

**Research Reports from Undergraduate Students
receiving support from the Shackouls Honors College
via the Honors Summer Undergraduate Fellowship Program**

Summer 2017

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Name: Amelia Andersson

Major: Biology Pre-Vet

Faculty Mentor, Department: Dr. Mark Welch, Biological Sciences

Title: *Salt Marsh Rescue: A Restoration Initiative Examining *Spartina alterniflora* Microsatellite Allele Lengths*

Summer Research 2017

The research conducted over the course of the summer consisted of identifying genetically diverse stock populations for restoration efforts of hurricane and oil damaged saltmarsh coastlands. *Spartina alterniflora*, a native cordgrass, was selected for its high petroleum tolerance and adaptability to the local climate. The initial plant collection consisted of 160 individuals representing 8 populations. We optimized PCR protocols for 21 microsatellite loci, however only 19 of those were genotyped as three loci were disregarded for lack of variation. Analysis of microsatellite variation within and amongst populations gave us a better understanding of the fitness and adaptability of this particular smooth cordgrass species. From this information we concluded that all eight *S. alterniflora* populations had high expected heterozygosity and thus high genetic diversity. With regards to molecular variance the percentages remained favorable for increased genetic diversity with 64% variance exhibited within individuals and 27% variance among populations. With this information we can confidently conclude that using *Spartina alterniflora* populations as a native stock within damaged coastal saltmarshes would be beneficial for restoration initiatives.

Fall Research 2017

As a continuation to the summer research we examined a second coastal species, a soft rush, *Juncus roemerianus*, based on its self-compatibility, in hopes of supplying another salt marsh plant to act as a genetically advantageous stock population. We

collected and isolated DNA across eight populations (160 total individuals) using the same protocols conducted on *S. alterniflora*. The allele lengths are currently being analyzed looking at 19 *J. romerianus* specific microsatellite loci; current preliminary analysis shows a positive trend in heterozygosity values across populations and within individuals. This is seen as the first few analyzed microsatellites show that all eight populations show high expected heterozygosity indicating high genetic diversity.

Additionally, we have added two populations of *S. alterniflora* and two populations of *J. romerianus* to increase our data set for more accuracy with regards to selecting the most diverse stock population. This adds 80 individuals to the 320 already analyzed individuals in addition to extending the geographical range, now spanning from Lake Pontchartrain, LA to Pensacola, FL. By providing two highly adaptable species of native saltmarsh plants, we bypass introducing a monoculture into these damaged marshlands, thereby increasing the overall fitness and genetic diversity of the existing and future saltmarsh populations.

Acknowledgements

The success of this research came from efforts from the University of Southern Mississippi's Gulf Coast Research Laboratory, the Department of Plant and Soil Sciences and the Department of Biological Sciences at Mississippi State University. Because of the funding received from the Shackouls Honors College I was able to better hone my laboratory skills as well as gain a better understanding of conducting research through to completion. By participating in this summer's research symposium I learned to analyze population genetics data by using various gene-sequencing programs and designing and presenting a scientific poster for the purpose of aiding current and future gulf coast conservation efforts.

Name: Rachel Booth

Major: Psychology

Faculty Mentor, Department: Dr. Andrew Jarosz, Psychology

Title: *The Read Scare: Reading Stereotype Threat in College Aged Males*

A common topic when discussing education is the gender gap in reading abilities. The Center on Educational Policy (Chudowsky & Chudowsky, 2010) found that in each grade and in each American state, girls outperformed boys on reading tasks. When children start primary school, teachers and parents assume that boys will require additional reading assistance compared to girls (Blair & Sanford, 2004). Furthermore, this disparity continues into secondary school. The Programme for International Assessment, an international survey given to 15 year olds, reported a reading gap between the genders that rates females 38 test points ahead of males – equivalent to a year’s worth of progress (OECD, 2014). This gap persists even into upper education as English majors are nearly 75% women (Siebens & Ryan, 2009).

