in response to treatment with NAC in fully confined spaces, while no discernable increase was seen in partially confined spaces. Fibroblasts exhibited slightly increased speeds in confinement, but not significantly so.

The frequency of nuclear blebbing, or bulb like protrusions seen extending from the nuclear lamina, decreased in both cell lines after treatment with NAC in fully confined spaces, again having no effect in partial confinement. The same trend was seen when looking at migratory phenotype; the protrusive phenotype, or the more aggressive migratory phenotype, was seen in higher frequency in full confinement after treatment with NAC. Both nuclear blebbing and cell phenotype were quantified by fixing cells using paraformaldehyde and staining the cells with two fluorescent markers: Hoechst, a marker that emits blue fluorescence upon excitation by UV light after binding to Adenine-Thymine regions of nucleic DNA, and Phalloidin, a peptide which binds to F-actin filaments in cell cytoplasm and emits green fluorescence after UV stimulation.

As nuclear blebbing typically coincides with NER, we transfected HT-1080 and fibroblast cells with a fluorescent reporter which allows for visualization of localized ruptures in real time. Inhibition of ROS markedly suppressed the incidence of NER in fully confined channels, suggesting an increase in cellular ROS levels may affect

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*Corresponding author: wck0016@auburn.edu nuclear lamina integrity. It has also been demonstrated that cell death in long term confinement (~3 days) is markedly suppressed in confined channels after treatment with NAC in fibroblasts.

Our results reveal that not only do ROS play a role in confined cell migration, but their concentration can also modulate migratory cell characteristics. As ROS have been shown to hyperactivate protumorigenic effects in elevated intracellular levels like increased cancer cell proliferation and angiogenesis, ROS have also been shown to induce tumor inhibiting characteristics in high concentrations; prolonged inflated levels of ROS can induce cancer cell death[9]. Better understanding the exact effects of ROS on both cancerous and noncancerous migration is an important step in working towards improving patient care. We hope to continue to investigate the effects of ROS by using a novel fluorogenic probe, CellROX, to visualize the localization of ROS within cells. As the ROS scavenger only had an effect in fully confined channels, we hypothesize that intracellular levels of ROS will be elevated in cells moving through full confinement as compared to cells moving through partial confinement.

Statement of Research Advisor

Collins' research has delineated previously unknown conclusions involving a complicated relationship between reactive oxygen species and confined cell motility. He has independently driven all aspects of this project and his efforts will allow for more in-depth exploration into confined cell migration.
- Dr. P. Mistriotis, Chemiscal Engineering, Samuel College of Engineering

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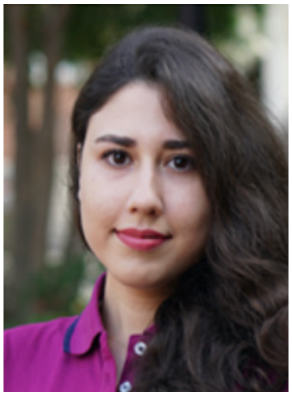
Authors Biography

Collins Keith is a senior in the department of Chemical Engineering at Auburn University. From Birmingham, Collins joined the Mistriotis lab in March of 2021, where he is conducting a project investigating the effects of Reactive Oxygen Species on confined cell migration as an undergraduate research fellow. Collins aims to pursue a M.D./Ph.D. program post-graduation



Farnaz Hemmati received her bachelor's and master's degrees in chemical engineering from the Iran University of Science and Technology (IUST). She has been a Ph.D. student in the Mistriotis Lab since January 2020, her research project focusing on uncovering the role of 3D confinement in cell behavior.

Farshad Amiri is a graduate student in the Department of Chemical Engineering at Auburn University. He received his bachelor's and master's degree in chemical engineering from the University of Tehran, Iran. Farshad joined the Mistriotis' lab in January of 2020 and is interested in combining engineering tools and concepts with advanced cell and molecular biology.

Panagiotis Mistriotis, Ph.D., is an Assistant Professor in the Department of Chemical Engineering and a Ginn Faculty Achievement Fellow in the Samuel Ginn College of Engineering at Auburn University. In his postdoctoral work, which was in part funded by an American Heart Association Postdoctoral Fellowship, he integrated cutting-edge μ-fluidics, imaging, and molecular biology techniques with mathematical modeling to uncover the underlying molecular mechanisms regulating cancer cell locomotion inside confining microenvironments.

An Investigation of the Sweep Effect on Corrugated Wings at Low Reynolds Numbers

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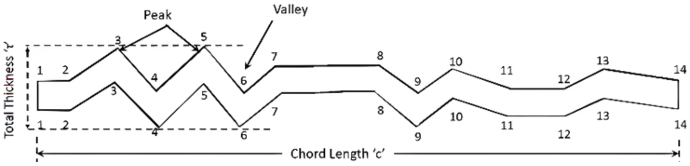
[1]Undergraduate Student, Department of Aerospace Engineering, Auburn University
[2] Graduate Student, Department of Aerospace Engineering, Auburn University
[3]Professor, Department of Aerospace Engineering, Auburn University

Modern-day living has been defined by automation, with more and more work being done by machines: warfare is no exception, wherein a large magnitude of effort is being generated around the globe to reduce the involvement of humans in risky missions. Unmanned Air Vehicles (UAV), also known as Remotely Piloted Vehicles (RPV) and drones have been used over battlefields since the War of Attrition; however, it was only in the past two decades that their use has glaringly been demonstrated during conflicts in Afghanistan, Iraq, and, most recently, in Ukraine. Micro Air Vehicles (MAV) are small UAVs measuring less than 15 cm in any dimension. The size limit directly impacts aerodynamics, requiring the design to be efficient enough to fully use available space while carrying its own weight and having some purposeful endurance. In this regard, nature provides some efficient and unique opportunities: insects use a thin membrane and corrugated-shaped airfoil wings to fly in a low Re regime.

From the aerodynamics point of view, dragonflies exhibit good glide and hover performance, nimbleness, and precision in executing maneuvering flight at a speed of up to 10·m/s with 2g sustainable acceleration and up to 4g instantaneous accelerations. The cross-sectional shape of corrugation in the wing varies in a spanwise direction. These corrugations trap vortices/eddies, helping in lift enhancement and stall delay. Furthermore, the vortices stay anchored in the bottom of the corrugation, shielding the wing from external flow, and consequently helping in lowering the viscous drag. In the year 2000, Kesel extracted three cross-sectional shapes from the dragonfly forewing. This was the Kesel-2 airfoil which serves as a reference for this study and is shown in Fig. 1.



Tests were conducted in the Brown-Kopel Engineering Student Achievement Center and the Davis Aerospace Building at Auburn University. The four models investigated in this research consist of rectangular planform Kesel-2 profile wings with an aspect ratio of two, serving as the baseline. The other models were obtained by introducing a constant sweep of 15, 30 and 45 degrees at the leading edge. The wind tunnel tests were carried out at three Reynolds numbers of 50,000, 75,000 and 100,000. The lift (L) and drag (D) were obtained from the normal (N) and axial (A) forces measured by the force sensor with a simple transformation:

$$L = N\cos\alpha - A\sin\alpha \tag{1}$$

$$D = N\sin\alpha + A\cos\alpha \tag{2}$$

Qualitative flow visualization was conducted in the close-loop water tunnel in the Vortex Dynamics Lab of Auburn University. A fluorescence powder mixed with sugar was deposited over the wing surface and was illuminated with a UV light to observe the flow features as shown in Fig. 2.

The research investigated the effect of leading edge sweep on a Kesel-2 profile corrugated wing having a small aspect ratio. The results show that the introduction of sweep helped delay the stall angle, and as a result, the maximum lift coefficient $C_{L,MAX}$ was also increased. The leading edge sweep without any taper also impacted the stalling behavior by making it sharper

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for the 45-degree sweep. The variance in lift coefficient *CL* showed a more steady lift when Reynolds numbers exceeded 75,000 for higher sweep angles. Flow visualization showed that eddies trapped in the corrugation valleys aided in keeping flow attached over the surface of the wing model, which resulted in a thick, virtual airfoil.

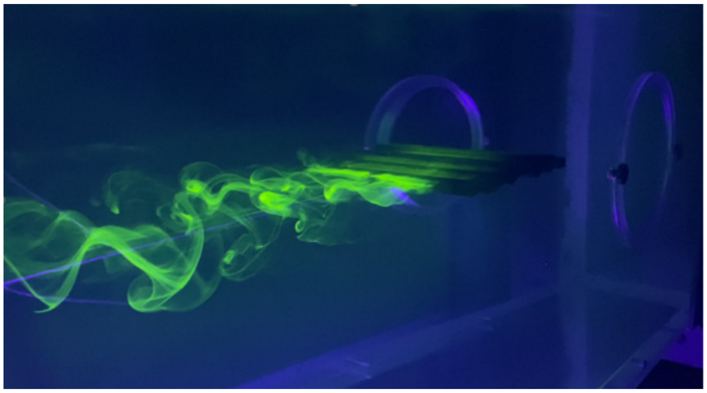

Fig. 2 Water tunnel flow visualization (flow direction from right to left).

Statement of Research Advisor

As a part of Vortex Dynamics Lab, Josh was introduced to and exposed to the fascinating world of Experimental Aerodynamics. During his research he learned to conceive idea through observation of the natural world and transform them into research question and drawing meaningful conclusion from his investigation. He learned to develop an experimental setup, wind tunnel testing to quantify the problem and flow visualization to study the flow physics.

- Syed Hassan Raza Shah PhD Canidate, Aerospace Engineering Department, Samuel Ginn College of Engineering

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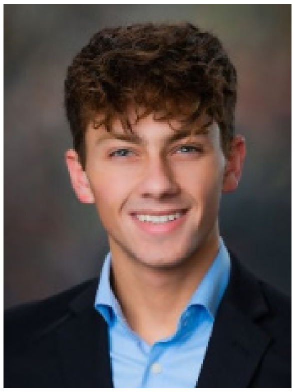
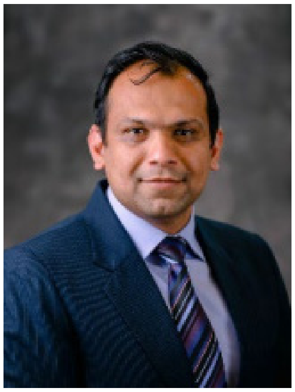
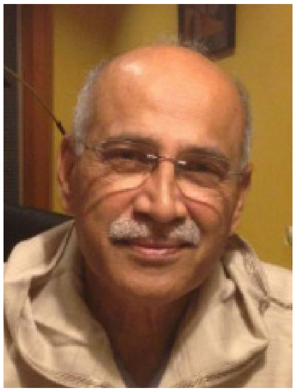
Auburn University Authors and Research Advisor Biography



Kacmarzyk H. Joshua is a senior-year student pursuing a B.A.E degree in Aerospace Engineering at Auburn University. Funded and advised by Dr. Ahmed in the Dept. of Aerospace Engineering, Joshua served as the primary author and was mentored by Dr. Anwar Ahmed and Syed Hassan Raza Shah for guidance and direction of the project and confirmation of results.



Syed Hassan Raza Shah is a PhD Candidate at Aerospace Engineering, Department. His research includes unsteady low Reynolds number aerodynamics and hydrodynamics of vertical axis turbine.



Dr Anwar Ahmed is a Professor at Aerospace Engineering Department. He has a strong background in experimental aerodynamics and fluid mechanics. In addition, he also has experience in laser diagnostics, anemometry, laser doppler velocimetry, PIV, flow visualization, and wind tunnel testing. His research includes aero optics of airborne lasers, boundary layers, viscous drag reduction, vortex-dominated flows, bluff body wakes, and synthetic jets.

Production of Biofuels Through Co-Pyrolysis of Blends of Biomass and Waste Plastics

Ayden J. Kemp[1,] ,and Sushil Adhikari[2]*

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[2] Professor, Department of Biosystems Engineering, Auburn University

In 2021, more than 40 million tons of plastic waste was produced in the United States of America. 34 million tons of which was not recycled or reused and was deposited into landfills or exported out of the country (EPA, 2022). This marks a massive loss of money, energy, and valuable resources from our society. The innate value stored in waste plastics can be reclaimed through either recycling or through various thermochemical processes, such as pyrolysis, which splits plastic polymers into smaller hydrocarbon molecules (Nagarjuna and Shrikanth, 2018). These molecules can then be used as ingredients or reagents for the manufacturing of various value-added products, used for energy production, or refined to produce fuels, lubricants, and asphalt among other products (EIA, 2022). Although some research has been conducted to determine the effectiveness of plastic pyrolysis, little research has been conducted regarding the possible synergistic or antagonistic effects of blending plastics with biomass, which is presently a common feedstock for pyrolysis.

If pyrolysis is to become a widespread waste management solution throughout the United States, it is inherently necessary that it be a cost-effective process. As such, performing co-pyrolysis of blended feedstocks is appealing because municipal waste streams contain various organic and inorganic waste products, and it is both time consuming and expensive to separate these various materials from each other (Burnley, 2007). Co-pyrolysis is the process of performing pyrolysis on mixed feedstocks. It has the potential to produce oil of higher quality than if either feedstock was pyrolyzed individually due to various synergic effects that can occur. If value-added products of sufficient quality and quantity can be achieved at a reasonable cost and energy expenditure through co-pyrolysis of the entire municipal waste stream, the need for landfills and non-renewable petroleum products will simultaneously decrease.petroleum products will simultaneously decrease.

This study investigated the effectiveness of co-pyrolysis of a simplified municipal waste stream modeled by longleaf pine (Pinus palustris) to represent organic waste and polystyrene to represent inorganic plastic wastes. In addition to varying the composition of the blended feedstock, various pyrolysis temperatures, and catalysts were also investigated to determine their respective effects on the yield and energy content of the pyrolysis oil produced.

Three different blends of feedstocks: 100% polystyrene, 100% pine, and 50% polystyrene and 50% pine blend were investigated. Additionally, pyrolysis was performed at three different temperatures: 450°C, 500°C, and 550°C; and with three different catalytic conditions: no catalyst, 10% bauxite residue (red mud) by mass blended with the feedstock, and 10% Zeolite Socony Mobil-5 (ZSM-5) by mass blended with the feedstock.

Polystyrene was purchased from Amazon in the form of clear disposable cutlery and ground into uniformly sized particles using a plastic granulator with a 1/8” screen. Pine was obtained from Auburn University forest tracts and dried, chipped, and ground into uniformly sized particles using a hammer mill with a 1/8” screen. The 50% polystyrene and 50% pine blend was blended on a by-mass basis and blended using an orbital shaker to form a homogeneous mixture.

Red mud was not reduced or calcined and was crushed and sieved through a No. 140 mesh sieve. ZSM-5 was ground into a fine powder using a planetary ball mill and passed through a No. 140 sieve. The catalyst feedstock blends were prepared as a 90% feedstock and 10% catalyst blend on a by-mass basis and blended using an orbital shaker to form a homogeneous mixture.

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A total of 27 experimental trials were performed to allow for each feedstock to be pyrolyzed at each combination of temperature and catalytic activity. Pyrolysis experiments were Auburn University Journal of Undergraduate Scholarship performed in a small-scale fixed-bed pyrolysis reactor at a heating rate of 50°C per minute up to the pyrolysis temperature and with Nitrogen purge gas flowing at 0.75 liters per minute through the reactor tube. The pyrolysis gases leaving the reactor tube passed through a four-unit condenser train sitting in an ice bath and through an electrostatic precipitator operating at 20 kV before being discharged to the atmosphere as seen in Figure 1.

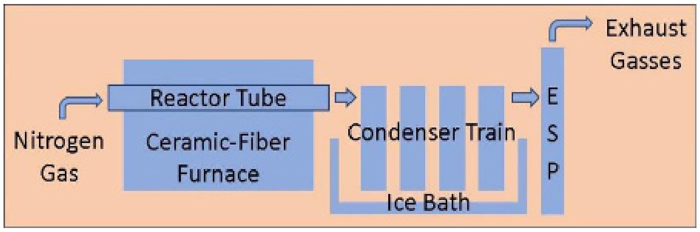


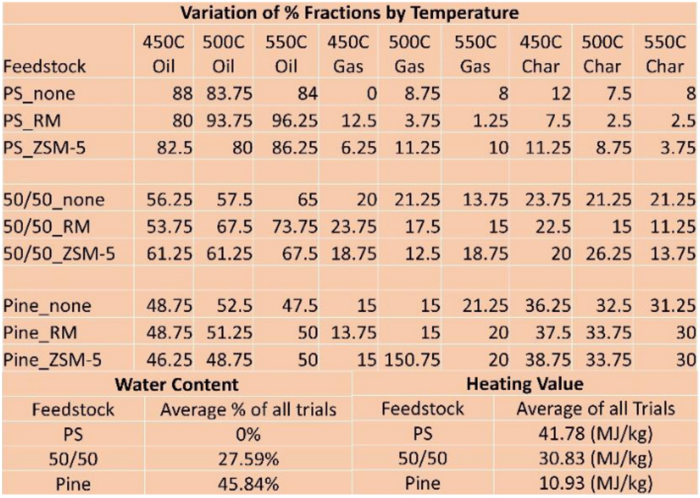
Fig. 1 Model of fixed-bed pyrolysis reactor used in this study.

In each trial without a catalyst, 40.0g of feedstock was loaded into the reactor tube. For each trial containing a catalyst, 44.5g of feedstock blend was used to ensure that 40.0g of the desired feedstock was present at a 90% feedstock to 10% catalyst ratio on a per mass basis. Each trial was run for three hours after reaching the desired pyrolysis temperature to fully pyrolyze all the feedstock in its entirety.

After the reactor had cooled down the percent mass of pyrolysis oil collected and char remaining in the reactor tube were measured and the percent mass of syngas was obtained by the difference. The pyrolysis oil collected was analyzed via Karl Fischer titration to determine the water content, through bomb calorimetry to determine the higher heating value and via gas chromatography-mass spectrometry to determine the chemical composition and hydrocarbon chain sizes of the pyrolysis oil produced.

The summarized results of the 27 trials performed over the course of the experiment are presented in Figure 2. Additionally, from the data collected via gas chromatography mass spectrometry it was determined that the polystyrene containing blends consisted of heavier atoms frequently containing 16 or more carbon atoms and the pine containing blends were composed of lighter aromatic compounds with oxygenated groups. Furthermore, it was observed that oil obtained from pyrolysis performed at higher temperatures and in the presence of catalysts contained more frequent occurrences of smaller and lighter hydrocarbons.

It was concluded that polystyrene pyrolysis produced both the largest oil yield and the pyrolysis oil with the highest energy content. Furthermore, it was observed that higher temperatures led to a higher oil and gas yield in polystyrene containing feedstocks and that 500°C was the optimal temperature for pyrolysis oil production from pure pine feedstocks. When pyrolyzed at temperatures lower than 500°C the pine produced more char and when pyrolyzed at temperatures higher than 500°C the pine feedstock produced larger amounts of gas.



Variation of % Fractions by Temperature

Feedstock	450C Oil	500C Oil	550C Oil	450C Gas	500C Gas	550C Gas	450C Char	500C Char	550C Char
PS_none	88	83.75	84	0	8.75	8	12	7.5	8
PS_RM	80	93.75	96.25	12.5	3.75	1.25	7.5	2.5	2.5
PS_ZSM-5	82.5	80	86.25	6.25	11.25	10	11.25	8.75	3.75
50/50_none	56.25	57.5	65	20	21.25	13.75	23.75	21.25	21.25
50/50_RM	53.75	67.5	73.75	23.75	17.5	15	22.5	15	11.25
50/50_ZSM-5	61.25	61.25	67.5	18.75	12.5	18.75	20	26.25	13.75
Pine_none	48.75	52.5	47.5	15	15	21.25	36.25	32.5	31.25
Pine_RM	48.75	51.25	50	13.75	15	20	37.5	33.75	30
Pine_ZSM-5	46.25	48.75	50	15	150.75	20	38.75	33.75	30

Water Content

Feedstock	Average % of all trials
PS	0%
50/50	27.59%
Pine	45.84%

Heating Value

Feedstock	Average of all Trials
PS	41.78 (MJ/kg)
50/50	30.83 (MJ/kg)
Pine	10.93 (MJ/kg)

Fig. 2 Summarized results of the percent mass fractions of oil, char, and gas (calculated by difference) as well as the water content and heating value of the pyrolysis oils produced.

Red mud increased the oil yield and decreased the char yield of polystyrene containing feedstocks. ZSM-5 increased the gas yield of polystyrene containing feedstocks and decreased the char yield. Red mud had little effect on the pure pine feedstock and ZSM-5 increased the gas yield of pine and decreased the char yield.

Most importantly, it was concluded that blending polystyrene and pine in a 50% and 50% ratio had an antagonistic effect on both the quantity of oil produced and the energy content of that oil. It is likely that some of the high energy content molecules produced by the pyrolysis of the polystyrene was either absorbed by the pine char or further cracked by the catalytic effects of the char into non-condensable gasses. Further study will be required to determine with certainty the exact cause of the decreased yield of the blended feedstocks.

Statement of Research Advisor

Ayden's research was conducted as part of the overall focus of the Center for Bioenergy and Bioproducts at Auburn University. We aim to produce renewable energy, biofuels, and other value-added products from biomass and various waste materials. Ayden's research on the co-pyrolysis of biomass and plastic wastes can be applied at a larger scale to blended waste streams to produce pyrolysis oil from municipal and industrial wastes. This oil could be upgraded or refined into various biofuel or biolubricant products.
- Sushil Adhikari, Department of Biosystems Engineering, College of Agriculture

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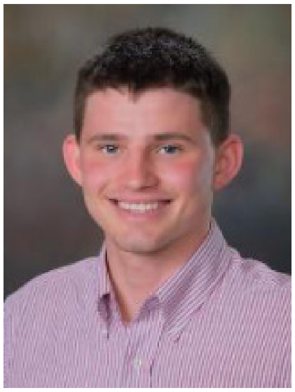
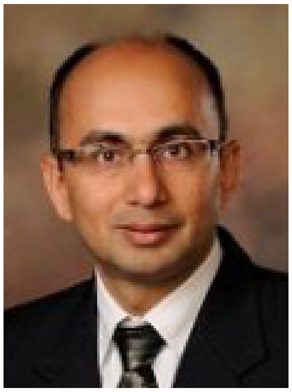
Authors Biography



Ayden Kemp is a junior pursuing a B.S. degree in Biosystems Engineering and a B.S. degree in Aerospace Engineering at Auburn University. His research focuses on pyrolysis of various feedstocks and on catalytic pyrolysis to improve yields and oil quality.



Sushil Adhikari is a professor of Bioenergy and Bioproducts in the Biosystems Engineering Department at Auburn University. He is also the director of the Center for Bioenergy and Bioproducts at Auburn University. He has received numerous awards and honors for both his achievements as a researcher and as a faculty member. His research interests include biomass gasification, biomass pyrolysis, hydrothermal liquefaction, and bio-oil upgrading.

Implementing a Flexible Event Pipeline to Improve User Experience in Sat-Tycoon

Emily Kimbrell[1,*] *and Daniel Tauritz*[2]

[1] Undergraduate Student, Department of Computer Science and Software Engineering Auburn University
[2] Associate Professor, Department of Computer Science and Software Engineering, Auburn University

Satellite Tycoon (Sat-Tycoon) is a multi-player strategy-simulation game where players act as satellite-internet providers. The focus of this project was to implement a flexible event pipeline into Sat-Tycoon. The market of megaconstellations providing internet services is rising and it is challenging to predict what business strategies will succeed in an industry dependent on a variety of physical and economic factors. Sat-Tycoon aims to create a virtual environment where these business strategies can be explored via players' actions. The original mechanics of Sat-Tycoon simulated indirect interactions between players through customer acquisition but lacked complex event scenarios that motivated players with truly challenging and insightful gameplay. The addition of an event pipeline enhances this gameplay by creating more engaging interactions that encourage players to formulate more robust strategies. To model these distinct scenarios, an event pipeline was constructed to generate events based on characteristics such as the duration of the event, the terrestrial region affected by the event, and the type of affected resources. Based on these generated characteristics, the pipeline then utilizes a program to determine which players are affected and carry out the effects of the event. Ultimately, the event pipeline communicates this event's effects to the player(s) so that they can utilize this information to refine their game strategy.

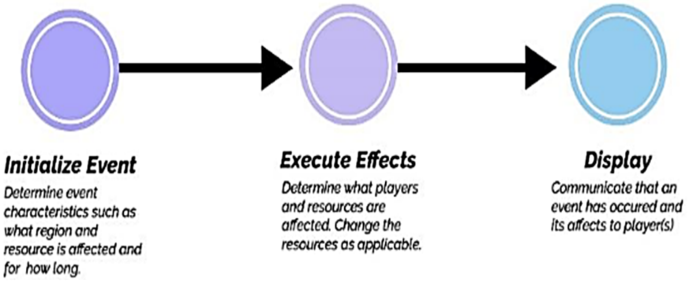


Fig. 1 Illustrates the sequential steps of generating an event in the event pipeline.

A JavaScript Notation Object (JSON), a file structure used to store and format data, was developed to contain the unique characteristics of an event while being abstract enough to simulate other types of events utilizing the same data structure. To determine which abstract characteristics should be specified in this data structure, the team created a list of categories of events that have a substantial impact on a satellite-internet provider's resources, revenue, and the target market's finances; these events included satellite collisions, natural disasters, magnetics storms, launch failures, and cyber-attacks. Considering these types of events, the abstract characteristics relevant in each event were the number of players affected, the type of affected resource, the duration of the event, the probability of the event occurring, and the affected region. A JSON file where each event category contains specific events described with abstract event characteristics. For example, the file contained multiple natural disaster events, some of which simulated earthquakes with varying magnitudes and locations. The JSON file can be expanded to include more variations of natural disasters like tornados and even more categories of events not originally considered.

Sat-Tycoon runs on a concurrent game loop in which variables like population, consumer demand, and players' revenues are updated at a consistent interval throughout the game. Utilizing this structure, a new function was added to roll for active events to create random obstacles in the game environment. At a set frequency, the game loop will generate a random number which will be compared against a particular instance of an event picked from the JSON file mentioned above. If the randomly generated number is less than the probability of that particular event occurring, then the effects of that event will be calculated. A program was developed to pull the characteristics of a particular event from the JSON file and calculate the effects for each

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player based on the event's characteristics. An example would be if an earthquake occurred in India, the program would calculate the distance between each player's ground stations and the location of the earthquake. If the program determined a ground station was in the affected region it would temporarily change the ground station status to inactive therefore this ground station would not be servicing customers and contributing to the player's revenue. Another function was created to handle updating the active events which will check if an event is still affecting the game environment. If the updating active events function determines that an event is no longer affecting the game environment because of the predetermined end date, the function handles reverting the affected resources to their original state if applicable.

Fig. 2. User interface displays which player's ground stations are affected by a natural disaster.

The last step of the event pipeline is communicating changes in events to players so that they can utilize this data to formulate their strategies. Sat-Tycoon had a pre-existing system for updating front-end displays for users. A function was created to compress the active events data to a simplified list. This simplified list of events was sent to the front end where relevant information was extracted and compared to previous events. If the front end detected a new event was added or an event had ended it would send a direct chat to the player notifying them of this change.

Statement of Research Advisor

Emily started contributing to the Sat-Tycoon project in fall semester 2021, focusing on human-computer interaction. In spring semester 2022, she became the lead developer of the graphical user interface, a significant escalation of responsibility. In the academic year 2022-2023, her focus has been on designing and implementing a flexible events pipeline to support environmental events such as natural disasters. Not only has this significantly increased the simulation's realism, it also is an important step toward making the game more fun for humans to player. Emily has engineered the pipeline in a flexible manner to facilitate adding events in future, hence her contributions may be expected to impact this project for a long time to come.

- Daniel Tauritz, Department of Computer Science and Software Engineering in Samuel Ginn College of Engineering

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Authors Biography

Emily Kimbrell is a junior-year student pursuing a B.E. degree in Software Engineering with a minor in statistics at Auburn University. She has been working on Sat-Tycoon for two years where she has played a key role in improving user experience through developing intuitive user interfaces and expanding game mechanics to create an engaging experience for players.

Daniel R. Tauritz is an associate professor in the Department of Computer science and Software Engineering, Interim Director of the Auburn Cyber Research Center, and Director for National Laboratory Relationships in the Samuel Ginn College of Engineering. His research interests include computational intelligence approaches to complex realworld problem solving with an emphasis on national security problems in areas such as cyber security, cyber physical systems, and critical infrastructure protection.

Auburn University Journal of Undergraduate Scholarship

An Analysis of the Effects of *Dobbs V. Jackson Women's Health Organization* On Voter Turnout

Gabriella LaRocca[1,], and Dr. Soren Jordan[2]*

[1] Undergraduate Student, Department of Political Science, Auburn University
[2] Associate Professor, Department of Political Science, Auburn University

Since the Supreme Court decision in *Dobbs v. Jackson Women's Health Organization,* abortion has become a major topic in both federal and state policy. The Supreme Court ruling removed abortion as a constitutional right, opening the floodgates for states to determine their own policies. Previously, abortion did not weigh very heavily as a policy issue, but this has changed since 2022. As states begin to put major restrictive and protective policies in place, the question is how representative are these policies of the populations that they serve?

Earlier polling conducted by the American National Elections Studies (ANES) revealed that prior to 2022, the majority of Americans rated abortion very low as a topic of concern for the United States' (US) government behind issues such as gun control and defense spending.[1] Similar polls in the 1980s showed that the majority of Americans agreed with the legality of abortion "as it is now".[4] However in 2020, an ANES survey showed Americans, while ranking abortion low as a policy issue, still felt that it should only be legal in certain circumstances (rape, incest, etc.).[2]

With the change in Supreme Court rulings, though, comes a change in abortion law. Many states enacted so-called "trigger laws" that immediately set severe restrictions on abortion policy within the state upon recission of the precedent set by *Roe v. Wade and Planned Parenthood v. Casey.* Ostensibly, these policy changes reflect the "will of the people" within the state, whereby more conservative or Republican states could adapt their state-level abortion policy to better represent public opinion on abortion within the state.

This linkage is completely untested, however. We do not know the extent to which changes in abortion policy, generally becoming more conservative, are actually representative of the will of the people who live within a given state. It is wholly possible that state-level legislatures are making restrictive abortion policy that few, if any, individuals in the state actually want. This hypothesis is additionally informed by existing research demonstrating that even the most conservative individuals typically support exceptions for certain circumstances (i.e. cases of rape or incest or when the life of the mother is in danger). These exceptions, however, are not common to all state abortion policy.

This research survey was designed to evaluate attitudes towards abortion across states and how these attitudes have translated into voting behavior. In November of 2023, I recruited a nationally representative sample of 1000 American adults, measuring their attitudes towards abortion generally, the circumstances in which they believed abortion should be permissible, their state of residence, and their perception of abortion policy in their state. Specifically, I asked whether abortion policy in their state triggers common emotional responses of anger and disgust. I measured these attributes on a one to five scale, where one is "does not at all describe my feelings" and five is "strongly describes my feelings." The survey was distributed to a random sample of American adults using the online distributor, Lucid Theorem.

The results revealed a wide range of emotions and responses to the survey with the total sample leaning slightly conservatively but overall being split evenly. Two emotions that the survey specifically probed were disgust and anger toward the individual's state abortion policy. The results were divided between male and female responses displayed in the anger maps seen in Figures 1 and 2. As shown in Figure 1, the majority of female respondents reported a mild level of anger towards their state's abortion policy. Women were angri-

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est, on average, in Arizona, Indiana, and Utah. These states are notable for their abortion policy as they all passed extremely restrictive policies that place the fetus as the sole concern. In Figure 2, the male respondents of these particular states show a deep contrast with each state indicating much lower levels of anger and Utah especially shifted to show no anger. The male map as a whole shows less anger in many states when compared to women with Wyoming being the only outlier. This is extremely relevant in understanding the lack of representation that these policies reflect but also the division between men and women on this issue. With the vast majority of females reporting a mild to severe level of anger, it is clear that most states are not listening to the constituents that are targeted by these policies: women. The data also shows that there is a divide in perspectives based on gender that could be playing a major role in policy decisions as the majority of states have male-dominated state governments.

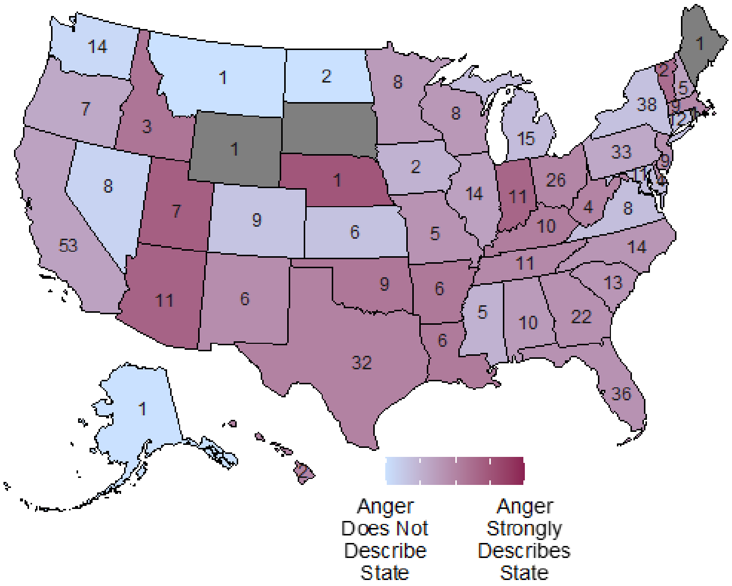

Figure 1. Average Level of Anger Towards State-Level Abortion Policy Among Women in Each State (# = Number of Respondents).

The results of the survey also showed that policies are not appropriately considering circumstances that voters view as acceptable exceptions to abortion restrictions. The leading reason that surveyed individuals gave for an acceptable justification for an abortion was a circumstance in which the woman's health is in danger. However, in states that are more conservative, such as Texas and South Carolina, restrictive abortion policy is being passed with no exceptions for the woman's health.[3] The next leading justification for abortion was in circumstances of rape or incest, which has become a highly contested exception to abortion restrictions. State governments have not appropriately accounted for these situations, and the data has shown that this is an exemption most constituents want in their state policy. The bar graph in Figure 3 reflects the reasons included in the survey in which an abortion would be acceptable and the percentage of total participants that chose each reason. An unexpected outcome from this question was that approximately 40% of participants stated that an abortion should be acceptable for "any reason." While this is by no means a majority, it is a higher percentage than state policies would lead individuals to believe.

Abortion attitudes and policies have been evolving for decades, but the data reveal that currently there is a significant gap between the policies being passed and the emotions of the constituents. The democratic integrity of state abortion policies should be questioned, as data reveals a serious lack of representation for citizens' true attitudes surrounding the issue. While subsequent analysis is necessary, the message is clear that abortion policy is not aligned with the wants and needs of the people to which it applies.

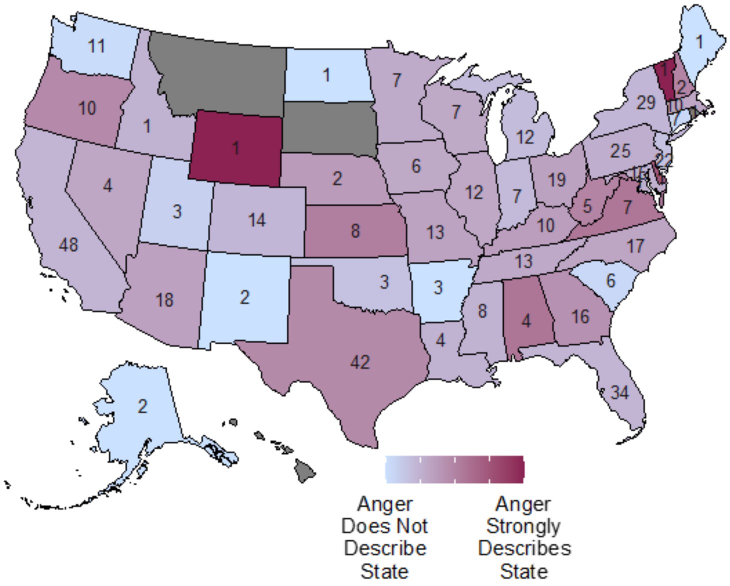

Figure 2. Average Level of Anger Towards State-Level Abortion Policy Among Men in Each State (# = Number of Respondents).

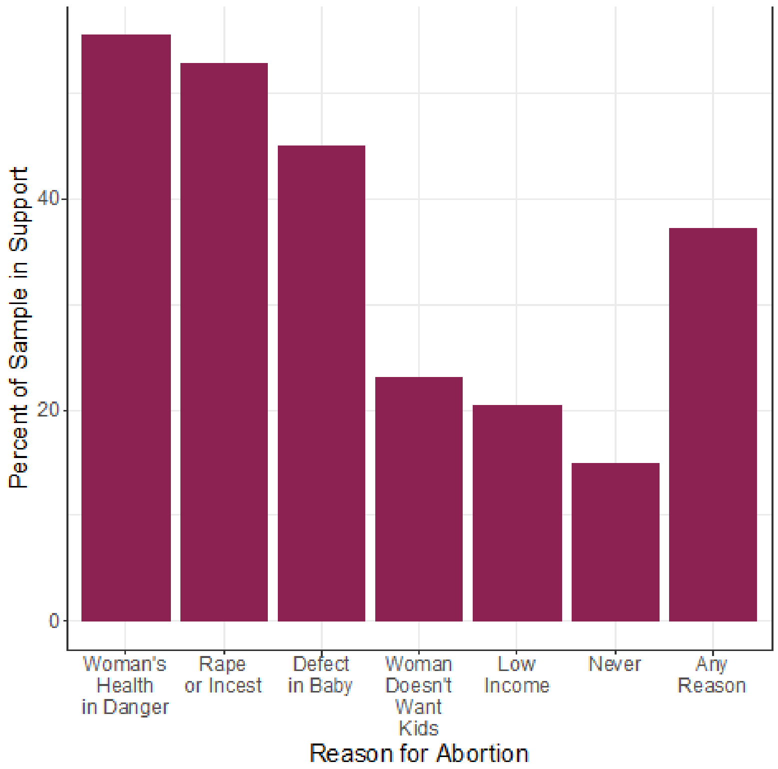

Figure 3. Percent of the Sample Who Believes Abortion Should Be Legal in a Given Circumstance.

Statement of Research Advisor

American abortion attitudes are at an inflection point. *Dobbs*, as a Court decision, serves as an opening for states to create new abortion policy as well as potentially generating a firestorm of criticism about the Court itself. However, we have little to no understanding of how Americans feel about these changes in abortion policy, either at the Court level or within their states specifically. Gabriella's original, poignant research helps address this gap by measuring American attitudes towards state-level abortion policy. This research is essential for our understanding of the extent to which abortion policy is a channel or representation for individuals in states, or if abortion policy showcases a fundamental disconnect between state legislators and their constituents.

- Dr. Soren Jordan, Department of Political Science, College of Liberal Arts

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Authors Biography

Gabriella LaRocca is an undergraduate student in the Department of Political Science who is pursuing a B.A. in political science with a concentration in international relations. She has previously been published as a co-author on a paper studying state investment as a result of the 1996 Safe Drinking Water Act in the American Society for Public Administration's 2023 conference.

Soren Jordan is an Associate Professor in the Department of Political Science and Director of the Ph.D. Program. He received his Ph.D. in Political Science from Texas A&M University in 2015. He studies partisan polarization and party conflict on high-profile social issues.

Analyzing the Infection Efficiency of CLRDV in *G. hirsutum* and *N. benthamiana* by Agroinoculation

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Cotton Leafroll Dwarf Virus (CLRDV) is a newly emerging plant pathogen in the United States and is the causative agent of Cotton Blue Disease (CBD). This virus has been previously described in Africa and South America (Cauquil et al., 1971). CLRDV was first detected in the United States in Alabama in 2017 and has been detected in 11 states across the Cotton Belt. CLRDV mainly infects cotton but has also been detected in 23 different weed species that are commonly found near commercial cotton fields (Sedhain et al., 2021). *Aphis gossypii* (cotton-melon aphid) is a vector for CLRDV and can acquire and transmit this virus within 75 minutes (Heilsnis et al., 2023). Cotton was worth over $346 million dollars in Alabama in 2022 and is the most common fiber utilized in textile manufacturing (USDA 2022). This crop has worldwide importance; therefore, studying CLRDV is a necessary step in preventing its spread and the destruction it may cause.

Viruses are unable to survive without their host and because of this studying them in a lab can be difficult. A copy must be made of the virus so that it can be stored in the lab and easily used in experiments. A CLRDV clone was previously made in Dr. Kathleen Martin's lab at Auburn University. The efficiency of this copy and its rate of infection were characterized in this study.

The CLRDV clone was grown in *Agrobacterium tumefaciens* for one to two days at 28°C. A 10mM MgCl2, 10mM MES buffer was made and the bacteria was mixed into it until an OD of 0.6-1.0 was reached. The solution then sat for one to two hours before the infiltration was completed with a needless syringe. Cotton (*Gossypium hirsutum*) and benth (*Nicotiana benthamiana*) were used in this study. Three replicates of ten cotton plants and two replicates of ten benth plants were infiltrated. For each replicate, for both cotton and benth, two plants were infiltrated with an empty plasmid backbone with no CLRDV insert as a negative control.

After infiltration, the plants were moved to a greenhouse and each replicate was stored in its own mesh cage to prevent infestation from aphids and other insects. After one month, root and leaf samples were collected from cotton and benth, respectively. The samples were stored in 2mL screw-cap tubes and immediately placed in liquid nitrogen. The samples were then stored at -80°C until RNA extraction was completed with a Total RNA Mini Kit (plant) from IBI Scientific. After extraction, RNA was stored at -20°C. Complementary DNA (cDNA) was synthesized using a Verso cDNA Synthesis Kit (ThermoScientific) from the RNA to run detection assays on the samples.

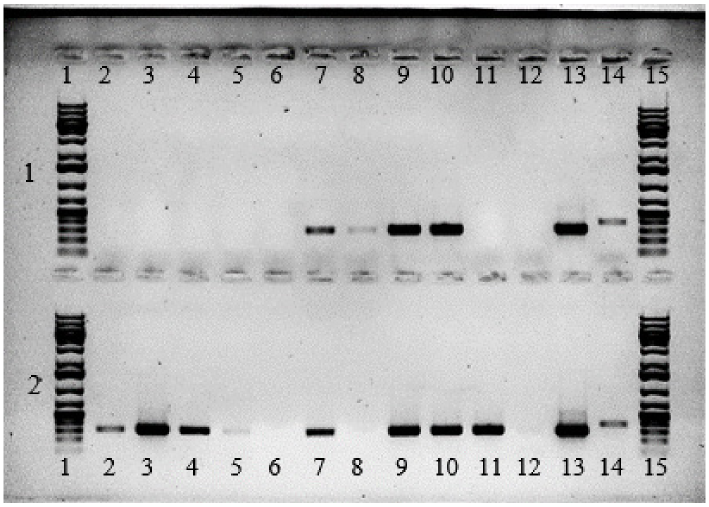

Fig. 1 This image shows a 1% agarose gel after PCR products have been run through it. In columns 1 and 15 on each row is a GeneRuler 1 kb Plus ladder, which helps denote the base pair size of bands in the gel. Columns 2-14 of both the top and bottom of the gel represent test and control samples.

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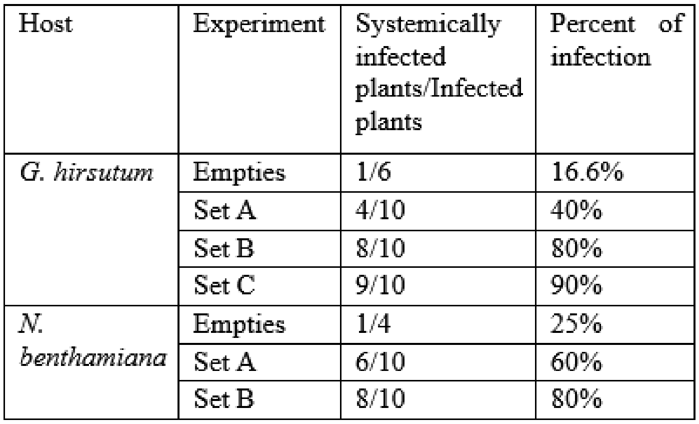
Polymerase chain reaction (PCR) was used to assess the infection status of each plant. A nested detection method, using two rounds of PCR, was utilized for maximum amplification of the products (Mahas et al., 2022). After the second round of PCR, the products were analyzed with a 1% agarose gel. A band with a size of 300 base pairs confirmed CLRDV infection in samples. One negative control and two positive controls were run through the nested detection assays to confirm the PCR. In **Fig. 1**, the first row of samples is acceptable because the negative control, located in column two, does not have a band. The second row of samples is not acceptable because there is a band in the negative control, meaning that the PCR products are likely contaminated. The bands in columns 13 and 14 on both rows are the positive controls that confirm both rounds of PCR were successful.

Table 1 This table represents the results of the nested detection PCRs of the CLRDV clone in both *G. hirsutum* and *N. benthamiana.*



Host	Experiment	Systemically infected plants/Infected plants	Percent of infection
G. hirsutum	Empties	1/6	16.6%
	Set A	4/10	40%
	Set B	8/10	80%
	Set C	9/10	90%
N. benthamiana	Empties	1/4	25%
	Set A	6/10	60%
	Set B	8/10	80%

The accumulated results of the nested detection PCRs are represented in **Table 1**. The rate of infection in cotton ranges from 40-90% but the rate of infection in benth ranges from 60-80%. In the empty samples, there was one cotton plant and one benth plant that each tested positive for CLRDV. All empty samples were expected to be uninfected since they were not infiltrated with CLRDV. Due to these results, work is still being done to confirm the rate of infection of this clone.

Statement of Research Advisor

Rachel has performed key studies to test the infection rate of a cloned version of Cotton leafroll dwarf virus (CLRDV) in *Nicotiana benthamiana* and *Gossypium hirsutum*. Before her contributions, it was difficult to determine the rate in which this viral copy could infect these two plant species. However, Rachel was able to optimize the RNA extractions, clean up both the cDNA synthesis and the PCRs to determine positives and negatives with more accuracy. Rachel's experiments have been critical in determining the differences and similarities of the United States CLRDV compared to the South American strains.

- Kathleen Martin, Department of Entomology and Plant Pathology, College of Agriculture

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Authors Biography

Rachel Livingston is a Senior pursuing a B.S. in Applied Biotechnology. She has been working in the Martin lab since Fall '22 and will continue to work until graduation. Since she began working in the Martin lab, Rachel has discovered an interest in plant pathology and virology and intends on pursuing an M.S. in Plant Pathology as her next challenge.

Dr. Kathleen Martin is an Assistant Professor in the Department of Entomology and Plant Pathology. She started her lab in vector entomology at Auburn in 2019. She works on the molecular aspects of insect transmission of plant viruses in the field. Her work focuses on Cotton leafroll dwarf virus, Soybean vein necrosis virus and Tomato spotted wilt virus. She started working on plant viruses during her Master's program at the University of Arizona and continued to work on viruses that also infect their insect hosts/vectors at the University of Kentucky where she completed her PhD in 2011.

Design and Construction of a Low-Cost Diamond Turning Lathe and Workflow for Ultra-Precision Manufacturing

Cyrus M. Lloyd[1,*], *Nicholas Browning*[2], *Jordan Roberts*[3]

[1] Undergraduate Student, Department of Aerospace Engineering, Auburn University
[2] Undergraduate Student, Department of Mechanical Engineering, Auburn University
[3] Senior Lecturer, Department of Mechanical Engineering, Auburn University

Diamond turning lathes (DTL's) are the state of the art in ultraprecision manufacturing and enable modern high precision mass production. They use monocrystalline diamond cutting tools in conjunction with nanometer precise kinematic frames to machine parts to sub-micron accuracies with optical quality surface finishes, seen in Figure 1. Limitations to the state of the art include cost and inefficient workholding techniques like vacuum chucks. A low-cost diamond turning lathe was developed concurrently with a novel kinematic coupling based workholding system to address these limitations and bring ultra-precision manufacturing capability to Auburn University. The goals for this project included less than 1 μm and 10 nm Ra (roughness average) form and surface roughness tolerances, respectively.