Research has suggested that this aptitude inequality could be caused by low self-concept (the belief that one can do a task well) in boys (Retelsdorf, Schwartz, & Asbrock, 2015), or by disinterest in the subject because reading is boring, difficult, and boys prefer TV (Sainsbury & Schagen, 2004). However, neither explanation attempts to address fundamental questions about the underlying reasons for boys’ underperformance in reading. Rather than attributing boys’ underperformance to innate gender differences in reading ability, as others have proposed, effects could be due to a stereotype threat (ST).

ST places people at risk of confirming a negative stereotype about a group with which they identify, leading to poorer task performance (Steele, 1997). Some work suggests that early differences in reading ability may indeed be due to stereotypes. For example, Pansu et al. (2016) demonstrated that third grade boys had poorer reading scores when they were placed under a negative reading stereotype than boys not under a stereotype. While there has been little consideration for stereotype threat in adult

males, research dedicated to identifying the mechanisms underlying males' underperformance at reading is crucial, particularly when considering the necessity of reading in daily life. The present study will therefore examine whether negative stereotypes exist for males on reading tasks, and whether these negative stereotypes effect reading ability.

Stereotype Threat

The ST phenomenon occurs when there is a societal perception of a group coinciding with an awareness of that belief from those included in the group (Aronson, Fried, & Good, 2002). In one of the few studies to consider a reading ST for boys, Pansu et al. (2016) demonstrated a reading ST effect for boys in their study. They assigned a reading test to 80 third graders, who were either told that the purpose of the study was to evaluate the children's reading ability, or to test out a new game. The gender by condition interaction revealed that the ST effect dramatically decreased boys' reading scores.

Though investigations of reading stereotypes in males are scarce, other common stereotypes have been studied, such as women underperforming in math (Spencer, Steele, & Quinn, 1998), minorities having lower intelligence (Aronson, Quinn, & Spencer, 1998), or Asians being superior at math (Aronson, Lustina, Good, Keong, Steele, & Brown, 1999). In each of the aforementioned groups, subjects only underperformed when under the ST (in Aronson et al., Whites underperformed and Asians over performed under ST). The abundance and range of ST research lends confidence to the theory that ST interferes with task performance.

There are large numbers of women and minorities effected by ST, resulting in performances that are not congruent with their optimal capacity in areas such as mathematics for women and intelligence tasks for minorities (Aronson, Quinn, & Spencer, 1998; Nguyen & Ryan, 2008; Steele, 1997). In their lab, Steele and Aronson (1995) found that because of ST, African Americans' standardized test scores decreased. Another probable effect of ST is a lack of diversity in science, technology, engineering, and math

fields. Furthermore, those who suffer from ST have decreased ambition in jobs requiring the stereotyped ability (Davies, Spencer, Quinn, & Gerhardstein, 2002). They also tend to have low self-esteem (Aronson & Inzlicht, 2004) and even poor health (Blascovich, Spencer, Quinn, & Steele, 2001).

The most frequently studied targeted group is women, with research exploring how minute the ST has to be to alter performance results. Findings show ST can be induced easily—even being in a math class with a female math-confident teacher induces stress in female students who want to live up to their teacher’s expectations (Shapiro, 2011). Likewise, simply having the individuals specify their own gender before a math task, having the experimenter note gender differences in the study, and the participant identifying with the task subject can result in similar effects (Good & Aronson, 2008; Keller, 2007).

Working Memory Capacity

In well studied domains like mathematical performance in women, the existence and activation of ST has been established thoroughly enough, such that the mechanisms underlying ST have become a focus of research. In particular, studies have explored the role of working memory capacity (WMC). Beilock, Rydell, and McConnell (2007) demonstrated that WMC may be a primary mechanism underlying the effects of ST. Participants in both a control and ST condition were presented with math problems which demanded high or low WMC to solve. There was an interaction between ST and high demand problems, demonstrating that ST took a toll on WMC. Their results indicated that WMC resources are depleted by ruminations over the perceived stereotype and that depletion in WMC leads to a decrease in women’s math solving abilities.