The design of the machine was carried out using principles of precision machine design laid out by Moore [1], Slocum [3], Smith [4], and others. The main subsystems of a two-axis diamond turning lathe are the spindle, the X axis, and the Z axis. To achieve the accuracy required, one must design a system that uses accurate guideways and bearings without mechanical contact between the elements, actuators that do not impart undue influence on these axes, and high-resolution feedback devices.

The opposed-cone air bearing spindle used for the work spindle was generously provided by Professional Instruments Co. (PICo), along with frameless BLDC motor components which were integrated for motorization. Custom hydrostatic bearings in a box way configuration were designed for the X axis, which was driven by an ironless linear motor. This was done in accordance with the theory and procedures laid out by Rowe [2]. A surplus aerostatic stage was used for the Z axis, driven by a unique non-influencing friction bar drive to achieve backlash free coupling with exact kinematic constraint. Both the X and Z axes used Heidenhain LIP-382 linear encoders with Zerodur scales. This enables sub nanometer position feedback resolution enabling ultra-precise servo control of the axes.

Fig. 1. Diamond turning a planar aluminum mirror.

The workholding solution consists of a quasi-kinematic coupling developed to act as a standard zero-point pallet system across machines, seen in Figure 2. A three-toothed coupling with six contact faces at 45 degrees emulates a traditional style of kinematic coupling but provides face-to face contact, significantly increasing rigidity. The loss of ideal kinematic contact is made up for by elastic averaging between faces. Parts can be taken on and off the lathe with sub-micron repeatability with this system, removing the need for manual alignment techniques.

Cost estimation of this design determined it can be manufactured for approximately $75k, a vast cost savings over other commercial options, which start well

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above $100k and can exceed 1 million dollars.

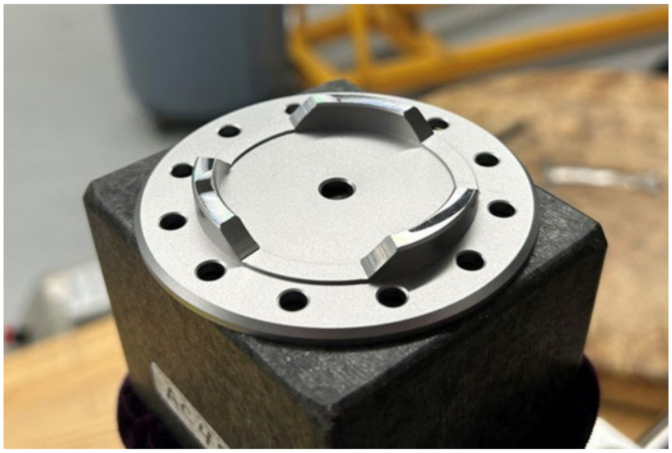

Fig. 2. The quasi-kinematic coupling used to eliminate inefficient workholding practices

The DTL was not only designed by the authors but also constructed, assembled, and tested in-house. Research and development in the field of precision machining was required to accomplish this. Tolerances held on key parts of the lathe, like the hydrostatic bearing components, define the maximum possible geometric accuracy of the machine. Thus, these must be machined to tolerances as tight as the lathe is meant to hold. The X axis guide rail and all hydrostatic bearing components were surface ground flat, square, and parallel to a tolerance of 1μm. A novel method of machining granite to flatness tolerances of less than 2.5 μm was also developed to aid in the construction of the machine base. One of the most critical components from a machining perspective is the flange that the spindle mounts to, as any out of flatness will distort the spindle stator, inducing error motion in the spindle. Using a Dover air bearing spindle, the spindle mount was rotary surface ground to a flatness of 0.5 μm.

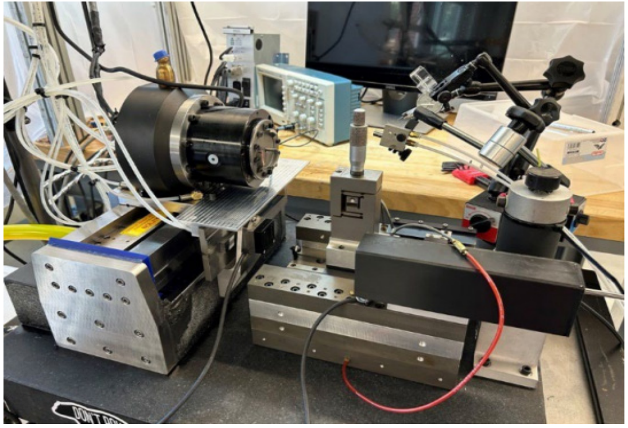

Fig. 3. The completed DTL on a vibration isolation table.

After machining, the DTL was assembled and aligned to similarly tight tolerances. The squareness of the two axes and co-axiality of the spindle to the Z are the most important parameters in this process. The finished lathe can be seen in Figure 3. More accurate mechanical alignment techniques are being developed but there is an opportunity to compensate for these errors in software as well. With these errors removed, the linear positional accuracy of the axes may be <125 nm over the 150 mm travel, the rated accuracy of the LIP-382 scales. Overall machine accuracy would then be thermal growth limited. Currently, the only significant source of heat is the oil hydrostatic bearing system. The nature of the Z drive is inherently thermally isolated, and the absence of high forces or dynamic movement means the Z, X and spindle do not generate appreciable heat on their own. For example, operating at 2000 rpm, the spindle draws ~2 Watts of power. The axes were all controlled via Granite Devices IONI-PRO servo drives. The spindle was run in velocity mode using a 10- bit rotary encoder. The X and Z axis were tuned and run in position control mode. The X axis maintained a position stability of 2 nm or less, while the Z had a positional stability of ~30 nm due to oscillations inherent to the air bearings used.

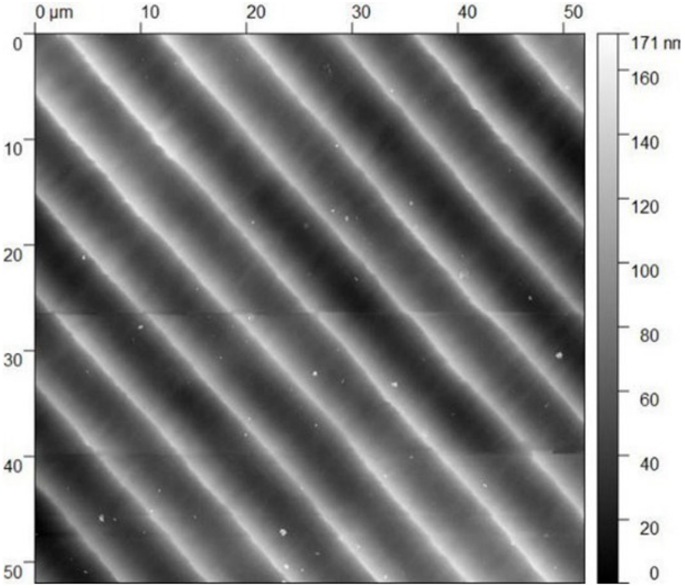

Fig. 4. AFM scan of copper part (500 rpm, 6 μm FPR).

Several test parts were turned using a monocrystalline diamond tool generously provided by Edge Technologies. These were inspected for form and finish via a Fizeau-type interferometry system, and close contact atomic force microscopy (AFM), respectively. As of current, the best finish form achieved is 1.5 μm and the best finish achieved is 14 nm Ra, defined in Equation 1. An AFM scan of one of the test parts can be seen in Figure 4. The pallet system coupling was also tested at this time, the results of which are shown in Table 1. It proved to be repeatable to under 0.5 μm.

$$R_a = \frac{1}{L}\int_0^L Z(x)dx \tag{1}$$

Table 1 Repeatability testing results for quasi-kinematic zero- point system.

Sensitive direction	Average total deviation from 0	Average mount-to-mount repeatability
Tilt	7 μrad (1.45 arcseconds)	---
Radial	423 nm (16.7 μ")	345 nm (13.6 μ")
Axial	523 nm (20.6 μ")	142 nm (5.6 μ")

There is still future work to be completed on the DTL. A control software enabling synchronous real time control of the axes is being developed to enable higher precision motion control and the machining of arbitrary mathematically defined aspheres. This software will also include error compensation features to remove almost all remaining geometric errors and incorporate a thermal error model.

Statement of Research Advisor

Cyrus has designed, manufactured, and verified an ultra- precision diamond turning lathe that is beyond the capabilities of machines currently on campus. The accuracy and precision of the manufactured parts, and their fits are orders of magnitude beyond even good undergraduate machining.

- Dr. Jordan Roberts, Department of Mechanical Engineering, Sameul Ginn College of Engineering

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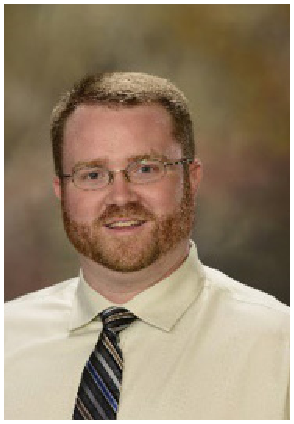
Authors Biography

Cyrus Lloyd is a Senior seeking his bachelor's degree in aerospace engineering at Auburn University and led the design and fabrication efforts for this project. His research interests include rocket propulsion, precision machine design, ultraprecision machining technologies, and all things precision engineering.

Nicholas Browning is a double major in Mechanical Engineering and History at Auburn University. They served as the CAD lead and their research interests include precision engineering, very flat objects, very round objects, esoteric firearms design, the Boer war, the Russo- Japanese war, tank combat, and wetland ecology.



Jordan Roberts, Ph.D. is a Senior Lecturer in the Mechanical Engineering Department at Auburn University. He serves as Director of the ME3D Polymer Additive Laboratory, and the Design and Manufacturing Laboratory, supporting traditional subtractive manufacturing in the ME curriculum and research efforts. He also serves as the faculty advisor to the Auburn Off-Road Team which competes in the BAJA SAE Collegiate Design Series. Teaching at Auburn since 2008, his interests are engineering education, hands on laboratory experiences, manufacturing, additive manufacturing, design for manufacture, materials characterization, and electronics packaging.

Control and Path Planning for an Unmanned Ground Vehicle in Simulation

Wesley Lowman[1,], Chad G. Rose[2], and Vahid Azimi[3]*

[1] Undergraduate Student, Department of Computer Science, Auburn University
[2] Assistant Professor, Department of Mechanical Engineering, Auburn University
[3]Staff Research Engineer, Controls, Gatik

With the prevalence of robotics in daily life expected to only increase, there exists many opportunities for the optimization of robotic system performance. One such area is the control and path planning of unmanned ground vehicles (UGVs). In robotics, path planning is used to generate a trajectory for a robot to move from one point to another in a 3D-reference coordinate system [2]. Essentially, this means creating a program to help the robot determine the most efficient way to travel from one point to another while accounting for all possible variables and obstacles. Control, on the other hand, ensures that the robot finds the most efficient way to remain on the planned path to get there; it acts as a "real-time" calibration method [7]. In addition to optimizing the performance of a UGV, developing and testing control and path planning solutions for it mitigates potential risks associated with both safety and cost.

This study designs a differential drive UGV in SolidWorks™ and configure it into a Unified Robot Description Format (URDF) file, configure a ROS2 package to host all of the project contents, design a simulation environment in Gazebo™, use OpenCV™ to design an overhead camera system with which the UGV will communicate, implement localization, mapping, path planning, and motion-planning programs in Python™, implement control in the ros2_control framework, and evaluate the efficacy of UGV path planning algorithms [3,5]. While the use of tools such as SolidWorks™, MeshLab™, and Blender™ provided a unique interdisciplinary experience in the completion of this project, the primary consideration is the control and path planning of the UGV itself. This study considers a UGV that is required to traverse from a known initial position to a desired target location while also navigating any potential obstacles it faces. For test settings, this study saw the creation of obstacle course environments for the robot to traverse. The first major step in enabling a path planning program for the UGV was to place a camera at the top of the Gazebo™ simulation environment (as shown in Fig. 1) and connect it to OpenCV™, providing the UGV with a utility that functions as a satellite camera.

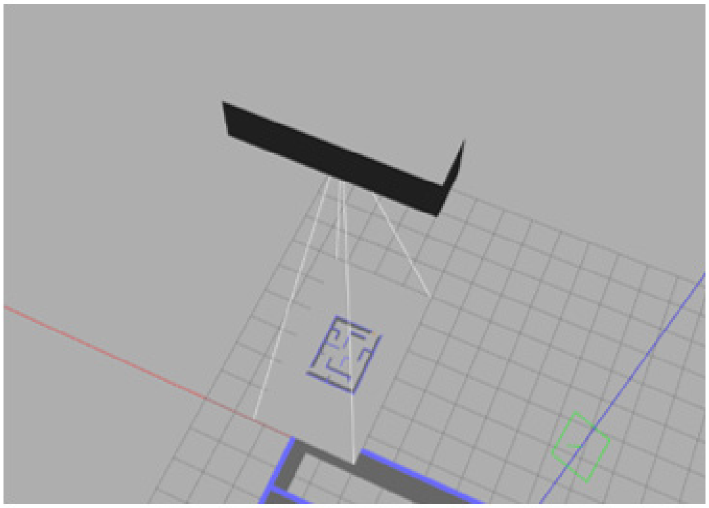


Fig. 1. Example of output from satellite camera inside the Gazebo™ world once OpenCV™ is connected.

After a given simulation environment was prepared, the next major component of the project was using Python™ and ROS2 libraries to develop programs to navigate the UGV. First, a localization program was developed that extracts the mask of all objects in the region of interest in the environment (as shown in Fig. 2) and then localizes the UGV through background subtraction and foreground extraction using an overlay image scan of the environment captured by the satellite camera [4].

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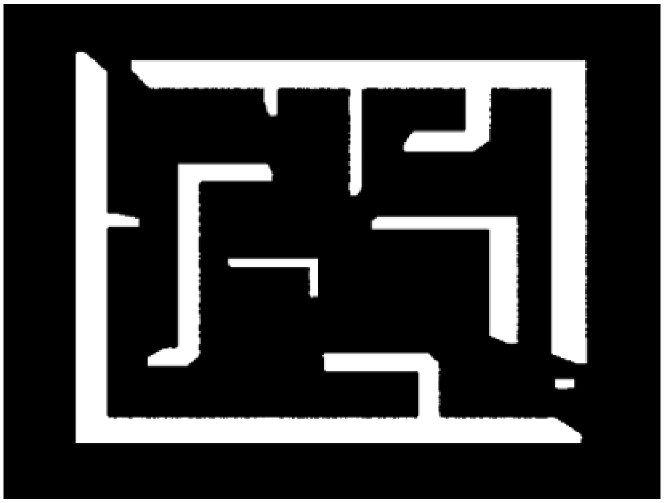

Fig. 2. Example of a region of interest mask output generated by this project's UGV localization program.

After this, this study implemented a mapping program for the UGV that would graphify the map by representing juncture points as nodes and connecting routes to such points as edges (as shown in Fig. 3). The program makes this possible by simplifying the environment itself into a grid and running a one-pass algorithm on itself [6]. The one-pass algorithm scans the grid from left-to-right and top-to-bottom and connects nodes that are neighbors, including all nodes that are connected diagonally.

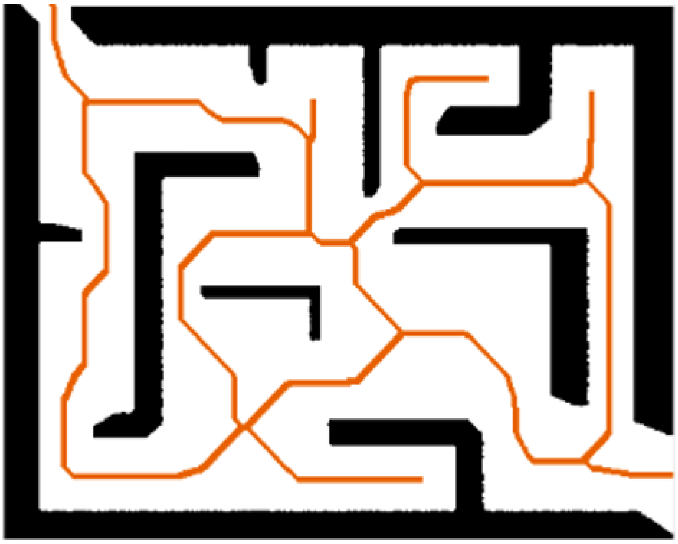

Fig. 3. Example of the map output generated after nodes in the graph of the simulation environment are connected.

Next, this study implemented 9 algorithms, including Dijkstra's algorithm, the A* algorithm, and A* variant algorithms into the UGV's path planning program. All these algorithms have the purpose of finding the shortest path in a graph, whereas the key difference between the Dijkstra's algorithm and the A* algorithm (and its variants) is that A* uses a heuristic function that gives priority to nodes that are more optimal. Last in the programming of the UGV was its motion planning program, which is a ROS2 program that commands the UGV to follow coordinate points on the shortest path (as shown in Fig. 4) generated by the path planning program.

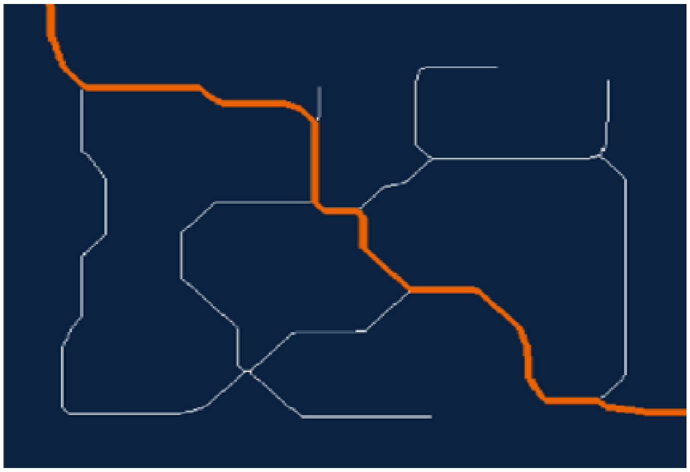

Fig. 4. Example of the shortest path output generated by the UGV's path planning program.

For control, the UGV is using a ROS2 framework known as ros2_control, which has allowed for a custom control system. This was done by creating a custom control file and coding in command interface objects for different joints of the UGV and connecting this file to the UGV's URDF file. All the previously mentioned programs are connected to a central navigator.py program, which is run in the Linux terminal to combine the many project components together; this program also provides a live feed, as shown in Fig. 5.

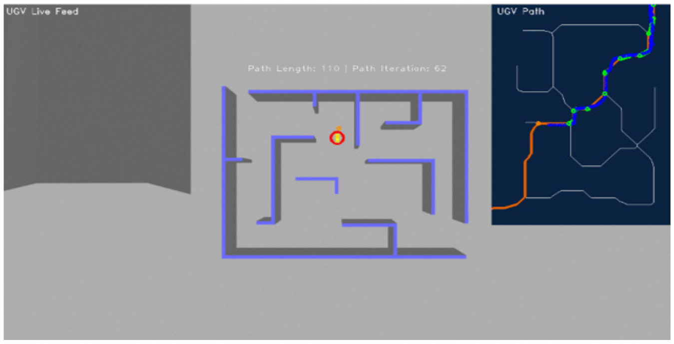

Fig. 5. Example of the live feed output displayed by the UGV's navigator.py program.

This project has already yielded a viable system for the control and path planning of a UGV in a simulated environment. An accurate map, along with a program that generates the most optimal path was developed for a ROS2 UGV. After testing, it is confirmed that the path the UGV follows is both feasible and efficient.

The performance of the UGV in 5 maps of increasing complexity (with each map tested 20 times), based on average values for path length (PL), computation time (CT), nodes visited (NV), smoothness (S), path safety (PS), path continuity (PC), memory usage (MU), path deviation (PD), and search space visited (SV) indicates that, of the algorithms tested, Theta* provides the most efficiency in the navigation of a UGV from a start point to a goal point, as shown below in Table 1 [1].

Table 1: Performance Summary of Path Planning Algorithms

Algorithm	**PL**	**CT (s)**	**$\log_{10}$(NV)**	**S**	**PS**	**PC**	**MU (MB)**	**PD (%)**	**SV (%)**
Dijkstra's	79.35	0.08	2.32	57.99	8.71	33.73	282.69	0.00	98.55
A*	79.35	0.04	2.18	58.11	8.71	33.73	283.38	0.00	76.48
Theta*	79.35	0.03	2.18	58.11	8.71	33.73	283.55	0.00	76.48
Beam Search	79.35	0.03	2.32	58.11	8.71	33.73	283.74	0.00	99.32
Weighted A*	79.35	0.03	2.18	58.11	8.71	33.73	283.93	0.00	76.48
Iterative Deepening A*	79.35	24.81	6.91	57.72	8.71	33.73	285.60	0.00	100.00
Bandwidth Search	79.35	0.03	2.32	57.99	8.71	33.73	286.11	0.00	98.55
Bidirectional Search	91.64	0.06	2.25	67.59	8.12	39.39	286.59	12.45	86.81
Ant Colony Optimization	89.60	0.77	4.97	70.20	8.56	36.65	288.33	10.44	100.00

Future work includes the validation of the efficacy of path planning algorithms tested in simulation by testing them with a TurtleBot 4 lite robot. In summary, this work will lead to results that will allow researchers to answer questions related to the validity of path planning algorithms in both simulation and the real world.

Statement of Research Advisor

Wesley's independent investigation into path planning algorithms, as well as the development of a simulation environment, used industry standard tools and approaches which make the results generalizable and interesting to the robotics community. The entire project has been self-motivated, independent, and high-quality.

- Dr. Chad G. Rose, Mechanical Engineering, Samuel Ginn College of Engineering

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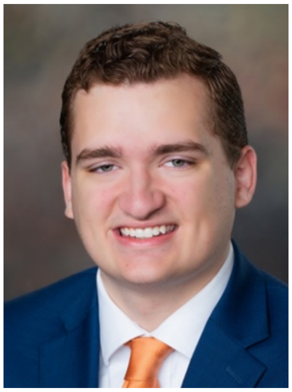
Authors Biography



Wesley Lowman is a junior-year student pursuing a B.S. degree in Computer Science at Auburn University. He has designed, developed this entire project. He specializes in algorithmic design, the primary focus of this project, but he also completed all mathematical and mechanical design components of the project as well.

Chad G. Rose, Ph.D. is an Assistant Professor in the Department of Mechanical Engineering. He holds a B.S. from Auburn University, with M.S. and Ph.D. from Rice University, all in Mechanical Engineering. Dr. Rose's research focus is on the design and control of robots to rehabilitate, augment, or assist human sensorimotor function.

Vahid Azimi received the M.Sc. and Ph.D. degrees in electrical engineering from the Georgia Institute of Technology in 2020. From 2020 to 2021, he was a Postdoctoral Research Fellow at Stanford University. From 2021 to 2022, he was an Assistant Professor at Auburn University. His research interests include robotics and autonomous driving. He is currently a Staff Research Engineer at Gatik, an autonomous driving company.

Functional genetic analysis of Single Nucleotide Polymorphisms in drug metabolism genes

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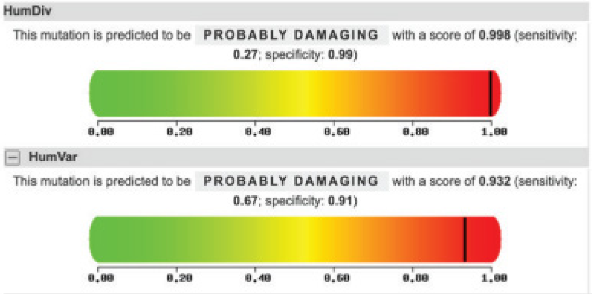
Single Nucleotide Polymorphism (SNP) is a variation of a nucleotide at a single position in a DNA sequence. Certain SNPs are associated with disease and can be used to provide a better understanding of how mutations affect function in the body [1]. One of the major causes of inter-individual differences in drug effects is genetic variations in drug metabolism enzymes (DMEs) [2]. Certain mutations could lead to the development of adverse drug reactions, caused by the change in efficacy or toxicity of the drug. Having this genetic information will aid in prescribing the best treatment for a beneficial outcome while also avoiding unwanted effects in a particular patient in a timely manner (also known as Precision Medicine)[3]. The objective of this research is to understand the pharmacogenomic biomarkers underlying variable drug response and differences in drug metabolism genes. Our SNP discovery work focused on the Indian subpopulations that have not yet been explored. Mutational analysis was conducted to find the most damaging mutations. This determined the SNPs that would be most effective to study for functional analysis using bacteria transformation. The results of this research will help in understanding how different sub populations compared to that of the original Human Genome Project results. Furthermore, it will attempt to explain how these genetic differences can affect disease predisposition, drug reactions, and metabolism.

This project's aims are broken down into two main phases. In **Phase 1**, genotype and allele frequencies were calculated from the sequencing data that has been previously generated by the Mitra Lab. In **Phase 2**, the mutation types (coding or non-coding regulatory SNPs) and resulting amino acid changes were evaluated using databases like National Center for Biotechnology Information (NCBI) and Ensembl. SNPs were then shortlisted for functional analysis based on the predicted effect on protein function using PolyPhen-2.

The results of this research will help in understanding how these genetic differences can affect drug metabolism and treatment outcomes, and also allow us to explore population differences in DMEs.

Following SNP discovery and validation in two separate datasets, information about each SNP's gene, chromosome position, alleles, clinical significance, gene consequence, flanks, and aggregate allele frequencies was collected from the NCBI SNP database (https://www.ncbi.nlm.nih.gov/snp/). The allele frequencies from reported SNP data were also calculated. The potential damaging effects of each SNP were evaluated using SIFT Prediction data (https://sift.bii.a-star.edu.sg/www/SIFT_dbSNP.html) and HumDiv and HumVar models from PolyPhen-2 data (http://genetics.bwh.harvard.edu/pph2/).



This mutation is predicted to be PROBABLY DAMAGING with a score of 0.998 (sensitivity: 0.27; specificity: 0.99)

This mutation is predicted to be PROBABLY DAMAGING with a score of 0.932 (sensitivity: 0.67; specificity: 0.91)

Fig. 1 Polyphen-2 data on SNP rs28399434 in CYP2A6, a drug metabolism gene.

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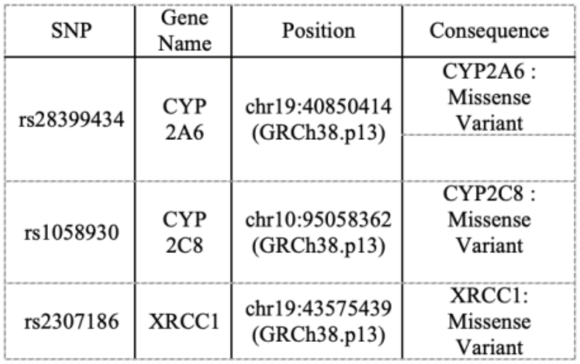
Information gathered about the genes associated with the listed SNPs includes drug label annotations and clinical annotations from PharmGKB (https://www.pharmgkb.org/). PharmGKB data included drug molecules and phenotypes already associated with the SNPS. If available, CPIC guidelines were noted (https://cpicpgx.org/). Finally, the genes were searched on GeneCards for more information about drugs already associated with the SNPs (https://www.genecards.org/). The reference sequence of each gene was found using NCBI gene data (https://www.ncbi.nlm.nih.gov/snp/). Each gene was then annotated to find the start of the gene, the exon positions, and the mutation positions.

A condensed list of SNPs was created and was used for the focus of further study [4, 5]. The SNPs were chosen based on damaging HumDiv and HumVar models, as well as deleterious SIFT predictions. The allele frequencies were also considered when creating the condensed list. In addition, the importance of the gene that the SNP references were considered based on its relation to drug metabolism and other cellular mechanisms like DNA damage repair pathways [6].

Table 1 Information about SNPs chosen for further research.



SNP	Gene Name	Position	Consequence
rs28399434	CYP 2A6	chr19:40850414 (GRCh38.p13)	CYP2A6 : Missense Variant
rs1058930	CYP 2C8	chr10:95058362 (GRCh38.p13)	CYP2C8 : Missense Variant
rs2307186	XRCC1	chr19:43575439 (GRCh38.p13)	XRCC1: Missense Variant

All PCR were carried out using reagents from New England Biolabs (New England Biolabs, Ipswich, MA, USA). A 25 µL reaction mix was made by adding 2.5 µL 10X Taq Buffer, 1 µL dNTP solution mix, 1 µL forward primer, 1 µL reverse primer, 0.5 µL Taq DNA polymerase, 100 ng DNA sample, and 17 µL purified water. The optimal annealing temperature was predicted by inspecting the GC content of the primer sequence to determine the melting point of the primers. A gradient was chosen to include the estimated optimal annealing temperature and temperatures above and below the estimated optimal annealing temperature. The initial denaturation step was at 95 °C for 7 min and 34 cycles of PCR consisting of denaturation at 94 °C for 30 sec. For primers used in the present reaction, an annealing temperature gradient was made using temperatures of 57 °C, 57.9 °C, 59.2 °C, and 61.1 °C. The rest of the cycling PCR reaction had an extension step at 72 °C for 45 sec for 30 cycles, and a final extension step at 72 °C for 7 min.

The reaction mix for the PCR was prepared the same as in the Gradient PCR above, adjusting the annealing temperature to 57.9 °C. Reaction mixes were also made for various multiple myeloma cell line DNA samples including U266P, JIM3, U266VR, RPMI8226VR, MMISVR, and UTMC2.

Bidirectional DNA sequencing was performed on SeqStudio Genetic Analyzer System with SmartStart (Applied Biosystems, Foster City, USA). The DNA samples were cleaned and prepared using 2 µL ExoSAP-IT (Thermo Fisher Scientific, Waltham, MA, USA) and 5 µL of the sample. The sample was incubated at 37° C for 4 minutes, 80° C for 1 minute, and held at 4° C. The cycling sample was prepared using 3.5 µL purified H2O, 2 µL BigDye Terminator, 1.5 µL BigDye Buffer, 1 µL primer, and 2 µL cleaned PCR sample. The samples were mixed and thermal cycling was run. After the cycling was completed, 45 µL SAM solution, 10 µL of XTerminator solution, and 10 µL of the cleaned sample was added to the well. The plate was sealed and vortexed for 30 minutes at 2000 speed. The plate was then centrifuged for 2 minutes at 2000 RPM. Sequencing results were exported and viewed using DNASTAR software (DNASTAR, Madison, WI, USA).

Bioinformatics analysis was done to analyze the frequencies of the SNPs between different Indian subpopulations. The first SNP analyzed was rs28399434, which was the original CYP2A6 mutation that was predicted to be damaging within a population and an individual. SNPs rs4997557 and rs8192730 were other mutations found after sequencing that warrant further research.

The results obtained from this dual-staged SNP exploration study exemplify the uniqueness of the Indian subpopulation clusters with respect to certain mutations, genotypes, and allele frequency patterns. It also shows the variation between different subdivisions of the country. These findings underscore the fact that the Indian population must be investigated for its plausible existence as a separate entity from the commonly inferred major global population clusters. The data generated from this study may have wide-ranging applications for further epidemiological and public health-related research on the Indian population.

In addition, several SNPs within our genes of interest show a predicted damaging effect on an individual and require functional validation within in vitro models, that we plan to do next using myeloma cell lines mentioned above. Continued research will include site-directed mutagenesis and transfection into mammalian cells. Additionally, these mutations may affect drug metabolism and require further functional study using a reference in-vivo model system.

Statement of Research Advisor

Katie's research involves the functional analysis of key drug metabolizing gene mutations using two parallel approaches: Bioinformatic analysis of high-risk variations, and recombinant DNA technologies. We are planning to further this work with a particular focus on world populations and under-served subpopulations.
-Amit K. Mitra, Harrison College of Pharmacy

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Authors Biography

Katherine G. Marlow is a junior-year student pursuing a B.S. degree in Genetics at Auburn University. She has played key research roles in understanding pharmacogenomic biomarkers in drug metabolism genes and DNA repair genes.

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Understanding the Association of CYP2A6 Gene Variations with Drug Resistance in Prostate Cancer

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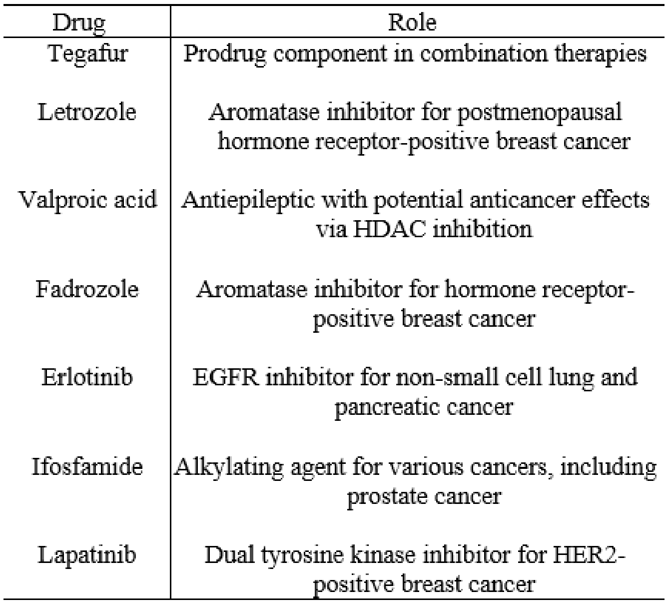
Pharmacogenomics is an emerging field of study that focuses on investigating the genetic basis of inter-individual variations in drug response, specifically linked to Single Nucleotide Polymorphisms (SNPs). SNPs are genetic variations/mutations at a single base position in a DNA sequence and are the most common type of genetic variation. Certain SNPs within drug metabolism enzymes (DMEs) could lead to the development of adverse drug reactions or toxicity following drug treatment, which we aimed to investigate [1]. Prostate cancer (PCa) is the second leading cause of cancer-related deaths among men in the US [2]. Treatment options for mCRPC patients are docetaxel or cabazitaxel (types of chemotherapy drugs) alone or in combination with other drugs or immunotherapy. However, it is typical that these chemotherapy drugs only slightly improve survival by 3-4 months in patients, often resulting in more aggressive variants of aggressive or lethal PCa [3]. Certain mutations in drug metabolizing enzymes (DMEs) could lead to the development of adverse drug reactions, caused by the change in efficacy or toxicity of the drug. Having this genetic information will aid in prescribing the best treatment for a beneficial outcome while also avoiding unwanted effects in a particular patient in a timely manner [4]. CYP2A6 enzyme is responsible for metabolizing a wide variety of drugs, including anti-cancer agents (Table 1). Discerning genetic diversity within the CYP2A6 gene may provide a unique resource in understanding the population-specific role of SNPs in drug resistance within prostate cancer, including aggressive PCa forms metastatic castration resistance PCa (mCRPC). Previously, we used DNA samples from ~2000 healthy individuals from >50 sub-populations across the world and performed targeted exon sequencing followed by multiple sequence alignment and bioinformatics analysis and identified several potentially relevant SNPs within CYP2A6.

Table 1. Anti-cancer drugs potentially metabolized by CYP2A6.



Drug	Role
Tegafur	Prodrug component in combination therapies
Letrozole	Aromatase inhibitor for postmenopausal hormone receptor-positive breast cancer
Valproic acid	Antiepileptic with potential anticancer effects via HDAC inhibition
Fadrozole	Aromatase inhibitor for hormone receptor-positive breast cancer
Erlotinib	EGFR inhibitor for non-small cell lung and pancreatic cancer
Ifosfamide	Alkylating agent for various cancers, including prostate cancer
Lapatinib	Dual tyrosine kinase inhibitor for HER2-positive breast cancer

Our overarching goal is to identify prostate cancer cell lines displaying variable responses to primary anti-cancer drugs. This critical step lays the foundation for understanding the interplay between genetic variations and drug sensitivity, paving the way for personalized therapeutic approaches. A key aspect of our study is to discern the association between cytotoxicity and the presence of functionally important CYP2A6 SNPs. By honing in on this specific gene, we aim to unravel its

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role in mediating drug response and potentially identify novel targets for therapeutic interventions.

Commencing our study, a thorough bioinformatic analysis was executed to discern patterns and potential functional ramifications of previously identified SNPs. This initial computational analysis laid the foundation for subsequent investigations, providing a comprehensive map of genetic variations within the prostate cancer context. Expanding our analytical scope, SNPs were selected based on their predicted impact on protein function. Additional SNPs were included based on their predicted effect on protein function using SIF and PolyPhen. So far, we have identified nine SNPs within CYP2A6 in several world subpopulations. Bioinformatics analysis revealed that several of these SNP may be deleterious in effect, including rs4997557 and rs8192730.

Next, we used a panel of prostate cancer cell lines, spanning a spectrum of aggressiveness, which were cultured and subjected to cytotoxicity assays using standard-of-care drugs (Fig. 1). To quantify the cell viability and response to standard-of-care drugs from the in vitro cytotoxicity studies, we utilized the MTT assay. The MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay is a widely used colorimetric assay employed in cellular and molecular biology to assess cell viability and proliferation. This assay is based on the reduction of the yellow tetrazolium salt MTT by mitochondrial dehydrogenases in metabolically active cells, producing a purple formazan product. The intensity of the color is directly proportional to the number of viable cells [5].

In our upcoming phases, we plan to employ quantitative PCR (qPCR) with TaqMan gene expression assays to correlate CYP2A6 gene expression with drug response in wild type and mutant prostate cancer cell lines.

TaqMan assays utilize a fluorogenic 5' nuclease probe that is specific to the target gene of interest. These probes are designed to anneal to the target sequence during the PCR amplification process. The 5' nuclease activity of Taq DNA polymerase cleaves the probe, releasing a fluorescent signal that is proportional to the amount of amplified DNA [6]. This real-time quantitative PCR (qPCR) technology allows for the accurate quantification of gene expression levels, enabling researchers to analyze changes in gene expression under different experimental conditions or in response to various treatments This advanced molecular technique will allow us to delve deeper into the mechanistic underpinnings of drug sensitivity, providing valuable information for the development of targeted therapies.

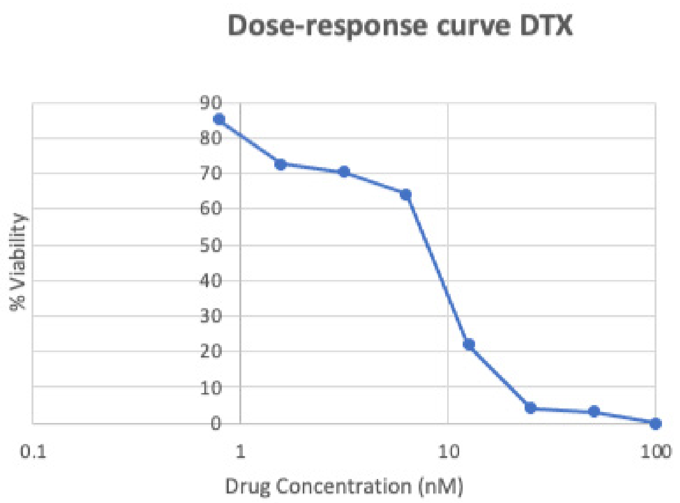

Figure 1. Dose-response curve illustrating the pharmacological effect of Docetaxel across a range of concentrations in DU145 PCa cell line.

As our study progresses, the integration of diverse methodologies and comprehensive analyses promises to unravel the complexities of prostate cancer genetics, ultimately contributing to the advancement of personalized medicine in the field of oncology.

Statement of Research Advisor

Katie's research involves the functional analysis of key drug metabolizing gene mutations using a combination of several dry-lab and wet-lab approaches: Bioinformatic analysis of high-risk variations, drug sensitivity studies and molecular biology-based validation of top SNP biomarkers. We are planning to further this work with a particular focus on world populations and under-served subpopulations.

- Amit K. Mitra, Harrison College of Pharmacy

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Authors Biography

Katherine G. Marlow is a senior-year student pursuing a B.S. degree in Genetics at Auburn University. She has played key research roles in understanding pharmacogenomic biomarkers in drug metabolism genes and DNA repair gene

Abigail Weir is a senior-year undergraduate pursuing a B.S. degree in Biochemistry at Auburn University. She has performed mutational analysis of mutations in DNA repair genes such as LIG1 and MSH2.

Razan Waliagha is a current third year dual degree PharmD./PhD. student at Auburn University Harrison College of Pharmacy. Her current work involves understanding the novel mechanisms of resistance to anti-cancer therapis in solid tumors.

Dr. Amit K. Mitra is an Assistant Professor at the Harrison College of Pharmacy at Auburn University. He is also the founding Director of the Center for Pharmacogenomics and Single-Cell Omics (AUPharmGx). Dr. Mitra's current research involves integrating single-cell multi-omics with in vitro drug

response modeling, and functional genomics with translational bioinformatics to investigate inter-tumor and intra-tumor (subclonal) heterogeneity to drug response in human cancers.

Auburn University Journal of Undergraduate Scholarship

Recruitment in a Pediatric Wellness Initiative, Nutrition Wellness

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[2] Managing Director Nourish Welness, Hunger Solutions Institute, Auburn University,

Minority individuals, particularly children, are disproportionately confronted with an increased risk for obesity, diabetes, and other chronic illnesses (Price et al., 2012). The healthcare system plays a critical role in treating and managing chronic disease. However, healthcare reach and access remain limited. Nourish Wellness is a flexible, clinical- community pediatric wellness initiative in a community- based clinical setting. Nourish Wellness partners with adolescents and their families to impact health routines, patterns, habits and long-term health. For this specific study, the objective was to describe participant recruitment for the clinical community-based pediatric wellness initiative. Those with eligibility for the program included individuals ages 5 to 16 years who have conditions or are at risk for conditions related to obesity, hypertension, and type two diabetes. Convenience sampling was conducted by primary care physicians, school nurses, and school counselors. Anthropometric and clinical measures were implemented for both patients and caregivers. Validated questions included a brief interview checklist that documented quality of life, demographics, and past/ current medical history of each participant and caregiver. Statistical analysis determined characteristics of those originally engaged in Nourish Wellness. Findings are presented and conclusions offered to inform the continued success of Nourish Wellness.

The Centers for Disease Control and Prevention estimate that 19 percent of children 2 to 19 years are obese. Children who are Hispanic and non-Hispanic Black have a higher obesity prevalence (26% and 22%, respectively) than children who are non-Hispanic white (who are around 14%) (Centers for Disease Control and Prevention, 2022). Obesity prevalence was 19 percent among children and adolescents in the lowest income group compared to 11 percent among those in the highest income group (Centers for Disease Control and Prevention, 2022). Children who are obese are at risk of developing cardiometabolic diseases and face significant quality-of-life challenges in the present and future. Healthcare system-based interventions have been limited in success of reach by their inattention to socio-contextual factors. Food insecurity, limited access to safe places to be physically active, and barriers to transportation to clinical and community resources are all critical systemic challenges traditionally found in communities with limited resources that contribute to higher obesity rates and inhibit adherence to healthy lifestyles. Therefore, clinical-community interventions must be expanded to populations facing health disparities. Additionally, clinical community interventions must be implemented in locations accessible to populations in the greatest need of improved health outcomes and quality of life.

The flexible, clinical-community pediatric wellness initiative gives children and their families an individualized wellness plan and connectivity with resources. A multidisciplinary team consisting of a pediatrician, nurse, pharmacist, dietitian, kinesiologist, child life specialist, psychologist, and social worker provides collaborative care, including an individualized wellness plan, to the child and his/her family. Nourish Wellness aims to partner alongside adolescents and their families, with the outcome that the children's health routines, patterns, and habits can be positively influenced in the long run.

The objective of the current study was to describe participant characteristics for a one-year clinical commu-

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*Corresponding author: kgm0054@auburn.edu nity-based pediatric wellness initiative, Nourish Wellness.

Participant characteristics were utilized to describe those who enrolled with Nourish Wellness. Those with eligibility for the program included individuals ages 5 to 16 years who have conditions or are at risk for conditions related to obesity, metabolic syndrome, hypertension, and/or type 2 diabetes. Exclusion criteria included anyone participating in another wellness or weight loss program. Researchers used convenience sampling. Primary care physicians, school nurses, and school counselors referred up to 40 patients.

Validated questions included on a brief interview checklist measured the quality of life, demographics, and past/current medical history.

The child intake form measured the child's habits, medical history, patient and family characteristics, date of birth, race, ethnicity, gender, primary care provider, and health insurance.

Participant current and past medical information included information on diagnosis and treatment of typical medical conditions, surgeries, allergies, and medications.

Anthropometric measures included participant height, weight, and body mass index. Both height and weight were measured using a scale and a stadiometer. The body mass index was calculated using participant weight and dividing it by the square of the height.

Researchers used SPSS to describe the characteristics of those originally engaged in the program, including frequencies and other appropriate descriptive statistics. Fourteen individuals participated in the study. The majority were male (n=10, 71.4%) and black or African American (n=8; 57.1%). Out of these 14 patients, 10 of the participants' ages were reported. The youngest participant was 10 years, and the oldest participants was 19 years. The mean age of all ten of the reported recruits was 14.36 years (sd=.054 years). All patients (n=14) reported having a primary care provider as well as health insurance, with the majority utilizing Medicaid (n=9; 64.3%).

Many of the patients were faced with chronic illness, diabetes (n=4; 28.6%), pre-diabetes (n=4, 0.50%), a history of heart disease in family (n=7; 50%), asthma (n=4; 28.6%), and abdominal, stomach, or digestive problems (n=4; 28.6%). Mental health conditions also were stated with patients reporting psychiatric, psychological, or emotional disorders (n=4; 28.6%), depression (n=5; 35.7%), and anxiety (n=8; 57.1%). Most of the recruits (n=9; 64.3%) had never participated in weight management practices in the past despite almost every patient (n=13; 92.9%) reporting that someone in the family is overweight.

The majority of the recruits (n=8; 57.1%) had a strong growth mindset (x=20.57, sd=3.897). The remaining patients (n=3; 21.4%) had growth with some fixed ideas or fixed with some growth ideas (n=3; 21.4%). No one had a strong fixed mindset.

Participants consumed between 1 to 4 snacks per day with an average of 2.29 snacks (sd= 1.139) per day. For servings of fruit per day, the patients consumed 0 to 6 servings per day. On average they consumed 1.57 (sd=1.651) servings per day. For servings of vegetables per day (n=12), patients ranged from 0 to 2 servings per day. The average was 0.75 (sd=0.64) servings per day. The number of dairy participants had ranged from 0 to 2 servings per day and on average participants had 0.86 (sd=0.863) servings per day. Patients (n=9) who reported having 12 oz. of sugar sweetened (ssw) beverages per day ranged from 0 to 4 12oz. beverages per day. Participants on average had 1.33 (sd= 1.413) 12 oz. beverages per day. Figure 1 shows some unique findings of participants' eating habits.

Most patients (n=14) who reported eating while watching tv or playing on device said they often did this (n=8; 57.1%). Secret eating (n=14) was reported by 35.7% (n=5) of participants.

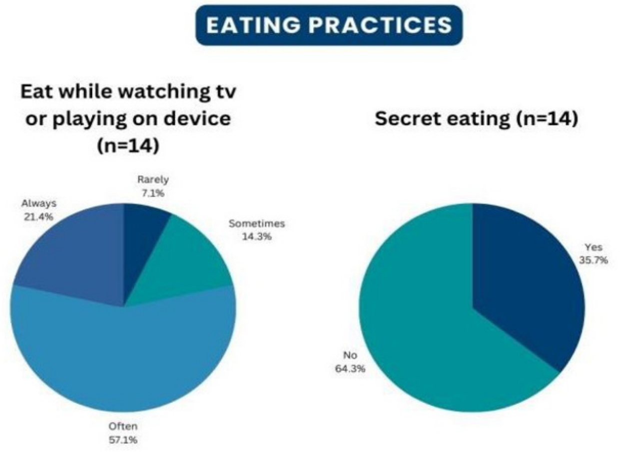

Fig. 1. Eating Practices of Nourish Wellness Recruits.