High working memory participants are most affected by ST because low working memory participants already operate at maximum capacity without an interference like ST. (Hutchison, Smith, & Ferris 2013). High WMC subjects ordinarily have enough capacity to manage WMC tasks because they use that large capacity to employ more complex strategies (DeCaro & Beilock 2010). Under ST, however, high WMC individuals use the

rest of their mental space to process the ST, and are reduced to using simple strategies like a low WMC participant, so they no longer have the advantage of using their larger capacity. Low WMC individuals, however, never have had the added advantage of greater space to process WMC tasks, and always used simple strategies, and so they are less affected. In other words, ST makes high WMC participants perform similarly to low WMC participants.

Although the studies outlined above examined the relationship between ST's effect on WMC during math problems, similar ST effects can be expected of WMC during reading problems since WMC is already known to be linked with reading ability. Past research has found that scores on complex memory tasks, in both children and adults, predict reading achievement (Cain, Oakhill, & Bryant, 2004; Swanson, 2003; Swanson & Howell, 2001; Waters & Caplan 1996). Thus, WMC should predict reading scores under normal circumstances.

The Present Research

The large reading gender gap and apparent reasons of self-concept and disinterest are reminiscent of prior misconceptions of female underperformance on mathematical tasks. In that scenario, a body of literature has demonstrated that many gender differences in math ability are caused by negative stereotypes towards females (Good & Aronson, 2008; Keller, 2007; Nguyen & Ryan, 2008; Shaprio, 2011; Spencer, Steel & Quinn 1998).

The present study will determine if ST impacts reading task performance for college males. Male college students will complete a reading comprehension task, either with or without instructions intended to induce ST. They will additionally complete two WMC tasks. If ST is truly the cause of decreased reading scores among males, then high WMC men under ST will score lower on the reading task than high WMC men in the control group, with low WMC men unaffected by the manipulation. In contrast, women's reading scores will not be affected no matter the group.

Method

Design

The study will be a 2 (gender of participant) X 2 (ST or no ST) between-subjects factorial design.

Participants

A G*power analysis predicted that with 80 participants (40 in each condition) and 85% power assuming $\alpha = .05$, the study could detect an effect of $d = .50$. Participants will be male and female college aged students, (M=20.0 years).

Materials

The Gates-MacGintie Reading Test (GMRT). The GMRT (Gates & MacGintie 1993) is a commonly used reading comprehension task. It comes in two parts, reading comprehension and vocabulary; both will be used. In the first portion, participants will read 11 passages and then answer 3 to 5 questions for each passage. Gates-MacGintie chose the passages from Arts and Science texts. The reading comprehension questions test both literal and inferential comprehension. Immediately following the reading comprehension, they will read 45 short phrases with a word underlined and choose from five options which option best serves as a synonym for the underlined word. Form S, level AR will be used. Participants will have 40 minutes to complete the task.

The Operation span. The automated Operation span (Ospan; Unsworth, Heitz, Schrock, & Engle, 2005) is a commonly used test of WMC. The automated Ospan requires participants to solve a series of math problems interleaved with unrelated letters that they are expected to remember. Following the math/letter presentation, they are asked to recall the letters in the correct serial order. Sets range from three to seven letters in length. The computer scores participants' accuracy by summing all letters recalled in the correct serial order. All subjects will receive the exact same Ospan questions but in a randomized order.

The Symmetry span. The automated Symmetry span (Sspan; Unsworth, Redick, Heitz, Broadway, & Engle, 2009) is another common WMC test. In this computer automated task, subjects decide if varying shapes are vertically symmetrical. In between images of shapes to judge, red squares pop up on a random location in a grid and must be remembered. The red squares are recalled after participants judge several shapes and see several red squares, by clicking on the appropriate spaces in a grid in the correct serial order. Each of these lists include two to five squares. The Sspan consists of three trials.

The computer scores participants' accuracy by number of correct cells subjects clicked in correct order. Scores are calculated by summing the number of red square locations correctly recalled in the correct order.

Demographics Sheet. Following the tests, participants will receive a demographics sheet to collect gender, major, and age. Thirteen questions regarding academic reading exposure, reading identification, and awareness of the stereotype accompany the demographics.