Physical activity practices of patients (n=14) were reported by days per week. The range was from 0 to 7 days per week. On average the patients exercised 3.64 (sd=2.590) days per week (sd=2.590).

The amount of screen time patients had in hours per day ranged from 2 to 16 hours per day. On average, participants spent 6.21 (sd=4.246) hours per day on a screen.

The systolic blood pressure of the participants (n=9) measured in mmHg was on average 110.78 mmHg (sd=7.513) and the diastolic blood pressure (n=9) was on average 68.67 mmHg (sd=6.928). Body mass index (n=8) ranged from 23 kg/m2 (healthy) to 41 kg/m2 (obese). The average body mass index of patients was 32.01 kg/m2 (sd=7.41) revealing that the patients were on average obese.

Limitations included recruitment through primary care physicians and lack of engagement with the Hispanic population. In terms of the body mass index, z scores should be calculated and compared as the study progresses.

Data reveal the average participant was male (n=10, 71.4%), black or African American (n=8; 57.1%), 14.36 years old, insured under Medicaid, had never participated in weight management practices in the past despite having a family member who is overweight, and had a strong growth mindset. The average participant also consumed 2.29 snacks, 1.57 servings of fruit, 0.75 servings of vegetables, 0.86 servings of dairy, and 1.33 12oz. ssw beverages per day. This data reveals a need for nutritional guidance for patients. The average patient exercised 3.64 days a week and spent 6.21 hours a day on a screen. One potential goal for patients could be to decrease screen time and add in more exercise. The average systolic blood pressure was 110.78 mmHg, and the average diastolic blood pressure was 68.67 mmHg. Finally, on average the patient would be obese with a body mass index of 32.01. As the study progresses, body mass index should be compared to reveal if there has been a change in the study.

Statement of Research Advisor

Kendall assisted in supporting baseline data collection, data analysis, and reporting for an Auburn University Creative Works and Social Impact Scholarship funded initiative. She was able to describe participant characteristics for a one-year clinical community-based pediatric wellness initiative, Nourish Wellness.

-Alicia Powers, Hunger Solutions Institute, College of Human Science

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Dr. Alicia Powers serves as the Managing Director for the Hunger Solutions Institute. Dr. Powers holds a PhD in Nutrition and Food Systems from The University of Southern Mississippi as well as a MS and BS in Nutrition and Food Sciences from Auburn University.

Monitoring TSWV in Alabama Peanut Fields

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Tomato spotted wilt virus (TSWV) is a plant virus transmitted exclusively by thrips, as seen in Figure 1. The symptoms of TSWV are wilted, young leaves, stunted growth, ring spots on leaves and pods, and reduced yields (Culbreath et al., 2003). Thrips transmit the virus in a persistent-propagative manner, meaning the adult insects can transmit the virus to new hosts for their lifetime because the virus infects and replicates within the insect tissues (LaTora et al., 2022). During the 1990s, up to 100% infected plants were observed in the southeast, and losses from the virus were estimated to be $12.3 million from 1996-2006 in Georgia peanuts alone (Riley et al., 2011). TSWV disease symptoms have been greatly reduced since the 1990s outbreak, primarily by resistant varieties, insecticides, and cultural practices (Kemerait, 2020). However, a resurgence of TSWV has been reported in the southeast and mid-south U.S. (Sundarai, et al, 2014). This research aims to quantify TSWV incidence in Alabama peanuts.

Fig. 1. Frankliniella fusca, also known as tobacco thrips

TSWV symptoms were monitored on small plot research trials in Headland, Brewton, and Fairhope during July of 2022. Up to 3-12 standard local varieties including Tuf 297, Flo 331, Flo T61, GA 06G, GA 16HO, AU 17, GA 20VHO, GA 14N, GA 12Y, GA 19HP, GA 18RU, and GA 09B were planted in research trials. Plots at Headland, Brewton, and Fairhope consisted of two, 25', 20', and 30' rows respectively. The middle two rows of each plot were visually inspected for symptoms caused by TSWV. Data was recorded as the number of row feet infected by counting the number of one-foot sections expressing TSWV symptoms and calculating the proportion of total row length infected (Culbreath et al., 1997). As seen in Figure 2, leaflets expressing symptoms were photographed and collected in a labeled bag with the location, date, row number, and cultivar. The samples were taken to the lab and placed in cold storage.

Fig. 2. Peanut plant expressing TSWV in Brewton

All samples taken to the lab tested positive for TSWV using RT-PCR. TSWV incidence was variable among the three locations. The average number of infected-row feet per plot calculated for Fairhope, Brewton, and Headland was 0.59, 2.45, and 0.26 respectively. Brewton experienced the most TSWV incidence, and there could be several reasons for that, such as increase temperature, humidity, and long dry seasons.

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Statement of Research Advisor

Lucinda gained valuable field research experience contributing to larger projects aimed at surveying the incidence of TSWV in Alabama peanuts. She assisted with rating plots for early-season crop damage caused by thrips vectors of TSWV, and learned how to recognize symptoms and rate incidence of TSWV in peanuts mid- to late-season when crop disease is apparent. Lucinda's efforts at three research stations helped to generate viable data on virus incidence in commercially available cultivars grown across the state that can be shared with stakeholder communities of interest.

- Dr. Alana Jacobson, Entomology and Plant Pathology, College of Agriculture

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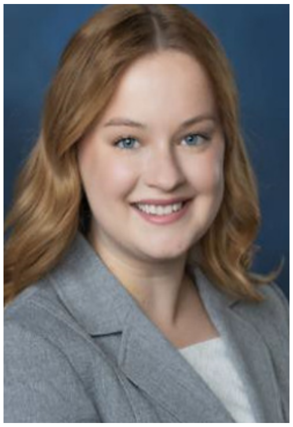
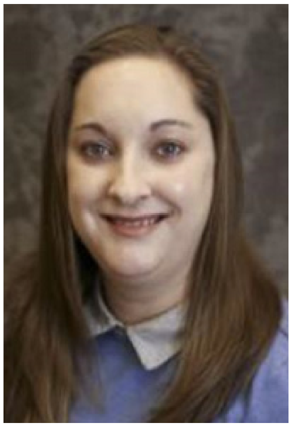
Authors Biography



Lucinda McEachin is a senior-year student pursuing a B.S.degree in Horticulture at Auburn University. She collected thrips feeding damage and subsequent TSWV infection data in Summer 2022. In Summer 2023, she will begin a master's program under Dr. Timothy Brenneman at the University of Georgia to study peanut seedling disease.

Dr. Alana Jacobson is an associate professor in the Department of Entomology & Plant Pathology at Auburn University. Her research program investigates the biology, ecology and management of insect pests and insect vectors of plant viruses.

Dr. Scott Graham is an assistant professor and Extension Specialist in the department of Entomology and Plant Pathology at Auburn University. His research focuses on developing integrated pest management solutions for insect pests of cotton, soybean and peanut.



Dr. Amanda Strayer-Scherer is an assistant professor and extension specialist in the Entomology & Plant Pathology department at Auburn University. Her research largely focuses on plant disease diagnostics and evaluating alternative approaches for managing diseases of tomatoes, such as bacterial spot, early blight of tomato, and late blight of tomato.

Dr. Kathleen Martin is an assistant professor in the Department of Entomology & Plant Pathology at Auburn University. Her lab studies plant viruses in the state of Alabama, including cotton leafroll dwarf virus (CLRDV), Soybean vein necrosis virus (SVNV), and TSWV.

Livleen Kaur is an MS Plant Pathology student at Auburn University under the supervision of Dr. Amanda Strayer-Scherer. She is working on Integrated Disease Management of peanut leaf spots. In Fall 2023, she will begin her Ph.D. at Penn State University to study phyllosphere microbiome under Dr. Kevin L. Hockett.

Claire Cooke is a master's student working under Dr. Scott Graham in the Department of Entomology & Plant Pathology at Auburn University. Her research is focused on assessing different management practices to control thrips and tomato spotted wilt virus in peanuts grown in Alabama.

Brad Miller is an Associate Research Director of the Brewton Agricultural Research Unit with a demonstrated history of working in the higher education industry. He is skilled in research, budgeting, customer service, higher education, and science.

Christopher Parker is an Associate Research Director of the Gulf Coast Research and Education Center in Fairhope, AL.

H. L. Campbell is a lab technician in the Department of Entomology & Plant Pathology at Auburn University.

Identifying Single Shift Quality Measures in the Case of Nursing Students

Kelly Moore[1,*], *Haneen Ali, PhD*[2]

[1] Undergraduate Student, Department of Political Science, Auburn University
[2] Associate Professor, Department of Political Science, Auburn University

What interactions, events, or environments have the authority to define a shift as "good" or "bad" in a future nurse's eyes? This project determines specific factors that significantly influence these nursing students' perceptions of their abilities, workloads, and stress. After determining a suitable instrument for data collection, interviews were then conducted with nursing students to identify key determinants of shift quality. Data was then synthesized to identify and evaluate the factors contributing to stress.

This research aims to (1) assess the degree to which nursing students can predict a single shift's potential level of stress through the comparison of the student's predicted perceived stressors at the start of the shift with their observed and experienced stressors at the time they clock out; and (2) analyze the factors contributing to perceived SSQ from a student nurse's perspective by identifying changes in indicators from discernable stressors before and after the shift. SSQ seeks to positively impact nursing workflow, improve patient safety, and reengineer shortcomings stemming from inadequate processes in healthcare.

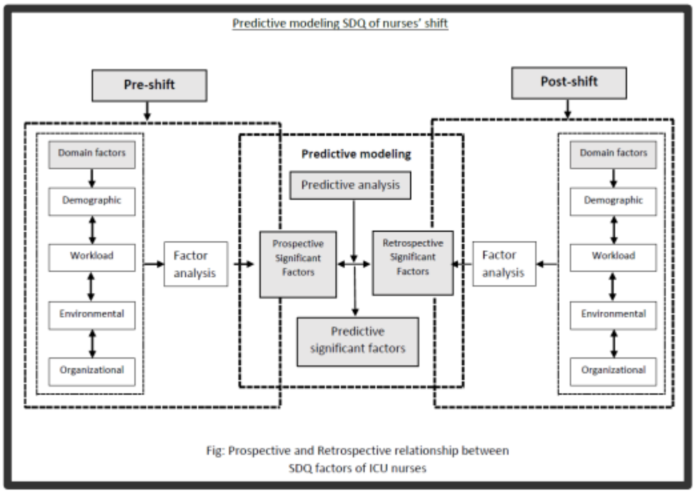


Fig. 1 SSQ predictive modeling.

This project seeks to evaluate how well nursing students can predict their level of stress in a single shift. The student's prediction of his or her perceived stressors at the beginning of the shift are noted. After the shift, observed stressors are recorded. The two student reports are then compared and analyzed.

Next in the process, variables are investigated and identified. These variables are factors that contribute to perceived single shift quality from a nursing students reported stressors in clinical settings. Changes in the single shift quality indicators from student stressor reports are identified for both the beginning and the end of shift reports provided by the students.

The ability to identify and explain daily stress factors for nursing students in clinical settings allows for our team to determine if there is a causal relationship between their perceptions of these stressors and their expectations of experiencing adversity physically and socially during a particular shift.

With this research, gaps in education and clinical training can be addressed more efficiently and accurately through the assessment of stress on overall student performance.

Figure 1 shows the pre-shift and post-shift domain factors that survey questions are sorted into categorically once answered by the nursing students. These factors are analyzed to find prospective and retrospective factors that appear to be significant in determining shift quality. The factors are then analyzed through predictive analysis to identify predictive significant factors.

The modeling also shows the prospective and retrospective relationship among SDQ factors of ICU nurses, specifically, as shown by the figure.

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Correlations found through pre- and post-shift surveys were examined through descriptive statistics. The majority of relations were found to be among workload, patient characteristics, internal environment, leadership, and external environment. The pre- and post-shift survey averages of domains were also compared, with nominal results.

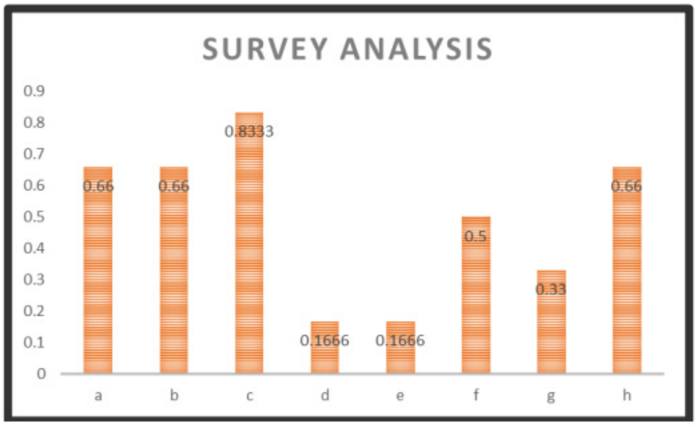

Fig. 2 SSQ survey analysis results.

The survey analysis results can be found above in figure 2. An explanation of letters a-h can be found in this section. Column a shows that 66% of the participants consented to being at their specified unit. Column b shows 66% of participants expected to have positive interactions with other clinicians during their shift. Column c illustrates that more than 83.33% of participants expected to have a good shift based on the race, gender, and first impression of the patients. Column d illustrates that 16.66% of the participants expected discrimination during the shift. Column e shows that 16.66% of the participants expected ingratitude during the shift. Column f illustrates that 50% of the nurses expected that course workloads could affect their quality of care. Column g shows that 33% of the students expected to feel unable to meet the clinical instructor's expectations. Finally, column h shows that 66% of the students expected when they encountered stressful situations to make plans, list priorities, and problem solve.

In the case of single shift quality analysis, perceived stressors were compared prior to and following shifts of student nurses in clinical settings.

Variables are continuing to be identified as more data is collected from participants and more changes in SSQ indicators become identifiable. At the current point in our research, there is a significant correlation found in two domains: between the internal environment and the overall rate, as well as the overall rate and coping strategies.

Statement of Research Advisor

This research seeks to improve the quality of care patients experience in clinical settings, as well as the efficiency of workflows in healthcare organizations. Further understanding the intricacies that cause shifts to be regarded positively or negatively by a nursing student allows us to contribute to these goals. The research team has been more successful because of the effort and work contributed by Kelly.

- Dr. Haneen Ali, Department of Political Science, College of Liberal Arts

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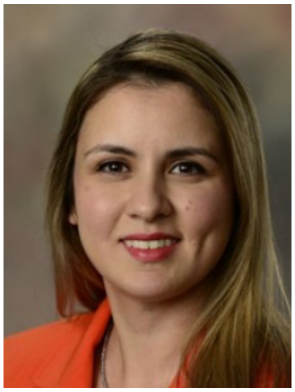
Authors Biography

Kelly Moore is a senior year student pursuing a B.S. degree in Health Services Administration at Auburn University. She has played key research roles in the single shift quality study as she has researched alongside Dr. Haneen Ali. Moore is from Muscle Shoals, Alabama, and is currently completing her internship requirement at UAB Huntsville Regional Medical Campus in the Office of Family Health, Education & Research. She has held numerous leadership positions on campus within the Student Government Association, Panhellenic Council, and Health and Hospital Administration Organization. She is honored to be an Undergraduate Research Fellow and credits this program with giving her the exposure to shortcomings in healthcare that will allow her to become a better healthcare administrator.



Haneen Ali is an associate professor in the Health Services Administration Program at Auburn University. She received her PhD in industrial and systems engineering from the State University of New York at Binghamton in 2016. Ali holds a BS in biosystems engineering and an MS in industrial engineering, and she is a certified Lean Six Sigma Black Belt. Her research areas of interest are in healthcare delivery systems, applications of systems engineering and Lean Six Sigma in healthcare, and human-computer interaction. She has been leading a wide spectrum of projects in the healthcare delivery systems. The focus of these projects can be broadly classified under (1) safety and quality of care, (2) process improvement and system redesign, (3) evaluation of work systems, and (4) technology and innovation.

The optimization of *Aphis gossypii* rearing and RNA extraction methods

Nicholas Mueller[1,], and Kathleen M. Martin[2]*

[1] Undergraduate Student, Department of Entomology and Plant Pathology, Auburn University
[2] Assistant Professor, College of Agriculture, Auburn University

Introduction

Aphis gossypii, the cotton-melon aphid, has an international distribution, being found on all continents except Antarctica. In warm weather, these aphids give live birth, and reproduce by parthenogenesis in the spring through fall, producing winged and wingless forms (Fig. 1) (Berim, n.d.). Cotton leafroll dwarf virus, or CLRDV, is transmitted in a circulative and persistent manner by *A. gossypii* (Michelotto & Busoli, 2003) and does not replicate inside the aphid (Heilsnis, 2020). CLRDV is the cause of Cotton Blue Disease, which causes leaf curling, stunted growth, reddening of petioles and veins, and reduced cotton yield (Conner et al., 2021). In 2018, CLRDV was first identified in Alabama, where it caused an estimated loss of $19 million (Conner et al., 2021). CLRDV is a positive-sense single-stranded RNA polerovirus, meaning its genome is made of a single strand of RNA (Avelar et al., 2020).

The RNA extracted from *A. gossypii* can be used in research of CLRDV with applications such as detection PCR, CLRDV quantification, transmission assays, RNA sequencing, and protein-protein interaction assays. Optimizing these *A. gossypii* rearing and RNA extraction methods can aid in the research of CLRDV and can one day help us discover new virus management techniques.

Methods

Two *A. gossypii* rearing methods on the Deltapine 1646 cotton variety were compared, a caged method (Fig. 2.A) imitating aphid greenhouse rearing methods on seedlings, and a confined method (Fig. 2.B) imitating field trial or transmission assay methods for larger plants that are difficult to cage. For the caged method, *A. gossypii* were reared on a tray of one-to-two week old cotton in a cage (Fig. 2.A). After one week, aphids were collected from three-to-four seedlings (wingless adults and nymphs) or the wall of the cage (winged adults). For the confined method, 50 wingless adult aphids were confined to one leaf on a mature cotton plant, older than six months, with a cone, coated with Fluon to prevent aphid escape, around

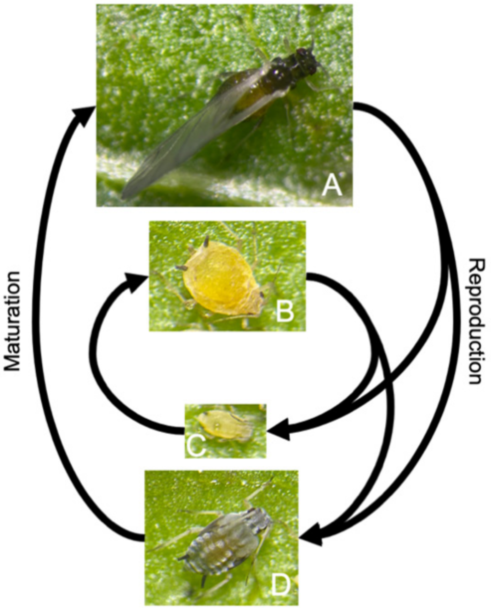


Fig. 1 *A. gossypii* parthenogenic life cycle with (A) winged adult, (B) wingless adult, (C) nymph of wingless adult, and (D) nymph of winged adult. Made in Microsoft PowerPoint.

Fig. 2 Caged method (A) and confined method (B) of *A. gossypii* rearing.

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*Corresponding author: mnm0059@auburn.edu the petiole and a mesh bag enclosing the leaf and cone (Fig. 2.B). The aphids were collected after 10-14 days from only the confined leaves. The rearing methods were assessed by the number of complete samples (100 adults, wingless or winged, or 300 nymphs) collected after 10 collections, as well as the ease of the rearing method.

Two common RNA extraction methods were compared, a chemical only RNA extraction method and a spin column assisted RNA extraction method. The chemical only extraction method used TRIzol Reagent, following the user guide (Invitrogen, 2023). The chemical only extractions were done with sample sizes of 25-75 mixed wingless and winged adult A. gossypii and 25-200 nymphs. The spin column assisted extraction method used the NucleoSpin RNA Kit, following the kit manual (Macherey-Nagel, 2023). The spin column assisted extractions were done with sample sizes of 50-150 winged or wingless adult *A. gossypi* and 50-300 nymphs. The RNA extraction methods were assessed by the quantity and purity of the RNA extracted for different aphid numbers, as well as the ease of the method. The quantity and purity were measured using a NanoDrop Microvolume Spectrophotometer (Thermo Scientific, 2023). The A260/280 ratio, or absorbance ratio at 260 nm and 280 nm, was used to measure the purity. Pure RNA should have an A260/280 value of ≥2.0.

Results

Between the two rearing methods, the caged method resulted in more complete samples collected across all three *A. gossypii* forms (Table 1). It is important to note that several of the leaves that aphids were confined to had died or fallen off the plant before any aphids were collected. As for the ease of the two rearing methods, the caged method was less time consuming to set up and easier to maintain.

Overall, the chemical only extraction method was able to extract more RNA per aphid on average than the spin column assisted extraction method, but the spin column assisted extraction method had a much higher average A260/280, indicating a higher average purity (Table 2). Once the spin column assisted extraction method was seen to result in purer RNA, separate wingless and winged samples were collected for RNA extraction to compare the two adult forms, which showed that the wingless adult aphids had on average more RNA extracted from them than the winged adult aphids (Table 2). Both extraction methods had inconsistent amounts of RNA extracted across samples of the same number and form of aphids. For example, the chemical only extraction with 25 mixed adult *A. gossypii* resulted in a range of total RNA extracted of 6.25-18.484 µg per sample. For the spin column assisted extractions with 100 wingless adults and 100 winged adults, the range of total RNA extracted was 16.664-59.265 µg and 9.02-23.32 µg per sample, respectively. To get similar amounts of RNA from adults, the chemical only extraction method required only a quarter the number of aphids as the spin column assisted extractions. For samples of 200 nymphs, the chemical only extraction resulted in 15.357 µg of total RNA while the spin column assisted extraction resulted in 4.496 µg of total RNA.

Table 1 Number of complete collections of A. gossypii forms per rearing method.

Aphid Form	Caged Method	Confined Method
Winged Adult	5	0
Wingless Adult	4	2
Nymph	3	1

Table 2 Number of complete collections of A. gossypii forms per rearing method.

	Chemical Only		Spin Column Assisted	
	Average RNA per Aphid (µg)	Average A260/280	Average RNA per Aphid (µg)	Average A260/280
Adult	0.382794	1.92	0.327098 (Wingless)	2.174 (Wingless)
			0.21312 (Winged)	2.136 (Winged)
Nymph	0.1711442	1.59525	0.0611283	2.1716666

Discussion

The caged method of rearing *A. gossypii* resulted in more complete aphid collections and is ideal for the greenhouse setting where smaller, younger cotton plants can be used. The softer tissues of the young plants may be preferable to the aphids, which would contribute to the higher aphid numbers. The mature cotton plant used in the confined method of rearing had older, tougher leaves. The age of the leaves on the mature plant may have also contributed to the early death and abscission of the leaves the aphids were confined to. Despite the lower number of complete aphid collections for the confined method, this method is still useful for field trials, transmission assays, or aphid confinement on large, uncaged plants. It may be necessary to use an excess of aphids and more confined leaves to be able to get the final number of aphids that is needed using the confined method.

Due to the amount of both adult *A. gossypii* forms needed for the spin column assisted extraction method needed in comparison to the chemical only extraction method, the chemical only extraction method may be ideal for experiments with low aphid numbers. It is possible to correct for the low purity of the chemical only extraction method with further purification steps if necessary. The spin column assisted extraction method may then be ideal for experiments where the purity of the RNA is a priority and there are more aphids available to extract the RNA from. The difference in RNA quantity across the replicated extractions with the same number and form of aphids is likely due to the natural differences in aphid size within each aphid form. The difference in average RNA quantity across adult aphid forms is expected due to the function of each form. The function of the wingless adult *A. gossypii,* which had the most RNA, is to reproduce rapidly, having multiple developing nymphs inside of them at once. The function of the winged adult *A. gossypii* prioritizes long distance movement over reproduction (Braendle et al., 2006).

By weighing the pros and cons of both *A. gossypii* rearing methods and both RNA extraction methods, one can determine the best methods to use for future experiments in the investigation of *A. gossypii*-CLRDV interactions. This was a critical first step towards a larger study aimed at blocking transmission in the field.

Statement of Research Advisor

Nick Mueller was able to identify the best method of rearing the cotton-melon aphid, Aphis gossypii, as a key first step in the ongoing studies of the transmission of Cotton leafroll dwarf virus (CLRDV) in the field. He was also able to identify a method of extraction of aphid RNA which will further our work on identification of aphid proteins that interact with the proteins of CLRDV. Nick's experiments represent a crucial first step at the beginning of a large and complex project about how this virus can move through the tissues of A. gossypii. Understanding this process will enable better recommendations as to how to stop this process to halt the spread of this virus in the field.

- Kathleen Martin, Department of Entomology and Plant Pathology, College of Agriculture

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Authors Biography

Nicholas Mueller is a recent Auburn University graduate with a B.S. in Applied Biotechnology from the College of Agriculture. Nicholas has worked for the Dept. of Entomology and Plant Pathology since May 2021, and worked in the Martin Lab from May to December of 2023 where he worked with *Aphis gossypii* and CLRDV. In June and July of 2022, Nicholas participated in the Summer Scholars Program at AgriTech at Cornell University investigating the transmission of Grapevine red blotch virus by *Spissistilus festinus*. His research interests include vector entomology and plant virology.

Dr. Kathleen Martin is an Assistant Professor in the Department of Entomology and Plant Pathology. She started her lab in vector entomology at Auburn in 2019. She works on the molecular aspects of insect transmission of plant viruses in the field. Her work focuses on Cotton leafroll dwarf virus, Soybean vein necrosis virus and Tomato spotted wilt virus. She started working on plant viruses during her Master's program at the University of Arizona and continued to work on viruses that also infect their insect hosts/vectors at the University of Kentucky where she completed her PhD in 2011.

Auburn University Journal of Undergraduate Scholarship

Philanthropic Innovations: A Review of the Literature

Reagan Myers[1,] and, Peter Weber[2]*

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[2] Associate Professor, Department of Consumer and Design Science, Auburn University

Organized philanthropy's capacity to innovate and have systemic impact has been invoked in recognition of philanthropy's limited resources as compared to the size of social problems (Ylvisaker, 1999). This disconnect has driven the search for impact and innovation in the past (Hammack & Anheier, 2013). Yet, most research on innovation and philanthropy is externally oriented.

Two-thousand, sixty-four articles were identified in a systematic literature review focused on philanthropic innovations. After removing two hundred and twenty duplicates, the remaining abstracts were hand-screened for relevancy by two authors, leading to the exclusion of 1,759 articles because they were focused on funding innovation or individual philanthropy, or the search word was used in a completely different context (e.g., "giving" appears often in "giving birth" or "giving reason"; "charity" is frequently used as a synonym of nonprofit organizations; and "innovations" was often used in reference to methodology or approach). Studies typically analyze philanthropic foundations or philanthropy funding innovations. We find that studies on innovations in organized philanthropy focus on innovative practices (program area), innovation in administrative structures, and building a culture conducive to innovation.

Among academic articles, there is a high reliance on case studies. It is noteworthy that the analysis of references in our initial corpus led to the inclusion of a significant number of practice-oriented publications (grey literature). Thirty-nine out of the seventy-two total articles included in the systematic literature review were included during the citation and reference search. Grey literature "comprises an increasing proportion of information relevant to research synthesis" and has become more prevalent as technology has created new opportunities for its distribution (Rothstein & Hopewell, 2009, p. 104).

Rothstein and Hopewell (2009, p. 104) define grey literature as "Just about everything not published in a peer-reviewed academic journal, whether or not it is produced by those for whom publishing is the primary activity." Although some researchers have expressed concern with including literature that hasn't been published in journal articles in research synthesis, Rothstein and Hopewell (2009) believe that peer review alone is not an indicator of its quality. Each piece of literature should be individually assessed for methodological quality when determining whether it should be included in research. Professionals who are not under pressure to publish in academic journals may produce reports of equal quality as those for whom publishing is incentivized. Scientific discovery and knowledge are not limited to traditional journal publications.

Grey literature is of great value for theorizing. Rothstein and Hopewell (2009) found that it may be more current than articles published in academic peer-reviewed journals. A comprehensive search of both peer-reviewed and grey literature also minimizes publication bias (Rothstein & Hopewell, 2009). Scholars must evaluate academic and practitioner literature when forming theories about philanthropic innovations.

Among the program opportunities for innovation in philanthropy, shared/blended value, donor-advised funds, prize philanthropy, impact investing, multi-year funding, collaboration/co-creation, venture philanthropy, and learning culture are all mentioned more than once. The use of multi-year funding, impact investing, venture philanthropy, and collaboration mentioned in *Foundation News* were all a response to shifts in govern-

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*Corresponding author: rem0072@auburn.edu ment funding or tax law.

Structural, financial, and administrative opportunities included program-related investments, the use of online platforms, and impact investing. Impact investing was included in this category if the author discussed investing from their endowment. The use of online platforms is a response to new technologies and is often used as a tool to connect funders with grant applicants.

This research highlights some potential avenues for innovations and the importance of grey literature in literature reviews. A more systematic way to include grey literature needs to be created.

Statement of Research Advisor

The project aimed to identify innovations in the grantmaking activities of philanthropic foundations. Reagan was in charge of all steps in the research project, from data collection to analysis and dissemination. She completed a systematic review of the peer-reviewed literature, thematically analyzing articles that discussed specific grantmaking innovations. This analysis led her to expand the project to incorporate grey literature serving the nonprofit sector with an applied and practitioner focus. By reviewing and analyzing more than 30 years of The Foundation News (the leading trade publication for foundation leaders), Reagan identified trends in foundation activities and paradigm shifts in grantmaking approaches from a historical perspective. She presented the different stages of this research at the 2022 Annual Conference of Association for Research on Nonprofit Organizations and Voluntary Action (ARNOVA) in Raleigh (North Carolina) and at 2023 Annual Conference of Association for Research on Nonprofit Organizations and Voluntary Action (ARNOVA) in Orlando (Florida). ARNOVA is the premier national conference for scholars interested in philanthropy and nonprofit organizations.
- Peter Weber, Department of Consumer and Design Science, College of Human Sciences

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Authors Biography

Reagan graduated in December 2023 with a double major in Human Development and Family Science as well as Philanthropy and Nonprofit Studies. She works for Our House, a nonprofit in Auburn, as the Volunteer and Program Coordinator.

Peter Weber is an associate professor of philanthropy and nonprofit studies and program coordinator of the Philanthropy and Nonprofit Studies (PNPS) Program at Auburn University. He holds a doctorate in Philanthropic Studies from the Indiana University Lilly Family School of Philanthropy, as well as a master's in history and a Master in International Studies in Philanthropy and Social Entrepreneurship, both from the University of Bologna in Italy.

Adaptation of a Microfluidic Device for Use in Scalable Cell Encapsulation

Ravi Nataraj[1,] , Yuan Tian[2] , Mohammadjafar Hashemi[3] , Elizabeth A. Lipke[4]*

[1] Undergraduate Student, Department of Chemical Engineering, Auburn University
[2] Postdoctoral Fellow, Department of Chemical Engineering, Auburn University
[3] PhD Candidate, Department of Chemical Engineering, Auburn University
[4] Mary and John H. Sanders Professor, Department of Chemical Engineering, Auburn University

Three-dimensional (3-D) cell culture models have gained recent interest in tissue engineering (TE) and drug discovery applications over traditional two-dimensional monolayer culture [1]. This is because 3-D culture models are more physiologically relevant and better able to mimic the human in-vivo microenvironment. Different cell applications, such as high-throughput screening, injectable cell delivery, and bioprinting, require the scalable production of 3-D systems, but current manufacturing approaches are inadequate. For example, using single-use 3-D bioreactors for scale-up cell production form aggregates that lack size and shape uniformity, resulting in cell structures with dissimilar functionalities. To overcome such challenges, TE methods – e.g. emulsification, photolithography, microfluidics, and micromolding – can create highly consistent microengineered hydrogels with tight spatial control, but microfluidics is especially promising because it uses a continuous-flow approach suitable for scale-up production needs [2].

Previously, our lab has established a novel microfluidic platform capable of producing 3-D engineered tissues by encapsulating cells within monodisperse poly(ethylene glycol)-fibrinogen hydrogel microspheres (MS) [3]. During MS encapsulation, an expensive, high-intensity visible halide lamp has been used for rapid photocrosslinking of the hydrogel; however, issues with light output consistency, heat regulation, lack of adjustable light parameters restricting photoinitiator choice, and bulkiness weaken platform scalability. Such drawbacks cause added maintenance costs, batch-to-batch variability, and may interfere with cell viability. Here, by leveraging an iterative and modular design strategy, we optimized the photocrosslinking module in our platform to support the high-throughput and scalable production of MS.

As an alternative to the halide lamp, high-watt LED modules (LEDSupply) were mounted on an aluminum heatsink assembly for heat dissipation, and light output was precisely controlled using a PWM (pulse-width modulation) dimmer. Optic lens focusers were used with LEDs to help collimate light and reduce unwanted light from clogging the microfluidic device due to premature crosslinking. Similar assemblies were created by altering LED type – visible or ultraviolet-A (UVA) – to accommodate various photoinitiator types (Eosin Y, LAP) for supporting robust crosslinking of different polymers specific to user needs. 3-D printed fixtures were designed to secure the power supply, dimmer, and lab jack to a 15x15 cm2 aluminum breadboard (THOR Labs). As proof of concept, HT29 colorectal cancer cells were encapsulated using both our original and optimized microfluidic platform, and cell viability was compared using live/dead staining. Images of live/dead stained HT-29 cancer cell MS from both platforms were captured using confocal microscopy.

The compact design of the optimized platform (Figure 1) helps minimize its footprint inside the biological hood.

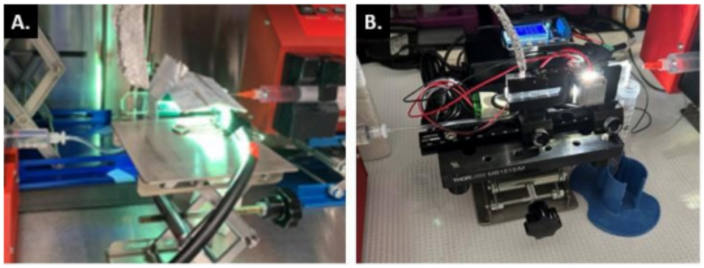

Fig. 1. A. Original and **B.** optimized microfluidic platform setup for acellular microsphere production.

The use of modular LED assemblies allows for quick compatibility with different photoinitiators. Fast ad-

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justability and reliable modularity support easy troubleshooting and efficient batch-to-batch transitions. Preliminary results of live/dead confocal microscopy to assess cell viability suggest fewer dead cells in MS produced by the optimized platform (Figure 2).

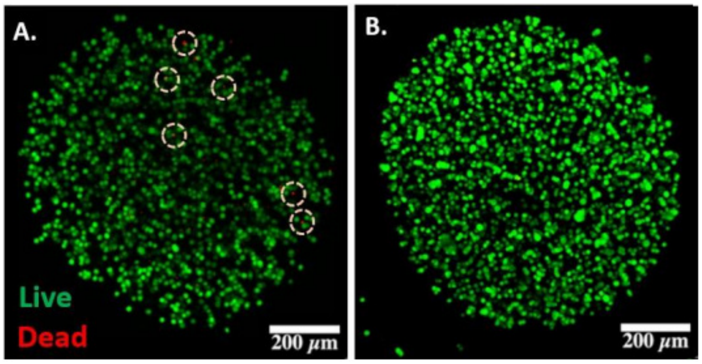

Fig. 2. Confocal microscopy image of a live/dead stained HT29 cancer cell microsphere produced from **A.** original and **B.** optimized microfluidic platform.

Overall, our adjustable and modular microfluidic platform provides quick compatibility with multiple photoinitiators, efficient batch-to-batch transitions, and easy troubleshooting during cell encapsulation. To validate if the above changes impact cell viability, additional assays and experimental tests will be performed to help provide insight into cell growth, metabolic activity, and microenvironment. Future optimization plans include implementing computer vision software to count real-time MS production and designing an automated MS distribution system into any size well plate for high-throughput drug screening applications. By improving both function and utility while maintaining its reliability, our platform has high potential to address large-scale cell production needs.

Statement of Research Advisor

Ravi has been instrumental in driving forward the establishment of a new, adjustable LED light source with consistent light intensity for photocrosslinking of engineered microtissues. Ravi has demonstrated a high capacity for innovation, problem solving, critical thinking, and leadership in the lab environment. His contributions were critical to advancing his light source project from initial design through multiple iterations to prototype.

- Elizabeth A. Lipke, Chemical Engineering, Samuel Ginn College of Engineering

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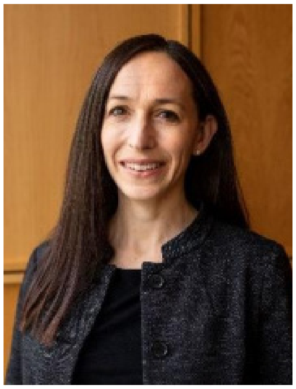
Authors Biography

Ravi Nataraj is a senior-year student pursuing a B.S. degree in Chemical Engineering at Auburn University. After joining the Lipke Lab, he has played key research roles in optimizing a novel microfluidic platform and has gained experience in computational analysis for characterizing the maturity of engineered cardiac tissue.

Yuan Tian, Ph.D. is a Postdoctoral Fellow in the Department of Chemical Engineering, Samuel Ginn College of Engineering at Auburn University. Yuan received his doctorate training from Dr. Elizabeth Lipke’s research group at Auburn University. Yuan’s research interest focuses on intravascular targeted cell delivery and scalable production of engineered tissues for drug discovery and regenerative medicine purposes.

Mohammadjafar Hashemi is currently a fifth-year PhD candidate in Chemical Engineering at Auburn University. He obtained his M.Sc. in Polymer Engineering from Sharif University in Iran. With his knowledge in these fields, he specializes in encapsulation of hiPSC microspheroids and cardiac differentiation.



Dr. Elizabeth A. Lipke is the Mary and John H. Sanders Professor in the Department of Chemical Engineering at Auburn University. Dr. Lipke completed her graduate studies at Rice University followed by a postdoctoral fellowship at Johns Hopkins University. Dr. Lipke's research focuses on the use of cell-material interactions to create cellular microenvironments that guide tissue formation and direct cellular function.

Expression and Characterization of the Luciferase of *Noctiluca scintillans*

Sean P. O'Hare[1,], Steven O. Mansoorabadi[2]*

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[2]Associate Professor, Department of Chemistry and Biochemistry, Auburn University

Dinoflagellates are an important group of microorganisms that are ubiquitous in the world's oceans. Many species can produce bioluminescent light, which occurs through the oxidation of dinoflagellate luciferin by the dinoflagellate luciferase (LCF), as depicted in Figure 1. LCF is an enzyme of great interest because it has the potential to be utilized as a reporter enzyme, a useful tool for detecting gene expression, studying infectious diseases, and monitoring cancer growth.

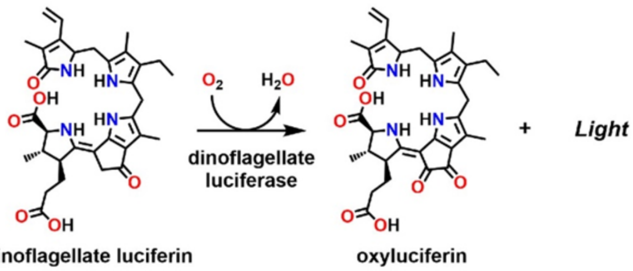

Fig. 1. Dinoflagellate bioluminescence reaction

We are specifically studying the LCF of *Noctiluca scintillans* (NS-LCF) due to its unique structure. While LCF typically contains three homologous domains, NS-LCF has two distinct domains (refer to structural comparison in Figure 2) (Liu & Hastings, 2007). As depicted in Figure 3, the first domain shares 65% sequence identity with domain 1 of the LCF found in the luminous dinoflagellate *Lingoludinium polyedra* (LP-LCF), and thus is labeled the LCF-like region (Liu & Hastings, 2007). The second domain, however, shares 40% sequence identity with the separately encoded luciferin-binding protein (LBP) of *L. polyedra* (LP-LBP), another essential component of the bioluminescence system, so it is denoted as the LBP-like region (Liu & Hastings, 2007). This distinctive structure of NS-LCF has led to the hypothesis that all other forms of LCF and LBP evolved from a NS-LCF-like progenitor (Liu & Hastings, 2007). Therefore, elucidating the structure and catalytic regions of NS-LCF and comparing them to other forms of LCF and LBP could explain how the functions of these proteins evolved over time.

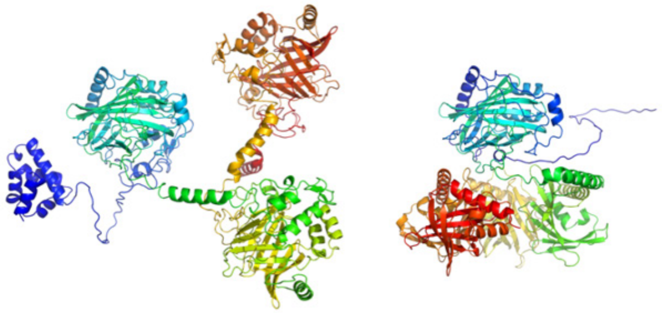

Fig. 2. Predicted structures of the canonical LCF from *L. polyedra* (left) and of NS-LCF (right)

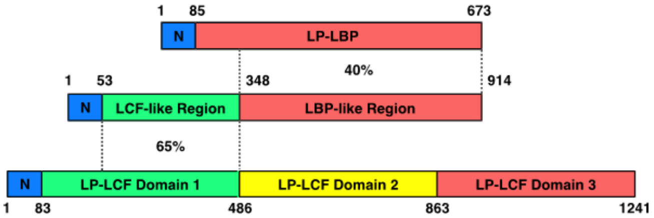

Fig. 3. NS-LCF domain structure in comparison to LP-LCF and LP-LBP

In this research, the focus was on expressing and purifying NS-LCF. To achieve this, a technique called heterologous expression was used. Heterologous expression involves inserting the gene of interest into a different host organism, in this case, *Echerichia coli*, which is a common bacterium used for protein expression (Kaur

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et al., 2018). To accomplish this, a technique called polymerase chain reaction (PCR) was first used to amplify the NS-LCF gene. Then, a technique called Gibson Assembly was performed to insert the NS-LCF gene into the Champion^{TM} pET-SUMO vector. A vector is a DNA molecule that acts as a carrier to introduce the target gene into the host organism (Nora et al., 2019). The pET-SUMO vector is designed to facilitate the expression of the target protein by adding a SUMO (small ubiquitin-like modifier) tag to the protein, which enhances protein solubility levels (Butt et al., 2005). After the construction of the plasmids containing the NS-LCF gene in the pET-SUMO vector, they were introduced into *E. coli* BL21 (DE3) cells for expression. BL21 (DE3) is a commonly used strain of *E. coli* that is known for its ability to produce large amounts of recombinant proteins (Robichon et al., 2011). Following expression, the SUMO-tagged NS-LCF protein was purified using a technique called immobilized metal affinity chromatography, which takes advantage of part of the SUMO tag to specifically capture and purify the NS-LCF protein from the mixture of proteins produced by the *E. coli* BL21 (DE3) cells (Falke & Corbin, 2013). Finally, the purified sample was analyzed using sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE), which is a technique that separates proteins based on their size using a gel and an electric field.

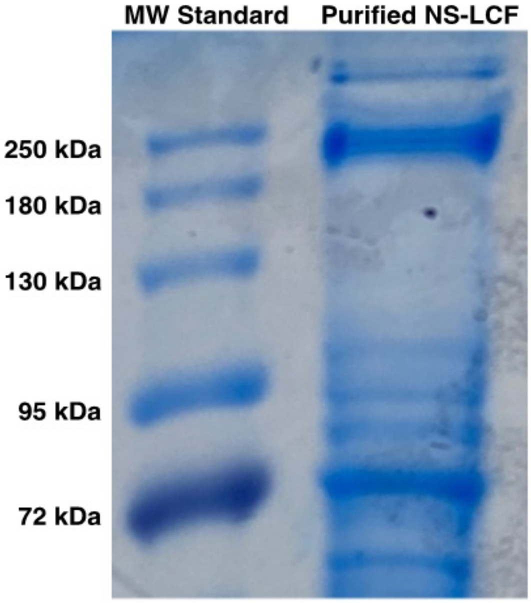

Fig. 4. SDS-PAGE analysis of IMAC-purified NS-LCF

SUMO-tagged NS-LCF has a molecular weight (MW) of 111 kDa, but looking at the SDS-PAGE gel (see Figure 4), no band corresponding to the expected molecular weight was observed. Instead, a prominent band was detected at the 72 kDa marker, which is likely indicative of the presence of DnaK, a common *E. coli* chaperone protein contaminant (Rial & Ceccarelli, 2002). This inference aligns with previous findings from the lab, although further confirmation will be sought using mass spectrometry. Additionally, a band was observed between the 180 and 250 kDa molecular weight markers, suggesting the possible presence of NS-LCF dimers, which would have a molecular weight of 222 kDa. This hypothesis is backed by data, as the structural prediction program AlphaFold indicates that the N-terminal region (front-most portion) of NS-LCF, which appears intrinsically disordered, may group together to form higher order oligomer complexes like dimers, trimers or dodecamers (see Figure 5). However, this assignment has not yet been confirmed.

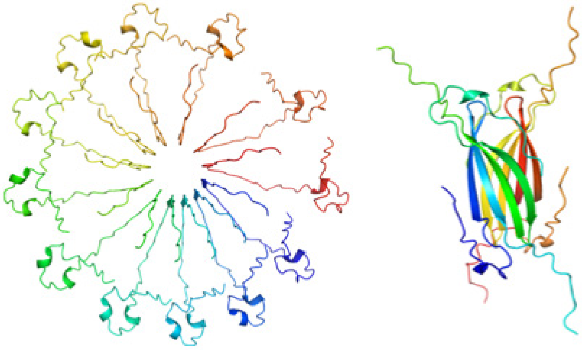

Fig. 5. Potential NS-LCF N-terminal trimer (right) and dodecamer (left) complexes

It is still unclear if NS-LCF has been successfully expressed and purified. It is possible that dimers have been isolated, but this needs to be further investigated. For future steps, we first plan to perform a western blot, an analytical technique used to identify specific proteins. This will allow us to validate that the protein we purified is NS-LCF. If successful, then we plan to run multiple different experiments to study NS-LCF. Structural analysis will first be conducted using X-ray crystallography to elucidate its three-dimensional structure. Mutational analysis will then be performed to determine the active site residues by selectively mutating specific amino acids and studying their functional impact. Finally, the pH dependence of the enzyme will be studied using fluorescence spectroscopy. Through these investigations we hope to gain an understanding of the enzyme's mechanism of action, laying the foundation for further research into the enzyme's potential use as a reporter enzyme.

Statement of Research Advisor

Sean's undergraduate research project is focused on understanding the mechanism of dinoflagellate bioluminescence. Dinoflagellates are a diverse group of freshwater and marine microorganisms that are simultaneously responsible for harmful algal blooms (red tides) and the 'phosphorescence of the sea' via a unique bioluminescence system consisting of a luciferase enzyme (LCF), a luciferin substrate, and a luciferin-binding protein (LBP). Sean began volunteering in the lab and started a new project focusing on a primitive luciferase that combines the functionalities of LCF and LBP in one protein in collaboration with a senior graduate student. After receiving an Undergraduate Research Fellowship, Sean has continued to work on this project independently, as his graduate student mentor left for a position at a biotechnology startup company, and he has made significant progress that sets the stage for future research in the laboratory.

- Dr. Steven O. Mansoorabadi, Department of Chemistry and Biochemistry, College of Math and Science

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Authors Biography

Sean P. O'Hare is a junior-year student pursuing a B.S. degree in Biochemistry at Auburn University. As a 2022-2023 Undergraduate Research Fellow, he played a key role in the research design, data collection, and analysis.