Manipulation check. As part of the demographic information following the study, there will be a questionnaire including three items: "On a scale from 1-10, how much do you agree with this statement: 'The ability in reading comprehension of my gender is worse than the ability of the other gender.'" (Martiny, Roth, Steffens, & Croizet, 2012); "On a scale from 1-10, how much do you agree with this statement: 'I was motivated to perform well on the reading comprehension task to help show that I am good at reading.'" (Yeung, von Hippel, 2008); and "On a scale from 1-10, how much do you agree with this statement: 'I was motivated to perform well on the reading comprehension task to help show that my gender is good at reading.'"

The first rating will be reverse coded before being analyzed with the other two ratings. The mean of the ratings collected from these questions should indicate if participants believed the stereotype while completing the tasks.

Procedure

The study will be administered at Mississippi State University. Participants will be recruited through the SONA-systems website and will be given course credit as compensation.

Sessions will hold one to four subjects at a time. Instructions for both conditions will be presented by both the experimenter speaking to the participants, and by the participants reading the instructions on a sheet of paper while the experimenter speaks. Stereotype threat instructions for the reading task will be adapted from Beilock et al. (2007). Both groups will read and hear:

“We are interested in reading comprehension. Most college subjects require advanced reading skills. However, not much is known regarding the mechanisms of reading abilities. This study is meant to discover what makes some people better at reading than others.”

In the control condition, participants will also read and hear:

“Your performance on the reading problems you are doing today will be compared to other students in the nation.”

In the experimental condition, subjects will also read and hear:

“As you may know, at most schools female students outnumber male students in majors requiring strong reading skills. There also seems to be a growing gap in academic performance between the two sexes. Unfortunately, there has not been a good explanation for this. Your performance on the reading problems you are doing today will be compared to female responses across the nation. Our specific research question is whether females are superior at all types of reading problems or only certain types.”

Participants will first complete the GMRT. Then, each participant will complete both the Ospan and the Sspan, with the order of WMC task presentation counterbalanced. Participants who complete the WMC tasks before other participants will be given a filler task of completing a maze to do silently, while they wait for other participants to finish. The manipulation will be checked after the experiment is

administered in a post-test questionnaire. After completing the post-test questionnaire, participants will be debriefed and the stereotype will be removed.

Results

The study will use SPSS to analyze gathered data in a 2 (condition type) x 2 (gender) General Linear Model to identify main effects and interactions between the conditions and genders, with WMC as a covariate. There should be a main effect for both gender (females should outperform males) and condition (scores will be higher under the control condition) as well as an interaction between condition and gender in which males under the ST condition underperform to females in either condition. Additionally, WMC will be positively correlated to reading scores in the no-threat control condition for males and females. It will still be correlated to females' scores but not correlated to males' scores in the ST condition, because high WMC males will be performing like low WMC males now, and the two will produce similar scores. The single mediator model using the procedure developed by Preacher and Hayes (2008) will be used.

Discussion

Should the results follow the hypotheses, this study will demonstrate that there is a reading ST against college aged males and it impacts their reading performance abilities. It will follow the work done by Pansu et al. (2016) and it will indicate that the poor reading test's results in older males (OECD, 2014) is a result of ST. Furthermore, it would lend credence to theory that processing ST activation uses WMC resources (Schmader, & Johns, 2003). Demonstrating a reading ST in college aged males will affect how males, teachers, and parents think of males' reading in all facets of life. Future research may explore implicit ST on males, dependencies on types of reading materials, or how to alleviate ST effects during reading.

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Name: Jennifer Fisher

Major: Biological Engineering

Faculty Mentor, Department: Dr. Kurt Showmaker, Institute for Genomics,
Biocomputing & Biotechnology

Title: *The Genome Sequencing, Assembling, and Annotation of the Corn Earworm
Helicoverpa zea*

Introduction:

Helicoverpa zea is crop pest that has several names including corn earworm, soybean podworm, bollworm and tomato fruit worm. This organism is a moth that has a complete metamorphosis. It is found throughout the United States; however, it causes most damage in the southern states. The Corn Earworm affects several crops such as corn, cotton, soybean and grain sorghum. The larva causes the damage to these plants by eating at important structures like the pods in soybeans and the bolls in cotton. It is a leading cause of insect damage to both cotton and soybeans.