Dr. Steven O. Mansoorabadi is the J. Milton Harris Associate Professor in the Department of Chemistry and Biochemistry at Auburn University. He oversaw all aspects of the fellowship project.

Small Business Digitization Before, During and After COVID-19 Pandemic

Audrey Osborne[1,] and Atiya Avery[2]*

[1] Undergraduate Student, Department of Information Systems and Technology, Auburn University
[2] Assistant Professor, Harbert College of Business, Auburn University

A supply chain can be defined as a system that facilitates the connections and flows among one or more partners, producers, wholesalers, retailers, or customers.3 This research aims to better understand the COVID-19 Pandemic's role in small business supply chain disruptions and digital solutions. Small businesses are essential to the American economy, employing nearly half of the U.S. workforce(2). Unfortunately, small businesses were one of the most impacted organizations by the Pandemic. As a result, small businesses were forced to engage in the digital transformation of their supply chains to further their survival. We saw examples of the digital transformation of small business supply chains through the increased use of digital communication technologies and digital platforms that enabled organizations to continue conducting business in their new environments. These digital solutions became essential for small businesses to continue.

When examining these small businesses and their digitization of business processes, it is important to look at how these processes have changed over time. This perspective was used in the creation of our research question: How has the digitization process for small businesses changed from before, during, to after the Pandemic? Using this question as the basis for all our research, we conducted a systematic literature review to better understand the evolution of small business supply chain information systems in the context of the COVID-19 Pandemic.

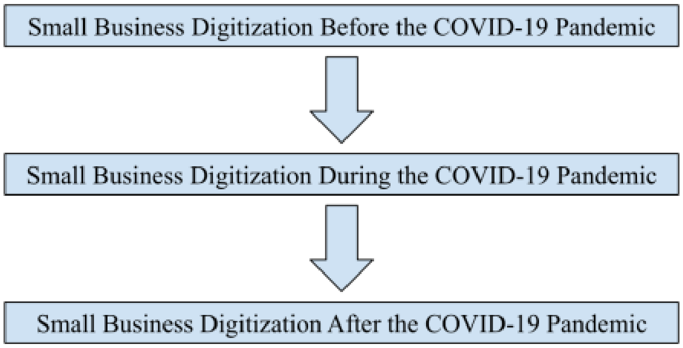

Fig. 1. Illustrates the research Framework of Small Business Digitization Periods

We used a structured systematic literature review to answer our research question. First, records were pulled from business, social science, and technology-related databases. Keywords and phrases such as "small businesses," "digitization," and "COVID-19 Pandemic" were identified and used during the process. Records were then assessed for their relevancy. Finally, records were organized by period as outlined in our framework: before, during, and after the COVID-19 Pandemic. This research's timeline of the COVID-19 Pandemic spanned from March 2020 through the end of 2021. We created a PRISMA diagram to allow our research to be replicated(6).

After screening our results for eligibility, we identified 33 records and counted the number of records from each period.

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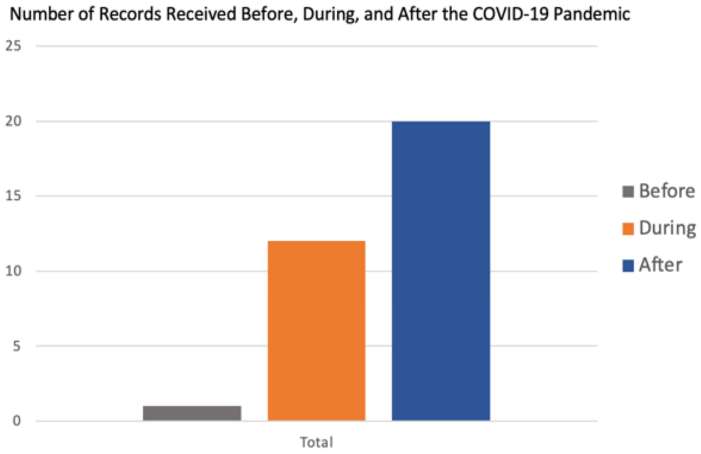

Fig. 2. Counts the total number of records written before, during, and after the COVID-19 Pandemic.

We created this bar chart as a visual representation to show the number of records related to the need for small business digitization written before, during, and after the COVID-19 Pandemic. The number of records written during and after the Pandemic is significantly greater than the number of records received before the Pandemic. This relationship quantitatively shows the Pandemic's role in sparking a need for the digitization of small businesses.

Next, we took the records from each period and extracted themes. Before the COVID-19 Pandemic, the focus was on the digital readiness of small businesses(8). When the Pandemic began, the discussion quickly shifted from the possibility of future digitization to the absolute need for digitization as soon as possible. We found that themes focused on using digitization to survive the COVID-19 Pandemic, using AI as a means of digitization, and opportunities to implement digitization in business processes(1,5,9). In the period after the COVID-19 Pandemic, new themes emerged. These themes focused on the digital solutions needed to survive the lasting supply chain disruptions, the increase in telework after the Pandemic, and sustainability through digitization(3,4,7). From these themes we can better understand how the narrative of small business digitization shifted from before, during, to after the COVID-19 Pandemic.

Before the COVID-19 Pandemic, there was little research surrounding small business digitization, likely because there was little need for small businesses to digitize. During the COVID-19 Pandemic, small businesses had to improve business processes and customer satisfaction with digitization solutions. After the COVID-19 Pandemic, a new normal surfaced. Employees continued to work from home and use digital platforms to work and communicate. COVID-19 has made a lasting impression on business processes. Most implementations, especially surrounding digitization, proved to last.

A more comprehensive answer to the research question can be found using an analysis of media portrayals of small businesses before, during, and after the COVID-19 Pandemic. Reviewing theory from the literature, creating focus groups, interviewing small business owners and employees, and soliciting a large-scale survey would also paint a broader perspective.

Statement of Research Advisor

This systematic literature review sought to better understand the evolution of the supply chain information systems that allowed small businesses to withstand the COVID-19 Pandemic. Results from a thematic analysis of selected research articles indicate that the literature focused on digital readiness in the period before the COVID-19 Pandemic. In the periods during the COVID-19 Pandemic overall themes related to specific technologies such as AI, Web 4.0, and survivability. In the period after the COVID-19 Pandemic, research focused on solutions to reduce disruptions and increase sustainability, among other themes. Future research in this area could benefit from the application of one or more theories on organizational survival, sustainability, and resiliency as well qualitative research data from small business owners and media portrayals.
- Atiya Avery, Harbert College of Business

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Authors Biography

Audrey Osborne is a junior at Auburn University pursuing degrees in Accounting & Information Systems Management. She is an undergraduate research fellow for the Department of Information Systems and Technology. She has presented these findings at the Southern Association for Information Systems as well as the Auburn Student Research Symposium.

Atiya Avery is an Assistant Professor of Information Systems Management at the Harbert College of Business at Auburn University. Her research interests include infrastructure governance, security breach mitigation and recovery, surveillance, and the changing nature of work. With a Ph.D. in Management Information Systems from the University of Illinois at Chicago, she also holds the Associate in Risk Management, Security+, and Certified Information Systems Security Professional (CISSP) designations. Dr. Avery enjoys working with student scholars as she always learns something new along the way.

Sequencing Sex Chromosome Telomeres to Quantify Degradation in Wild Lizard Population

Brynleigh E. Payne[1],, and Tonia S. Schwartz[2]*

[1] Undergraduate Student, Department of Biological Sciences, Auburn University
[2] Associate Professor, Department of Biological Sciences, Auburn University

Telomeres are protective sequences of DNA located at the end of a chromosome that are pertinent to the maintenance of cell survival. Knowledge of the sequences of telomeres on sex chromosomes is especially limited due to their highly repetitive nature and high GC content. We optimized a method to sequence chromosome specific telomeres in the lizard, *Anolis sagrei*. Nanopore sequencing allows a single, long read through the telomere providing chromosome level information that is not acquired through other quantification methods such as qPCR. The aims of this project are to answer these questions: (1) What effect does sex have on telomere length across the lifespan? (2) Do the telomeres on the X and Y chromosomes degrade at different rates? I hypothesize that because women tend to live longer than men, and female lizards live longer than male lizards [1,3], the telomere lengths on sex chromosomes will be longer and degrade more slowly over time in females (i.e., the X chromosome), relative to the Y chromosome in the males.

To address these questions two sequencing trials were planned. The first trial took an adaptive sequencing approach to only enrich for telomere sequences in a sample size of three hatchlings and three adults, consisting of both males and females. Once the sequencing data was collected, it was moved onto Auburn University's high-performance computer, Easley. High Accuracy Basecalling was performed using Guppy (v.6.4.6). In order to assess the quality of the sequence data, FastQC was run on each of the barcoded samples. Each sample met the Nanopore requirement for good quality reads. A summary of the basecalled data was collected using Nanoplot. The total number of reads sequenced was 19,353 and the average read length of those reads was 6,785 bp (Fig 1).

Fig. 1 Nanoplot graph of the distribution of sequenced read lengths

PoreChop (v.3.8.6) was applied to cut off adapters and barcodes, and the data quality for each sample was assessed again with FastQC. The PoreChop data was then mapped to the AnoSag2.1 genome assembly as a reference with Minimap2 (v.2.26). [4]

Findings from the first trial suggest that although the adaptive sequencing collected tandem repeats, many did not map to the ends of the reference genome. This is possibly due to unsequenced regions between the ends of the assembly and where the telomeres begin. We are currently testing other bioinformatic approaches for cataloging and quantifying the telomere repeats sequenced. [2] Due to this delay in the bioinformatic stage of analysis, telomere quantification from the first sequencing trial is still underway.

Moving forward, in the second trial, I will perform a revised Nanopore sequencing method, with the addition of TeloTags to target the telomere lengths in longitudinal blood samples, from the "Field Aging Anoles

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Dataset," to look at sex specific differences at the telomere level of the chromosome. [5] The Field Aging Anoles Dataset is from a mark-recapture study on a wild island population in Florida, in which the individuals were tracked throughout their lifespan. The sample size for this sequencing trial is four males and four females each with three blood samples from across their lifespans.

This research will provide insight on the relationship between sex and telomere length at the level of each chromosome, and how these change with senescence. In addition to filling a gap in knowledge, this research will improve the quality of the *Anolis sagrei* draft genome assembly.

Statement of Research Advisor

The field of aging biology has limited vertebrate models to study sex-specific aging, and we have limited understanding of telomere dynamics in reptiles. This is the first study to sequence sex-specific chromosomes and quantify changes in chromosome-specific telomeres for any reptile. Upon completion of this project, Ms. Payne will have made a major contribution in our ability to use reptiles as a model for sex-specific aging in the field of comparative aging biology as a whole.
- Dr. Tonia Schwartz, Department of Biological Sciences. College of Science and Mathematics

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Authors Biography

Brynleigh E. Payne is a senior-year student pursuing a B.S. degree in Genetics at Auburn University. She has been a member of The Schwartz Lab of Functional and Ecological Genomics since the Spring 2021 semester and is a Summer 2023 Undergraduate Research Fellow. Her research area of interest is in the biomedical field, specifically in diseases related to the aging process.

Dr. Tonia Schwartz is an Associate Professor in the Department of Biological Sciences. Her Lab of Functional Genomics addresses questions about how animals respond to environmental stressors. She served as a mentor to Ms. Brynleigh Payne as she conducted her research on the sex specific telomeres.

Auburn University Journal of Undergraduate Scholarship

Fabrication of Self-Standing Bio-Based Films Containing Hemicelluloses and Pectin

Evie Pearson[1,], Fatimatu Bello[2], Maria S. Peresin[3]*

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[2]Visiting Research Scholar, College of Forestry, Wildlife and Environment, Auburn University
[3]Associate Professor, College of Forestry, Wildlife and Environment, Auburn University

It is no secret that plastics—particularly single-use plastics— are deeply ingrained into our world and lives today. This is problematic for various reasons, including health concerns (Endo, et al. 2005; Andrady, 2011; Cox, et al., 2019), marine litter (Willis, et al., 2018), and plastic waste causing disproportionate effects for those in developing countries (Browning, et al., 2021).

A commonly used type of single-use synthetic plastics is transparent, flexible films. While recycling is possible (though uncommon), there can be a decline in quality of the recycled material (Horodytska, et al., 2018). Additionally, synthetic-based plastics are non-renewable and non-biodegradable causing various environmental concerns. To potentially replace these materials with a more sustainable alternative, research focused on the development of biodegradable composite films using polymers such as pectin and hemicellulose commenced.

Pectin is a natural material obtained from plants (commonly from fruits), and it is an edible polysaccharide that is commonly used in the food industry (Chen, et al., 2020). Hemicellulose is another natural polysaccharide that is found in plants and constitutes up to 35% of the biomass in plants (Egüés, et al., 2013; Gírio, et al., 2010). Since polysaccharides are promising materials to create oxygen barriers, both pectin and hemicellulose are materials of interest for film application (Gröndahl, et al., 2004).

The purpose of the following research is to develop biocomposite films using a combination of galactomannan (a type of hemicellulose) from tara gum and different sources of pectin (apple and soybean hulls) as potential alternatives for traditional synthetic films. To develop the films, solutions containing varying ratios of tara gum and pectin (apple or soy pectin) with glycerol (at an amount of approximately 25% of total film solid weight, which was 0.5 g) as plasticizer were prepared. The compositions are displayed in Table 1. The solutions were stirred on a magnetic stirrer for 1 hour at 50 ^{0}C. The solutions were then poured into polystyrene petri dishes and dried in an oven at 35°C for 5 days. The films were then characterized using various analytical techniques.

Table. 1. Film Compositions

Hemicellulose (% of Solids)	Pectin (% of Solids)
0	100
20	80
40	60
60	40
80	20
100	0

**Note: The amount of glycerol and ultrapure water remained constant at 25 wt.% and 40ml, respectively, in all formulations.*

Preliminary characterizations were done on the films, and, for the purpose of this highlight, the most prominent results will be discussed. All characterizations took place after films remained in a desiccator at least overnight.

Film thickness was measured ten times with micro calipers on each film. The average of the ten measurements was then taken to obtain the thickness value for each composite film. Values are displayed on Table 2. The thickness ranged from 0.071mm to 0.133mm. Though

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the films were prepared with a constant mass of material, there are many different factors that influence the thickness such as drying conditions and interactions between materials used in the films (Sood & Saini, 2022), so this will require further investigation.

Table. 2. Film Thickness

Film Thickness (mm)			
Apple Pectin/Hemicellulose Composite Films		Soybean Hull Pectin/Hemicellulose Composite Films	
Film (% Pectin)	Thickness (mm)	Film (% Pectin)	Thickness (mm)
0*	0.09	0*	0.09
20	0.09	20	0.09
40	0.08	40	0.13
60	0.08	60	0.07
80	0.07	80	0.07
100	0.09	100	0.09

**100% hemicellulose films*

The contact angle of water was measured on a selection of the films. More investigation is necessary to obtain a comprehensive view of this characterization, but the results from the soybean hull pectin composite films could indicate a potential lignin contamination due to increasing zero-time hydrophobicity as pectin content increases. The film with 100% hemicellulose had a zero-time contact angle of 40.30°, while that with 100% pectin had an initial contact angle of 67.23°.

FTIR analysis was performed for each of the films, and the data from the 100% and 60% pectin films and 100% hemicellulose films is displayed on Figure 1 and Figure 2 for apple pectin/hemicellulose composite films and soy pectin/hemicellulose films, respectively. Both spectra indicate the presence of the peak at 3400 to 3300 cm^{-1}, indicating the OH stretching vibration of inter- and intramolecular hydrogen bonding (Sood & Saini, 2022), whereas the bands between 3000 and 2500 cm^{-1} is related to the CH, CH_2, and CH_3 stretching and bending vibrations (Egüés, et al., 2013). The intense peak observed around 1740 cm^{-1} corresponds to the absorption of the esterified carboxylic groups (Sood & Saini, 2022) of the pectin, whereas the absorbance band around 1200 to 980 cm^{-1} could be ascribed to the presence of hemicellulose (Cerqueira, et al., 2011). A peak around 1515 cm^{-1} in the soybean hull pectin/hemicellulose spectra can be attributed to the aromatic vibrations (Boeriu, et al., 2004). This could indicate presence of lignin in the soybean hull pectin, although further characterizations are required to ascertain the claim.

Overall, developing flexible composite films with the materials in the percentages is possible, which could provide the opportunity to diversify application fields. Moving forward, more films will be made to obtain more comprehensive data. The films will also be subjected to mechanical testing.

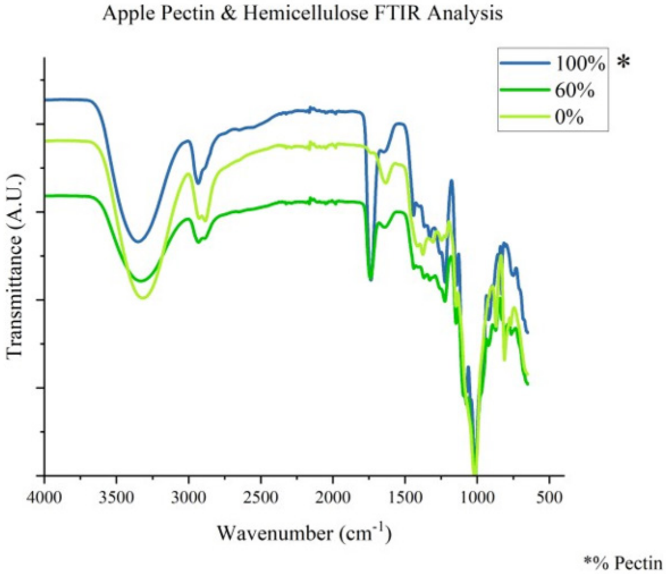

Fig. 1. FTIR Spectra of Apple Pectin Composite Films

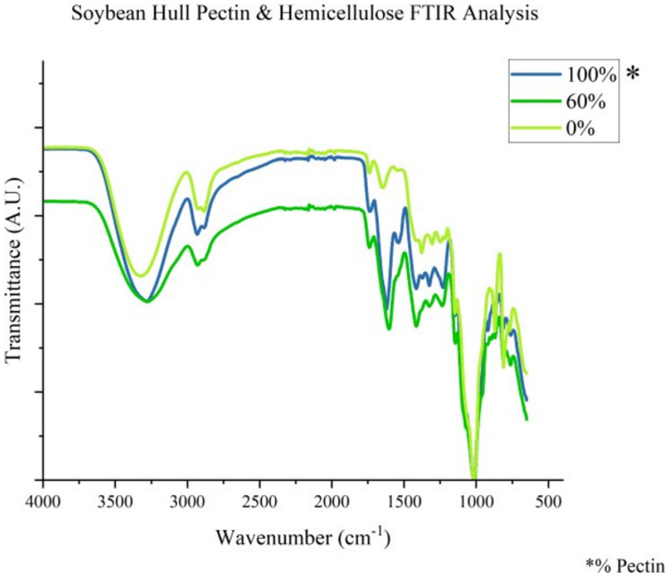

Fig. 2. FTIR Spectra of Soybean Hull Pectin Composite Films

Statement of Research Advisor

Evie has actively developed strategies to develop formulations to cast composite films, while overcoming challenges related to deaeration of the solutions and homogenization to improve film formation. Additionally, Evie has planned and executed experimentation, data collection and analysis. During this period, Evie has shown a great level of maturity in carrying independent work, as well as critical thinking.

- Maria Soledad Peresin, College of Forestry, Wildlife and Environment

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Authors Biography

Evie Pearson is a junior-year student studying Sustainable Biomaterials and Packaging at the College of Forestry, Wildlife and Environment. She has been working in the AU Sustainable Bio-Based Materials lab as an Undergraduate Research Fellow.

Dr. Fatimatu Bello is a Visiting Research Scholar at the College of Forestry, Wildlife and Environment at the AU Sustainable Bio-Based Materials Lab.

Dr. Maria Soledad Peresin is an associate professor at the College of Forestry, Wildlife and Environment. She leads the research initiatives at the AU Sustainable Bio-Based Materials Lab.

Using Neural Networks to Solve Forward and Inverse Problems of Second-Order Ordinary Differential Equations

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[2] C Harry Knowles Endowed Professor, Department of Mathematics and Statistics, Auburn University

Differential equation models are ubiquitous in physics and engineering, and solving them efficiently and accurately is an important task in modern applied mathematics. With the growing success of AI and machine learning in recent years, building deep-learning solvers that could give solutions to these problems in real-time is plausible and exciting. The goal of this project was to develop efficient machine learning algorithms that could accurately predict the solution to second-order ordinary differential equations given the coefficients, the forward problem, and predict the coefficient given the solutions, the inverse problem. The differential equations that this project aimed to solve have the following form:

$$\frac{d}{dx}\left(a(x)\cdot\frac{du}{dx}\right) = f(x), \quad x \epsilon (0,1) \tag{1}$$

To clarify, for some predetermined *f(x),* the forward problem is to solve for *u(x)* given coefficient *a(x)*, and the inverse problem is to solve for *a(x)* given *u(x)*. For simplicity, we assumed the boundary condition $u(0)=0=u(1)$.

In order to develop machine learning algorithms to solve this problem, we first needed to generate data to train them on. To do this, we developed a finite difference solver in MATLAB to compute the solutions of the differential equations numerically. This solver was built using the centered difference approximation, allowing for efficient solving of a tridiagonal linear system [2].

Next, we generated many random coefficients *a(x)* to run through the difference solver to find the corresponding *u(x)* for each one. We found that the coefficient needed to be continuous, smooth, and positive, so we used the Karhunen-Loeve (K-L) Expansion [3] to generate many different pseudo-random coefficients.

The K-L Expansion we used is given by:

$$a(x) = \mu + \sum_{k=1}^{100} \lambda_k \cdot \xi_k \cdot \cos(k\pi x), \tag{2}$$

where, $\lambda_k = 1/k^2\pi^2$ and ξ_k is a random variable. By testing with trial and error, we found that using a mean $\mu=4$ and pulling each ξ_k from the normal distribution, N(0,50), gave the best results for our purposes. We also assume the following source function:

$$f(x) = 200 \cdot (x^2 - x) \cdot \sin(10x). \tag{3}$$

With this all coded in MATLAB and decided, we were able to efficiently generate data to train our machine learning algorithm consisting of 5,000 pairs of coefficients *a(x)* and their corresponding solutions *u(x)*, each with 100 steps from 0 to 1, or 99 data points in between.

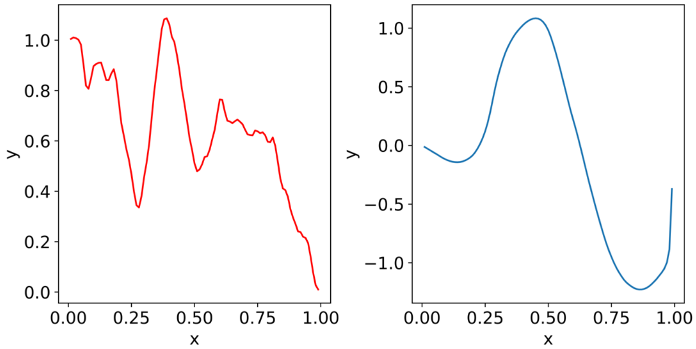

Fig. 1 An example pair of coefficient *a(x)* (left) and solution *u(x)* (right)

Once the data was generated in pairs as shown in Fig-

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*Corresponding author:jtp0064@auburn.edu ure 1, work began on constructing neural networks in Python using the PyTorch library to find the map from *a(x)* to *u(x)*.

The first task was to develop autoencoders to reduce the dimensions of both *a(x)* and *u(x)*, so we could find the map between them in the new low dimension. Autoencoders are special kinds of neural networks designed to reduce the dimensions of some set of data. They consist of two parts: the encoder to get to the low dimension, and the decoder to get back to the high dimension. These are adjusted simultaneously by running an input through both and using back-propagation with a cost function defined as the difference between the input and the output of the autoencoder [1].

We found that the most effective autoencoders for both *a* and *u* did not use a traditional activation function but one simple linear transformation to the low dimension. The a autoencoder could reduce the coefficient from 99 to 15 data points with 3 digits of accuracy, and the *u* autoencoder could reduce from 99 to 25 with the same accuracy.

Once these autoencoders were developed, we could work on the network to map the coefficient to solution (the forward map). Although we pursued training all autoencoders and this map together, we found that we had more accurate results when training both autoencoders and the map in the low dimension separately. We also found through testing on another generated dataset that we needed more data to train on, so we generated 100,000 coefficient-solution pairs.

Ultimately, by training on this new data set, we were able to train a network (as shown in Figure 2) so that it had an average mean squared error of 0.01 between the low-dimension solution and the network's predicted solution, and an average error of 0.02 between the true high-dimension solution and predicted solution of the test data. The network consisted of 5 layers of neurons, first with 30, then 50, 100, 50, and 30 neurons in the layers and the rectified linear unit activation function between them.

After work on the forward problem, we did similar work on the inverse problem using the same generated data, just looking for the map from *u(x)* to *a(x)*. This problem proved more challenging, as the coefficient had more features that the model needed to learn from fewer features in the solution *u*.

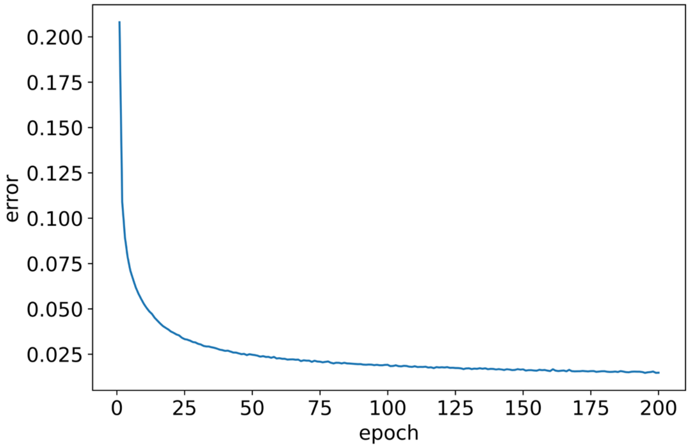

Fig. 2 A plot showing the error for each epoch of the forward network during training.

Because of this, we found that we needed a much larger network, consisting of 7 layers increasing to 1000 neurons, so that the model had the necessary degrees of freedom to accommodate such a map. We also found that, although it was about twice as expensive in terms of training time, training directly from *u(x)* to *a(x)* in the high dimension without using autoencoders proved more accurate than reducing each again. Ultimately, after completing the training (Figure 3), we were able to produce an average mean squared error of 0.009 between the network's predicted coefficient and the true coefficient in the inverse problem as well. The first layer was 99 neurons, then 200, 500, 1000, 500, 200, and 99 neurons, and we once again used the rectified linear unit activation function.

In conclusion, we were able to develop algorithms that could predict both forward and inverse problems with high accuracy. This work suggests that newly built neural network architecture can efficiently obtain solutions to a broad variety of differential equations. Further research must be conducted to test whether such neural networks can be used to solve the more complex partial differential equations; however, this project shed some light on attacking those problems.

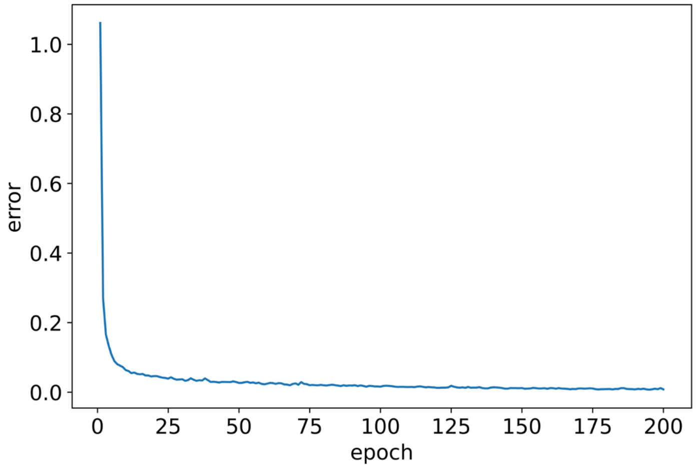

Fig. 3 A plot showing the error for each epoch of the inverse network during training.

Statement of Research Advisor

Jacob Pennington has developed a reduced-order based neural network for solving the forward and inverse problems in differential equations. He independently generated the training data using the finite difference method and trained the network using the stochastic gradient method in Pytorch. Through numerous numerical tests, it is shown that the new neural network is able to represent the forward and inverse maps for differential equations. The work sheds light for future investigation for the modeling of more complicated mathematic models using the reduced-order based networks.
- Dr. Junshan Lin, Department of Mathematics and Statistics, College of Sciences and Mathematics

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Authors Biography

Jacob T. Pennington is a junior-year student pursuing a B.S. in Applied Mathematics at Auburn University. He plans to graduate in Spring 2024 and continue to work and learn in data science and machine learning while pursuing his M.S. in Data Science and Engineering the following year.

Junshan Lin is the C Harry Knowles Endowed Professor in Department of Mathematics and Statistics at Auburn University. He joined Auburn University in 2013 as an assistant professor, and was promoted to associate and full professor in 2018 and 2023. His research focuses on applied and numerical analysis, and scientific computation. He develops mathematical tools to solve scientific problems for waves in novel devices and materials, inverse wave scattering and imaging, computational inverse and optimal design problems. He has published over 40 papers in applied and computational mathematics journals and has delivered over 100 talks in a variety of international conferences and universities worldwide.

Computational Analysis of the Peptide Hydrolysis Pathway of Serine Proteases: Novel Reaction Engineering Perspectives

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Comprising more than one third of all proteases, serine proteases are the largest known category in the protease enzyme subclass. These enzymes are ubiquitous in nature, are present in all known organisms, and can be active under temperatures ranging from 4˚C to 65˚C. Additionally, serine protease-based products occupy over 90% of the current global protease market, spanning household detergents, waste management, leather processes, food processing, biomedical applications, and more. However, issues behind the hydrolysis reaction mechanism via this enzyme have arisen recently in literature—particularly regarding a high-energy transition state called the "histidine (His) flip." We propose an alternative, charge-neutral (with no charge separation) step that potentially allows for a more favorable reaction pathway. Better understanding this new hydrolysis reaction pathway will allow us to develop more accurate reaction rate law expressions to increase the efficiency of industrial processes involving these enzymes.

Investigation of the serine protease reaction pathway involves implementing a quantum mechanics (QM) cluster analysis on the enzyme active site, employing density functional theory (DFT) methodology. QM-cluster calculations allow for a more accurate and higher theoretical level and free transition state (TS) determination, as opposed to just a free energy surface, for example. To choose how big of a cluster to include, we decided to include all amino acid residues that are directly involved in the catalytic process, as well as all neighboring amino acids that are important to maintain the active site topology and those participating in hydrogen bonding with the reacting atoms. We propose that the inclusion of all these factors provides a robust model with minimal geometry restriction (i.e., freezing of the atoms at the boundary of the cluster).

This project is still ongoing, but we have discovered certain preliminary results regarding the serine protease reaction pathway. Our reaction coordinate results are in accordance with the historical reaction profile shape but seem to be overestimating the activation barriers as compared to literature. We expect that increasing the cluster size will result in lowering these energies. Our proposed alternative mechanism has indeed yielded a more favorable reaction profile, and we will continue to investigate this new profile by calculating its corresponding transition states, along with comparing against profiles calculated with other density functionals.

The impact of this study is to provide more efficient reaction parameters for chemical processes using serine proteases, from length scales ranging from industrial bioreactors to drug design. From our calculations, we will soon be able to determine the reaction rate constants, which could eventually be used in reaction rate law expressions. An effective reaction rate law would enable better prediction of many reaction properties, such as how much reactant is needed, what concentrations of reactants is ideal, or how long it would take for the reaction to proceed—all highly important factors when optimization large-scale bioreactors or targeted drug delivery dosages.

Statement of Research Advisor

Dylan Pollard has contributed to ongoing research efforts in computational modeling of catalysis, working closely with Ashraf Ali and group members. The project gave him the opportunity to connect fundamental chemical

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engineering and chemistry concepts to real-world applications.
- Dr. Andrew J. Adamczyk, Chemical Engineering, Samuel Ginn College of Engineering

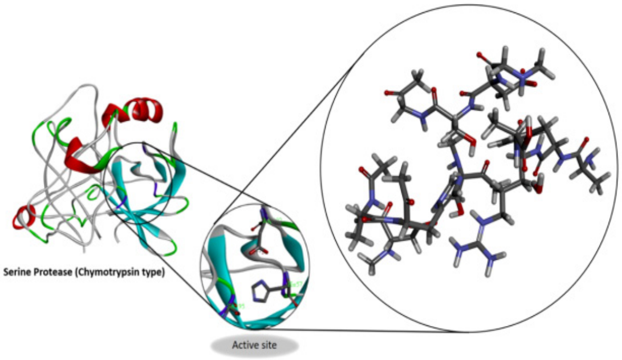

Fig. 1. QM-cluster active site of serine protease used in this study.

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Authors Biography

Dylan Pollard is a senior at Auburn University majoring in chemical engineering and physics. He will attend the University of California, Santa Barbara for their PhD program in chemical engineering. His undergraduate research included heterogeneous/ enzymatic catalysis and machine learning (REU).

Dr. Andrew Adamczyk is an assistant professor in the Dept. of Chemical Engineering at Auburn University. He has been at Auburn since 2018 and conducts research using computation chemistry and physics, kinetic modeling, and reaction engineering principles to better understand complex reacting systems.

Dr. Ashraf Ali is a postdoctoral researcher in the Kieslich Lab in the Dept. of Chemical Engineering at Auburn University. He recently received his PhD at Auburn University. Ashraf uses mathematical optimization, and data science to predict how molecular changes affect their therapeutic properties.

Characterization of a Viral Suppressor of RNA Silencing Encoded by CLRDV-AL

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Cotton leafroll dwarf virus (CLRDV) is an infectious agent of Cotton Blue Disease. CLRDV is a member of the genus Polerovirus (Delfosse et al., 2014). CLRDV has six open reading frames (ORFs). Among them, ORF 0 encodes P0, which was identified as a viral suppressor of RNA silencing (VSR). CLRDV strains that were prevalent and caused severe yield loss in the cotton industry in African and South American countries had noteworthy differences among their VSRs, the P0 proteins (Agrofoglio et al., 2019). VSRs allow the virus to infect the host by disrupting the RNA silencing process, a major conserved mechanism, in which dsRNA is cleaved into siRNA by Dicer (Baulcombe, 2004; Wassenegger, 2002).

A new CLRDV strain has been isolated from Alabama and the rest of the United States Cotton Belt. To understand the pathogenicity of the Alabama strain of CLRDV (CLRDV-AL), our project aimed to characterize a CLRDV-AL encoded VSR, P0 protein, by expressing various recombinant P0 proteins via *Agrobacterium*-mediated infiltration to examine them for silencing suppression potency, intracellular localization, and self-interaction.

Sequence alignment comparing CLRDV-AL to the previously isolated strains from South American countries indeed showed some mutations within the domain known for VSR function (Agrofoglio et al., 2019).

To verify the P0 protein's ability to suppress the RNA silencing, P0 was concurrently expressed next to the VSRs from other viruses along with a green fluorescent protein (GFP) in *Nicotiana benthamiana* 16c plants, a transgenic line that constitutively expresses GFP (Fig. 1). This assay demonstrated that P0 protein of CLRDV-AL is not a potent silencing suppressor compared to other VSRs such as P19 and HC-Pro known for their strong silencing suppression.

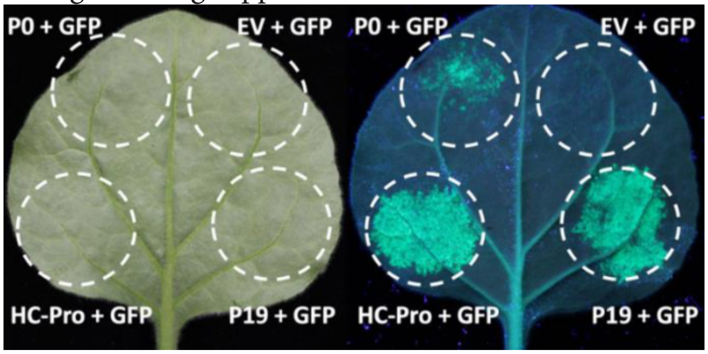

Fig. 1. GFP silencing and its suppression in GFP-transgenic N. benthamiana plants.

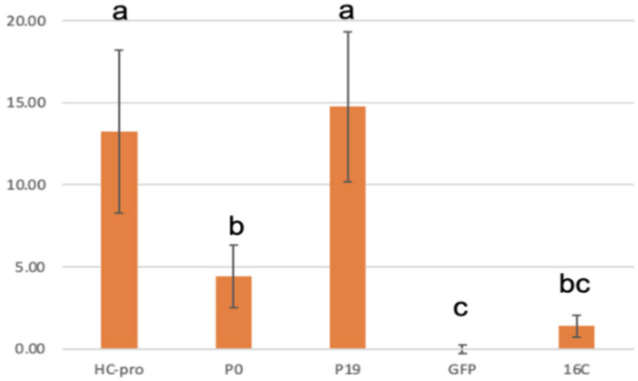

Fig. 2. The P0 protein of CLRDV-AL is a weak VSR.

Infiltrated leaf tissue showing suppression of GFP silencing was examined using a fluorescence microscope. The fluorescence intensity was calculated from more than 15 images per treatment using Region of Interest (ROI) on ImageJ, and the relative intensity was analyzed by a one-way ANOVA test in R (Fig. 2; significant difference, $p < 0.01$, was denoted by letters).

As some VSRs are known to form a dimer that interacts with small-interfering RNAs, the self-interaction of P0 proteins was examined using the yeast-two-hybrid

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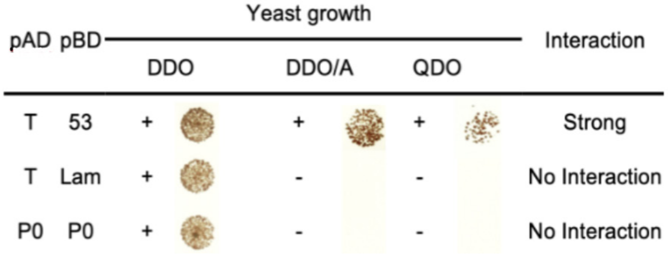
(YTH) assay (Fig. 3). No growth of the co-transformed yeast cells on the selective media implied no homo-dimerization of CLRDV-AL P0 proteins.



pAD	pBD	Yeast growth			Interaction
		DDO	DDO/A	QDO	
T	53	+	+	+	Strong
T	Lam	+	-	-	No Interaction
P0	P0	+	-	-	No Interaction

Fig. 3. Self-interaction of CLRDV-AL P0 protein. A pair of pAD-T and pBD-53 is a positive control. A pair of pAD-T and pBD-Lam is a negative control.

The intracellular localization of P0 investigated by expressing GFP-tagged P0 proteins in the plant cells using a fluorescence microscope revealed the possibility of P0 protein being a membrane-bound protein (data not shown). Hence, considering YTH is not a suitable method for the membrane proteins, the homo-dimerization of P0 proteins is still in question.

Our study showed that VSR encoded by CLRDV-AL has interesting characteristics that differ from well-known VSRs. More studies may be needed to identify the cause of such differences further.

Statement of Research Advisor

Bailee was an inaugural member of the AU plant virology lab, and she continued her research as an undergraduate research fellow. Bailee led and conducted experiments in this project, from constructing various clones to testing them in plants and yeasts. A graduate research assistant, Mary Akinyuwa, assisted her with acquiring and analyzing the data. This research demonstrated peculiar characteristics of the protein encoded by newly isolated Polerovirus.

- Sung-Hwan Kang, Entomology and Plant Pathology, College of Agriculture

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Authors Biography

Bailee K. Price is a senior-year student pursuing a B.S. in Biomedical Sciences at Auburn University. She was a research assistant and, subsequently, a research fellow in the Plant Virology laboratory. She has played key research roles in the alignment of sequences, cloning of constructs, agroinfiltration, and YTH assays.

Mary F. Akinyuwa is a Ph.D. student at Auburn University. Her research focuses on the molecular characterization of viral proteins. She earned M.Sc. in Plant Health from the European Erasmus Mundus program. She has contributed to the study by assisting with microscopy, YTH assay, and analyses of fluorescence images.

Sung-Hwan Kang, Ph.D., is an assistant professor of plant virology at Auburn University, where he began working in 2020. He earned his Ph.D. in Microbiology and Molecular Biology at the University of Nebraska. His research interest includes the molecular mechanism of host infection by viral pathogens in plants.

Investigating Invisible Labor in Tabletop Role-Playing Game Actual Play

Olivia J. Price[1,], Emily C. Friedman[2], Chase A. Bringardner[3]*

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[2]Postdoctoral Researcher, Department of English, Auburn University
[3]Assistant Professor, Department of Theatre and Dance, Auburn University

The popularity of Tabletop Role-Playing Game (TTRPG) streaming has grown exponentially in the last few decades, making way for a new hybrid between film, theatre, and television: Actual Play (AP). These transmedia shows incorporate different aspects of each entertainment model to deliver TTRPGs in the form of a livestreamed or pre-recorded broadcast. Audiences are invited to watch a group of people gather to play a game and maintain a narrative throughout an episode. An Actual Play often works to establish the atmosphere of these imagined circumstances. Viewers often interact with the Actual Play participants in some way: they may be able to donate and change the trajectory of the narrative, make live comments, or vote for their favorite player. However, invisible labor remains concealed throughout the production process. Who works behind the scenes of Actual Plays, and how is invisible labor orchestrated in a genre that continues to transform?

Fig. 1. Production shot from Hyper RPG's KOIIOK. Photo from Hyper RPG's website.

Actual Play production groups like Critical Role, Dimension 20, and Hyper RPG (Figure 1) have garnered large fanbases for the quality of their shows. Lighting, scenic, audio, and camera effects are deployed to further entrench the audience and players in the ongoing narrative; this develops a suspension of disbelief similar to live theatrical performance. So long as that labor is hidden in some way, the dissonance between product and labor remains.

With a limited pool of previous research to draw upon, firsthand accounts from participants who conduct invisible labor are the defining trait of this project. While there has been some scholarly exploration of Actual Play, this specific focus on invisible labor has seen little previous research. Dr. Alex Chalk's "Mapping an online production network" was integral in establishing a working vocabulary and general trajectory. Dr. Christin Essin's invaluable Working Backstage (on the choreography of Broadway's backstage labor) provided a general framework within which interviews would be conducted. Her qualitative oral interview strategies were drawn upon for the purposes of this project, refitted for the context of Actual Play.

This project's interviews were conducted via Zoom and in- person with several Actual Play production team members of different scales. Some interviewees were practitioners of invisible labor outside of AP (film, television, theatre), while others were hobbyists who gravitated toward it by their involvement in the TTRPG community. These unique perspectives come together to influence the nebulous shape of AP, with different practitioners and their strategies informing others to produce inimitable works of all scales.

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Fig. 2. Off-camera shot from Hyper RPG's KOIIOK. Photo from Hyper RPG's website.

The differing scales of Actual Plays are key to understanding how a labor framework comes to fruition: budget, location, modality, and time frame decide exactly how labor is to be sourced and organized. An AP that follows the television model may be produced entirely in a filming studio with 10 to 15 team members (Figure 2). A show that is produced virtually (via Zoom or a similar online platform) may be orchestrated entirely by one person running audio and camera effects remotely. These modalities form a spectrum, which presents striations in labor demands that are difficult to cleanly categorize. No two productions are the same.

Revealing the invisible, or off-camera, labor of Actual Play acts as a mirror to the state of entertainment. This project has only led to more questions: how agile must invisible labor be, depending on the modalities and scale of a production? How can social media platforms be used to acknowledge the efforts of invisible labors and, in turn, increase the public's perception of a show's production value? These questions will be answered through further study and more conversations with more Actual Play participants.

These interviews, along with the gradual compilation of a resource bibliography and exploration of academic works, have become the premise for scholarly research on invisible labor in Actual Play. New works in the AP space will continue to generate conversation on how labor occurs in digital and physical environments. The modalities of labor continue to transform in the performance field post-pandemic; this growth combined with the exponential popularity of Actual Play will produce new perspectives on how labor can be sourced and organized in transmedia spaces. This project is meant to serve as a basis on which other scholars may build their studies and as a living, evolving collection of resources and ideas for coming expansion.

Statement of Research Advisor

Asking questions about craft and labor largely unexplored in this genre, Olivia Price conducted informational interviews and made site visits to better understand the contexts for backstage/off-camera work in the world of performed tabletop roleplaying games, or "actual play." This research allows us not only to better understand the nature of this performance form (which is practiced by both amateurs and professionals on the same platforms), but also creative labor in new digital media more broadly.

- Dr. Emily C. Friedman, Department of English, College of Liberal Arts

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Authors Biography

Olivia J. Price is a senior-year student pursuing a B.A. degree in English Professional and Public Writing and a B.F.A. degree in Theatre Design and Technology at Auburn University. As a theatre student, she studies performance and actively participates as a force of backstage labor in the lighting and scenic fields. Her research on invisible labor and its presence in media will continue to expand outside of her undergraduate career.

Emily C. Friedman is an Associate Professor of English at Auburn University. An eighteenth-centuryist and book historian by training, her current work focuses on the long history of creativity outside commercial mass media, from never-published manuscript fiction of the 18th and 19th centuries to creator cultures of the 21st. Her current book project is Improvised Worlds: Digital Storytelling through Play.

Chase A. Bringardner is a Professor of Theatre at Auburn University and the Chair of Auburn's Department of Theatre & Dance. His research interests include regional identity construction and intersections of race, gender, and class in popular performance. He has contributed articles and reviews to publications such as Theatre Topics, Theatre Journal, Studies in Musical Theatre, Theatre Symposium, and Southern Theatre. He has also published chapters in volumes including The Oxford Handbook of the American Musical, The Cambridge Companion to American Theatre since 1945, and The Great North American Stage Directors, Volume 4: George Abbott, Vinnette Carroll, and Harold Prince (where he also served as co-editor). He is the president of the Association for Theatre in Higher Education (ATHE).

Emotional Regulation and Suicide Risk in Adolescents Adjudicated for Illegal Sexual Offenses

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[2] Assistant Professor, Department of Psychology & Sociology, Texas A&M University-Kingsville

Suicide is an important risk factor for incarcerated youth given the high rates of trauma experienced (OJJDP, 2020). Trauma has a significant effect on the onset of suicidal ideation, or thoughts and feelings related to suicide (Lannoy et al., 2022). Adolescents adjudicated for illegal sexual behavior (AISB), experience significantly more trauma, making them potentially more susceptible to suicidal ideation (Seto & Lalumiere, 2010). Emotional regulation, or one's ability to recognize and understand emotional states and respond in an adaptive way, is another correlate of suicide prevalent in AISB (Berman & Knight, 2015). One correlate is hyper-responsiveness, or an overreaction to emotionally triggering stimuli (Carthy et al., 2010). In youth and adult populations, this form of emotional distress was positively correlated in both the presence of and severity with suicidal ideation (Neacsiu et al., 2018). The current study sought to establish a link between suicidal ideation and self-reported hyper-responsiveness to trauma in a sample of AISB.

Data was collected from a sample of AISB (n=165) at a court mandated residential treatment facility in the southeastern United States. The Millon Adolescent Clinical Inventory (MACI; Millon & Davis, 1993) is a 165-item self-report questionnaire used to assess clinical mental health symptoms and personality features in adolescents from 13-18 years of age. Thoughts and behaviors related to suicide were measured using the suicidal ideation scale. The Trauma Symptom Checklist for Children (TSCC; Briere, 1996) is a 54-item self-report questionnaire used to assess the presence of trauma symptoms in children ages 8-16. The hyper-responsivity scale was used to assess heightened emotional responses to trauma.

Linear regression was used to evaluate the relationship between reported suicidal ideation and the trauma symptom scales. The overall model was significant, F(2, 164) = 38.90, p = .001, indicating a significant positive association between suicidal ideation and hyper-responsivity (r = .502, p < .001) as seen in the scatterplot results depicting in Figure 1.