The corn earworm (*Helicoverpa zea*) was used in a study about insect pest of soybean in the Southeastern United States (Alabama, Arkansas, Louisiana, Mississippi, North Carolina, Tennessee, and Virginia) (Heatherly 2016). In Mississippi, corn earworm has caused significant soybean crop damage on an annual basis. Annually, over the years 2011-2015, the corn earworm infested on average about half (47.90%) of the soybean acres in the Southeastern region of the U.S. causing an average estimated loss of \$ 143.45 million to the soybean producers during this time frame. Estimates for percent of soybean acres infested and annual losses for state of Mississippi that are available for a longer time span (2009-2015), show an average infection rate of 37.68% and an average loss of \$21.77 million per growing year. Although, the corn earworm causes a considerable amount of damage every year very little is known about its genomics.

There is already genomic research being done on plants to determine genes and other genomic factors that might lead to better crop production. These studies have considered

what genes can produce stronger and more fruitful crops (Bevan et al 2017). These studies have also determined how plants can avoid attacks from pests (Bevan et al 2017). This research is insightful, but the plant is only half of the biotic interaction. Because of this a need to understand the genomics of the pest has arisen. Furthermore, the genomes of the pests are much smaller than the host plants (Challis et al 2016), thus making the genomic analysis cheaper and less complex. By sequencing the pests that attack the crops, we gain insight into the fundamental biology of the pest that can be used in future studies with the pest. Currently, there is one published genome of the corn earworm on the National Center for Biotechnology Information (NCBI) website. The goal of this project is to better understand the corn earworm's biology through sequencing.

To develop our method for sequencing this genome, we looked at a study on the Eastern Tiger Swallowtail to develop our method for this project. The Eastern Tiger Swallowtail is a Lepidoptera organism like the soybean looper. In this study, they built a model genome from a wild Eastern Tiger Swallowtail in a single Illumina lane (about 60 Gb) (Cong et al 2015). They used DNA from adult thoracic muscles. They annotated the genome and found several genes that produce different functional proteins. From that genome, they determine proteins that control when the Eastern Tiger Swallowtail adult will come out of its pupae (Cong et al 2015).

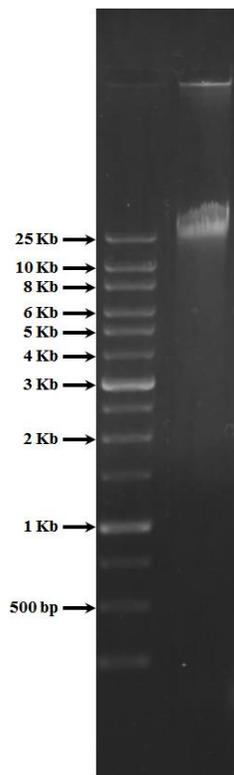
It is interesting to note the amount of research and development that has been done to decrease the impact of this insect in these crops. There are several insecticides that have been developed; however, there is evidence of resistance to the insecticides. There has been development of Bt cotton plants which contain a gene of a bacterium that produces the Bt toxin which is harmful to most insects. Again, there is evidence of the corn earworm developing resistance to the Bt toxin. There is research that looks at the method of managing the crops. However, there is one published genome of the corn earworm. By sequencing another corn earworm, we will better understand its genetic diversity.

Results from the DNA preparation and Sequencing:

A sample of the Corn Earworm was collected, the DNA was extracted, and visualized with gel electrophoresis (Figure 1). The results from the gel electrophoresis shows evidence of high molecular weight DNA. The construction of the libraries for the Corn Earworm was built by the Novogene from this DNA. These sequencing libraries were constructed by Illumina Truseq Nano DNA HT Sample preparation kit. The following graphs provide insight into the quality of sequence data that we have collected.

Overall, the quality of the raw reads was very effective and have low percentage of error (*Data Quality Summary*). The Quality Scores ranged from 30 to 40 (*Quality Score Distribution Along Reads*). The different type nucleotide bases results show the relationship between AT base pairing and CG base pairings (*Bases Content Along Reads*). Overall, there seems to be low amount of error from the raw reads (*Classification of Raw Reads*). These results show strong evidence that our raw reads provide good sequence data.

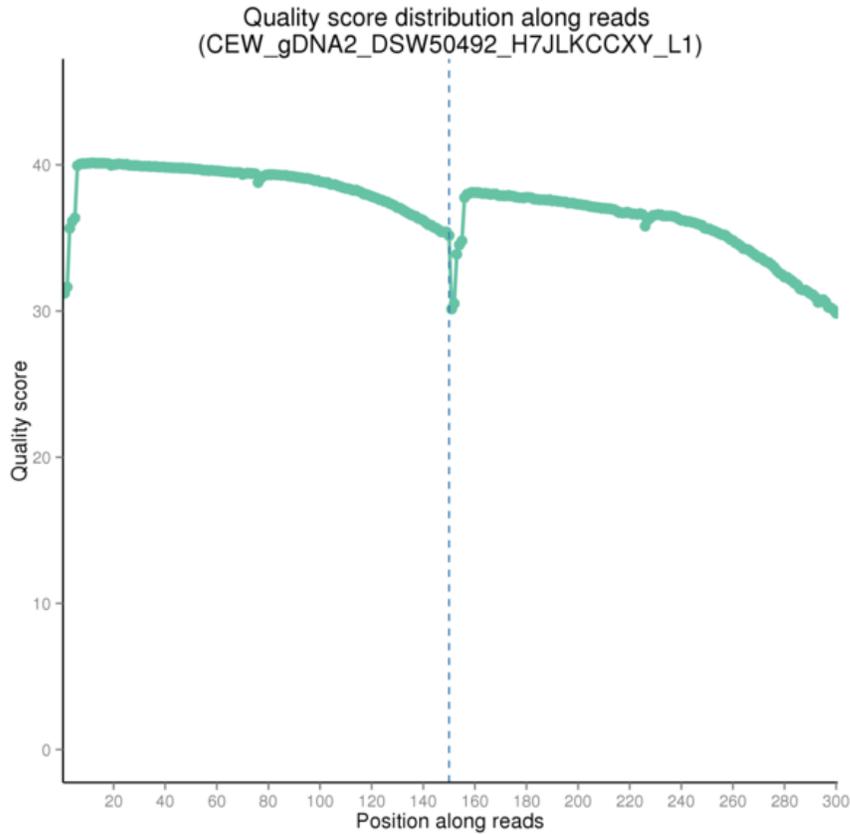
Gel Electrophoresis Results from the Corn Earworm Sample