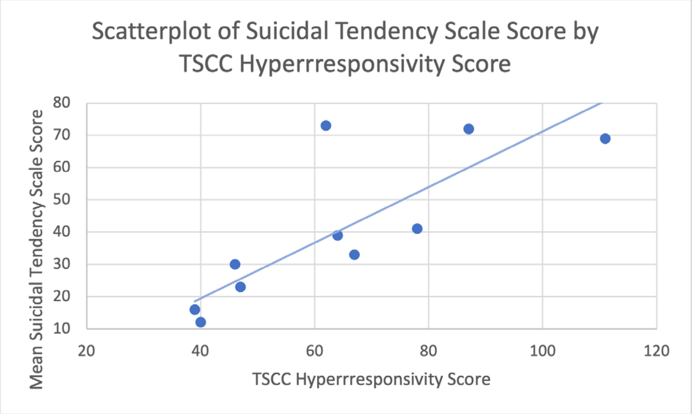

Fig. 1 Linear association of suicidality and a hyper-responsivity to childhood trauma

This positive relationship between self-reports of suicidal ideation and features of hyper-responsivity implies that those who respond externally to stress may be at a higher risk for suicidal ideation. This supports previous data that heightened emotional states as a response to emotionally triggering stimuli are related to suicidal ideation, highlighting the interaction between traumatic life events, maladaptive coping strategies, and suicide risk (Neacsiu et al, 2018). AISB may be at a higher risk for suicidal ideation due to the increased presence of emotional dysregulation and traumatic life events (Seto & Lalumiere, 2010), as well as a lack of outlets for young men to express emotion. Facilities treating AISB may

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implement more proactive approaches in addressing ideation in treatment, rather than an entirely reactive approach of close monitoring once symptoms spiked.

Statement of Research Advisor

Madeleine independently started this project after joining my lab as a Research Assistant a year earlier. After working with the archival data for a while, she found some variables of interest, and set about designing a research question of her own. She presented this data locally at the AU student symposium and regionally at the Southeastern Psychological Association's annual conference in New Orleans, LA in April 2023.

- Kelli Thompson, Department of Psychology, College of Liberal Arts

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Authors Biography

Madeleine Rein is a Senior-year student pursuing a degree in Psychology at Auburn University. She was awarded a Research Fellowship for the 2023-2024 school year. Her research interests include suicide, trauma exposure, and mental health in forensic clincal settings.

Kelli R. Thompson is an undergraduate alumni from Auburn University. She is the former Director of the Juvenile Delinquency Lab at Auburn University. During her time at Auburn she mentored more than a half-dozen Undergraduate Research Fellows through her lab. She is dedicated to helping students find their way into the field of psychology through research. She is now an Assistant Professor of Psychology at Texas A&M University-Kingsville where she continues a strong tradition of student mentoring.

Effect of Preservation Method on Nutritive Value of Kudzu Forage

Diva Rigney[1,], Abbigail R. Hines[2], Courtney Heaton[3] and W. Brandon Smith[4]*

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[2] Graduate Student, Department of Animal Sciences, Auburn University, Auburn University
[3]Lecturer, Department of Animal Sciences, Auburn University, Auburn University
[4]Assistant Professor, Department of Animal Sciences, Auburn University, Auburn University

Kudzu *(Puerarira montana [Lour.] Merr.*) is a drought tolerant perennial leguminous vine native to Asia. The species was brought to the United States as an ornamental crop that became a solution for soil erosion during the Dust Bowl when southern farmers were encouraged to plant the now invasive species. In the 1950s, kudzu was removed from the cover crop list, and was later labeled as an invasive plant species by the USDA (Everest et al., 1999). Early research on kudzu as a pasture crop found that it has a high nutritive value and nitrogen-fixation ability. The leaf was found to have a higher nutritive value than what was recommended by the National Research Council (Glass and Al-Hamdani, 2016). The leaf has been found to be rich in crude protein at 17.5% (Corley et al., 1997) which is comparable to alfalfa values at 18.7% (NRC, 2012). The leaf has also had similar neutral detergent fiber (NDF) and acid detergent fiber (ADF) values, 48.1% and 38.2%, (Corley et al., 1997) to that of alfalfa, 46.0% and 36.9% respectively. (NRC, 2012). However, research on kudzu was abandoned for years, making animal data on the usage limiting (Gulizia et al. 2019). Recent efforts in sustainable agriculture have renewed interest in the potential use of kudzu.

The purpose of this study was to evaluate the effects preservation method on nutritive value and digestibility of kudzu forage. Our experiment was conducted as a completely randomized design. A single treatment factor (preservation method) was employed with two levels (fresh or sun-cured [representing the haying process]).

For this experiment, we selected a stand of kudzu on a private property in Auburn, Alabama. Two independent plots at this location were identified for harvest. Herbage was sampled from each plot by hand-clipping at a quadrat (0.25 m^2) four random locations within each plot to determine biomass. Total herbage was removed using a two-wheeled tractor (BCS Model 853, BCS American, Oregon City, OR) fitted with a sickle-bar mower attachment. Fresh kudzu was immediately removed from each plot. Sun-cured kudzu (representing the haying process) was removed once a target moisture of 20% was achieved (determined by microwave testing).

Samples of forage from each level of the treatment factor were dried at 50°C in a forced air oven for 72 h following collection. Oven-dried samples were ground to pass through a 2-mm screen using a Wiley mill, and a subsample was ground to pass through a 1-mm screen. Fiber fractions (NDF and ADF) were assayed sequentially according to the procedures of Vogel et al. (1999) using an ANKOM2000 and ANKOM DELTA Fiber Analyzers. Acid detergent lignin (ADL) was assayed on the ADF residues according to the procedures of AOAC (2000). Crude protein (CP) was measured using the Kjeldahl method (AOAC, 2000). In vitro true disappearance (IVTD) was also measured (Vogel et. al 1999) using the ANKOM DaisyII incubator.

Data was analyzed using SAS v. 9.4 (SAS Institute, Inc., Cary, NC, USA). All response variables were analyzed using the generalized linear mixed models procedure (PROC GLIMMIX) in SAS. For measures of nutritive value, the model included the fixed effect of preservation method. For in vitro true disappearance, the model included the fixed effect of preservation method and the random effects of incubation vessel and inoculum source. Denominator degrees of freedom were adjusted

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using the second-order Kenward-Roger approximation method (Kenward and Roger, 2009). Least squares means were computed for the main effect of preservation method. The α-level for mean differences was set at 0.05. Means separations were performed based on F protected t-tests using Tukey-Kramer's HSD (Kramer, 1956).

There was no statistically significant effect of preservation method on NDF (P = 0.45), ADF (P = 0.50), ADL (P = 0.39), or CP (P = 0.79) concentrations (Table 1). However, sun cured kudzu had a greater ($P < 0.01$) IVTD than did fresh kudzu (Figure 1).

Table 1. Nutritive value of fresh and sun-cured (hay_ kudzu harvested in Auburn, AL.

Preservation method	NDF %	ADF %	ADL %	CP %
Fresh	54.50	40.00	20.10	11.52
Hay	51.65	37.48	14.96	11.13

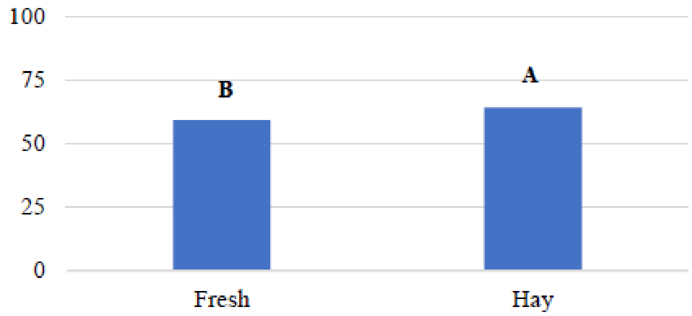

Fig. 1. In vitro true disappearance (IVTD) of fresh and sun-cured (hay) kudzu forage harvested in Auburn, AL.

To understand the context in which kudzu forage may be beneficial for livestock operations, it is helpful to compare it to more commonly used leguminous species. According to NRC (2012), alfalfa presents NDF, ADF, and CP concentrations of 46%, 37%, and 19% respectively. Similarly, perennial peanut has been documented to have NDF, ADF, and CP concentrations of 46%, 34%, and 11%, respectively (Eckert et al., 2010). In our study, regardless of preservation method, kudzu had greater NDF concentrations and similar ADF concentrations, while CP concentrations were more similar to perennial peanut than to alfalfa. Seasonality has also been shown to play a significant role in nutritive value of kudzu forage. The kudzu harvested in our study would be considered late season (harvested in October 2022). A study by Gulizia et. al (2019) found that kudzu leaves in late season had NDF, ADF, and CP concentrations of 45.7%, 26.2%, and 26.7%, respectively. The differences in our samples and those of Guliza et al. (2019) are likely due to their samples only containing the leaf portion of kudzu and our samples containing both leaf and stem portions. While dry matter demand was influenced based on age variability, the rumen degradability of kudzu was similar across early and late season kudzu. However, early season kudzu was found to be more rumen degradable than late season kudzu as the plant is younger with limited stores of carbohydrates. Producers could utilize this information to manage kudzu growth for the purpose of livestock browsing. The research of Guliza et al. (2019) showed that kudzu is a nutritious and highly degradable legume for the ruminant diet.

In summary, while preservation method of kudzu forage had no effect on nutritive value parameters (NDF, ADF, ADL, or CP), there was a measurable improvement in digestibility in the sun-curing (i.e., haying) process. Regardless of treatment, nutritive value and digestibility estimates obtained from this experiment are interpreted to mean that kudzu may represent a viable, low-quality roughage for use in ruminant livestock production systems

Statement of Research Advisor

Diva's work with an unorthodox and novel forage species is setting the foundation for further work in the Ruminant Nutrition Laboratory at Auburn University. Data from her experiment will form the basis for future student endeavors in novel forage and byproduct feeding systems, ultimately contributing to a more efficient and sustainable beef production model for Alabama. Diva aided in the development of the research protocol and was solely responsible for the assays described herein. The skills that she developed through this experience will serve her well in her next stage as a ruminant nutrition master's student.

- Dr. Brandon Smith, Assistant Professor, College of Agriculture

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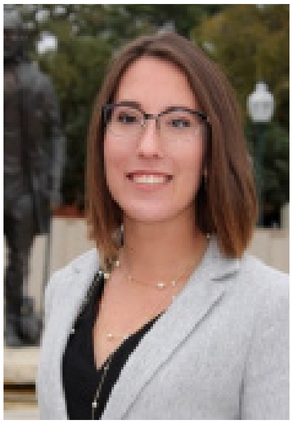
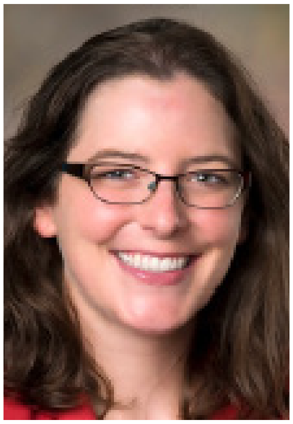
Authors Biography

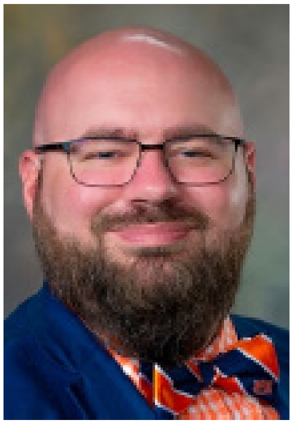
Diva Rigney is a senior pursuing a B.S. degree in Animal Sciences at Auburn University.



Abbigail Hines is PhD student pursing a PhD in Ruminant Nutrition at Auburn University.



Courtney Heaton is a lecturer and Equine Extension Specialist in the Department of Animal Sciences at Auburn University.



W. Brandon Smith is an assistant professor of Ruminant Nutrition in Forage Systems in the Department of Animal Sciences at Auburn University.

Assessment of Early-Stage Thermal Manipulation on Broiler Chicken Muscle Satellite Cell Population Densities at Transfer and at Hatch

J. Wesley Rogers[1], Brittany L. Hutson[2], Martha Rueda[2], Jeremiah D. Davis[3], Joseph L. Purswell[4], Charles W. Starkey[5] and Jessica D. Starkey[6,]*

[1] Undergraduate Student, Department of Animal Sciences, Auburn University
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Multi-stage hatching egg incubators are challenging to manage but still common throughout the US broiler industry. It is difficult to satisfy all embryonic temperature requirements in systems where late-stage embryos must be kept from overheating while ensuring early-stage embryos are not at sub-optimal temperatures.

Preliminary data generated by our research group at Auburn University showed improvements in performance and meat yield when incubation temperature was increased to 38.6 °C from embryonic day (ED) 4 to 11 as opposed to lowering it to 36.4 °C compared with a 37.5 °C control. It was hypothesized that incubation temperature differences impacted satellite cell (SC) activity in our previous study and led to the differences in performance and meat yield. Muscle SC are muscle specific stem cells that serve as the rate limiting step in post-hatch hypertrophic muscle growth. Therefore, the objective of this study was to assess the effect of thermal manipulation during early-stage incubation (ESI) on SC heterogeneity in broiler chicks at transfer and hatch to explore the mechanism responsible for increased meat yield in our previous study.

Broiler breeder eggs (n = 2,160) were incubated at 37.5 °C from embryonic day (ED) 0 to 3. On ED 4, COLD incubator setpoints decreased to 36.4 °C, HOT incubator setpoints increased to 38.6 °C, and control incubators remained 37.5 °C (n = 2 incubators per treatment). On ED 11, all incubators were set to 37.5 °C until ED 18 when eggs were transferred to hatchers. At transfer (ED 18) and hatch (ED 21), pectoralis major (PM) and biceps femoris (BF) muscle samples were collected from 6 chicks per treatment. Samples were immunofluorescence stained to facilitate taxonomy of SC populations expressing the myogenic regulatory factors and SC markers, MyoD, MRF4, and Myf5, by fluorescence microscopy.

Data was analyzed as a 1-way ANOVA with the GLIMMIX procedure of SAS. Means were separated at $p \leq 0.05$ with the PDIFF option. Tendencies were declared when $0.0501 \leq p \leq 0.10$. Chicks from COLD incubators had the greatest density of MyoD+:Myf5+ SC in their BF ($p = 0.0261$) and tended to have a greater density of MyoD+:MRF4+ SC in their PM muscle ($p = 0.0562$) compared with chicks from HOT incubators at transfer on ED 18. On ED 21, chicks from HOT incubators had the greatest density of MyoD+:MRF4+:Myf5+ SC in their PM muscle ($p = 0.0406$). Temperature gradients as small as 1.1 °C during ESI altered BF SC populations in chicks at transfer and PM SC populations at both transfer and hatch.

Overall, these results indicate that thermal manipulation during ESI can influence SC population kinetics in both PM and BF muscles of modern, fast-growing, high-yielding broiler chicks at ED 18 and 21. Further investigation is needed to understand the longer-term effects on SC populations and the cell signaling pathways involved over time during the post-hatch grow out period to explain the meat yield responses observed in our previous work.

Statement of Research Advisor

J. Wesley Rogers' work improves our understanding of how relatively small changes in environmental temperatures during broiler chicken in ovo development

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impact skeletal muscle development and growth as well as help provide the foundation for future studies aimed at exploring the role of skeletal muscle stem (satellite) cells in the Wooden Breast meat quality defect currently plaguing the global broiler chicken meat industry.
-Dr. Jessica Starkey, Department of Poultry Science, College of Agriculture

Sample of Authors Biography

J. Wesley Rogers is a senior pursuing a B.S. degree in Animal Sciences with a minor in Poultry Science. He plans to continue his academic career as a master's student in the AU Poultry Science Department studying muscle biology under Dr. Jessica Starkey starting in the summer of 2023. He ultimately plans to earn a Ph.D. and work as a monogastric physiologist.

Dr. Jessica Starkey is an Associate Professor in the Department of Poultry Science. Dr. Starkey's research program is focused on how nutrition, management, and disease impact the cellular and molecular regulation of satellite cell-mediated skeletal muscle growth in domestic livestock.

Effects of Accented Speech on Listening Effort and Speech Perception in College Students

Sophia Rosene[1,] and Sridhar Krishnamurti [2]*

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[2] Professor of Audiology, Department of Speech, Language, and Hearing Sciences, Auburn University

As the United States is becoming more multicultural and diverse, Americans are becoming more exposed to foreign accents. According to Van Engen and Peelle (2014), degraded speech caused by foreign accents requires additional cognitive processes for listener comprehension; the brain must recruit more neurons from the cingulo-opercular attention network when under stressful listening conditions. Furthermore, an increase in cognitive load can cause an increase in pupillary dilation (Porretta and Tucker 2019). Because of this, our study was able to use pupillometry to objectively measure whether more listening effort and cognitive load are required when listening to an accented speaker versus an unaccented speaker.

There were three main aims to our study: Aim 1 was an acoustic analysis of accented versus unaccented speech, Aim 2 tested the effects of accented speech on listening effort using pupillometry, and Aim 3 measured speech perception (speech intelligibility and speech comprehensibility).

The first step of our study was to acoustically analyze audio recordings of accented and unaccented speech by creating spectrograms in Adobe Audition (Fig. 1). The audio recordings contained 40 sentences total: 20 spoken by a male and a female from the United States whose native language was English (unaccented speech); 20 spoken by a male and a female from Québec, Canada whose native language was French (accented speech). The spectrograms showed that accented speakers paused more frequently between words than unaccented speakers. This resulted in clear differences in speech timing, which can impact speech understanding (Smith and Rathcke 2010). Accented speakers also produced mispronunciations, which caused slight distortions in the spectrograms. However, pitch and loudness were not significantly different between accented and unaccented speakers (a female was compared to a female and a male was compared to a male).

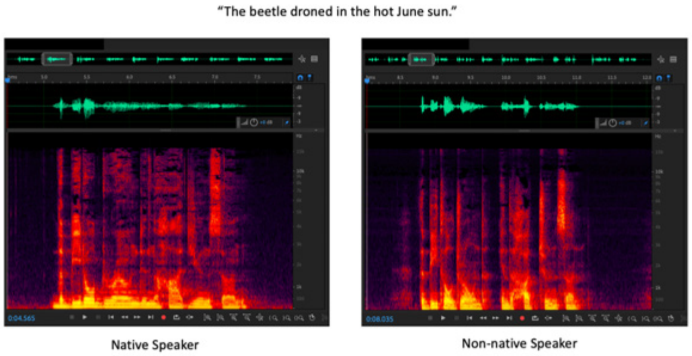

Fig. 1 Spectrograms show a native speaker of English (unaccented) and a non-native speaker of English (accented) saying "The beetle droned in the hot June sun."

After the audio recordings were acoustically analyzed, we began to collect data. The study was approved by Auburn University's Human Subjects IRB. We recruited nine American, college-aged students whose native language was English to participate. Before participating, subjects were administered vision, audiometry, and tympanometry tests to ensure they had normal vision, hearing, and middle ear function. Luminescence tests were also completed to ensure normal pupillary response to light. Next, the participants completed the pupillometry listening task. During the task, the participants listened to the audio recordings of accented and unaccented speech as they wore Micromedical Videonystagmography (VNG) eye goggles, which measured their initial and final pupil diameters (Fig. 2). Participants would hear a sentence and repeat back what they heard verbatim, which was scored for accuracy. This gave us speech intelligibility scores (how well someone is understood when speaking). The participants would also be asked to rate how difficult it was to understand

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each speaker on a scale from 1 to 5 (1 being very easy; 5 being very difficult). This subjective data gave us information on speech comprehensibility (how easily the listener can understand what the speaker is trying to say). All the while, the eye goggles were measuring changes in pupil diameter.

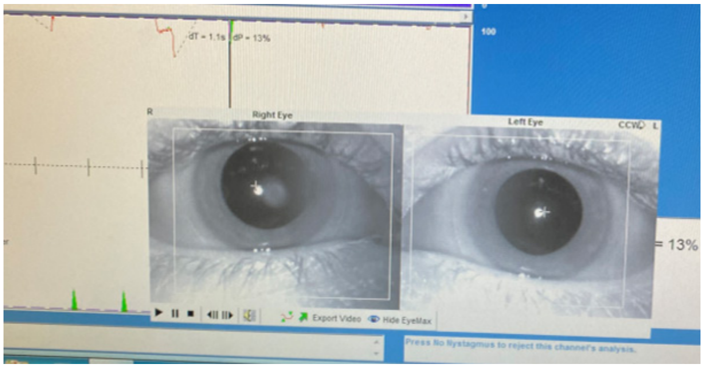

Fig. 2 Micromedical Videonystagmography (VNG) eye goggles measured initial and final pupil diameter during the pupillometry listening task.

After collecting the data, we averaged speech comprehensibility ratings for each speaker. For males, the unaccented speaker received a 1.2 while the accented speaker received a 2.2. For females, the unaccented speaker received a 1.2 while the accented speaker received a 2.3. Therefore, the participants found the unaccented speakers to be very easy to understand and the accented speakers to be more difficult to understand. While there were notable differences in speech comprehensibility, speech intelligibility scores were not significant.

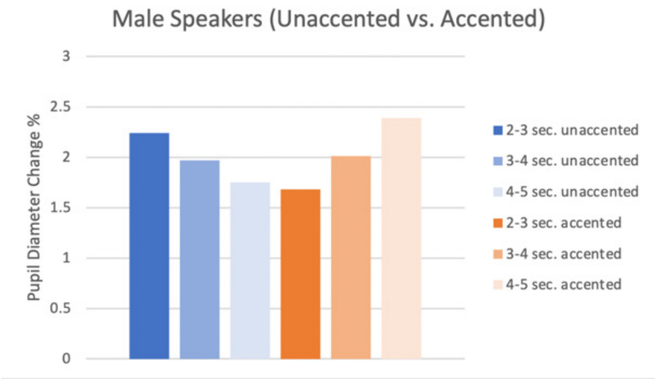

Fig. 3 Pupil diameter change by time interval for the unaccented and accented male speakers.

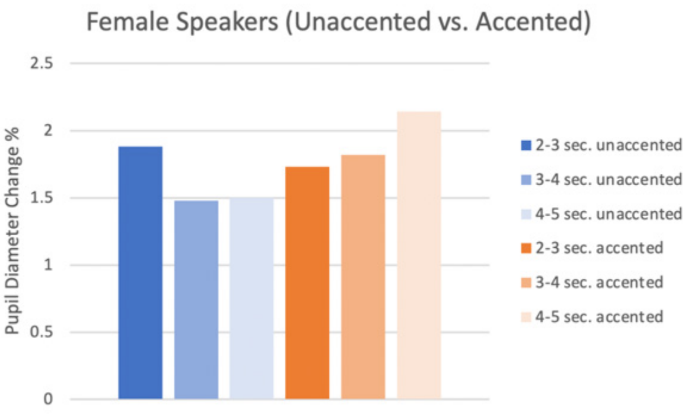

Fig. 4 Pupil diameter change by time interval for the unaccented and accented female speakers.

Lastly, statistical analyses were completed using IBM-SPSS software Version 23. The between-subjects independent variable was unaccented speech versus accented speech. The within-subjects independent variable was time interval during the task (2-3, 3-4, and 4-5 seconds). The dependent variable was the change in pupil diameter measured in percentage. These variables can be seen in Figures 3 and 4. The repeated measures ANOVA procedure was completed to look for significant differences across the six means for each speaker (Table 1). Paired T-test comparisons were completed to look for significant differences between unaccented and accented speech conditions (Table 2).

There were statistically significant differences when comparing the male accented speaker to the male unaccented speaker (Table 1). The male accented speaker caused greater pupil diameter changes in listeners, meaning he required greater listener effort and more cognitive load. Furthermore, the 4-5 second time interval showed statistically significant differences for both male and female speakers (Table 2), which means accented speech caused greater changes in pupil diameter than unaccented speech at this specific time interval. We believe peak dilation was consistently occurring at the 4-5 second time interval because at that moment, the speaker was finished saying the sentence, and it was time for the listener to repeat back what they had just heard; this brief moment of stress was creating the largest changes in pupil diameter that we were seeing, and listening to accented speech was proving to be more stressful than listening to unaccented speech. Greater changes in pupil diameter from listening to accented speakers can also be attributed to the poor speech comprehensibility ratings they received from listeners. Lastly, we found that our participants required more processing time to listen and respond to accented speech than they required for unaccented speech.

Table 1 ANOVA Results.

	dF	F	sig
Female Speakers (accented vs. unaccented)	5	1.85	0.10
Male Speakers (accented vs. unaccented)	5	2.14	0.05*

Table 2 Paired T-test Results.

Talker	Interval	Probability of Significance
Female	2-3 seconds	0.6
Female	3-4 seconds	0.2
Female	4-5 seconds	0.007*
Male	2-3 seconds	0.04*
Male	3-4 seconds	0.8
Male	4-5 seconds	0.03*

We can reasonably and objectively say that accented speech can cause greater changes in pupil diameter, require more listening effort, and place greater cognitive demands on a listener than unaccented speech. Accented speech can also take a longer time to process. Finally, listeners find accented speakers more difficult to understand in general. With these findings, we can better understand ourselves and the ways we react to degraded speech and stressful listening situations.

Statement of Research Advisor

Sophia Rosene has a passion for research in human listening behavior, and this is reflected in her selection of 'accented speech' as a variable in listening for college-aged students. She willingly learned the methodology for pupillometry and conducted the testing and analysis required for all participants. We appreciate the support for this study from the Undergraduate Research Fellowship Program in terms of mentoring, funds for participants, and providing a forum for presenting our results.

- Sridhar Krishnamurti, Speech, Language, and Hearing Sciences

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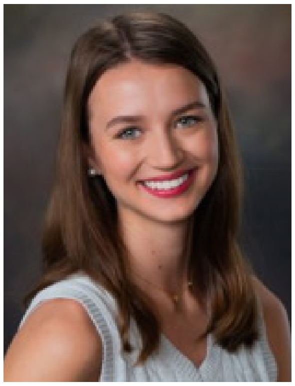
Authors Biography



Sophia Rosene is a senior-year student pursuing a B.S. degree in Speech, Language, and Hearing Sciences at Auburn University. She will begin the master's program in speech-language pathology at the University of Alabama in the Fall of 2023. She is interested in accented speech and foreign languages.

Sridhar Krishnamurti is a professor of Audiology in the department of Speech, Language, and Hearing Sciences at Auburn University. He has authored and co-authored articles and book chapters in electrophysiology, aging, hearing conservation, auditory processing disorders, and hearing aids.

Maternal Attachment & Family Relations in Court-Involved Youth

Jackie A. Sandell[1,],and Kelli R. Thompson[2]*

[1] Undergraduate Student, Department of Psychological Sciences, Auburn University
[2] Assistant Research Professor, Department of Psychological Sciences, Auburn University

Family attachment patterns, potentially disrupted by traumatic childhood experiences, could serve as a potential explanation for the development of antisocial behavior. The current study examined associations between self-reported maternal attachment styles and family relations, as measured by childhood trauma and family discord, in a sample of adjudicated adolescents with illegal sexual behavior (AISB).

There is a strong link between maternal overcontrol, hostility, and rejection and later antisocial behavior, including juvenile delinquency (Schroeder & Mowen, 2014). AISB reports higher rates of traumatic child abuse experiences, indifferent paternal caregiving styles, and more insecure attachment styles (Yoder et al., 2017). Psychological distress is experienced by a significant number of justice-involved youth with parenting styles and exposure to violence in the home both influencing this relationship (Jaggers et al., 2021). AISB have reported issues with disrupted parental communication and family separation, as well as experiences in family-specific emotional abuse and neglect above and beyond their peers (Seto & Lalumiere, 2010).

Data was collected from a pretreatment evaluation of male youth (n=529) adjudicated in a court-mandated residential treatment program for illegal sexual behavior. Ages ranged from 12-21 with an average of 15.65 and modal grade of nine. Attachment styles were measured using the Measure of Parenting Styles (MOPS), a 30-item measure used to perceive parenting styles using three subscales: indifference, abuse, and overcontrol (Parker et al., 1997). Responses are scored on a 4-point scale from 0 to 3. A higher score is indicative of a higher use of that parenting style/behavior. This study utilized only the maternal scales to isolate the impacts of maternal vs. paternal differences. The Millon Adolescent Clinical Inventory (MACI), a 160 item self-reported inventory format with 31 scales measuring various personality styles and clinical syndromes frequently encountered among adolescents in clinical settings (Millon et al., 1993).

Linear regression was used to determine if maternal indifference, abuse, and/or overcontrol could predict self-reported abuse and family discord. For family discord, a measurement of family conflict and indirect trauma exposure, the overall model was significant, F (3, 528) = 8.08, p = .001, R2 = .04. The maternal indifference scale (t = 2.77, p = .006) carried all the variance in the overall attachment model with the abuse (t = 0.67, p = .501) and over-control (t = 0.88, p = .380) scales not registering as significant predictors. For the child abuse scale, a measurement of more direct trauma exposure, the overall model was significant, F (3, 528) = 23.44, p = .001, R2 = .12. The indifference (t = 3.04, p = .003) and abuse (t = 3.13, p = .002) scales carried significant variance in the overall attachment model, with the over-control (t = 0.91, p = .365) scale not registering as a significant predictor.

Because the maternal indifference scale was a significant predictor in both family relations models, the statistical relationship has been visually depicted in Figures 1 and 2. For both family discord and childhood abuse, as maternal indifference increased so did the youth's self-report of negative family experiences.

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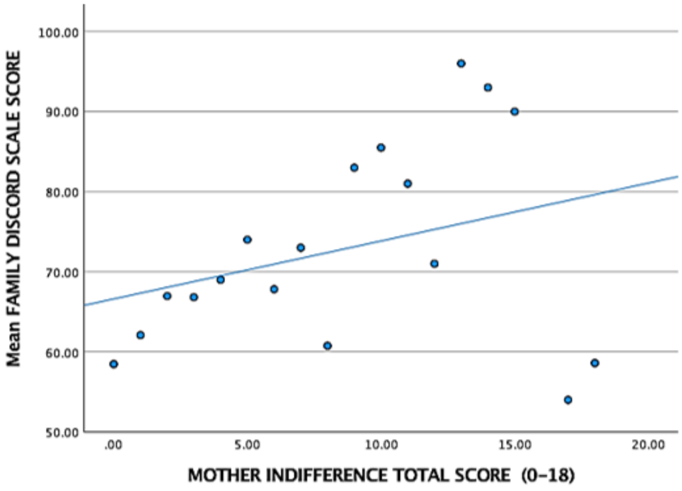

Fig. 1 Scatter Plot of Family Discord Scale by Mother Indifference Total Score.

A similar relationship was found between self-reported child abuse and maternal indifference. Overall, results indicated a significant positive association between self-reported childhood trauma or family discord and maternal attachment patterns.

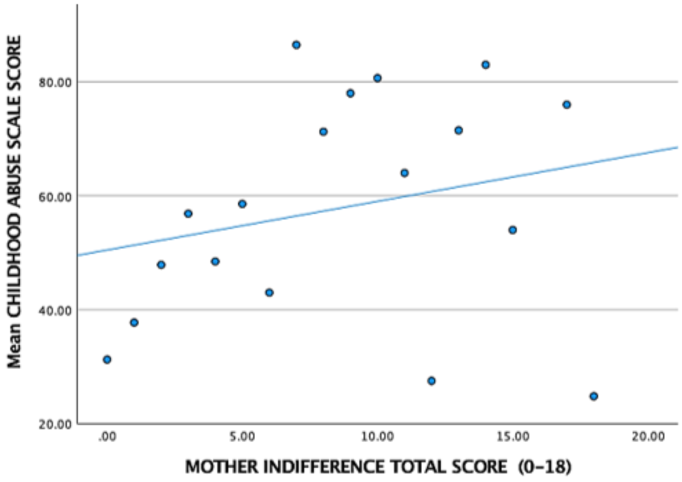

Fig. 2 Scatter Plot of Childhood Abuse Scale by Mother Indifference Total Score.

These results support previous findings on attachment styles and family relationships. A hostile, indifferent, or fearful maternal attachment can result in behaviors that represent attention seeking, intimacy avoidance, or anxious attachment styles (Bartholomew & Horowitz, 1991). This can lead to social and behavioral problems in adolescence, when youth begin modeling the social attachment patterns taught to them during childhood. Often those who experience unhealthy maternal attachment styles had a mother figure who experienced depression or victimization (Schmidt et al., 2021). Witnessing a parent struggle with severe mental illness within the home early in life may lead to an increased risk of emotional and behavioral issues later (Kitzmann et al., 2003). This could imply that another focus for clinicians could be mental health services for mothers of these youth.

The clinical implications of these results suggest male adolescents may experience negative parenting styles differently when analyzed separately from maternal behaviors. This study highlights the need for assessments of parenting styles which parcels out negative experiences from mothers vs. fathers separately, rather than simply asking about their parents collectively. In addition to this, it is clear that mental health services which focus on family attachment styles could improve the therapeutic process, but adequate assessment tools are needed. This data was cross-sectional in nature; therefore, no causal links can be made between parenting styles of family relations. Future studies should investigate longitudinal trends for causal links, as well as paternal attachments styles for similar or unique patterns.

Statement of Research Advisor

The Juvenile Delinquency Lab is supported by a more than 20-year public-public partnership with the Alabama Department of Youth Services. Jackie's project used archival data from the life of the program. This original research was a course credit final project and has been presented locally at the Auburn University student research symposium and regionally at the Southeastern Psychological Association in New Orleans, LA.

- *Kelli R. Thompson, Department of Psychological Sciences, College of Liberal Arts*

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Authors Biography

Jackie Sandell is a senior year student graduating Magna Cum Laude in Spring 2023 with a B.A. in Psychology from Auburn University. She was involved in Dr. Kelli Thompson's Juvenile Delinquency Lab and has collected data to assist with numerous research projects in addition to her own, especially those with a focus on parenting styles. Her future goal is to receive a Ph.D. in Clinical Psychology. Her interests include forensic psychology, recidivism risk, and the assessment and treatment of illegal sexual behavior.

Kelli R. Thompson was an Assistant Research Professor in the Department of Psychological Sciences at Auburn University. She is now working at Texas A&M University – Kingsville. While at Auburn University, her lab specialized in applied clinical research and she was particularly committed to undergraduate mentoring. She is an alumna from Auburn and has a Master of Divinity from Fuller Theological Seminary and a doctoral degree from the University of New Orleans. Her lab at Auburn taught the importance of science and civic engagement through creative scholarship such as this.

Environmental Design and Urban Economics in the Montgomery Peacock Tract

Aubrey Sanders[1,], Robert Sproull[2]*

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[2]Assistant Professor, Department of Architecture, Planning and Landscape Artchitecture, Auburn University

In 1850 the Montgomery, Alabama Peacock Tract neighborhood was a slave plantation. At its height in 1960, it was the African American cultural and commercial heart that powered the Civil Rights Movement. Since 1964, economic and environmental conditions of the Peacock Tract have declined dramatically. Much of the blame has targeted the residents, who are held responsible for high crime rates, unemployment and delinquency (Yawn, 2018). Instead of blaming the victims, this article seeks to clarify the impacts of centralized government planning on the downfall of the Peacock Tract. The results show overwhelming evidence that racially motivated government planning was used to systematically dismantle the social infrastructure that allowed the Peacock Track to otherwise thrive.

Social infrastructure is generally defined as the social and environmental structures which facilitate the improvement and sustention of both physical and human capital. It makes cities engines of social connection, learning, and economic opportunity (Latham, 2019). Additionally, social infrastructure benefits from agglomeration economies; a higher concentration of social infrastructure produces compounding social and economic benefits (Glaeser, 2009). Without social infrastructure, it may be impossible for goods and information to be exchanged, decreasing the potential for social connections and business opportunities.

Previous research has highlighted two government initiatives that have targeted the Peacock Tract. The first initiative was the use of redlining maps by the Federal Housing Administration and Home Owners Loan Corporation, which cut off the Peacock Tract from federally insured loans (Edwards, 2018; Nelson, 2023). The second initiative was the construction of I65 and I85 through Montgomery in 1964, and its connection to a political conspiracy to displace the leaders of the civil rights movement and African American voters (Retzlaff, 2019). What is unclear however, is how the demolition of a fraction of the building stock in the Peacock Tract led to a major decline across its entirety. Longtime residents of the Peacock Tract have repeatedly emphasized the importance that the loss of social infrastructure played in the neighborhood's decline, however little formal research on this topic exists (Khari, 2021).

To understand the effects of the I65 and I85 construction on the Peacock Tract's social infrastructure, streets, housing and social infrastructure were mapped for the years 1953 (Figure 1) and 2022 (Figure 2) using geographic information software. A density heat map of social infrastructure was generated for both years to see agglomeration economies.

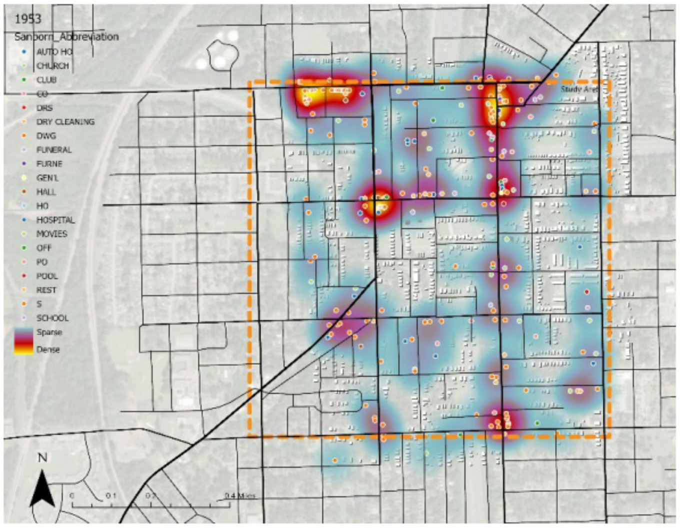

Fig. 1 Peacock Tract social infrastructure in 1953.

Fig. 2 Peacock Tract social infrastructure in 2022.

The results support Retzlaff and the residents' anecdotal claims that I65 and I85 were major disruptors to social and economic sustainability. Additionally, the results show that social infrastructure in the Peacock Tract relied heavily on a complex system of agglomeration and networking. The placement of the I65 and I85 interchange demolished and disconnected the four largest social infrastructure hotspots, leading to a chain reaction of social infrastructure closures and home vacancies across the neighborhood.

For every unit of social infrastructure demolished, 3.63 other social infrastructure units soon closed, and 12.02 homes soon vacated. 53 units or 22% of social infrastructure was demolished for I65 and I85. 137 units of social infrastructure closed soon after. By the year 2022, 189 units or 78% of social infrastructure had been lost. The diversity of social infrastructure dropped from 20 to just 12 categories, with the greatest loss coming from private businesses. For every housing unit demolished, 1.93 other homes were soon vacated. For every 5 housing units demolished, 1 social infrastructure unit soon closed. 670 homes or 31% of housing stock was demolished for I65 and I85. 626 homes vacated soon after. By the year 2022, 1,296 homes or 59% of housing stock had been lost.

Due to threats of displacement, future advancements to replace lost social infrastructure should seek to include the residents. Insight article demonstrates, resident anecdotes are too often overlooked by researchers yet may provide critical insight into imbedded local challenges. A special thank you to all the residents of the Peacock Tract for welcoming Auburn University to conduct research, and to Professor Robert Sproull for generous aid in mapping and research.

Statement of Research Advisor

Aubrey's project highlights a critical issue on the negative effects of highway planning on minority neighborhoods during the middle of the 20th century. The location of the study, Montgomery's Peacock Tract community, proves that no place was immune to the type of institutionalized discrimination often occurring during this period - including those of historic civil rights significance. Aubrey investigated the state of the community's social infrastructure prior to the introduction of I65/I85 and compared it to what exists today. The results, presented through striking graphics and a compelling narrative, support similar research findings from institutions around the country, and the project's outcomes call for further inquiries into the current condition of cities throughout the United States - *Robert Sproull, Environmental Design, College of Architecture, Planning and Landscape Architecture*

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Authors Biography

Aubrey Sanders is a senior research fellow of the Auburn University B.Sc. Environmental Design program and a Master of Urban Planning Student at the Harvard Graduate School of Design. Aubrey has been recognized for their ongoing research and practice in urbanism

Robert Sproull is an assistant professor in Environmental Design and a registered architect. His current research and teaching investigates the overlap between critical and social infrastructure systems with a particular focus on how highways have affected cities throughout the United States.

Post-Occupancy Evaluation of Evidence-Based Design in a Louisiana Healthcare Facility

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Using evidence-based design in women's healthcare facilities contributes to the betterment of user's comfort and the promotion of overall wellbeing. Different design aspects affect women's emotional and physical states (Jiang et al., 2022). One of the most effective means of healing architecture is thoughtful use of daylight because biophilic design has been proven to promote healing(Simosen et al., 2022). By studying successful projects and applying tactics to future projects, designers can create effective spaces that cater to the real needs of staff and patients (Obeidat et al., 2022). Utilizing connections with contacts who work on the fourth and sixth floors of a women's hospital in New Orleans will allow the researcher to analyze the effectiveness of evidence-based design in practice. The researcher hypothesizes that the results will be positive, but areas of improvement are likely to be identified. Using post occupancy survey data from a third-party medical practice survey organization, the researcher reviewed patient satisfaction data to determine what areas of the hospital design could be improved for future design. Future implications of these results include the possibility of increased importance of executing evidence-based design and the continuation of learning how to provide the most efficient design. The success or failure of evidence-based design on this project can inform future research.

Design for healthcare settings continues to evolve as new research is conducted, and new information comes to light. Evidence-based healthcare practices emerged in 1996 and the practice was introduced by Kirk Hamilton at the Center for Health Design (CHD) board meeting in 2003. Evidence-based design can most simply be defined as: the process of designing and building a physical environment based on scientific research to achieve the best possible outcome (Peavey and Wyst, 2017). It is most often used in healthcare design practices and the Evidence-Based Design Accreditation and Certification (EDAC) has become widely recognized.

Research is always being conducted, so it is crucial for designers to stay knowledgeable on current research findings in order to create the best possible design solutions for clients. Thoughtful design can meet the practical needs and promote healing and wellness. Due to the ever-changing medical field, designers must create adaptable and flexible environments that allow for growth and change as research evolves (Leavitt and Trent-Adams, 2020).

This task was taken on ten years ago in a health system in New Orleans, Louisiana. The health center was designed using evidence-based practices to create a built environment that met the communities' real needs. The hospital supports women's health in varying ways, including an alternate birthing center and a neonatal intensive care unit. One decade later the hospital is still supporting this urban community.

Fig. 1. Labor, Delivery, and Recovery Room
Image courtesy of the Louisiana Health System and partnered architecture firm.

The purpose of this research is to utilize a literature review and a review of floor plans and presentation views to understand how effective the applied evidence-based design is and to learn how the design could be more

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successful in the future. Fairly early for its time, this Louisiana health system employed the use of evidence-based design, only ten years after the concept was introduced in 2003 at the CHD board meeting. Evidence-Based Design applications found on the Labor and Delivery 6th Floor includes, but are not limited to: daylight in all patient rooms, alternate birthing options within each delivery room, centralized nursing station, serene color palettes, and thoughtful overall design for patients, family members, and staff.

The research was conducted remotely involving both a literature review and review of floor plans and presentation views. The literature review portion focused largely on the current state of the American healthcare system and how these disparities directly affect women and the design of women's birthing facilities (Anderlini, 2018). For example, it has been found that chronic illnesses are more prevalent in women than men (Boersma et al., 2018). The review of floor plans and presentation views studied the use of evidence-based design concepts read about in the literature review.

Since research is continually being conducted and new technology emerging in the healthcare space, there are always updates that can be made. However, as far as healthcare design is concerned, this Louisiana healthcare system is very advanced and designed for maximum flexibility. There is much to be learned from the forward thinking and flexible design of this health system. Post-occupancy reviews are of utmost importance because they allow designers to learn from precedents and understand what aspects of a design are most successful.

Statement of Research Advisor

Claire's research examines an academic foundation to conduct a post-occupancy evaluation of an interior design project based on the principles of evidence-based design. While post-occupancy evaluations are common within the field of interior design, few reflect back on the evidence-based design goals of the project as their starting point. In that, this novel approach may allow for reformation of the post-occupancy evaluation method.

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Authors Biography

Claire Sisson is a senior-year undergraduate student pursuing a B.S. degree in Interior Design at Auburn University. She has played key research roles in healthcare design and evidence-based design research.

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A Biophysical and Biomechanical Study of the Central Rod Domain of Dystrophin

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Abstract

The purpose of this project was to predict accurate, high resolution tridimensional structures for the spectrin-repeats (SR) of the central rod region of dystrophin. These structures can then be utilized in in-silico single molecule force spectroscopy experiments, such as Steered Molecular Dynamic Simulations to understand the mechanical properties of those mechanosensing proteins. The region of interest of the protein dystrophin is the central rod domain, which contains 24 SR regions that can be divided into four fragments: SR01-05, SR06-10, SR11-17, and SR18-24. Utilizing an artificial intelligence based molecular modeling software named AlphaFold, the individual structures of each SR were created. It was determined that these structures were accurate after careful inspection via sequence and structural alignment with the crystal structure of SR01. Accurate structures containing two adjacent SR regions were obtained using AlphaFold for SR01-02 through SR23-24. Superimposing these regions upon one another resulted in an accurate structure for each of the four fragments of the central rod domain of dystrophin. After combining the superimposed regions as a template with a sequence alignment in the software MODELLER, a single structure file was generated for each fragment, demonstrating that it is possible to obtain accurate structures of the entire central rod domain of dystrophin.

Key Words: Dystrophin, Spectrin-Repeat (SR), Molecular Dynamics, Molecular Modeling.

Introduction

Muscles consist of proteins that enable contraction to produce force and allow an organism to move. Almost all of the energy utilized in the cell is consumed in this contraction process, with the rest of the energy being used by a significantly smaller portion of the cell that is reserved for preservation of the cellular integrity. The dystrophin glycoprotein complex (DCG) plays a vital role in cellular integrity as it links microtubules, thin and intermediate filaments with other key components of the extracellular matrix. Within the DCG, dystrophin (427 kDa) is the protein that attaches cytoskeletal components and the protein dystroglycan, stabilizing the sarcolemma [1].

The function of the DCG can be disrupted by means of mutations within the dystrophin gene, resulting in a mutated form of dystrophin. This is known as Duchenne's Muscular Dystrophy (DMD), which is the second most common genetic disease, as it affects one out of every 3,500 males born. The fatal dystrophinopathy can be caused by chromosomal rearrangement or deletion at the dystrophin locus by missense, point, or nonsense mutations. There is no known cure for DMD, and life expectancy ranges from mid twenties to early thirties [2-4].

Dystrophin has four main functional domains: an actin binding domain, a central rod domain, a cysteine-rich domain, and a carboxyl-terminus domain[5]. While these aforementioned domains have been shown to be important in mechanical linkage of dystrophin, previous studies have demonstrated that presence of the C-terminus and N-terminal actin-binding domain is not necessary for the localization of dystrophin at the sarcolemma[6-9]. Previous studies have found that the central rod domain of dystrophin is vital in rescuing the phenotype in the mouse model of Duchenne's Muscular Dystrophy, which is commonly referred to as the mdx

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*Corresponding author: trs0044@auburn.edu model. In those studies, microdystrophin that contained 8 spectrin-repeats (SR) more efficiently rescued the phenotype of mdx as compared to the microdystrophin that contained only four SR, thus demonstrating the impact of the central rod domain on the phenotype of dystrophinopathies [10-14].

Dystrophin's central rod domain consists of 24 SR, which are ~110 amino acid motifs of triple alpha helices folded into small rods that are approximately five nm in length[15,16]. In order to understand more about the molecular mechanism by which dystrophin stabilizes the sarcolemma, a previous study broke up the 24 SR into four fragments: SR01-05: 338-938th, SR06-10: 939-1466th, SR11-17: 1464-2210th, and SR18-24: 2209-3044th [17]. Upon breaking up the central rod domain, each fragment was stretched. The unfolding/refolding dynamics of these fragments was determined, and the mechanical properties of those fragments were quantified.

Molecular dynamic (MD) simulations can be utilized to determine the biophysical and biomechanical properties of proteins down to an atomistic level, at which it can provide unfolding/refolding dynamics of mechanosensing proteins[18- 20]. A limitation of MD simulations, however, is that they are reliant upon accurate, high resolution structural data [21-23]. As of this writing, there does not exist an accurate protein structure file of the central rod domain. The artificial intelligence based software AlphaFold could serve as the key to solving this problem, as previous studies have shown that the software was able to predict a near-native protein fold based upon its genetic sequence [24].

Within the scope of this project, AlphaFold can be utilized to create accurate protein structure files for the central rod domain of dystrophin. Upon ensuring the accuracy of these protein structures, they can then be used in MD simulations to obtain the mechanical properties of each fragment of the central rod domain, and the entire length as well.

Methods

Determination of Residues

In order to create accurate protein structures using AlphaFold, the residues of each SR must be selected and an appropriate fasta file created. The sequences for each individual SR of the central rod domain were retrieved from the protein sequence database UniProt [25].

Creation and Confirmation of Individual and Paired Spectrin-Repeats

Upon retrieving appropriate sequences per each single SR region and each paired SR region, AlphaFold version 2 was used through the Visual Molecular Dynamics (VMD) QwikFold plugin batch mode to create models for each SR region and paired region[27-28]. An example of the single SR structures generated is seen in Fig. 1, and an example of a paired SR region is seen in Fig. 3. In order to ensure that the structures created were accurate, each individual SR created by AlphaFold was compared to the crystal structure of the first spectrin-repeat, SR01, deposited on the Protein Data Bank (ID:3UUN)[29]. This superimposition is seen in Fig 2. Using the molecular modeling system VMD the crystal structure of SR01 was superimposed upon each individual SR to obtain structural and sequence alignment data [30].

Creation of Each Region: R1: SR01-05, R2: SR06-10, R3: SR11-17. R4: SR 18-24

Upon determining the accuracy of each individual SR as well as each paired adjacent SR's, the adjacent SR's were superimposed upon one another to form each region of the central rod domain. An example of the superimposed doublets forming a region is pictured in Fig. 4. While the generated superimposed structure is an accurate representation of the region, it is not a single structure file, which is necessary to run MD simulations. To turn each superimposed region into a single structural file, the individual PDB files that comprised the superimposed regions were saved in their specific coordinates as templates. Using the sequences of each one of the superimposed structures as well as the sequence of the entire region, a sequence alignment was run through the web-server PROMALS3D, which has been shown to outperform a number of existing methods for constructing multiple sequence or structural alignments using both reference dependent and reference-independent evaluation methods[31]. The templates and sequence alignment were combined in MODELLER, which is an effective tool for comparative modeling of protein three-dimensional structures [32-35]. After running MODELLER, the structure with the highest discrete optimized protein energy (DOPE) score was selected and a single accurate, high resolution structure of each region was obtained. The resulting structures for Region 1, 2, 3, and 4 are pictured in Fig. 5, Fig. 6, Fig. 7, and Fig. 8 respectively.

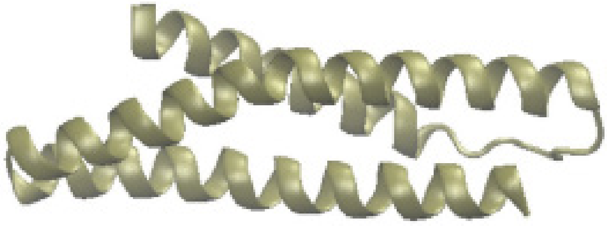

Fig. 1. Example of an AlphaFold generated structure for an individual spectrin-like repeat (SR). Represented in cartoon and colored in tan is the AlphaFold generated structure of SR06.

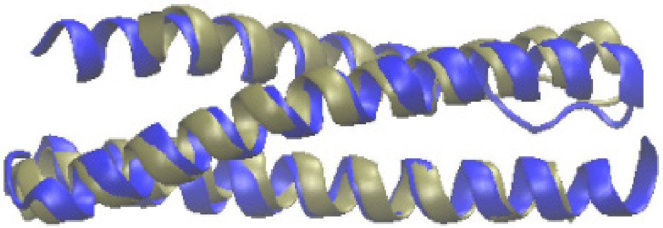

Fig. 2. Crystal structure of SR01 (blue) superimposed upon the AlphaFold generated structure of SR06 (tan). We notice the conservation of the triple alpha helical motif.

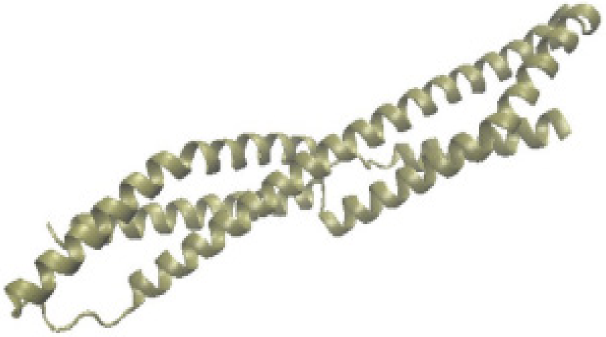

Fig. 3. Adjacent AlphaFold generated structure for SR06-07.

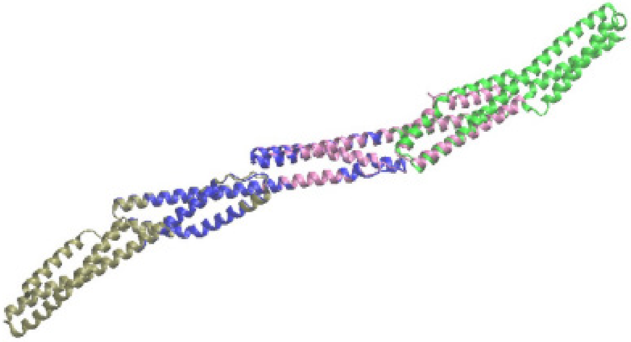

Fig. 4. Adjacent SR's superimposed structures that compose Region 2: SR06-07 (tan), SR07-08 (blue), SR08-09 (pink), and SR09-10 (green).

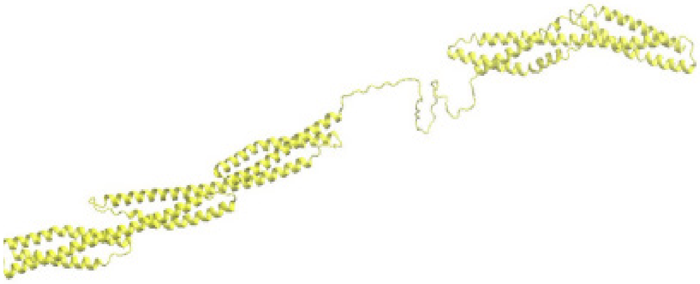

Fig. 5. MODELLER generated structure of Region 1:SR01-05.

Fig. 6. MODELLER generated structure of Region 2: SR-6-10.

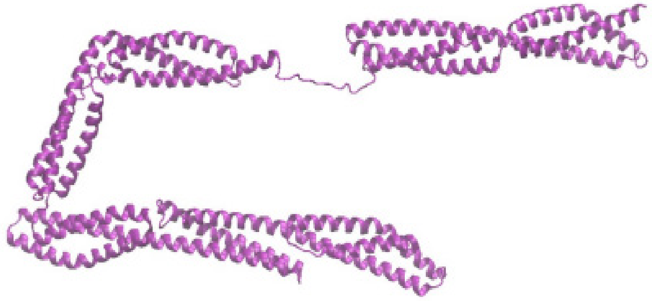

Fig. 7. MODELLER generated structure of Region 3: SR11-17

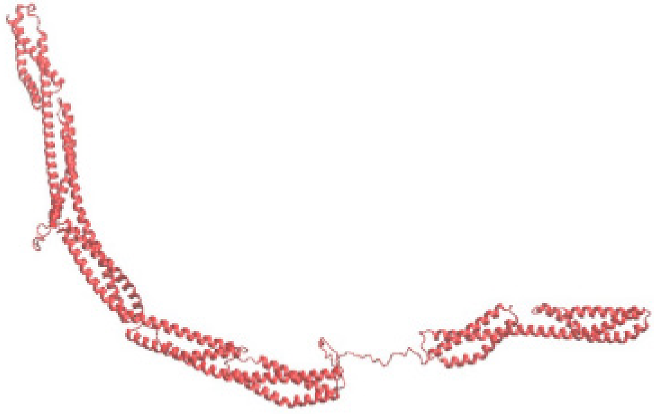

Fig. 8. MODELLER generated structure of Region 4: SR18-24.

Conclusions

At the time of writing this paper, there does not exist an accurate protein structure of the central rod domain of dystrophin. Accurate structures of paired adjacent spectrin repeats were created upon determining the accuracy of each individual spectrin repeat. Each paired SR doublet maintains the consistent structure of a triple helical motif consisting of a rod-like shape. By superimposing each adjacent pair upon one another, an accurate structure of each of the regions was created. The full structure maintains the expected structure of the entire fragment, as it maintains the triple helical motif and forms the rod-shaped protein structure. Creating accurate protein structures using AlphaFold allows for the use of MD simulations to determine biophysical and biomechanical properties of proteins at an atomistic level. These findings demonstrate that our protocol allows us to obtain tridimensional structure models that are accurate. These structures are currently being utilized in Steered Molecular Dynamic simulations in order to obtain biophysical and biomechanical data of the central rod domain of dystrophin.

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Nomenclature

SR - Spectrin-like Repeat. MD - Molecular Dynamics. DOPE - discrete optimized protein energy. PDB - protein data bank.

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Authors Biography

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Dr. Diego E. B. Gomes is a postdoctoral researcher at Auburn university. Diego holds a PhD in Biophysics from the Universidade Federal do Rio de Janeiro (Brazil). He is currently working on developing QwikFold, a VMD interface for AI based structural biology software. QwikFold will be integrated into a new version of QwikMD, which is also under development by Dr. Gomes. Besides that, he is working on mechanical properties of nanobodies, proteins that are under development for diagnosing and fighting cancer.

Dr. Priscila S. F. C. Gomes is a postdoctoral researcher at Auburn University. Priscila holds a dual-PhD in Biophysics from the École Normale Supérieure de Cachan (France) and the Universidade Federal do Rio de Janeiro (Brazil). Her main research interest is on the use of bioinformatics and molecular dynamics tools to investigate bacteria and virus adhesion. Dr. Gomes has recently contributed to understanding how mechanical properties of the COVID spike protein has evolved since the SARS-CoV-1 outbreak in early 2000s

Dr. Rafael C. Bernardi is an Assistant Professor of Biophysics at the Department of Physics at Auburn University. Before joining Auburn's faculty, Dr. Bernardi was a Postdoc (2012-2017), and then a Research Scientist (2017-2020), at the Beckman Institute at the University of Illinois. Dr. Bernardi is co-Investigator of the NIH Center for Macromolecular Modeling and Visualization, which is known worldwide for the development of NAMD and VMD software. Dr. Bernardi's main research interest is on protein mechanics, and how protein complexes behave under mechanical load. Such problems are very important in many areas of biomedicine, including bacterial adhesion during infection, viruses interaction with human proteins, and enzymatic activity in the gut microbiome.

Linear Enamel Hypoplasia in African Enslaved Individuals from Newton Plantation, Barbados

Katie E. Smith [1], and Kristrina A. Shuler [2]*

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The presence of Linear Enamel Hypoplasia (LEH) in dentition has been repeatedly linked to early life stressors, including malnourishment and effects of weaning. As such, LEH is commonly used in bioarchaeology to measure the effects of childhood stress in past populations. In this study, we examined dental samples from the Newton Plantation Burying Ground in Barbados (ca. 1660-1820) for LEH presence and age at disruption. LEH bilateral maxillary and mandibular first molars, canines, and central incisors were hand-scored by both authors, followed by inspection with a Dinolite W-20 digital microscope at 20x and a hand lens at 10x. LEH was measured using Mitutoyo digital needle-point calipers calibrated to .01mm from the defect's center to the CEJ. The total of 96 teeth from 17 individuals was scored. Antemortem tooth loss could not be assessed. LEH (n=6) was present in four individuals, two of whom displayed multiple defects. Based on Rose and Goodman (1991), LEH age at disruption ranged from 0.459 – 3.85 years. Malnutrition, environmental stressors, and other factors are well-documented archivally among the Barbadian enslaved, and these data suggest stress that started during early childhood. The presence of LEH only in individuals with isotopic signatures (Schroeder et al., 2009) of Barbadian birthplace supports the prediction of especially high stress for individuals born into enslavement. These findings contribute to more than 40 years of bioarcheological research at Newton Plantation and provide new insights into early childhood stress.

Key Words: Newton Plantation Burying Ground, Barbados, Linear Enamel Hypoplasia, LEH, malnourishment, weaning, environmental stressors, bilateral, maxillary, mandibular, first molars, canines, central incisors, antemortem tooth loss, isotopic signatures, age at disruption, bioarchaeology.

Newton Plantation in Barbados, West Indies was established in the mid-17th century during an economic boom of commercial production of sugar. Sugar was highly sought after in the West Indies, particularly in Barbados where approximately 45,000 enslaved Africans were forced to the colony as laborers to support the production of sugar, rum, and other commodities. In the early 1970s, an unmarked slave cemetery was rediscovered on the grounds of the former Newton Plantation. Archaeological excavations by Jerome Handler et al. (1978) revealed a total of 104 skeletons. More than 40 years of bioarchaeological data have provided insight into the health and life experiences for the enslaved people who lived on Newton Plantation (Shuler et.al 2019), including evidence of non-specific stress in early childhood that resulted in dental growth arrest. Linear Enamel Hypoplasia (LEH) are defined as enamel defects that can appear as either grooves or pitting upon the labial enamel surface of the teeth; such defects have been linked to a variety of stressors, including malnutrition and infectious diseases that result in disruption of enamel formation during childhood (Franklin et.al 2022, 223). Previous studies from Newton reported modest rates of LEH (20% Corruccini et.al 1985; 19% Ritter 1991; and 17% Shuler 2005) based on clearly palpable enamel defects (Shuler et al. 2019, 273). Research in this study assesses the presence of LEH in a separate sample of individuals from the plantation and takes up other issues that have not been previously explored: the age at which individuals experienced the LEH stress episode, and whether LEH occur with greater frequency by birthplace (Barbados or Africa). Questions concerning early childhood stressors and how it may have impacted the enslaved people's health are addressed in this study. Frequency of LEH within the dental sample from Newton Plantation, calculation of age at disruption of LEH events, and comparisons of LEH events between Barbadian v. African born individuals can offer

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further bioarchaeological data for understanding the lives of past individuals on the Newton Plantation and enslaved early colonial Caribbean populations.

In this study, dentition from the 1997-1998 excavation sample were assessed for the presence or absence of LEH. We analyzed all available permanent, bilateral maxillary and mandibular central incisors, canines, and first molars. A total of 17 individuals in the sample could be scored for at least one of the aforementioned tooth types. Teeth were inspected under oblique lighting by both authors working together. Any identified LEH defect was further examined using a Dinolite W-20 digital microscope at 20x and a separate 10x hand lens. Measurements were taken using Mitutoyo digital needle-point calipers calibrated to .01mm from the defect's center to the cemento-enamel junction (CEJ). Data were recorded in an Excel spreadsheet by burial number and tooth number. Antemortem tooth loss could not be recorded from this sample. The age at development for each enamel defect was calculated using regression formulae in Rose and Goodman (1991, 288-289).

Age at formation= age at crown completion - [(years of formation/crown height) x defect height (from CEJ)]

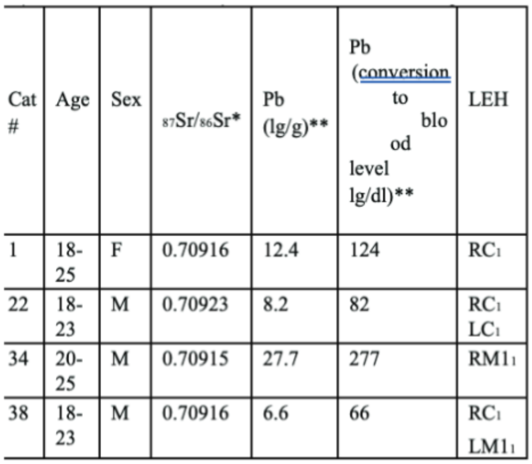
A total of 6 LEH were identified from 17 individuals in this study. LEH Burials 38 and 22 were the only individuals to have multiple defects. Burial 38 showed defects on both the upper right central incisor and the lower left first molar. Burial 22 showed defects on the upper left canine and the lower right canine (Figure 1). LEH were found on all tooth types: a higher frequency was shown in canines (1/3). The frequency of individuals with LEH present was .04 of those who could be scored. LEH age at disruption for the individuals ranged from 0.459-3.85 years. For each tooth type, their age at disruption ranges were:

- First molars range = 0.4487-2.4359 years
- Central incisors = 0.8081 years
- Canines = 0.6250-2.8125 years

The results of the study also showed a higher rate of LEH presence in Barbadian born individuals than African born based on previously reported isotopic values for these individuals (Schroder et al., 2009: 553).

Fig. 1 Image displaying LEH on the lower right permanent canine of Bu 22 (photo by Katie E. Smith).

Table 1. Table depicting LEH present individuals / tooth number present / measure of LEH to cemento-enamel junction / age at disruption / place of origin for individual / strontium (*Schroeder et al. 2009) and lead levels (**Schroeder et al. 2013) for individuals in this sample.



Cat #	Age	Sex	$_{87}$Sr/$_{86}$Sr*	Pb (lg/g)**	Pb (conversion to blood level lg/dl)**	LEH
1	18-25	F	0.70916	12.4	124	RC$_1$
22	18-23	M	0.70923	8.2	82	RC$_1$ LC$_1$
34	20-25	M	0.70915	27.7	277	RM1$_1$
38	18-23	M	0.70916	6.6	66	RC$_1$ LM1$_1$

The stressors such as malnutrition, environmental toxins, weaning, and multiple other factors are well documented among the Barbadian enslaved, as previously supported through studies at the Newton Plantation (Shuler et al., 2019). LEH presence in individuals with multi-isotopic signatures of Barbadian birthplace supports former predictions of particularly high levels of early childhood stress for those who were born into enslavement, including exposure to toxins such as lead (Schroeder et al., 2013) and potentially to ethanol from rum (Shuler & Schroeder, 2013). In this study, the LEH data at Newton Plantation shows that enamel defects were impacting children as early as 0.4 years of age and continued to impact them up to 3 years. Moreover, when combined with the published isotopic data, the LEH data from this small sample tentatively suggests that children who were born on the island may have been under a different type of stress than those who were later imported during adulthood. One factor in this may be exposure to an extremely toxic substance, lead, which has been documented in nearly all of the Barbadian born but absent from the African-born children at the site (Schroeder et al., 2013). Exposure has been linked to lead-tainted rum consumption, with toxins passed to children possibly in utero and/or during breastfeeding (Shuler & Schroeder, 2013). Regardless of the route, this likely would have contributed to high rates of physiological stress including, but not limited to, LEH and other indicators that have been reported from this site (Shuler et al., 2019). Such findings and former research upon the remains found at the plantation are accredited with over 40 years of former bioarchaeological research. This data study provides new advances towards dental studies and LEH analysis within Newton Plantation and other bioarchaeological sites/studies of the African Diaspora and trans-Atlantic slavery.

Acknowledgements

This study was supported by the Auburn University Undergraduate Research Fellowship Program. Thanks, are also given to the Barbadian Museum for supporting research upon the skeletal remains from the Newton Plantation.

Statement of Research Advisor

Katie did an excellent job with her project this year. She spent extensive time in the lab learning the intricate details of dental morphology, assisting with the collection of new data on enamel defects, and exploring recent scholarship in biological anthropology and bioarchaeology. Katie will expand upon this work over the next year by assessing a larger sample from the site and synthesizing the results with more than 40 years of published data from the Newton Plantation archaeological site. Katie's work is contributing valuable new data on early childhood stress experiences of enslaved individuals who lived on a 17th-18th century plantation in the Caribbean.

- Kristrina Shuler, Anthropology, College of Liberal Arts

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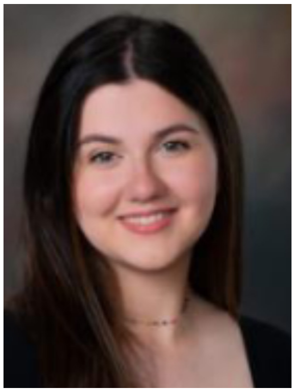
Authors Biography



Katie E. Smith is a senior-year student pursuing a B.S. degree in Anthropology at Auburn University. She is the assistant bioarchaeology lab director under Dr. Kristrina Shuler and the head student leader for CSI: Auburn. Her primary research focus has been studying dental morphology and linear enamel hypoplasia's upon a pre-colonial enslaved population from Barbados.

Kristrina A. Shuler is an associate professor in the department of Sociology, Anthropology, and Social Work at Auburn's College of Liberal Arts. She is a biological anthropologist (bioarchaeologist) whose primary focus is upon health and nutrition in early colonial populations from the Caribbean, Southeastern U.S., and Latin America.

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Linear Enamel Hypoplasia in a Commingled Archaeological Sample From Newton Plantation, Barbados

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Abstract

Bioarchaeological research of Linear Enamel Hypoplasia analysis at Newton Plantation Burying Ground (ca. 1660-1820) has revealed ample evidence for early life stressors such as malnourishment and weaning. Following my previous research on this site, the current study examines enamel growth defects in the form of Linear Enamel Hypoplasia and their timing of disruption within a subset of commingled dental remains from the Newton Plantation. Bilateral maxillary and mandibular first molars, canines, and central incisors were evaluated without magnification and then inspected using a Dinolite W-20 digital microscope at 20x as well as a hand lens at 10x. Measurements of identified growth defects were taken using Mitutoyo digital needle-point calipers calibrated to 0.01 mm from the defect's center to the cemento-enamel junction. Of the 173 teeth that were scored, 26 teeth showed the presence of LEH. Based on regression formulae by Rose and Goodman (1991), the LEH age at disruption ranged from 0.3846 to 2.87 years. Such data suggest stress began during early childhood for the Barbadian enslaved. Although the remains were commingled during the 1970s by archaeologists working at the site, the high presence of Linear Enamel Hypoplasia in this collection contributes further data to more than 40 years of bioarchaeological research on childhood stress at Newton Plantation, as well as commingled remains analysis.

Key Words: Newton Plantation Burying Ground, Barbados, Linear Enamel Hypoplasia, malnourishment, weaning, environmental stressors, bioarchaeology, dental anthropology.

Introduction

During the mid-17th century, Newton Plantation in Barbados, West Indies, as many as 45,000 people were enslaved and forcibly relocated by the British from Africa to serve as labor for the production of sugar, rum, and other commodities. Archaeological excavations and craniodental studies performed by Jerome Handler and Robert Corruccini (Shuler 2019) on the plantation in the early 1970s revealed a total of 104 skeletons. Such studies and results provided over 40 years of bioarchaeological insight into the health and livelihood of the enslaved people living on the plantation (Shuler et al. 2019).

Dental evidence provided insight into early childhood dental growth arrest. Specifically, Linear Enamel Hypoplasia (LEH), which is a type of enamel defect that appears as macroscopic grooves and/or pitting on the labial enamel surface of the tooth. Defects such as these are linked to a variety of stressors, including malnutrition and infectious diseases, often resulting in the disruption of enamel formation during one's childhood (Franklin et al., 2022, 223). These defects are often referred to as "nonspecific" due to their incomplete nature; although they can reveal evidence of some form of physiological stress occurring during childhood, it is difficult to ascertain what specifically causes their eruption (Steinberg et al., 2015, 452). Weaning has also been noted as a possible stressor for enslaved individuals during this period, but such has not yet been proven within a single population (Corruccini et al. 1985, 706). Previous studies, including my former undergraduate study, reported modest rates of LEH (20% Corruccini et al., 1985; 19% Ritter, 1991; and 17% Shuler, 2005) based on clearly palpable enamel defects measured by specific methods (Shuler et al., 2019, 273). For this sequential study, LEH prevalence was assessed and recorded within a commingled sample of dental remains exca-

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vated from Newton Plantation. Unlike the articulated collection, LEH assessment and age-at-disruption have yet to be recorded within the commingled set of dental remains. Although commingled and having seemingly little to no other historical data for the collection, much data and insight can still be gathered for further bioarchaeological studies surrounding Newton Plantation. References to my former study concerning early childhood stressors and environmental impacts within the population are also addressed in this article. The measurement of LEH frequency and age-at-disruption within the commingled dental sample from Newton Plantation can offer further bioarchaeological insight for understanding the lives and health of past individuals living upon Newton Plantation, as well as enslaved precolonial Caribbean populations.

Methods

In this study, a commingled sample of dental remains recovered during the 1997–1998 excavation was assessed for the presence or absence of LEH. The teeth are believed to have been originally excavated and subsequently reburied by archaeologists in the 1970s, resulting in the disarticulation and commingling of individuals.

In this study, the commingled dental remains were assessed for the presence or absence of LEH. Given the nature of the remains, certain methods concerning proper research analyses of commingled collections were used. Because there is no formal itemized list concerning the dental remains, the first step was to create a dental inventory categorized by tooth type, number, and side (RM1) following procedures outlined in Beck et al. (2019). This included dividing the dental remains by tooth type rather than burial type on the Excel spreadsheet.

All permanent, bilateral maxillary and mandibular central incisors, canines, and first molars in the commingled sample were assessed by me for LEH presence. A total of 173 teeth in the sample could be scored for at least one of the aforementioned tooth types. The teeth were inspected under oblique lighting, and any identified LEH defect was further examined using both a Dinolite W-20 digital microscope at 20x and a separate 10x hand lens. Using Mitutoyo digital needle-point calipers calibrated to .01mm, measurements of LEH were taken from the defect's center to the cementoenamel junction (CEJ). All data was recorded in an Excel spreadsheet, organized by tooth number and LEH presence or absence. Age at development for each enamel defect in the sample was calculated using regression formulae from Rose and Goodman (1991, 288–289).

Results

In total, 173 teeth were identified and analyzed for the presence of LEH under oblique lighting and using 20x and 10x magnification. Of the 173 teeth, a mix of 26 bilateral maxillary and mandibular first molars, canines, and central incisors showed defect evidence of LEH. Measurements for the LEH were taken using the Mitutoyo calipers and later used to calculate age-at-disruption with the age-regression formulae from Rose and Goodman (1990). Being a commingled sample, burial numbers cannot be noted, so tooth types and their associative numbers were used to specify which remains showed signs of LEH and those which did not.

Age at formation = age at crown completion – [(years of formation/crown height) x defect height (from CEJ)

LEH defects were not found on all tooth types; specifically, left maxillary first molars, right mandibular first molars, right mandibular canines, left mandibular central incisors, and left mandibular first molars were found to be absent of LEH presence during data collection. A higher frequency was shown in bilateral maxillary and mandibular canines (3/8). The second-highest frequency of LEH was found in the central incisors (1/8). The total frequency of individuals who showed the presence of LEH and were able to be scored was 1/7, or .15. The range for LEH age at disruption was found to be between 0.384 and 2.87 years.

For each tooth type, their age at disruption ranges were:

- First molars range = 0.3846 years
- Central incisors = 0.8081-2.8735 years
- Canines = 0.6250-2.1568 years

Discussion and Conclusion

Malnutrition, environmental impacts, weaning, and other factors are archaeologically commonly found within the bioarchaeological contexts of the Barbadian enslaved, particularly in studies at the Newton Plantation. Such was also shown to be true in my former undergraduate research study; here I found that LEH presence in individuals with multi-isotopic signatures of Barbadian birthplace supports former predictions of significantly higher levels of early childhood stress for those born into enslavement, including exposure to toxins such as lead (Schroeder et al. 2013) and, potentially, to ethanol from rum intake (Shuler and Schroeder 2013). The results from this study of the measurements of LEH presence in the commingled collection of remains show that children as early as 0.3 years of age were continuously impacted by this severe level of stress up until 3 years of age. Researchers estimation of age at disruption has been repeatedly argued for its validity; according to Hillson and Bond (1997), this measurement shows an "expression of the pattern of enamel layers" rather than the exact timing of a stress episode the individual encountered in their lifetime. Although isotopic data are unable to be taken within this sample, one can easily conclude that many of these individuals experienced severe stress in their early childhood. This therefore results in the development of LEH defects on the enamel surface of the labial teeth (Shuler et al. 2019). Higher frequencies in canines and central incisors are also congruent with the results of my former study. Studies of dental asymmetry trends are congruent with field theory, which entails that "key" teeth, which tend to be the most mesial tooth in each class, tend to show less asymmetry than others. These teeth, however, are more likely to display minor environmental and genetic defects than others (Townsend et al. 2015). Figure 1 depicts a comparison of the frequency of LEH results within canines from both my former and current research studies. Although weaning and other research arguments have not provided sufficient evidence of such, it is reasonable to assume that such is one of the reasons for higher mortality in non-adults during these periods, and therefore it could be possible to assume the eruption of dental enamel and hypoplasia prevalence later on in life (Wasterlain et al. 2018). Understanding the impacts of childhood within a bioarchaeological context is essential, as it "should be contextualized within cultural understandings of the trajectory of the entire life course from conception to death" (Mays et al. 2017). LEH as a whole is an essential piece of a bioarchaeologist's toolkit for discovering not only the lifestyle of an individual but also the environmental impacts resulting from these physiological stressors. Analysis of LEH has been used within several contexts of bioarchaeological studies, ranging from forensics, primatology, and archaeological analysis (Steinberg et.al 2015, 458). An example of this is a study looking at the changes in health due to transitions from hunting and gathering societies to agriculture at Dickson Mounds (Steinberg et al. 2015, 457). Results showed that there was an increase in LEH presence during the population transition to subsistence (Steinberg et al., 2015, 457). The study of LEH and other enamel defects is essential to bioarchaeology and biological anthropology as a whole. Through LEH analysis, one can answer critical questions surrounding the health and lifestyle of human populations and primates, as well as transitions in agriculture and subsistence practices (Steinberg et.al 2015, 461). The findings from this study, along with former research, are undoubtedly accredited with 40 years of former bioarchaeological research surrounding the Newton Plantation. The data found offers new opportunities for bioarchaeological dental research and LEH analysis within commingled dental samples. Therefore, providing a platform for studies of Barbadian enslaved peoples and trans-Atlantic slavery.

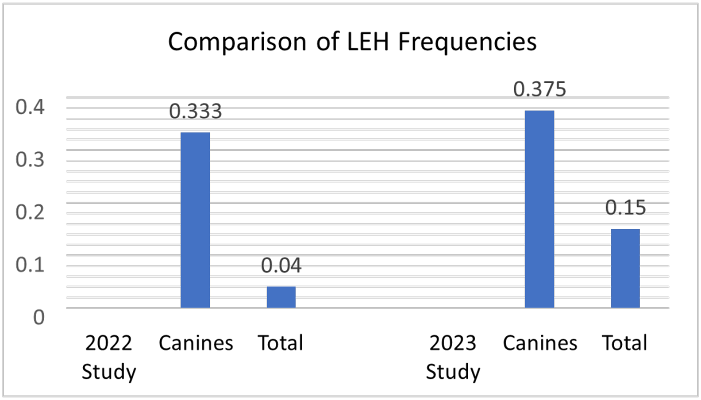

Figure 1. Chart depicting the comparison of LEH frequencies of canines, and the total number of teeth observed in my former 2022 fellowship study versus my current fellowship study.

Statement of Research Advisor

This is Katie's second undergraduate research project with dental anthropology and bioarchaeology on the Newton Plantation site. She expanded and did an excellent job in planning and carrying out this second project largely on her own. Through extensive time in

the lab, Katie has been improving her skills at tooth identification and analysis. She has also expanded her knowledge of both dental development and archaeology of the African Diaspora through more in depth reading of the scholarship that serves to contextualize this study. Katie's work will contribute valuable new data on early childhood stress experiences of enslaved individuals who lived on a 17th-18th century plantation in the Caribbean.
-Kristrina Shuler, Department of Anthropology, College of Liberal Arts

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Authors Biography

Katie E. Smith is a senior-year student pursuing a B.S. degree in Anthropology at Auburn University. She is the assistant bioarchaeology lab director under Dr. Kristrina Shuler and an intern in Auburn's NAGPRA lab. Her primary research focus has been studying dental morphology and linear enamel hypoplasia's upon a pre-colonial enslaved population from Barbados.

Kristrina A. Shuler is an associate professor in the department of Sociology, Anthropology, and Social Work at Auburn's College of Liberal Arts. She is a biological anthropologist (bioarchaeologist) whose primary focus is upon health and nutrition in early colonial populations from the Caribbean, Southeastern U.S., and Latin America.

Food Insecurity: What can TikTok reveal about Hunger in the American Condition?

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The challenges brought by the 2020 COVID-19 Pandemic revealed the immense struggle millions of United States citizens face amidst hunger and poverty. Currently, food insecurity in the United States effects roughly 10 percent of all households. This rate reflects no marked improvement from the rate in 2001, thus revealing stagnation and the need for deeper examination into the problem of hunger in the United States and the struggle faced by those living in food insecure conditions. This research aims to study the lived experiences behind food insecurity in the United States to provide a crystalized picture of the challenges and cycles present in hunger-stricken communities. Presenting an in-depth portrayal of hunger experiences will establish a foundation from which policymakers can develop informed, relevant solutions to food insecurity. Researchers developed software code to collect and synthesize TikTok posts related to a viral stitch about hunger and poverty in the United States. The researchers manually transcribed 170 TikTok posts from the original synthesized data. The data was then coded through the qualitative approach of thematic analysis for the purpose of identifying themes. The emerging themes identified in the data provide new insight into the lived hunger experience in the United States. These findings provide new information for researchers to find more effective solutions to the hunger crisis.

The United States is one of the most powerful and wealthy nations in the world [3]; however, food insecurity is still very prevalent. This is due to many factors, including a lack of research on the lived experience of food-insecure citizens. The purpose of this research is not to present numerical data on the number of people in need to gain more funding. The purpose is to understand the lived experiences of those suffering from food insecurity and provide faces to the data to alleviate the hunger crisis more effectively in the United States.

The current literature available does not portray the full picture of food insecurity in the United States. The data available is largely based on numerical representations of the hunger crisis. Moreover, there is an underrepresentation of lived hunger experiences in literature. The current data and literature available have not led to beneficial programs to alleviate the number of food-insecure persons in the United States. With negligible change from 2020, there is 10.2 percent of households or 33 million people suffering from food insecurity in the United States in 2021.

Additionally, the literature also suggests that the lack of government responsibility has resulted in an increase in feeding programs run by non-profit organizations. The lack of involvement by the governments in capitalist nations, such as the United States, has led to the needs of food insecure citizens being missed or miscommunicated [5].

TikTok is one of the fastest-growing social media platforms, with 3 billion downloads in the world in August 2020. Out of those 3 billion downloads, there were upwards of 1 billion active monthly users around the world [2]. Due to this growth, TikTok has become a place where people get their news and discuss topics with other users. The comment section on any given TikTok post shows engagement with the content as well as the emergence of communities within the platform. The interactive platform and the discreet manner of accessing information [4] has turned TikTok into a place for social change and political action. Between 2019 and 2020 countless adolescents utilized TikTok to mobilize

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social change and institute a new culture of advocacy and political learning [1]. This new culture of advocacy among adolescents with the use of an entertaining and discreet platform has resulted in more awareness in younger generations.

Researchers used the hashtag #growinguppoor that went viral in 2021 to collect data for this study. The hashtag was being utilized by users of TikTok to share their testimony of growing up in poverty or in low-income households. The videos related to users' lived experiences with hunger were especially interesting to our research team. After identifying the viral stitch, researchers created code to collect and synthesize the related videos from TikTok. Out of the 545 videos downloaded, only the top 200, based on view count, were selected for manual transcription. Following manual transcription, the researchers sorted through the transcribed videos and removed all transcripts not directly pertaining to hunger. This resulted in 170 video transcripts.

Researchers utilized a constant comparative method to analyze the transcripts and developed a series of codes. The codes were then defined and transferred to a codebook. This codebook was used by two third-party coders to test inter-coder reliability. The final codes were then summarized into an aggregated column graph, including codes from the original coders and the third-party coders. See Figure 1 for Summary of Code Analysis.

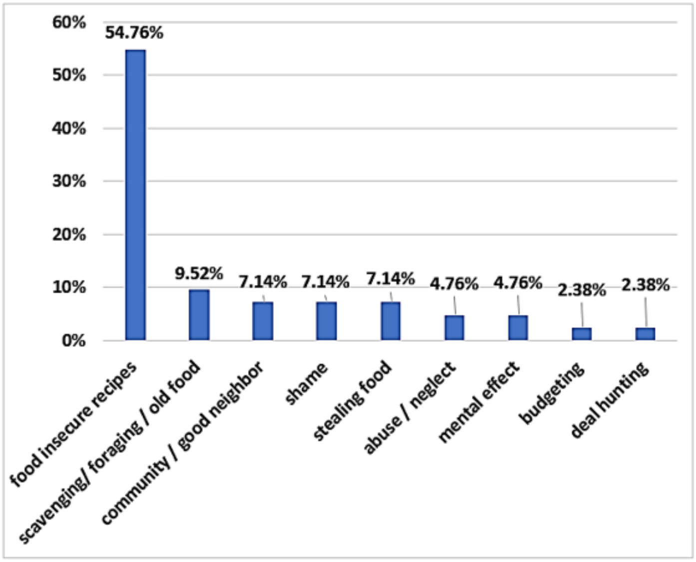

Fig. 1 Summary of Code Analysis

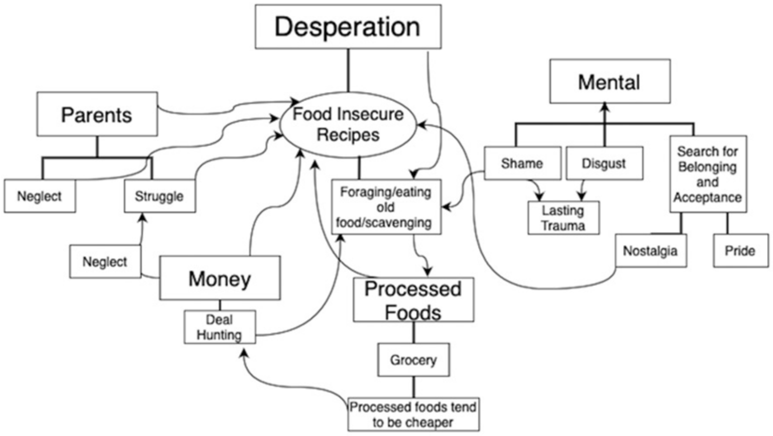

Fig. 2 Thematic Map.

With the analysis of the aggregated column graph, two researchers developed a thematic map to interpret code themes. See Figure 2 for Thematic Map.

The initial thematic map developed by researchers was analyzed again by two researchers and resulted in a final web of codes chart. See Figure 3 for Web of Codes Chart.

In the final round of thematic analysis three researchers refined the web of codes chart into the finalized map of overarching themes. These themes were Nutrition, Desperation (experienced when in food insecurity), Enduring Mental Effects, Parental Experience, and Assistance. See Figure 4 for Finalized Overarching Themes.

The emerging themes provide researchers with new insights into the lived hunger experience in the United States, which will allow researchers to find more effective solutions to the hunger crisis in the United States.

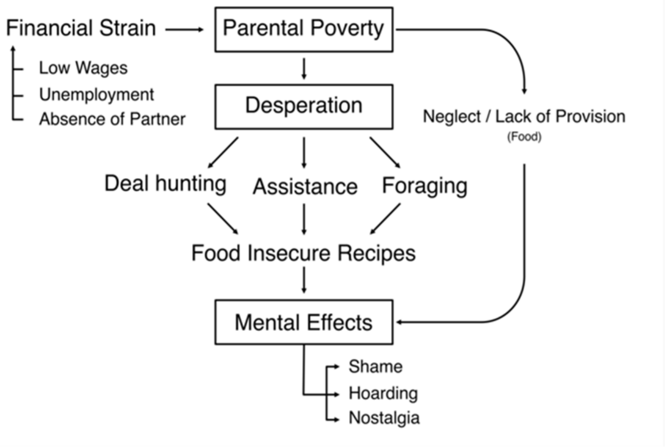

Fig. 3. Web of Codes Chart

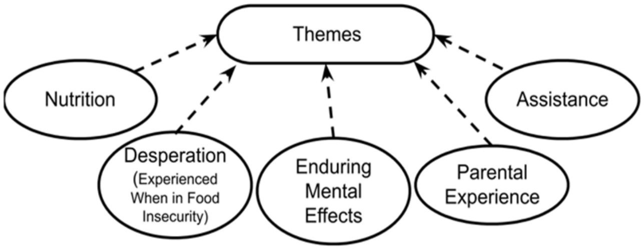

Fig. 4. Finalized Overarching Themes

Keywords: food insecurity, hunger, social media, TikTok, thematic analysis

Statement of Research Advisor

Beginning in the Summer of 2023, Serena has provided contributions to our study of learning about the lived hunger experience in the United States through a viral TikTok stitch. Her role, in addition to being a third-party coder and collaborating with two researchers to create a thematic map, was to develop a literature review. The literature review provides background and insight into the current literature available relating to food insecurity in the United States and using social media as a tool for social change.
- Kate Thornton, Department of Global Education, Auburn University College of Human Sciences

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Authors Biography

Serena T. Tedesco is a senior-year student pursuing a B.S. degree in Global Studies with a minor in Business at Auburn University. She is a 2023 Auburn Undergraduate Research Fellow. Serena has a passion for social impact studies and hunger research.

Adam J. Book is a Ph.D. candidate in the Department of Consumer and Design Sciences at Auburn University. He studies the quality of life among consumers in areas of product interaction and nutrition.

Kate Thornton, Ph.D., serves as the Director of Global Education in the College of Human Sciences at Auburn University. Thornton earned her Ph.D., MBA, and an MS in Consumer Affairs from Auburn University. She also holds a BS in Biochemistry and a BFA in Painting from Clemson University. Thornton has received many academic accolades, including being named a Rhodes and Marshall Scholar finalist and Algernon Sydney Sullivan Award recipient. Her interest and commitment to solving problems of hunger and poverty stemmed from adopting her children from Ethiopia.

Maggie Tennant holds a BS in Global Studies in Human Sciences from Auburn University and is pursuing graduate studies in the Netherlands. She focuses her research on hunger and equitable food access.

Python Developed GUI with AI-Aided Object Classification

Jacob Thornton[1,], Toyafel Ovee[2], Jean- François Louf [3]*

[1]Undergraduate Student, Department of Chemical Engineering, Auburn University
[2]Graduate Student, Department of Chemical Engineering, Auburn University
[3]Assistant Professor, Department of Chemical Engineering, Auburn University

Soft robotics is a growing field of research that aims to circumvent the typical limitations of conventional robotics [1], but that also comes with some limitations. In particular, imparting mechanosensing abilities to soft robots is extremely challenging. Current methods for mechanosensing fall short in their ability to respond to presented stimuli reliably and are not practical for real world applications; but how to impart mechanosensing abilities to a system lacking a nervous system? Interestingly, plants solved this problem a long time ago by leveraging poroelasticity. Upon touch, soft tissues are squeezed, inducing an overpressure in the plant's vasculature locally that will spread within milliseconds to the cells that control growth, triggering an ionic response afar from the stimulated area [2]. Inspired by plants, this project aims to design a smart skin generating pressure gradients and ionic signals upon deformation and enabling robots to deduce the firmness or softness of an object.

The Nature Inspired Fluids and Elasticity (NIFE) Lab built a robotic arm with such smart skin made of a soft, elastic, commercial material known as EcoFlex, with embedded microfluidic channels to allow for an overpressure to be generated upon touch(see Fig.1).

To control the soft robot we developed a GUI using Python to move the motors, handle and display pressure and displacement data, and perform tests on the object of interest(see Fig. 2).

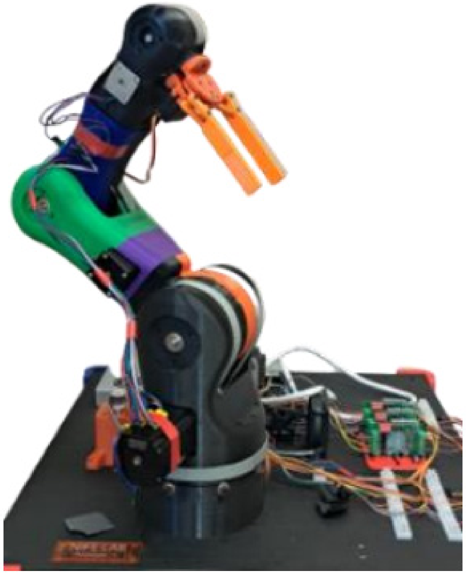
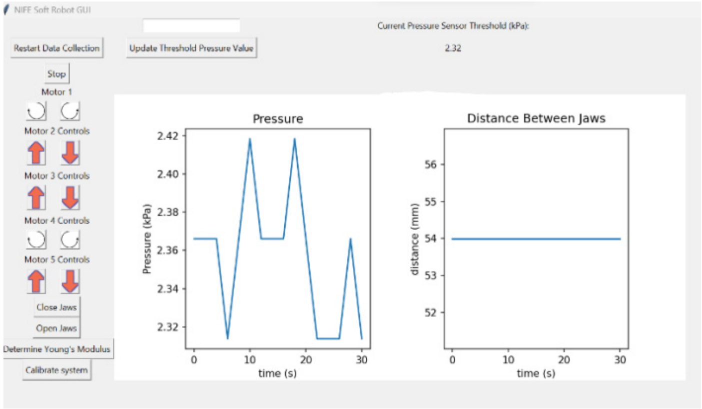


Fig. 1 NIFE lab mechanosensing soft robot



Current Pressure Sensor Threshold (kPa):
2.32

Fig. 2 Soft robot GUI

Utilizing the pressure and distance between jaws data from the program in conjunction with Equation 1

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*Corresponding author: jrt0047@auburn.edu from contact mechanics, we can calculate the effective Young's Modulus E * (Pa) of the system being squeezed.

$$\frac{3\pi PR^{1/2}}{4} = E^{*}d^{1/2} \qquad (1)$$

In Equation 1, P is applied pressure in Pascals, R is radius of the spherical object in meters, and d is the total deformation in meters. Using the effective Young's Modulus determined in Equation 1 and Equation 2, the effective Young's Modulus E * 2 of an object can be determined.

$$\frac{1}{E^{*}} = \frac{1}{B_1} + \frac{1}{E_2^{*}} \qquad (2)$$

To test the abilities of our soft robot to measure the diameters of different objects, we conducted experiments on eight objects and repeated each experiment five times. We then confronted our measurements to data obtained using a caliper (see Fig. 3) and found that we could measure diameter with 10% accuracy

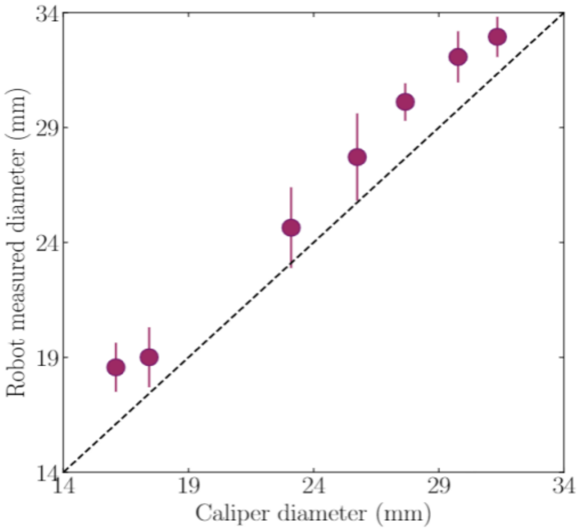

Fig. 3. Robot measured diameter compared to Caliper diameter.