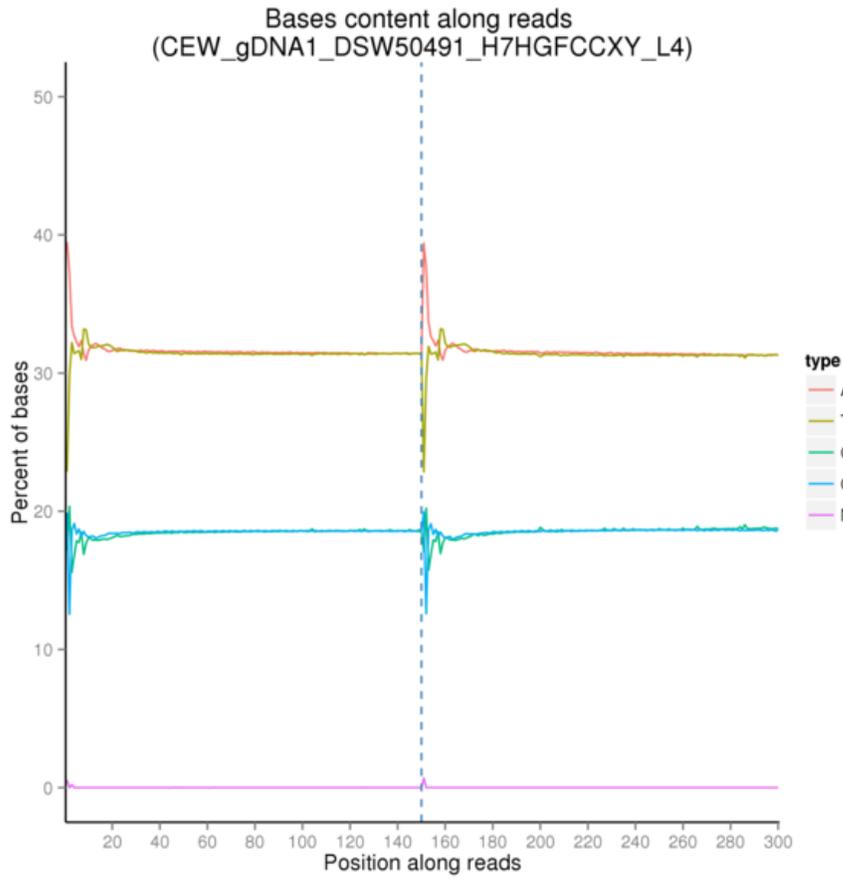
Data Quality Summary

SAMPLE NAME	LIBRARY	LANE	RAW READS	RAW DATA	EFFECTIVE (%)	ERROR (%)	Q20 (%)	Q30 (%)	GC (%)
CEW_gDNA1	DSW50491	H7HGFCCXY_L3	84244758	2.53E+10	99.88	0.01	96.21	91.26	36.98
CEW_gDNA1	DSW50491	H7HGFCCXY_L4	78897907	2.37E+10	99.89	0.01	96.4	91.61	36.98
CEW_gDNA1	DSW50491	H7HGFCCXY_L1	78421327	2.35E+10	99.89	0.01	95.72	90.38	36.98
CEW_gDNA1	DSW50491	H7HGFCCXY_L2	82326586	2.47E+10	99.89	0.02	95.5	90.03	36.98
CEW_gDNA2	DSW50492	H7JLKCCXY_L3	1.12E+08	3.36E+10	99.79	0.02	94.91	88.89	36.75
CEW_gDNA2	DSW50492	H7JLKCCXY_L1	90600061	2.72E+10	99.77	0.02	94.19	87.65	36.78
CEW_gDNA2	DSW50492	H7JLKCCXY_L2	1.03E+08	3.1E+10	99.8	0.03	94.97	88.97	36.77

Quality Score Distribution Along Reads

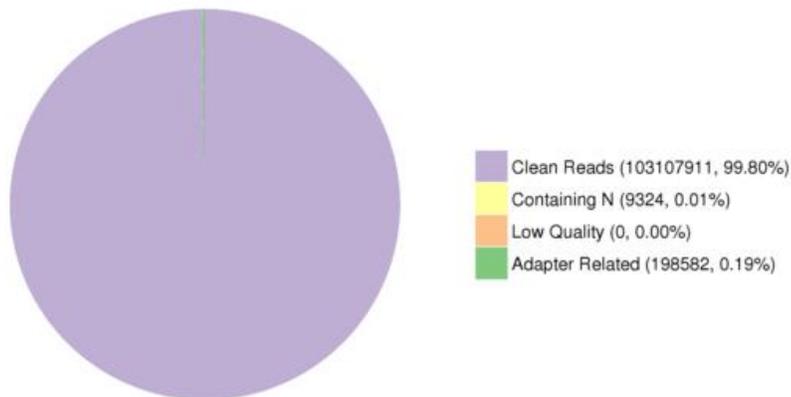


Bases Content Along Reads



Classification of Raw Reads

Classification of Raw Reads
(CEW_gDNA2_DSW50492_H7JLKCCXY_L2)



Current Materials and Methods for Flow Cytometry:

I have been developing the methods for the flow cytometry with Dr. Krish Krishnan, assistant professor in the entomology department at Mississippi State. Wei Tan a research associate at the vet school has helped with the running of samples through the NovoCyte 3000.