Following our geometrical test, we conducted experients to measure the Young's modulus of a sphere. By collecting data points at different deformations and applied pressure readings, a line of best fit was used to estimate the effective Young's modulus E* of the system (in Pascals), where the effective Young's modulus is the slope of the line of best linear fit, as shown in Figure 4.

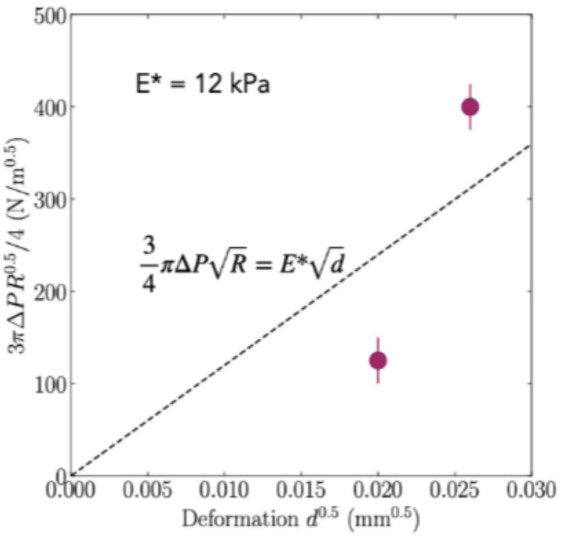

Fig. 4. Effective Young's modulus of the system.

From Figure 4 and Equation 2, we determine the effective Young's Modulus of the sphere of ecoflex to be E * 2= 20 kPa.

To determine the accuracy of this calculation, we performed a compression test using an Instron machine used in conjunction with contact mechanics theory to measure the effective Young's modulus of the sphere being tested using Equation 3.

$$\frac{3F}{4R^{1/2}} = E^{*}d^{3/2} \qquad (3)$$

Where F is the force in Newtons. In this case, E* is E*2, as the Young's modulus of the Instron plate is significantly greater than that of the testing objects (>4 orders of magnitude). The resulting measurements are displayed in Figure 5, where the slope represents the effective Young's modulus.

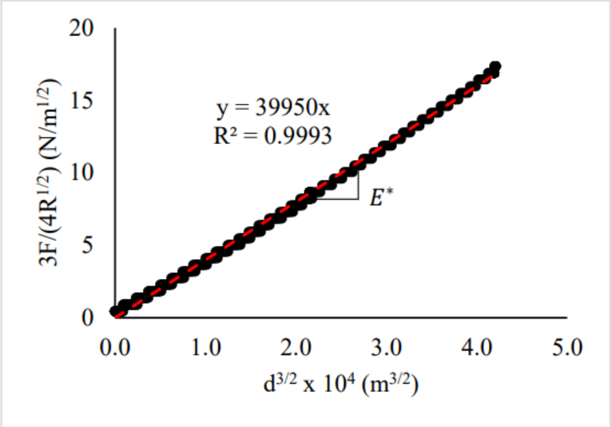

Fig. 5. Young's modulus calculated by Istron machine

From Figure 5 the effective Young's Modulus of the Ecoflex sphere is determined as 40 kPa. While this value is twice that measured using our soft robot, finding comparable measurements is encouraging. We will improve our measurements by using more accurate servomotors to capture the object's size and associated overpressure more accurately. Following these changes, the soft robot will be connected to a biological system consisting of an ionic solution chamber and nerve cells for biomedical applications.

Statement of Research Advisor

Jacob developed a GUI to control a 3D-printed robotic arm and simultaneously extract pressure and displacement measurements. He was very autonomous in this project and required little supervision to write the code in Python. He also performed mechanical experiments and data analysis that will be incorporated into a manuscript for submission soon. He was very autonomous, motivated, and did great work in the lab.

- Dr. Jean-François Louf, Chemical Engineering, Samuel Ginn College of Engineering

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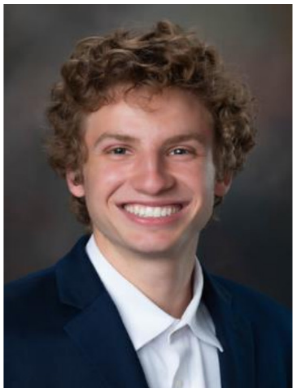

Jacob Thornton is a senior-year undergraduate student pursuing a bachelor's degree in chemical engineering. He has made significant contributions to the software utilized in the NIFE Lab soft robot project.

Tofayel is Graduate Research assistant and graduate student in the department of Chemical Engineering, Auburn University. He received a bachelor degree in Chemical Engineering and Polymer Science from Bangladesh. He is working with NIFE Lab under the supervision of Jean-François Louf. His key research interests are Soft robotics, Ionic hydrogel, 3D printing, prototyping devices etc.

Jean-François Louf is an assistant professor in chemical engineering at Auburn University working on poroelastic problems inspired by nature.

When Courts Disagree with Clincians: An Investigation with High-risk Youth

Cameron Tice[1,], Kelli R. Thompson[2], Kathryn Babbitt[3]*

[1] Undergraduate Student, Department of Psychology, Auburn University
[2] Assistant Research Professor, Department of Psychology, Auburn University; Research Director; Alabama Department of Youth Services
[3] Undergraduate Student, Department of Psychology, Vanderbilt University

Adolescents with Illegal Sexual Behavior (AISB) are responsible for a substantial number of sex crimes; however, the vast majority do not go on to reoffend as adults (Chaffin, 2008). AISB undergo extensive, progression-based rehabilitation before a secondary evaluation by the courts. As a progression-based rehabilitation, youth complete treatment only after clinicians observe significant improvement in the adolescent and deem them safe to return to their communities. Thanks in part to the success of this rehabilitation, recidivism rates for AISB fall consistently under three percent five years following adjudication (Cardwell, 2016). In additional to their low likelihood of reoffence, youth are also in a critical developmental period. Adolescents subject to the registry are more likely to experience harassment, adverse physical and mental health outcomes, and trouble maintaining stable housing (Harris et al., 2016). Therefore, it is imperative that the Juvenile Court System subject adolescents to the registry only in the extreme cases deemed appropriate by trained clinicians.

Using a wholistic report from a clinical team postrehabilitation, the courts assign a risk level to each adolescent. This risk level helps to determine whether the adolescent will be on the Juvenile Sex Offender Registry. Through the Sex Offender Registration and Notification Act (SORNA), states are incentivized to utilize a public, juvenile sex offender registry for adolescents 14 years of age or older if the offense was at least as severe as the federal crime of aggravated abuse (81 Fed. Reg. 50552). This study aims to investigate the relationship between the Alabama Juvenile Court System and a clinical team's recommendation regarding AISB.

The clinical team recommendations assessed in this study were given by a team of trained mental health professionals, representing a thorough evaluation of each adolescent. Evaluations are provided to the presiding juvenile court to help determine youth registry and public notification guidelines. Our sample is comprised of 86 male AISB who completed a court-mandated residential treatment program, the Accountability-Based Sex Offense Prevention Program (ABSOPP) between the years 2018 and 2022. To operationalize the degree of agreement between clinical team recommendations and court outcomes, risk assessment reports from the clinical team and juvenile courts records were assessed. Court files containing the corresponding risk level for each adolescent were obtained through the Alabama Department of Youth Services. The clinical team provided an evaluation of risk at "Low," "Medium," or "High," while the court evaluations ranged from "N/A," "Exempt," "Low," "Medium," or "High." A rating of N/A signifies the type of offense was not under consideration for the Juvenile Registry, while "Exempt" signifies the offense was under consideration, but the Juvenile Court ultimately determined the youth exempt from any registration.

Additional demographic data were coded from the Clinical Risk Assessment Files, including Age, Length of Stay, DSM Diagnoses, Trauma History, and Number of Trusted Friends. For this population of AISB, the average age of entry was 15.67 years. The average length of stay was 1.80 years. 68.6% reported a history of Trauma and half the population was given a DSM diagnosis. Of those with DSM diagnoses, 27.91% were diagnosed with a depressive disorder, 6.98% an anxiety disorder, and 23.26% for PTSD. The high rates of internalizing symptoms are consistent with previous studies on AISB (Seto & Lalumière, 2010). Additionally, 18.3% reported

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feeling as if they had no one in their lives they could trust.

As expected in a progression-based rehabilitation program, the clinical team gave each of the outgoing adolescents a risk level of "Low." The court assigned risk level for each adolescent is represented in Figure 1. With only three cases identified by the courts as higher risk than recommended by the clinicians, there was over 95% agreement between juvenile courts in Alabama and the clinical team. Of the three AISB who were assigned a Risk Level above the clinical recommendation, all ranged from 17 to 18 years of age, and each displayed some form of significant externalizing behavior during their time at the residential correctional facility. One case continued to deny the offense happened which may have not favored well with the judge. Among the three, there was no common county or jurisdiction. Additionally, there was no common thread between offense type, race, DSM diagnosis, or trauma history.

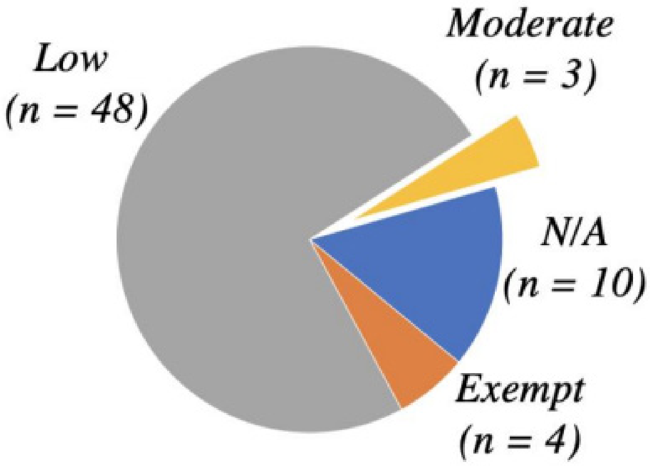

Fig. 1 Court Assigned Risk Levels

Investigating the instances where courts disagree with trained clinicians can give better insight into the rationale of the court, translating to a fairer court system where professionals are trusted, and harmful prejudices are ignored. This study suggests the Alabama Juvenile Court System consistently values the opinions of clinicians regarding AISB. Due to the relatively small percentage of disagreement between the clinical team and courts among this population, it is recommended that future investigations incorporate a larger sample size to obtain a more comprehensive understanding of potential disparities.

Statement of Research Advisor

Cam's research was supported by a more than 20-year public partnership with the Alabama Department of Youth Services and Auburn University. He has been a part of the Juvenile Delinquency Lab for a year and a half. During which time, he has presented at the Southeastern Psychological Sciences Annual Meeting, as well as at the Association for the Treatment of Sexual Abusers Annual Conference. He has advocated for juvenile registry reform with US Congressional representatives, Senators Katie Britt and Tommy Tuberville of Alabama. *- Kelli R. Thompson, Department of Psychological Sciences, College of Liberal Arts*

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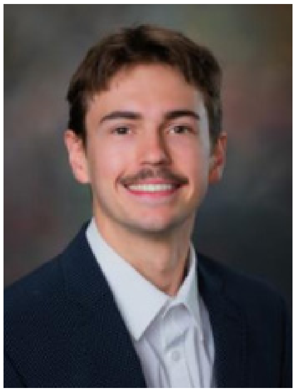
Authors Biography



Cameron Tice is a Junior pursuing a degree in Biomedical Sciences at Auburn University. Cam was selected as a College of Liberal Arts Undergraduate Research Fellow for 2022-2023. He has also represented Auburn University proudly in NCUR's Scholars Transforming through Research program and as a 2023 Goldwater Scholar.

Kelli R. Thompson was an Assistant Research Professor in the Department of Psychological Sciences at Auburn University. She is now working at Texas A&M University – Kingsville. While at Auburn University, her lab specialized in applied clinical research and she was particularly committed to undergraduate mentoring. She is an alumna from Auburn and has a Master of Divinity from Fuller Theological Seminary and a doctoral degree from the University of New Orleans. Her lab at Auburn taught the importance of science and civic engagement through creative scholarship such as this.

Kathryn Babbitt is a junior pursuing a degree in Psychology on the Honors Track at Vanderbilt University. She has been involved with Auburn's Juvenile Delinquency Lab for one year. At Vanderbilt, she is a member of the Park Clinical Neuroscience Lab researching schizophrenia and other psychotic disorders. Following graduation, she plans to pursue her Ph.D. in clinical psychology.

Characterization of Unsaturated Lipids Using Ambient Ionization Techniques (Paper Spray Ion Mobility-Mass Spectrometry (PS-IM-MS))

Alexis Toney[1,], Kimberly Kartowikromo[2], Ahmed Hamid[3]*

[1] Undergraduate Student, School of Science and Mathematics, Auburn University
[2] Graduate Student, School of Science and Mathematics, Auburn University
[3] Assistant Professor, School of Science and Mathematics, Auburn University

Abstract

The study of lipid isomers is becoming of great importance as various diseases such as diabetes and cancer can be identified by discriminating the ratio of double bond lipid isomers in biological samples. This study focuses on the development of a direct, fast, low-cost, and reliable method applicable to biological matrices in differentiating double bond lipid isomers utilizing paper spray ion mobility-mass spectrometry (PS-IM-MS). The IM based separation alone cannot discriminate all three of the PC lipids analysed in a mixture, even using the multiplexing mode. Therefore, an epoxidation reaction with m-CPBA was performed on the various lipids to form epoxides at the double bond position. This product was further dissociated with PS-MS/MS that resulted in unique diagnostic ion pairs. The fragmentation of the di-epoxide product for PC 18:1(6Z)/18:1(6Z) resulted in the two diagnostic ion pairs with m/z of 634.4 and 660.4, respectively. The fragmentation of the PC 18:1(9Z)/18:1(9Z) di-epoxide product also resulted in the diagnostic ion pairs with m/z of 676.5 and 692.4. Although PS-MS/MS was successful in discriminating various double bond lipid isomers with diagnostic ion pairs, the PS-MS of the lipids already exhibited diagnostic ion pairs with no epoxidation or fragmentation. Further analysis of the lipid isomers with ion mobility and computational methods will determine if the nature of ambient ionization correlates to the diagnostic ion pairs in PS-MS.

Introduction

Lipids are vital parts of biological systems and can function as energy storehouses, hormone regulators, components of cell membranes, chemical messengers, and much more (Ahmed, Saba, et al., 2018). Lipids can be classified as saturated or unsaturated as are structurally diverse with a variety of isomerism in the headgroup, chain length, sn-position, double bond positions, and geometry of double bonds (i.e., cis vs. trans) (Olajide, O. E., Donkor, B., & Hamid, A. M., 2022). Recent studies have shown that the characterization and identification of lipids are of great importance as cancerous and diseased tissue can be discriminated based on lipid structural differences, such as a higher presence of certain double bond configuration. Determining the double bond position in lipid isomers is beneficial considering that previous studies determined that a higher ratio of the double bond at position 11 to that of position 9 in PC (36:1) and PC (34:1) lipids can distinguish normal and cancerous tissue (Cao, Wenbo, et al., 2020).

Since lipids are structurally diverse with a variety of isomerism structural analysis is challenging only utilizing mass spectrometry (MS), especially double bond position isomers with the same mass over charge (m/z) ratio. Recent MS methods have been able to determine the double bond position in unsaturated lipids, such as ultraviolet-photodissociation (UVPD), ozone-induced dissociation (OzID), and many others but require modification to the mass spectrometers' setup (Williams, Peggy E., et al., 2017). To combat this, chemical methods including epoxidation with meta-Chloroperbenzoic acid (m-CPBA) will develop epoxides at the various double bond positions, and the product can be further dissociated with tandem mass spectrometry resulting in unique diagnostic ion pairs correlated to the double

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bond position. An illustration of this method can be seen in Figure 1. Utilizing ion mobility mass spectrometry (IM-MS) with epoxidation methods is of great advantage considering that discrimination of double bond isomerism is difficult only employing high resolution mass spectrometry.

Ion mobility mass spectrometry (IM-MS) is a very popular analytical technique used to separate ions in the gas phase depending on size, shape, and charge based on the balance of forces that effect the motion of an ion: the electric field and drag force created by collisions with the buffer gas, such as N_2 in this case (Burnum-Johnson, Kristin E., et al., 2019). Figure 2 shows the schematic illustration of the Agilent 6560 Ion Mobility- Quadrupole Time of Flight- Mass Spectrometer. This instrument is coupled with paper spray ambient ionization, where the sample is loaded onto a small triangular piece of paper and ions are generated directly for analysis by applying spray solvent and a high voltage to the wetted paper is of high interest (Liu, Jiangjiang, et al., 2010). Figure 3 shows the photographic illustration of the paper spray ambient ionization inlet. By combining ion mobility mass spectrometry with ambient ionization, we hope to develop a direct, fast, low-cost, reliable method for discriminating double bond isomers applicable to biological matrices.

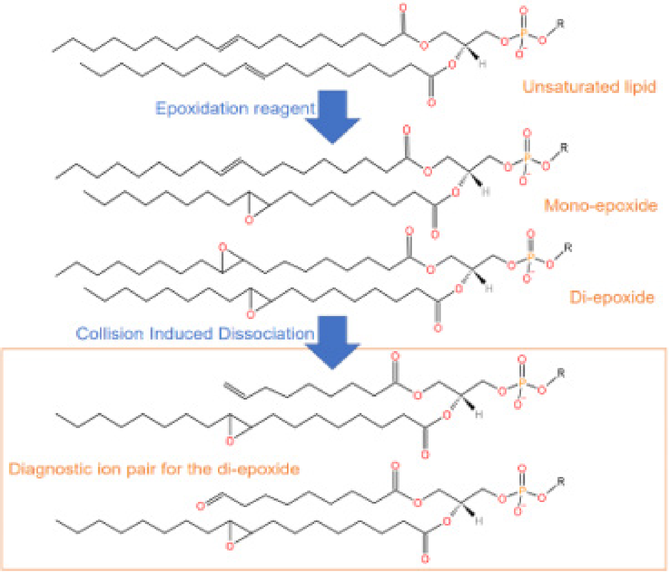

Figure 1. Schematic illustration of the epoxidation products and diagnostic ion pairs for an unsaturated lipid.

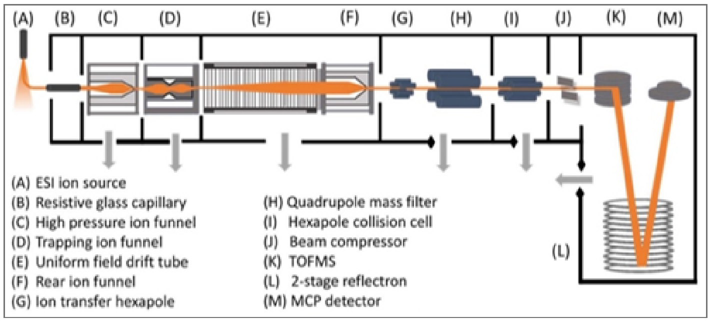

Figure 2. Schematic illustration of the Agilent 6560 Ion Mobility- Quadrupole Time of Flight- Mass Spectrometry instrument.

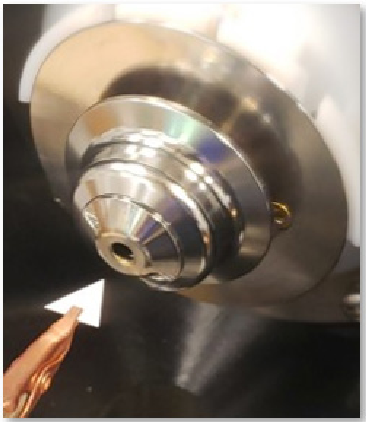

Figure. 3. Photographic illustration of the paper spray ambient ionization inlet

Methods

The unsaturated lipids analyzed in this study include PC 18:1(9Z)/18:1(9Z), PC 18:1(6Z)/18:1(6Z), PC 18:1(9E)/18:1(9E), PG 18:1(9Z)/18:1(9Z), and PG 18:1(9E)/18:1(9E). Each unsaturated lipid sample standard was prepared in IPA/ACN/H2O (2:1:1, v/v/v). For MS, IM-MS, and MS/MS, 2 µL of 5 ppm unsaturated lipid standard was used with each trial performed, while IM-MS (multiplex) used 2 µL of 1 ppm unsaturated lipid standard for each trial. Each trial used 15 µL of IPA solvent for the ambient ionization. Tables 1 and 2 display the parameters and values for the optimized paper spray MS and IM-MS conditions.

Table 1 Optimized paper spray MS and IM-MS conditions.

Parameter	Value
Drying Gas Flow Rate	8 L/min
Drying Gas Temperature	250 °C
Fragmentor	400 V
Vcap (positive mode)	4,500 V
Vcap (negative mode)	3,500 V
Spray Shield	Multi bore vortex

Table 2 Continued optimized paper spray MS and IM-MS conditions.

Parameter	Value
Trap Release Time IM-MS (Single-Pulsed)	150 µs
Trap Release Time IM-MS (Multiplex)	200 µs
Trap Fill Time IM-MS (Single-Pulsed)	20,000 µs
Trap Fill Time IM-MS (Multiplex)	3,900 µs
Multiplex Sequence Length	4 bit
Paper Distance to MS Inlet	6 mm
Paper Size	8 mm x 10 mm (width x length)

For the epoxidation reactions the parameters and conditions mentioned above were used, but the unsaturated lipid was left to react with the m-CPBA on the triangular piece of paper. This epoxidation rection was optimized based on the solvent system of the reagents, reaction time, and the volume and concentration of the epoxidation reagents. Table 3 and Figure 4 shows the parameters of the PS-IM-MS epoxidation optimization as well as the different reaction times and solvent systems.

Table 3 Parameters of PS-IM-MS epoxidation optimization.

Parameters	Value
Reaction Time	5 minutes
Solvent System of m-CPBA	IPA/ACN/H_2O (6:13:1, v/v/v/)
Volume of m-CPBA	2 µL
Concentration of m-CPBA	10,000 ppm

Results and Discussion

The IM-MS (single-pulsed) of the three PC lipids along with the mixture found in Figure 6 shows the minimal difference in drift times for the double bond isomers. The PC 18:1(9Z)/18:1(9Z) and PC 18:1(9E)/18:1(9E) exhibits closer drift times to that of PC 18:1(6Z)/18:1(6Z). The IM-MS (single-pulsed) of the PC mixture in Figure 7 only has one peak for the drift time, which means that these double bond isomers cannot be discriminated only using IM-MS (single-pulsed). The IM-MS (multiplex) in Figure 8 demonstrates two peaks in the drift time. This is because the resolving power of the Agilent 6560 in single-pulse is ~60. With multiplex mode the IM data, after deconvolution through PNNL software, can be further processed via a high-resolution demultiplexing tool (HRdm) resulting in an increased resolution to enhance IM separation of the isomers with a resolving power around 200. Although this process resulted in a higher resolution, only one out of the three PC lipids could be separated reflecting structural similarities among the lipid isomers. For the epoxide reaction on the PC lipid, Figure 5 shows the highest intensity of the di-epoxide product, 818.6 m/z, for the PC 18:1(9Z)/18:1(9Z) at 5 minutes. This optimization of reaction time was used in the PS-MS/MS for PC 18:1(6Z)/18:1(6Z) and PC 18:1(9Z)/18:1(9Z) as well as the mixture for IM-MS. For the IM-MS the drift times are shown for the lipid, mono-epoxide, and di-epoxide in Figures 9 and 10. The drift time for the lipid as well as the epoxide product varies minimally, and the separation of these products would be difficult. The fragmentation of the di-epoxide product for PC 18:1(6Z)/18:1(6Z) resulted in the two diagnostic ion pairs with m/z of 634.4 and 660.4, respectively. The fragmentation of the PC 18:1(9Z)/18:1(9Z) di-epoxide product also resulted in the diagnostic ion pairs with m/z of 676.5 and 692.4. The conformation of unique diagnostic ion pairs for each PC lipid proves that the double bond lipid isomers can be differentiated using PS-MS/MS on the di-epoxide products.

Although PS-MS/MS of the di-epoxide products was successful, the PS-MS of the PC lipids exhibits some of the diagnostic ion pairs without any epoxidation reaction or fragmentation, shown in Figure 11. LC-MS was then used to further analyze the PC lipids and found that no diagnostic ion pairs were present. This indicates that the diagnostic ion pairs found in PS-MS might have been the result of the nature of ambient ionization.

Since ambient ionization occurs in atmospheric conditions and applies high voltages to ionize the analyte, it is possible that dissociation was induced because of the high voltages. Other investigations with PS-MS on the epoxidation and fragmentation of the lipids needs to be conducted. Further analysis of this reaction will be studied by comparing the drift times of the diagnostic ion pairs found in PS-MS and PS-MS/MS along with computational methods to predict the fragmentation patters of the various lipids.

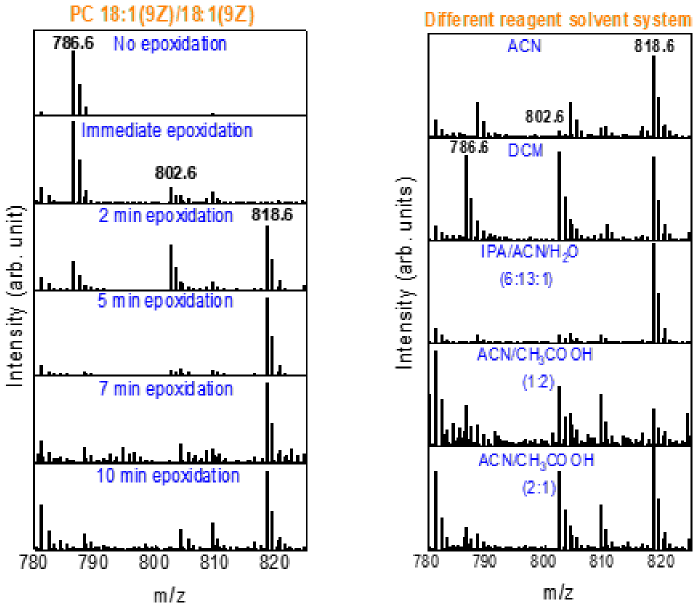

Figure 4. The optimization of the reaction times with m-CPBA and different solvent systems with PC 18:1(9Z)/18:1(9Z).

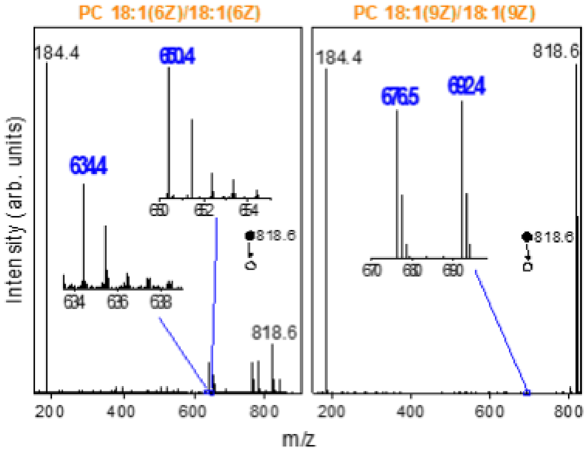

Figure 5. PS-MS/MS of the PC 18:1(6Z)/18:1(6Z) and PC 18:1(9Z)/18:1(9Z) of the diepoxide products.

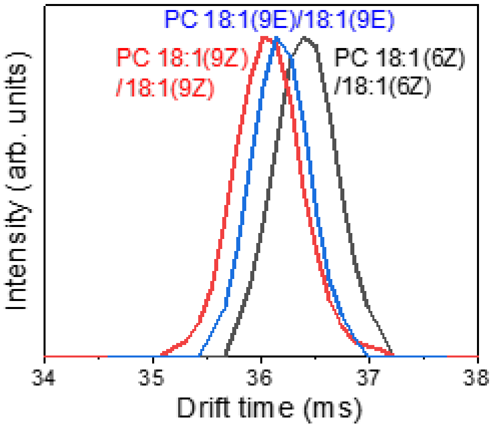

Figure 6 IM-MS (single-pulsed) PC 18:1(9Z)/18:1(9Z), PC 18:1(9E)/18:1(9E), and PC 18:1(6Z)/18:1(6Z).

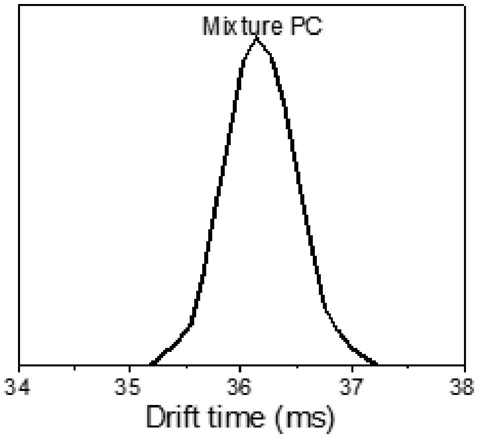

Figure 7 IM-MS (single-pulsed) of mixture of PC lipids.

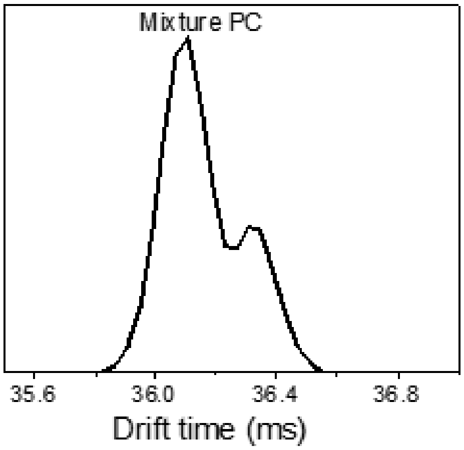

Figure 8 IM-MS (Multiplex) mixture of PC lipids.

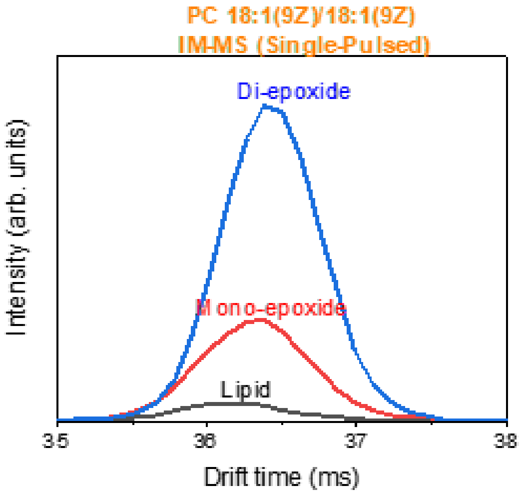

Figure9 IM-MS(single-pulsed)ofPC18:1(9Z)/18:1(9Z) unsaturated lipid, mono-epoxide, and di-epoxide products.

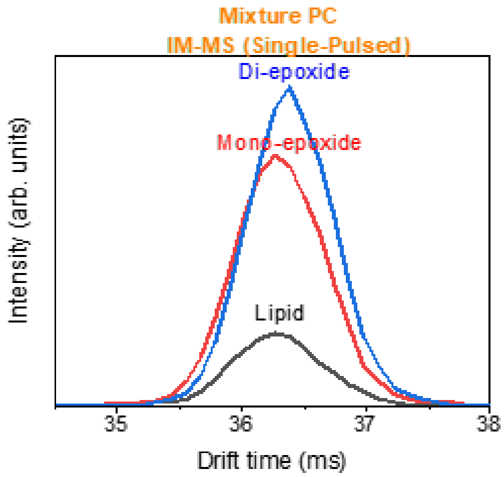

Figure 10 IM-MS (single-pulsed) of PC lipid, mono-epoxide, and di-epoxide mixture.

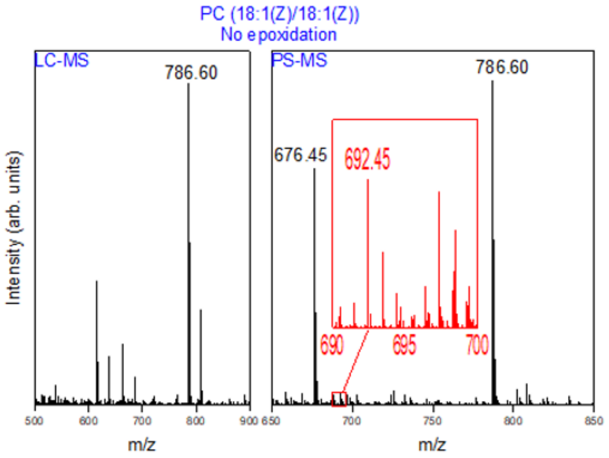

Figure 11. LC-MS and PS-MS of PC 18:1(9Z)/18:1(9Z) without performing epoxidation reactions. PS-MS shows diagnostic ion pairs of 676.45 m/z and 692.45 m/z along with the lipid, 786.60 m/z. LC-MS only exhibits the lipid, 786.60 m/z.

Statement of Research Advisor

Alexis's research studies were focused on the development and assessment of novel ambient ionization ion mobility mass spectrometry methods and their application in the study of epoxidation reaction of unsaturated lipids. She started with an extensive literature survey that led to the choice of several sets of lipid isomers that are challenging to analyze using the current mass spectrometry methods and implemented paper spray method developed in our laboratory in the differentiating them. Differentiating these lipid isomers can be used in the diagnosis of various diseases.

- Ahmed M. Hamid, Chemistry and Biochemistry, College of Sciences and Mathematics

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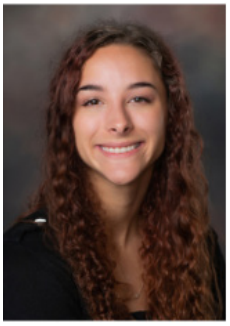
Authors Biography



Alexis Toney is a senior-year undergraduate student pursuing a B.S in Chemistry with a minor in philosophy of religion at Auburn University. She has played a key role in the discrimination of various double bond position isomers using ambient ionization and computational methods in hopes to predict the fragmentation patterns of the lipids. She will be attending a chemistry graduate program after graduation.

Kimberly Kartowikromo is a second-year graduate student in the Department of Chemistry and Biochemistry at Auburn University. Her research focuses on environmental and clinical applications of ambient ionization ion mobility mass spectrometry in discriminating the double bond isomers in lipids.

Dr. Ahmed M. Hamid is an assistant professor in the Department of Chemistry and Biochemistry at Auburn University. His analytical research primarily focuses on environmental and clinical applications of ion mobility mass spectrometry, as well as developing portable novel mass spectrometry instruments.

Auburn University Journal of Undergraduate Scholarship

Phonological Skills in the Spontaneous Speech of Children Who Do Not Stutter

Katie E. Wallace[1],, Katelyn G. Gilson[2], Meghan E. Stinnette[3], Gregory J. Spray[4]*

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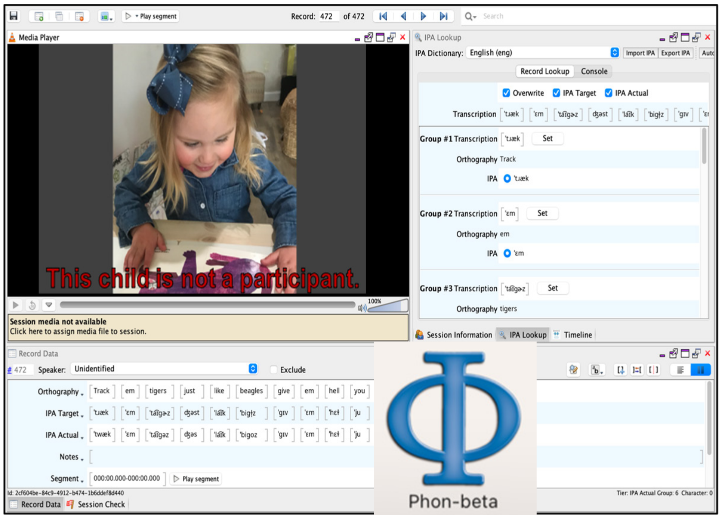
[2] Undergraduate Student, Department of Speech, Language, and Hearing Sciences, Auburn University
[3] Graduate Student, Department of Speech, Language, and Hearing Sciences, Auburn University
[4] Assistant Professor, Department of Speech, Language, and Hearing Sciences, Auburn University

Previous studies have reported that differences in phonological abilities may exist between children who stutter and children who do not stutter (Paden et al., 1999; Spencer & Weber-Fox, 2014). Studies have used nonword repetition tasks (a test where the participant is asked to repeat sounds in the form of made-up words) to differentiate young children who stutter from other groups based on production accuracy (Anderson et al., 2006; Hakim & Bernstein Ratner, 2004). However, these studies have not observed differences in phonological abilities in school-aged children (Smith et al., 2012; Spray, 2020; Weber-Fox et al., 2008). This study also differs from previous studies because it calculates phonological measures using spontaneous speech, rather than individually produced words. Spontaneous speech gives a more holistic view of the participant's speech (because the utterances are longer and more natural), in comparison to the production of single words.

Our hypothesis in this study is that children who stutter will exhibit reduced phonological accuracy in spontaneous speech compared to children who do not stutter. This is measured by phonological mean length of utterance (PMLU) and proportion of whole-word proximity (PWP) (Ingram & Ingram, 2001).

For this portion of the study, speech samples from 10 monolingual children between the ages of 30-50 months of age were transcribed into the software CLAN (MacWhinney, 2000) and Phon (Rose & MacWhinney, 2014). These transcriptions are publicly available through FluencyBank (Bernstein Ratner & MacWhinney, 2018). The inclusion criteria for the children who do not stutter includes: monolingual English speakers, within 1.5 standard deviations of the mean on speech-language tests, no history of learning delay, a minimum of 75 spontaneously produced utterances greater than two words each, and no previous history of stuttering.

One of the softwares used in this study, Phon, was a program that completes phonological analysis and calculates PMLU and PWP. After each speech sample was transcribed in CLAN, it was imported into Phon. Figure 1 illustrates Phon and an example transcription. Each word was reviewed within the speech sample to ensure proper phonetic transcription using the international phonetic alphabet (IPA). If a child's production of a word was incorrect, alterations to the IPA target were made. After transcription was completed, Phon calculated phonological accuracy and complexity.



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IPA Dictionary: English (eng)

☑ Overwrite ☑ IPA Target ☑ IPA Actual

Transcription: ˈtɹæk ˈɛm ˈtaɪ͡gɚz ʤəst ˈlaɪ͡k ˈbigɫz ˈgɪv

Group #1 Transcription: ˈtɹæk
Orthography: Track
IPA: ● ˈtɹæk

Group #2 Transcription: ˈɛm
Orthography: em
IPA: ● ˈɛm

Group #3 Transcription: ˈtaɪ͡gɚz
Orthography: tigers

472 Speaker: Unidentified ☐ Exclude

Orthography	Track	em	tigers	just	like	beagles	give	em	hell	you
IPA Target	ˈtɹæk	ˈɛm	ˈtaɪ͡gɚz	ʤəst	ˈlaɪ͡k	ˈbigɫz	ˈgɪv	ˈɛm	ˈhɛɫ	ˈju
IPA Actual	ˈtwæk	ˈɛm	ˈtaɪ͡gəz	ʤəs	ˈlaɪ͡k	ˈbigoz	ˈgɪv	ˈɛm	ˈhɛɫ	ˈju
Notes										
Segment	000:00.000-000:00.000									

Id: 2cf604be-84c9-4912-b474-1b6ddef8d440

Tier: IPA Actual Group: 6 Character: 0

Fig. 1 Example of IPA target and IPA actual transcriptions in the Phon software.

To calculate PMLU, Phon assigns 1-point to each consonant and vowel produced in a word. There is an additional point given for each correct consonant produced in the target production. This results in a calculation of a target PMLU, which is what the child attempted to produced, and an actual PMLU, which is what the child

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actually produced.

Each speech sample was reviewed by two highly-trained Phon users. If issues arose, a qualified third party was consulted to ensure validity and reliability of results.

An independent samples t-test was used to determine whether between-group differences existed for phonological measures that are normally distributed. A Mann-Whitney U-Test was used for phonological measures that are not normally distributed. All results for phonological measures were considered significant at $p < 0.05$. Table 1 shows group averages calculated during the study.

Table 1 Differences between tPMLU, aPMLU, and PWP of children who stutter and children who do not stutter

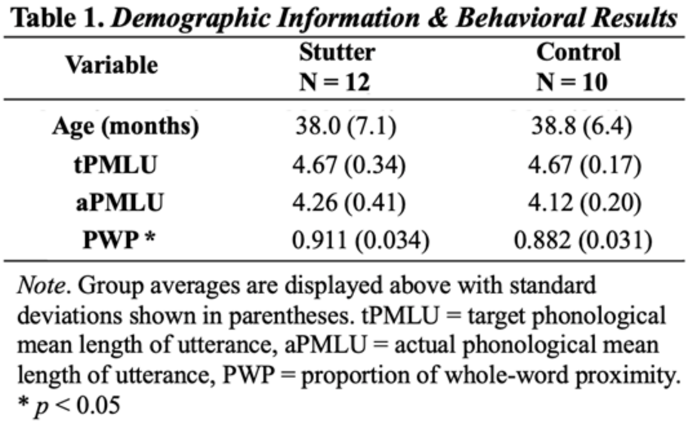

Table 1. ***Demographic Information & Behavioral Results***

Variable	Stutter N = 12	Control N = 10
Age (months)	38.0 (7.1)	38.8 (6.4)
tPMLU	4.67 (0.34)	4.67 (0.17)
aPMLU	4.26 (0.41)	4.12 (0.20)
PWP *	0.911 (0.034)	0.882 (0.031)

Note. Group averages are displayed above with standard deviations shown in parentheses. tPMLU = target phonological mean length of utterance, aPMLU = actual phonological mean length of utterance, PWP = proportion of whole-word proximity.
* $p < 0.05$

The results of this study support our hypothesis that children who do not stutter exhibit increased phonological accuracy in spontaneous speech when compared to children who stutter. Figure 2 depicts a comparison of the two groups.

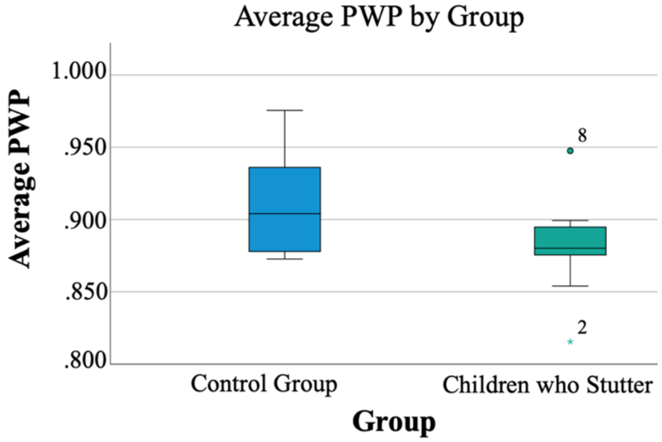

Fig. 2 PWP is higher for control group in comparison to children who stutter

This report is one part of a multi-phase study. The data collected in this study is being used in comparison to children who stutter to determine differences that between groups.

Results from this study were presented at the 2023 American Speech-Language-Hearing Association Convention in Boston, MA and the 2024 Speech and Hearing Association of Alabama Convention in Birmingham, AL.

Overall, the results of the study add to the mounting evidence that children who stutter may exhibit delayed maturation as it relates to phonological speech production.

Statement of Research Advisor

Katie Wallace made significant contributions to the project by transcribing speech samples of children who do not stutter. This transcription process included converting orthography into phonetic symbols, which were required to be highly accurate. In addition, Katie reviewed transcriptions completed by another research assistant who transcribed the utterances of children who stutter. Finally, Katie presented these findings at a national/international conference and a regional conference.

- Gregory Spray, Speech, Language, and Hearing Sciences, College of Liberal Arts

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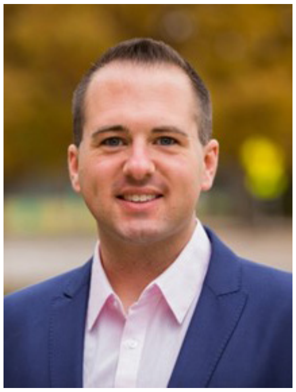
Authors Biography

Katie E. Wallace is a senior-year student pursuing a B.S. degree in Speech, Language, and Hearing Sciences at Auburn University. She has played a key research role in transcribing the sessions from 10 children who do not stutter into Phon. Katie is a member of multiple research laboratories at Auburn University and was a Peer Mentor at the BRAIN Program at Children's Healthcare of Atlanta.

Katelyn G. Gilson is a senior-year student pursuing a B.S. degree in Speech, Language, and Hearing Sciences at Auburn University. She transcribed the sessions from 12 children who stutter into Phon for this research study. Katelyn is an undergraduate research assistant in Auburn's Speech, Neurophysiology, & Attitude Perceptions (SNAP) Lab.

Meghan E. Stinnette is a graduate student in the Department of Speech, Language, and Hearing Sciences at Auburn University. She received a B.S degree in Communication Sciences and Disorders from Radford University in 2022. She aided in analyzing and preparing data for this report.



Gregory J. Spray, Ph.D., CCC-SLP is an assistant professor in the Department of Speech, Language, and Hearing Sciences in the College of Liberal Arts. He is the director of the Speech, Neurophysiology & Attitude Perceptions Laboratory (SNAP Lab) at Auburn University.

Virtual Tour of Auburn University's African American History

Courtney F. Weeks[1], and Robert Bubb[2]*

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[2] Lecturer Department of Human Sciences, Auburn University

African American experiences are a rich part of Auburn University's history that is not freely told. Current campus tours do not include African American experiences that helped create the university as we know it today. This concern has motivated this research initiative to create a virtual tour of Auburn University that places a spotlight on these stories. It will be assumed that the corresponding author will represent the paper. The objective of this project is to highlight fourteen points of interest on Auburn's campus that hold African American significance.

Preparation for this project began during the Spring semester of 2022. Two undergraduate students in the College of Human Sciences at Auburn University, Courtney Weeks and Kalandra Blake served as Co-Directors for the research to Preserve African American Stories and Traditions (rPAAST) research group under the mentorship of Human Sciences Lecturer Dr. Robert Bubb. Seventh and eighth-grade students from Auburn Junior High School interested in participating in this research registered for a school club entitled "Friends of Baptist Hill." This name was inspired by the students 'service work done at Auburn's first African American cemetery, Baptist Hill cemetery. Under the teaching and supervision of rPAAST co-directors, each student was responsible for researching one of the fourteen points highlighted in the virtual tour. For the final semester assignment, students invited their friends and family to walk the tour of Auburn's Campus and present their findings. The student's findings will be featured as summaries embedded in the virtual tour.

Fourteen points are featured on the virtual tour (Fig. 1). These points will highlight: Bessie Mae Holloway, Bo Jackson, Cam Newton, Harold A. Franklin, Harold Melton, John Reese, Josephus Bell, Josetta Brittain-Matthews, and Thom Gossom. The final point will be the NPHC Legacy Plaza which is currently under construction. It is expected to be completed in September of 2022, and we will revisit the site then to update imaging.

Fig. 1. Junior High Students presenting their research on Auburn athlete, Bo Jackson.

The National Pan-Hellenic Council (NPHC) is composed of nine African American Greek Organizations, also known as "the Divine 9". These organizations are Alpha Kappa Alpha Sorority Incorporated, Alpha Phi Alpha Fraternity Incorporated, Delta Sigma Theta Sorority Incorporated, Kappa Alpha Psi Fraternity Incorporated, Omega Psi Phi Fraternity Incorporated, Zeta Phi Beta Sorority Incorporated, Phi Beta Sigma Fraternity Incorporated, Sigma Gamma Rho Sorority incorporated, and Iota Phi Theta Fraternity incorporated.

Auburn University has a chapter for all nine organizations. Six of the nine NPHC organizations are active on

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campus as of Spring 2022. These organizations are Delta Sigma Theta (Kappa Upsilon chapter), Omega Psi Phi (Sigma Delta chapter), Alpha Phi Alpha (Omicron Kappa chapter), Phi Beta Sigma (Kappa Zeta chapter), Sigma Gamma Rho (Omicron Iota chapter), and Alpha Kappa Alpha (Kappa Chi chapter).

The NPHC Legacy Plaza will be located near the center of Auburn's main campus. Its goal is to "provide a space on campus that gives homage to the legacy of Black Greek Letter Organizations and African American culture at Auburn University (Greek Life, Auburn University)." It will feature nine markers to honor all organizations of the Divine 9. It is estimated to be completed in September 2022. We will complete this portion of the tour once the plaza is completed.

The Friends of Baptist Hill club for the Fall 2021 – Spring 2022 term was composed of twelve seventh and eighth graders attending Auburn Junior High School in Auburn, Al. Co-Directors from the research to Preserve African American Stories and Traditions program, Human Sciences students.

Courtney Weeks and Kalandra Blake, conducted research in the community to gather stories to teach to the students. Junior High students were given the opportunity to conduct their own research on their designated story. Students in this club were encouraged to take their knowledge outside of the classroom. Cemetery clean-up at Baptist Hill Cemetery was hosted by the club and supervised by the student Co-Directors. Students would spend hours of their weekend cleaning up the first African American cemetery in Auburn. Students also presented their work for the Fall 2021 semester at a presentation night for the Auburn community, where many of the people featured in the stories were present (Fig. 2). Reverend Willie Muse, who was the pastor of the first African American church was present for the student's presentation he did on him. Auburn's first African American firefighter, Jesse Strickland, and the wife of the first police officer, Estella Dunn, were also present for the student's presentations.

The Junior High students were encouraged to share their knowledge in an effort to spread awareness of Auburn's African American history. They also played a large role in creating this incredible resource to aid this goal.

Fig. 2. Auburn Junior High Students and rPAAST co-director Courtney Weeks posing at one of the sites of their presentation.

Procedures

The first stage of planning this project occurred in the early Fall of 2021. We began by identifying the sites we wanted to explore and study. We did this by researching at the City Hall, speaking with community members, and conducting research using ancestry databases. We prepared fourteen stories to be studied and taught to Junior High Students at Auburn Junior High School. These students were given assignments and challenged with creating a creative piece to honor that story.

When selecting the story's place on campus, each space was selected by considering the significance of each spot. For example, John Reese does not have a marker on Auburn's downtown area. It is understood that he had a great impact on establishing Toomer's Drugs. Therefore, his spotlight will be placed at that location. Another highlighted story, Mr. Harold A. Franklin, does have a marker on Auburn's campus. It is located just adjacent to the University library, and his spotlight will be placed there.

3D imaging was created using a compatible camera (Insta360 one X2 camera) and taking multiple images to create a 360 effect. We used Matterport software for 360 rendering to curate the tour.

Summaries for each spotlight were embedded at an appropriate spot. These summaries were curated by members of the Friends of Baptist Hill Club at Auburn

Junior High School during the Spring 2022 semester.

Discussion

Partnerships that helped bring this project into fruition include the Caroline Marshall Draughon Center for the Arts and Humanities, HDFS department, Biggio Center, Office of Inclusion and Diversity, Auburn City Schools, and the History Department. The Caroline Marshall Draughon Center for the Arts and Humanities donated the Matterport subscription and provided the Friends of Baptist Hill club a place for their Fall 2021 presentation night (Fig. 3).

Flaws from this project can be improved for future updates and improvements. The most notable challenge was that the camera and software were not created for outdoor spaces. This rendered the project because the majority of the tour features outside markers. The software only allows one hundred shots per space, which required us to split the tour into five different spaces instead of just one central tour. Finally, lighting was a factor in image capturing and resulted in the best images being captured between the hours of 5:30 am and 6:30 am. This created a small window for image capturing.

Plans for this project include updating the NPHC plaza once completed, adding additional spaces, displaying the virtual tour across campus, and opportunities to educate the community on Auburn's African American history.

There are an additional seven to eight locations on Auburn's campus that can be researched and added to the virtual tour. For the Fall 2022 semester, Auburn Junior High students will explore these stories with the addition of Auburn High School Auburn University Journal of Undergraduate Scholarship students. rPAAST will begin teaching classes at AHS in addition to AJHS, spreading more knowledge on Auburn's African American history and creating more content for the virtual tour. AJHS students (Friends of Baptist Hill club) will continue their work on researching stories and service to the Baptist Hill cemetery, while the AHS will have focus on researching and creating creative content for the Virtual Tour.

rPAAST plans to partner with the Office of Inclusion and Diversity to provide opportunities for the virtual tour to be accessible on campus. The Cross-Cultural Center for Excellence (CCCE) is located on the second floor of the student center. It is popular for minority students to mingle and stop by between classes. With help from the Biggio center, we plan to place a floor-standing iPad mount in the CCCE for students and guests to interact with the virtual tour.

From this project, we hope to inspire more opportunities for education on Auburn's African American history. The Friends of Baptist Hill club at Auburn Junior High School will receive an increase in membership numbers for the next semester, which will produce an opportunity for more stories to be researched and included in the virtual tour. rPAAST hopes to expand to neighboring schools in an effort to provide interactive educational opportunities. Current campus tours will be asked to incorporate this feature into their program for guest and prospective students to utilize.

Fig. 3. Junior High students and Courtney Weeks on the night of their presentations for Fall 2021.

Statement of Research Advisor

Courtney Weeks has worked vigorously and produced great work throughout this research period. The future of this project will produce great opportunities for African American stories to be researched and spread throughout Auburn's campus and community.
-Robert Bubb, College of Human Sciences

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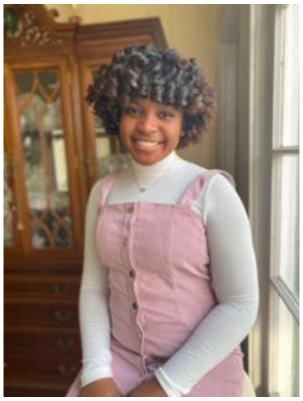

Courtney F. Weeks is a Summer 2022 graduate from Auburn University with a B.S. degree in Human Development and Family Science. She has played key roles in researching and teaching Auburn's African American History. She is from Birmingham, Al. Her professional goal is to work with non-profit organizations in Community Outreach.

Robert Bubb is a lecturer of statistics and research methods in the College of Human Sciences at Auburn University. His research focus is working alongside the community to research, preserve, and present local African American history.

Exploiting Genetic Traits of Plant Defense Mechanisms Against Phytoparasitic Nematodes

Benjamin W. Welsh[1,], Simrandeep Kaur[2], and Sang-Wook Park[3]*

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Phytoparasitic nematodes (PPN) cause extensive damages to essential food crops. These pests have been estimated to cause the annual loss of 173 billion U.S. dollars, accounting around 12.3% of global food production (Gamalero and Glick, 2020). Nematicides offer some relief, but their economic costs greatly exceed their utility, as well as concerns over toxicity to helpful organisms, insects, and mammals (Gamalero and Glick, 2020). In this study, we examine and characterize plant defense responses to PPN, in order to develop inexpensive and effective genetically resistant cultivars.

Salicylic acid (SA) has long been considered as a major plant defense hormone against PPN. SA signaling activates hypersensitive response (HR) that is effective at suppressing the spread of pathogenic microorganisms, and presumably PPN (Branch et al, 2004). Earlier, it was suggested that reactive oxygen species (ROS) production is an indication of HR which stems from SA signaling. In line with this scenario, previous studies showed some accumulations of ROS at the infection site of PPN (Branch et al, 2004). However, in our recent study, cotton roots inoculated with *Rotylenchulus reniformis* did not show any HR nor even localized cell death. While ROS accumulations were induced in high amounts, HR characteristic of SA signaling did not occur. Previous studies may have mischaracterized cell death from PPN feeding as HR.

Oxo-phytodienoic acid (OPDA) signaling may play a role in plant defense responses against PPN due to its roles for signaling redox reactions and root hair growth, which our recent study found that the amount of root hairs may play a role in tolerance to PPN (Liu and Park, 2021). OPDA is a precursor to jasmonic acid (JA), which antagonizes SA signaling. In order to assess OPDA's role in plant defense response, transfer DNA insertion knockout (KO) mutant Arabidopsis plants disrupting OPDA, SA, JA signaling and biosynthesis were grown in MS Gelrite plates and inoculated with PPN. These mutants include *cyp20-3*, the loss-of-function of *CYP20-3*, a small plastid protein that interacts with OPDA and intricately coordinate defense gene expressions. Interestingly, *cyp20-3* display severe inhibition of root hair growth (Liu and Park 2021) and impairs the activation of plant defense response against a range of pathogens and pests. Another mutant grown was *2cpa*, which disrupts *2CPA* (*2-cysteine peroxiredoxin A*), which in turn, reduces toxic byproducts of photosynthesis like H_2O_2. A recent study in our lab found H_2O_2 in high amounts when PPN were inoculated. *NPR1* (*Nonexpressor of PR1*) KO and *JAR1* KO were also grown to test SA signaling and JA isoleucine biosynthesis in a plant defense response to PPN. Wild type (WT), the genotype characterizing what is "normal" for *Arabidopsis*, was grown as a control. Seeds were sterilized and pipetted onto plates. MS Gelrite plates with five sterile seeds each were kept at 22°C for two days and were then grown for two weeks in a 12-hour light/dark growth chamber.

Meloidogyne hapla, a root-knot nematode, were harvested at the Auburn University Center for Advanced Science, Innovation and Commerce (CASIC) in Dr. Lawrence's lab. Eggs were then kept in a nematode hatchery, a container with a mesh strainer, at slightly above room temperature on a heating pad for two weeks so that stage two juvenile (J2) nematodes could hatch and develop. J2 *M. hapla* nematodes will seek a host and infect it more commonly at this stage. After the two-week period, *M. hapla* would be strained and sterilized. *M. hapla* would be sterilized by filtering through a vacuum flask with a mercury chloride solution and streptomycin solution. Autoclaved water would be filtered down as well, and

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sterile *M. hapla* were then inoculated onto M.S. Gelrite plates containing aforementioned genotypes. Plates were then wrapped with tinfoil to simulate dark light conditions of roots suitable for nematode growth and kept in the growth chamber for fifteen days.

M. hapla creates root galls/knots, or deformations in roots, and these root galls were counted for each plant inoculated under a microscope. Figure 1 shows root galls on *2cpa*, where large abnormal bumps on roots (root galls) exemplify where a female nematode has penetrated the root system and has begun laying eggs. After root galls were counted, roots were then weighed in mg. Roots were weighed after counting, and then were weighed after being dried. Root gall to root weight measurements were used to assess the level of infection of *Arabidopsis thaliana*.

Fig. 1 Root galls were counted and then compared to root weight. Root galls are abnormal bumps on roots and in this context, are caused by the root-knot nematode *M. hapla*.

While our study is not complete, our preliminary results (see Figure 2) show that *2cpa* seems to have more root galls and more average root galls per mg than WT. Root hairs on *2cpa* seem to be a little closer to root galls than on WT. Although, *cyp20-3* was found to have similar amounts of root hairs before inoculation while having a lack of root hairs after inoculation.

Once more results come in, implications can be justified more strongly. For now, *2CPA*, which reduces H_2O_2 into H_2O, can be deemed important for a plant defense response to PPN such as M. hapla. As *2CPA* is related to *CYP20-3*, and *CYP20-3* has roles in plant root hair signaling, *CYP20-3* will likely be found to be important in a plant defense response, but more data from this ongoing study is needed to derive such a conclusion. Finally, if both *CYP20-3* and *2CPA* are considered to be important in tolerance against PPN, improvements to OPDA signaling will be necessary for a genetically modified resistant cultivar.

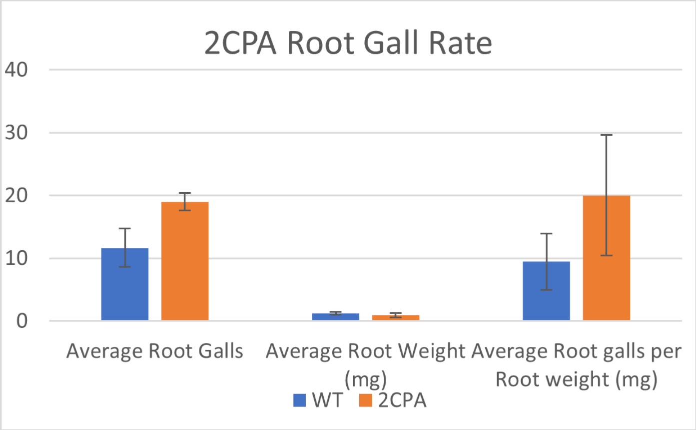

Fig. 2 Above shows our current data on *2cpa* KO that was inoculated with *M. hapla*. Blue bars show WT's root galls, weight, and root gall per root weight ratio, while orange shows *2cpa* KO's.

Statement of Research Advisor

Ben Welsh has done a great work in developing and establishing a standard pathosystem and assay protocol of plant parasitic nematode pests using a model plant, Arabidopsis thaliana. Based on this tool, we are now able to explore molecular details in plant and nematode interactions, which will provide noble insights on how to develop new crop cultivars that upgrade their own defense capacity against the pest infestations.

- *Sang-Wook Park, Department of Entomology and Plant Pathology, College of Agriculture*

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Authors Biography

Benjamin Welsh is a sophomore-year student pursuing a B.S. degree in Applied Biotechnology at Auburn University. He has been working on this project since early spring. He has a passion for studying potential cases for genetic modification for increased crop yields.

Simrandeep Kaur is a graduate student in the Department of Entomology and Plant Pathology at Auburn University. She received a B.S. (hons) Agriculture at Punjab Agriculture University, India.

Dr. Sang-Wook Park is an associate professor in Entomology and Plant Pathology at Auburn University.

Auburn University Journal of Undergraduate Scholarship

A Case Study of Crop Insurance Fraud in Alabama

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Crop insurance is insurance purchased by farmers to cover their potential farming losses caused by natural disaster, market fluctuation, or both. Crop insurance is a critical component of United States agricultural policy and farmers' risk management tools. However, due to the asymmetric information an insurance customer may have, crop insurance suffers from insurance fraud made by customers. Crop insurance fraud damages the trust between insurers and farmers, imposing economic consequences on both sides. Little research has been done on crop insurance fraud in the United States, specifically in Alabama. The purpose of this study is to provide a compilation of qualitative information that clearly delineates the causes and consequences of crop insurance fraud. This research will contribute to understanding the issue and seeks ways to address the crop insurance fraud issue in Alabama.

For this research project, publications relating to crop insurance are reviewed, cases of crop insurance fraud in Alabama are identified and studied, and interviews are conducted to learn more about crop insurance fraud and the previously identified cases. The main consensus in the publications reviewed is that more regulations on crop insurance are needed to deter fraud. Park et al. (2021) details how to deter fraud with the Risk Management Agency's spot check list (SCL), which uses data mining to identify insured farmers with anomalous crop loss compared to similarly situated producers. The insured producers identified on the SCL will receive more monitoring and inspections. The authors found that since its implementation, the SCL had made a positive impact on farmers: On average, counties with one additional producer included in the SCL tended to have decrease the county-level loss ratio (i.e., total indemnity payments divided by total premium) by 1.4%.

One of the interviews conducted is with an anonymous source involved with the Anna Marie Knowles case. Knowles was a U.S. Department of Agriculture employee at the Farm Service Agency office in Dothan, Alabama. She filed a claim through the federal crop insurance program where she allegedly falsely reported that a drought had caused her to lose the majority of her squash crop. During the interview, the source said that Knowles was "claiming that she planted so many acres, but the reality was that there was no market for the squash. If she was successful, where was she going to sell the squash?" After looking at prices proceeding with the planting date of the squash, the source concluded that it would have made more economic sense to have planted other crops.

In the other interviews, crop insurance and the SCL were discussed. One of the interviewees emphasizes that fraud not only hurts the crop insurance program, but it also hurts other farmers who want to purchase crop insurance. A majority of the concerns with fraud are solved by the SCL program. Moving forward, an effective way to deter crop insurance fraud in Alabama is to implement the SCL program in all counties and further study the impact of SCL on farmers' behavior.

Statement of Research Advisor

Lindsey Wessel explored the institutional background of the federal crop insurance program in the United States and studied an important issue of the program: insurance fraud. She investigated the possible causes and remedies for crop insurance fraud by reading relevant literature and by interviewing crop insurance agents, researchers, and people involved in some actual crop insurance fraud cases. Her work contributes to our understanding of crop insurance fraud issues in Alabama and in the United States.

- Ruiqing Miao, Department of Agricultural Economics and Rural Sociology, College of Agriculture

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Authors Biography

Lindsey Wessel is a senior-year student pursing a B.S. degree in Agricultural Business and Economics at Auburn University. She has played a key research role on exploring crop insurance fraud in Alabama.

Ruiqing Miao is an associate professor in the Department of Agricultural Economics and Rural Sociology of the College of Agriculture. His research focuses on the interaction between agricultural production and its environment, aiming to understand and quantify 1) agriculture's impact on land use, water use, water quality, and biodiversity, and 2) how agricultural production is affected by farmers' behaviors, public policies, agricultural innovation, technology adoption, and climate change.

Impact of Different Comonomers (PEGMA, PEGMEA, AND PEGMEMA) on Solute Co-transport in PEGDA and PEGDA-AMPS Membranes

Ryan Wozniak[1],[*],and Bryan S. Beckingham[2]

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[2] Associate Professor, Department of Chemical Engineering, Auburn University

CO_2 emissions have become an important environmental concern due to the increasing usage of various fossil fuels that release CO_2 upon combustion.[1] Therefore, researchers are working on finding methods to mitigate CO_2 emissions into the atmosphere. The three main methods to reduce atmospheric CO_2 are CO_2 capture, CO_2 storage, and CO_2 conversion.[2] This research focuses on CO_2 conversion by using an electrochemical cell that converts CO_2 by a reduction process into various, low carbon footprint chemicals and fuels such as carbon monoxide, methanol, ethanol, formate, etc.[2] In particular, the electrochemical cell has two half-cells, an anode and cathode that are separated by a polymer membrane known as an ion-exchange membrane (IEM). The reduction reaction occurs in the cathode, and an oxygen evolution reaction occurs in the anode. The IEM must selectively permeate the hydron molecule from the anode half-cell into the cathode half-cell for the reduction reaction to occur. However, the IEM must also be highly impermeable to all other molecules in the described reactions to avoid significant efficiency losses in the electrochemical cell.[3]Therefore, researching and characterizing various membranes is essential in determining an effective IEM.

The current research focuses on investigating single solute transport (sodium formate and sodium acetate) through a cation exchange membrane consisting of poly(ethylene glycol) diacrylate (PEGDA) and acrylamido-2-methyl-1-propanesulfonic acid (AMPS). In these membranes, different comonomers are implemented to determine their relative impacts on the membrane's water volume fraction and permeability. These comonomers are poly(ethylene glycol methacrylate) (PEGMA), poly(ethylene glycol methyl ether acrylate (PEGMEA), and poly(ethylene glycol ethyl ether methacrylate) (PEGMEMA). The first set of polymer membranes without AMPS had a constant pre-polymerization water content mol percent of 20% with varying comonomer and PEGDA mol percent. The second set of membranes with AMPS had a constant pre-polymerization water content mol percent of 20%, constant PEGDA mol percent of 54.4%, and varying comonomer and AMPS mol percent.

The first characterization method was implemented to measure water uptake and water volume fraction of the different polymer membranes. This method consisted of soaking the membranes in distilled water and weighing them at their "swelled weight". The membranes were then vacuum dried and weighed at their "dry weight". The dry membranes' hydrostatic weight was then measured to determine the water volume fraction of the membranes. The resulting data is displayed in Figure 1 and Figure 2.

The second characterization method was implemented to measure the permeability of the different polymer membranes. A diffusion cell was set up with one side filled with distilled water and measured by an FTIR probe that measured conductivity. The other side was filled with a 1M solution of either sodium formate or sodium acetate. The conductivity was measured over five hours and best fit with the Yasuda model to extract the permeability values of each solute. The resulting data is displayed in Figure 3 and Figure 4.

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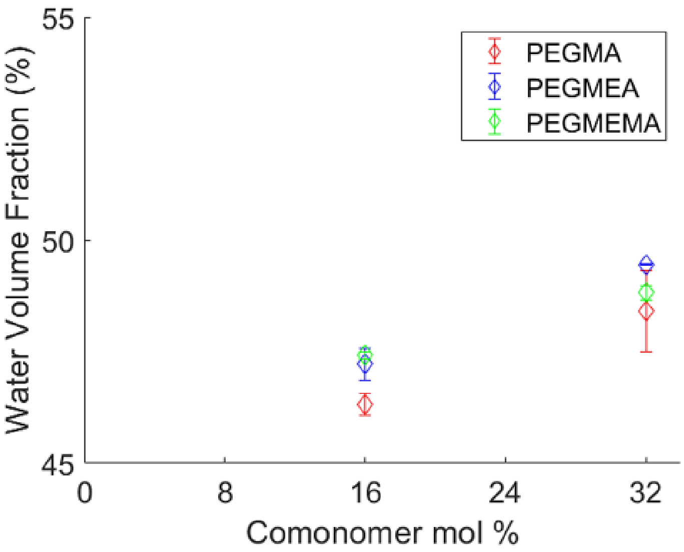

Fig. 1 Water volume fraction vs. comonomer mol percent with no AMPS

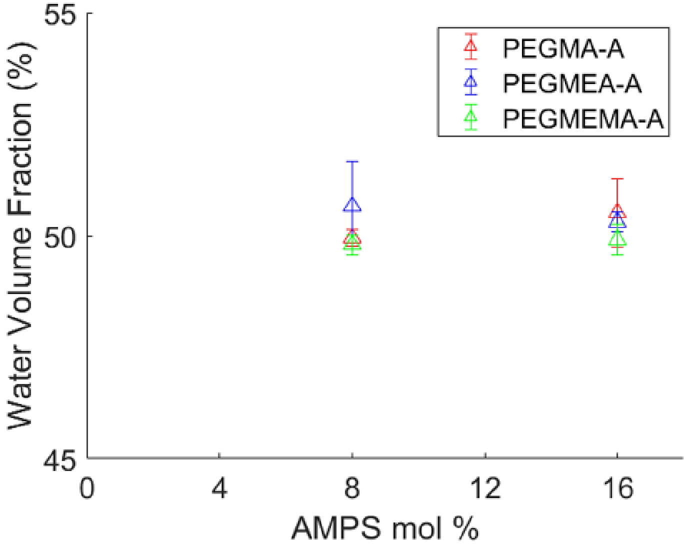

Fig. 2 Water volume fraction vs. comonomer mol percent with AMPS

Results from the first characterization method indicate that water volume fraction increases with increasing comonomer mol percent. Results from the second characterization method indicate that, in the case of sodium formate without AMPS, PEGMEMA has a higher permeability than PEGMA, and PEGMA has a higher permeability than PEGMEA at 16 mol percent. Further trials are being run at 32 mol percent to see if these trends are upheld. In the case of sodium acetate without AMPS, all three comonomers have roughly the same permeability at 16 mol percent.

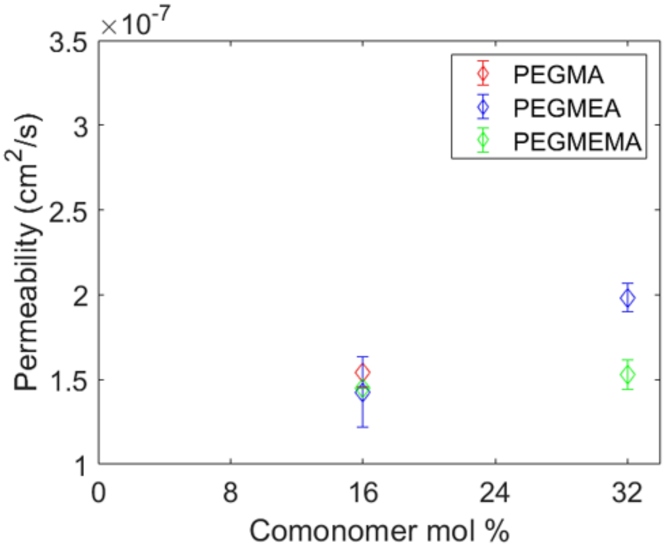

Fig. 3 Permeability vs. comonomer mol percent with sodium acetate and no AMPS

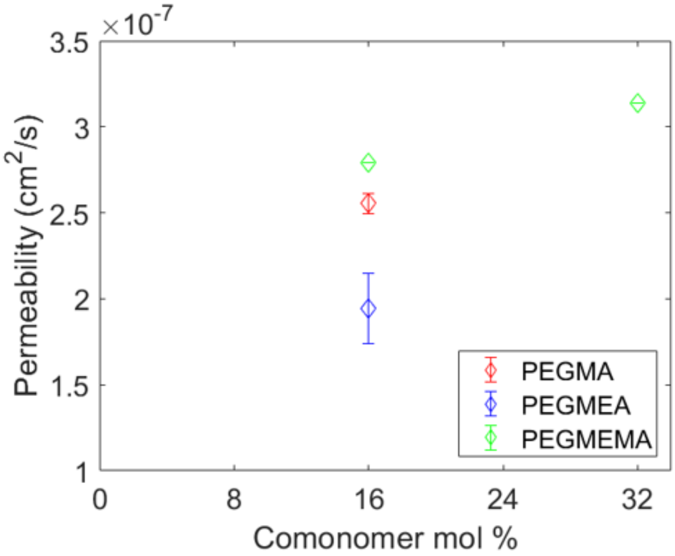

Fig. 4 Permeability vs. comonomer mol percent with sodium formate and no AMPS

Further trials are being run at 32 mol percent, but early data suggests that PEGMEMA membranes have a lower permeability than PEGMEA membranes. Trials using PEGDA-AMPS membranes will be run in the future to determine permeability values with varying AMPS and comonomer mol percents.

Statement of Research Advisor

Mr. Ryan Wozniak investigated how the chemistry of polymer networks could be used as a handle for tuning the polymer membrane behavior in solar fuels devices. Solar fuels devices convert carbon dioxide into chemicals or fuels such as methanol, acetate, and formate.

Ryan synthesized two series of polymer membranes (with and without ionic groups) and characterized their water uptake and permeability to formate and acetate. Overall, his work showed that water content could be controlled through the neutral comonomer content, but that even at similar water contents these different neutral comonomers had different impacts on the permeability of the solar fuels product molecules. This type of behavior is poorly understood, but important as the ability to design membranes with desirable permeability characteristics relies on knowledge of these kinds of structure-property relationships with Ryan's work adding to our growing knowledgebase.
- *Bryan S. Beckingham, Department of Chemical Engineering, Samuel Ginn College of Engineering*

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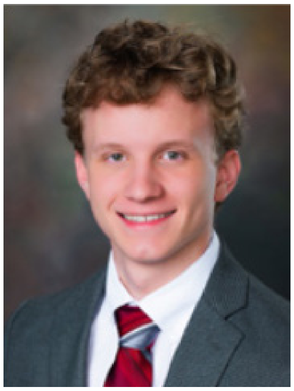

Ryan Wozniak is a junior-year student pursuing a B.S. degree in Chemical Engineering at Auburn University. He has played a key role in conducting research on single solute transport in PEGDA and PEGDA-AMPS membranes.

Dr. Bryan S. Beckingham is an Associate professor in the department of Chemical Engineering and is Director of the Center for Polymers and Advanced Composites. His research focuses on leveraging synthetic polymer chemistry and materials characterization to inform design of novel polymer materials, with an emphasis on polymer membranes, hierarchically structured matter and additive manufacturing of polymer functional polymer systems.

Development of Research Tools: In Search of Heifer Fertility Biomarkers

Morgan A. Young [1,], Hector A. Fajardo [2], and Paul W. Dyce[3]*

[1] Undergraduate Student, Department of Animal Sciences, Auburn University
[2] Graduate Student, Department of Animal Sciences, Auburn University
[3]Associate Professor, Department of Animal Sciences, Auburn University

Often in the cowcalf industry, a proportion of selected heifers (bovine females that have not yet calved) fail to become pregnant following their first breeding season. When a producer raises a heifer to full reproductive maturity or purchases a reproductively mature heifer and she is unable to calve, the cost that it took to raise or purchase that heifer is not fully recovered. This is detrimental to the producer and the overall beef industry. Infertility in the beef industry is estimated to cost over $4.7 billion annually (Prevatt et al, 2018). When replacement heifers are selected, they are chosen based on many genetic and phenotypic factors including body condition, age, disposition, reproductive tract score, and the performance of their parents. Even after taking these factors into account, a proportion fails to become pregnant in their first breeding season.

The objective of this research project is to investigate different candidate antibodies to potential biomarkers that were previously identified as different in fertile and sub-fertile heifers, at the transcript level. In this project we are investigating differences in protein expression in the endometrial tissue of fertile and subfertile heifers. The overall goal is to develop fertility-based biomarkers in heifers. For this specific project, only protein levels in the endometrial tissue will be investigated.

A group of Angus and Angus-crossed heifers were put through an estrous synchronization and artificial insemination (AI) program. This was then followed by natural service (NS), by placing them with a fertile bull, for two additional estrous cycles. After completion of the program, the heifers were grouped as either fertile (pregnant from AI), pregnant from NS, or subfertile (failed to become pregnant). In previous research from our lab, using samples from these heifers, RNA based molecular targets were identified that were expressed differently between the fertile and subfertile groups of heifers. In this current project, six biomarkers were evaluated including pannexin 1 (PANX1), connexin 43 (CX43), interleukin 6 (IL-6), tumor necrosis factor alpha (TNF-α), delta and notch-like epidermal growth factor-related receptor (DNER), and growth arrest and DNA damage inducible gamma (GADD45G). The protein level expression for each marker was evaluated using sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE) and Western blotting techniques. The antibodies for the markers were applied to the blots and the bound quantities were analyzed and com-pared between the two groups of heifers. Image Lab software was used to determine the relative quantity of the proteins using densitometry, then raw values were statistically compared using a t-test and GraphPad Prism software.

In previous research done in our lab, it was found that there is a significant difference between fertile and sub-fertile heifers for the biomarkers chosen. For IL-6 and TNF-α, there were significantly different mRNA transcript levels in the white blood cells between the two groups (Phillips et al, 2018). The granulosa expression profiles between fertile and sub-fertile heifers were significantly different (p value < 0.05) for DNER and GADD45G (Hollingsworth et al, 2023). Due to these previously detected differences, we were interested in investigating whether any of these markers were different at the protein level in endometrial tissue. However, there was no significant statistical difference between the fertile and subfertile groups for any of the markers we tested (Figures 1, 2, and 3). Based on these results, we can conclude that Panx 1, Cx43, IL-6, TNF-α, DNER, and GADD45G are not expressed differently at the protein level in the endometrial tissues of heifers with differing fertility. This study focused specifically

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*Corresponding author: may0015@auburn.edu on protein expression in endometrial tissue, but the Dyce Laboratory is currently investigating other tissues and targets.

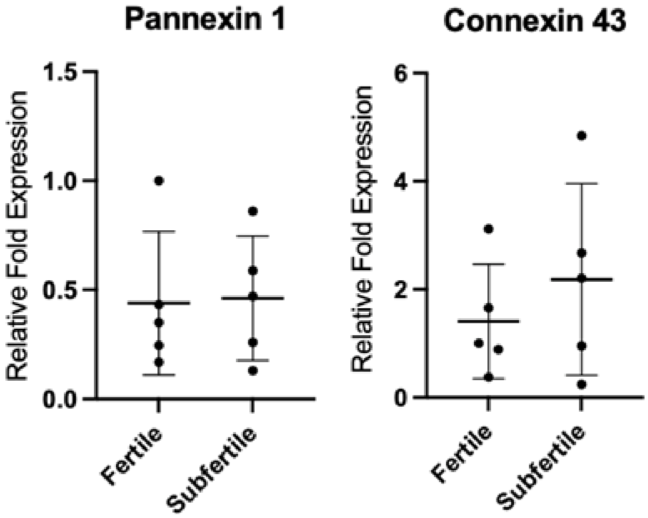

Fig. 1 Comparison of protein level expression of Pannexin 1 and Connexin 43 in endometrial tissue between fertile and sub-fertile heifers.

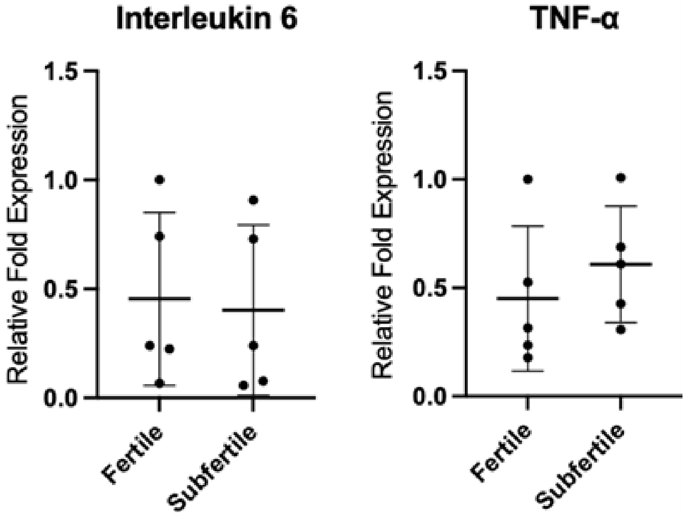

Fig. 2 Comparison of protein level expression of Interleukin 6 and TNF-α in endometrial tissue between fertile and sub-fertile heifers.

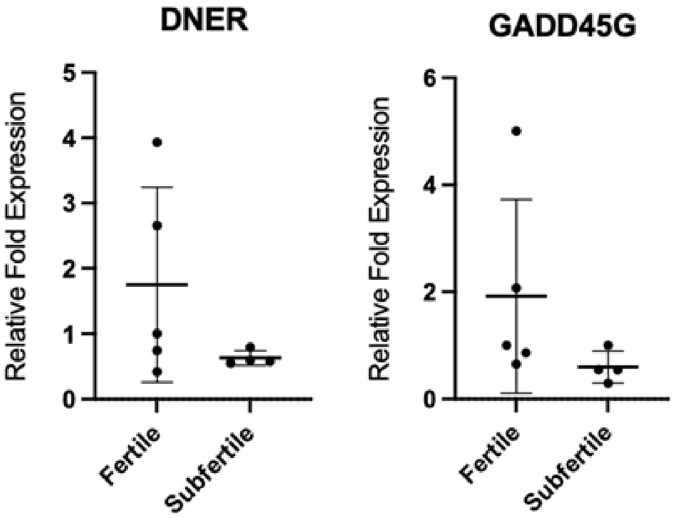

Fig. 3 Comparison of protein level expression of DNER and GADD45G in endometrial tissue between fertile and sub-fertile heifers.

Statement of Research Advisor

Over the past year Morgan has worked to gain protein isolation and analysis skills. Her work culminated in testing potential protein biomarkers in the endometrial layer of fertile and sub fertile beef heifers. This highlight will permit examination of other tissues in heifers at various stages of development.

- Paul Dyce, Department of Animal Sciences, College of Agriculture

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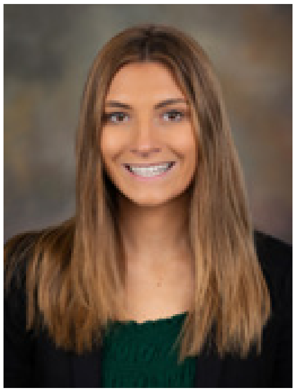
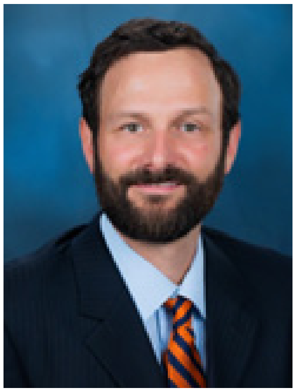


Morgan A. Young is an undergraduate student graduating in May of 2024. She is pursuing a B.S. degree in Animal Sciences Pre-Veterinary Medicine at Auburn University. She joined the Reproductive Biology Lab in May 2023 with a research focus on proteins.

Hector A. Fajardo is a graduate student in the College of Agriculture at Auburn University. He received a B.S. degree in Agricultural Science and Production at Zamorano University. He has experience in molecular techniques and farm management. His current responsibilities include working with scientists to develop field tests that improve fertile heifer selection. He is from Honduras and enjoys traveling and seeing other cultures.



Dr. Paul W. Dyce is an Associate Professor of Reproduction and Development in the Department of Animal Sciences at Auburn University.

Exposure to Counterstereotypical Scientist Role Models Impact How Students Relate to Scientists

Rachel M. Youngblood[1,], Robin A. Costello[2], Emily P. Driessen[3], Amelia Rose Radocha[4], Melissa Kjelvik[5], Elizabeth Schultheis[5,6], Ash Zemenick[5,7], Marjorie Weber[8], Cissy J. Ballen[9]*

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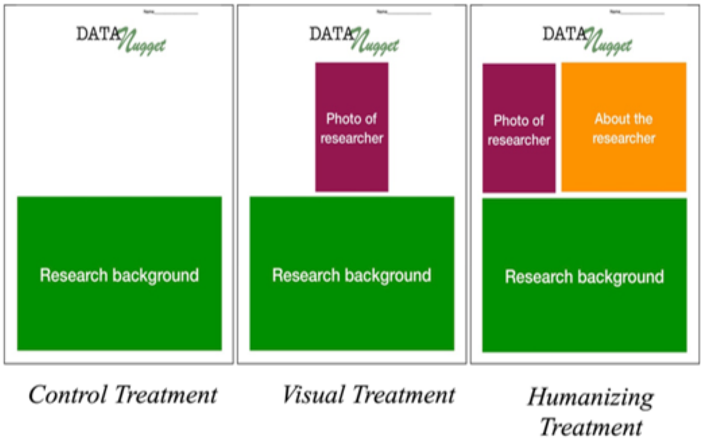
The representation of scientists in biology curricular materials does not reflect the demographic composition of society or of biology students (Wood et al., 2020). However, the presence of relatable role models benefits students who possess identities that are excluded in science by increasing their persistence and success in science disciplines (Schinske et al., 2016; Seymour et al., 2019). Due to the importance of role models within science classrooms, we investigated how students relate to scientists in biology, and specifically scientists who possess counterstereotypical identities. Specifically, we asked (1) does the amount of information given about a counterstereotypical scientist affect how students relate to scientists in undergraduate biology courses? and (2) what about counterstereotypical scientists do students relate to most?

To answer these questions, we implemented three treatments in introductory undergraduate biology courses across the country. These treatments involved data literacy activities created by Data Nuggets (datanuggets.org) paired with scientist profiles created by Project Biodiversify (projectbiodiversify.org). We manipulated scientist profiles to contain varying levels of information about counterstereotypical scientists. In treatment one (the control treatment), the data literacy activities were not accompanied by any information about the scientists; in treatment two (the visual treatment), the activities included pictures of the scientists; in treatment three (the humanizing treatment), the activities included pictures and extended 'About Me' sections with humanizing information (i.e., hobbies, interests, obstacles faced) (Fig. 1). Throughout the semester, students were given three different data nuggets of the same treatment at different time points.



Control Treatment *Visual Treatment* *Humanizing Treatment*

Fig. 1 Example of data nugget layout with varying amounts of scientist information.

We collected data through Qualtrics surveys administered immediately after students completed each activity. Students responded to the prompt, "Describe how you related to the featured scientist, if at all." We thematically coded 1574 student responses from 34 biology instructors across the United States. We created twenty-four codes within four major categories. These four categories included (1) student relates to diverse

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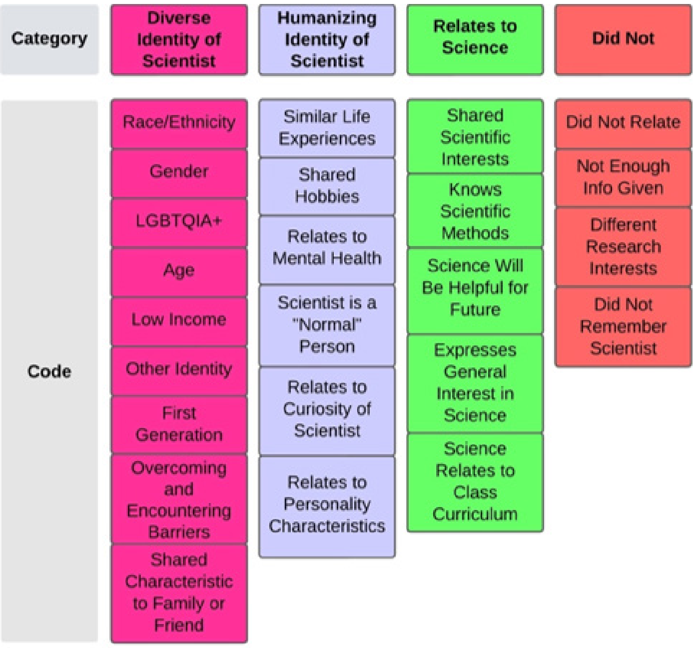
identities of the scientist, (2) student relates to humanizing elements of the scientist, (3) student relates to the science rather than the scientist, and (4) student did not relate (Fig. 2).

After thematically coding all student responses, we used logistic regressions to quantify the impact of treatment on how students related to the featured scientist. In both the control treatment, where no scientist information was given, and the visual treatment, where only a scientist photo was given, students were more likely to relate to the science rather than the scientist ($\chi2 = 5.47$, $p = 0.065$). In both the visual and traditional treatments, students most identified with the scientists' scientific interests (53%), the process of scientific methods (28%), and sharing a general interest in science (14%). Students within the humanizing treatment were most likely to emphasize the scientists' counter-stereotypical identities ($\chi2 = 11.54$, $p = 0.003$; Fig. 3). Here, students most often identified with the scientists' gender (57%), LGBTQIA+ status (18%), and how the scientists overcame barriers (39%).



Category	Diverse Identity of Scientist	Humanizing Identity of Scientist	Relates to Science	Did Not
Code	Race/Ethnicity Gender LGBTQIA+ Age Low Income Other Identity First Generation Overcoming and Encountering Barriers Shared Characteristic to Family or Friend	Similar Life Experiences Shared Hobbies Relates to Mental Health Scientist is a "Normal" Person Relates to Curiosity of Scientist Relates to Personality Characteristics	Shared Scientific Interests Knows Scientific Methods Science Will Be Helpful for Future Expresses General Interest in Science Science Relates to Class Curriculum	Did Not Relate Not Enough Info Given Different Research Interests Did Not Remember Scientist

Fig. 2 Codes used to analyze open-ended student responses to the prompt "Describe how you related to the featured scientist, if at all".

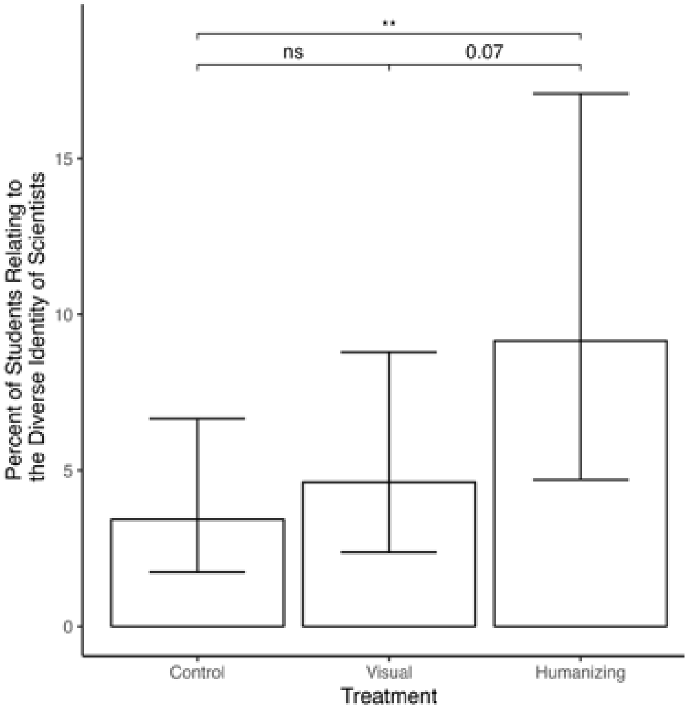


Fig. 3 Percent of students who relate to scientists' diverse identities by treatment type. $^{**}p < 0.01$.

This research highlights the importance of humanizing scientific role models within undergraduate biology courses. By humanizing scientists, we create opportunities for students to see themselves in science while presenting contemporary science as accessible to all.

Statement of Research Advisor

RYM groomed, coded, analyzed, and visually depicted all qualitative data presented in this research. She mentored several other undergraduates and assisted in a graduate-level course with CJB that emphasized qualitative methods in biology education research. Her contributions were critical to clarifying our novel understanding of how relatability to scientists benefits students, and several additional peer-reviewed publications will result from her efforts.

- Cissy Ballen, Department of Biological Sciences, College of Sciences and Mathematics

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Authors Biography

Rachel M. Youngblood is a senior-year student pursuing a B.S. degree in Exercise Science at Auburn University. She has played key research roles in researching the role scientific role models play in undergraduate Biology courses. She plans to pursue Occupational Therapy school after graduation.

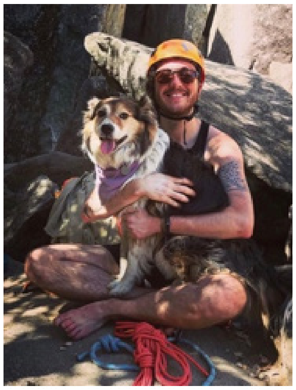
Robin A. Costello is a postdoctoral researcher in Cissy Ballen's lab at Auburn University. She received her PhD in evolutionary biology from the Brodie lab at the University of Virginia. Her postdoctoral work empirically identifies classroom interventions that promote equitable postsecondary STEM education.

Emily Driessen is a PhD candidate at Auburn University She earned a B.S. in Microbiology from North Dakota State University and a M.S. in STEM Education from the University of Kentucky. She is currently in her final year of a Biology PhD, studying in Cissy Ballen's lab where she focuses on how to best support the achievement and success of all students in post-secondary biology, recognizing structural barriers and historical biases.

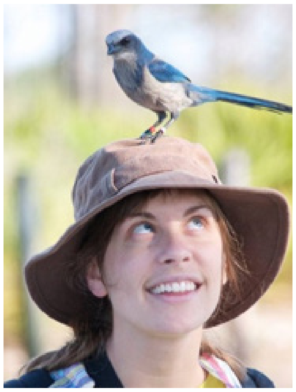
Amelia is a graduating senior at Colorado College with a bachelor's degree in Organismal Biology and Ecology. She is passionate about equity and equality, especially in regard to education and food access. After college, she plans to serve through the Peace Corps in Guinea, where she will focus on both of those issues.

Elizabeth Schultheis (she/her) is the Education and Outreach Coordinator for the Long-Term Ecological Research program at the W.K. Kellogg Biological Station, and the co-founder of Data Nuggets. Elizabeth received her PhD from Michigan State University in Plant Biology and Ecology, Evolutionary Biology and Behavior, and completed a postdoc in science education research. Her work includes outreach, research, curriculum development, and professional development for teachers and scientists.

Melissa K. Kjelvik is a science education research specialist at Michigan State University. She is a co-founder of Data Nuggets and a content editor for Project Biodiversify and has been working with educators, curriculum developers, and education researchers for over 10 years to create, innovate, and disseminate effective resources to increase data literacy and representation of scientists in K-16 classrooms.



Ash Zemenick is the Manager of Sagehen Creek Field Station where they support researchers, educators, students, and the community members as they immerse themselves in a very gorgeous and special slice of the Sierra Nevada. They are also proud to be the Director and Co-Founder of Project Biodiversity.



Marjorie Weber is an assistant professor in the Ecology and Evolutionary Biology department at the University of Michigan. Her lab focuses on the evolutionary ecology of species interactions. She is the co-founder of Project Biodiversify, a program for increasing equity in undergraduate biology classrooms.

Cissy Ballen is an assistant professor in the department of biological sciences at Auburn University. Her lab conducts discipline-based education research broadly focused on biology education and STEM equity.

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