Materials:

1. Tissue Sample- head of the insect
2. 1 ml of Galbraith buffers
 - a. Amount for 100ml
 - 0.41g of Mg
 - 0.88g of Sodium Citrate
 - 0.41g of MOPS
 - 100 ul of Triton x-100
 - 1 small grain of Ribonuclease A
3. 2ml Dounce tissue grinder with A pestle
4. 20 µml nylon mesh filter cap
5. 5ml round bottom tubes
6. 50 µg Propidium Iodide Solution
7. Flow cytometer- NovoCyte 3000

Methods:

Cut off the heads of the insect. Place head in 1ml of ice-cold buffer. Take micropipette and take head out of tube with some of the buffer. Place head in tissue grinder. Stroke until the head is no longer visible. Wash with filtered water between samples. Add 50 µg of PI solution and cover tube with Aluminum foil. Filter the sample through a 20 µml mesh into 5ml tubes. Have the samples stain for 3hrs. Run samples through the Novocyte 3000. Develop a ratio using the known genome size and the mean fluorescence of the known and unknown sample. Then calculate the unknown genome

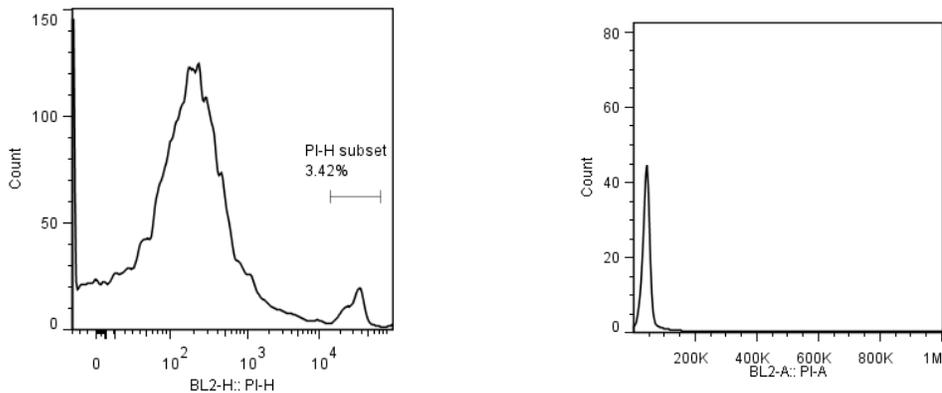
sizes (this is because of the linear relationship between the fluorescence and the genome size).

First Trial Results:

For the first run of samples we had 5 males and 5 females *Drosophila melanogaster* (fruit flies). These were a good first test samples because their genome is known. It was a good way to check and see if our methods were good. However, after running the samples, we noticed that the samples were not completely stained. The stain time for the sample needs to be increased for the next trial. Once we see the samples are being produced well we will start using this method to estimate the genome sizes of different insects.

Results from Male 1 in Trial 1:

The first figure shows that most of the sample was not stained. The second graph shows the number of nuclei that was stained and what the fluorescence was.



Future Developments from this Research Fellowship:

The next goals for our projects is to finish the development of the flow cytometry methods and begin to discover new genome size estimations of several insect sizes and begin the genomic annotation of the Corn Earworm. The results of this project will develop into two manuscripts for publication, a presentation at Mississippi Entomology Association (MEA), and a poster at the Spring Honors Research Symposium.

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Name: Noah van Hartesveldt

Major: Geoscience

Faculty Mentor, Department: Dr. Brandon Barton, Biological Sciences

Title: *Potential new avenues for expediting recovery of long-dead Acropora Palmata skeletons*

Background:

Acropora palmata (Lamarck 1816) have been the primary shallow water, reef building coral of the Caribbean for nearly 10,000 years. Following an outbreak of white band disease in the 1980's and subsequent, frequent bleaching events and hurricanes, A. palmata has yet to exhibit a basin wide recovery (Gladfelter 1982, Aronson & Precht 2001, Manfrino et al. 2003, Eakin et al. 2007). Various factors are hypothesized to account for this failure, but a peculiar, highly efficient mode of reproduction may be able to help expedite recovery. Resheeting, defined as the larval recruitment and recolonization on long dead A. palmata skeletons, has been suggested to decrease recovery time (Jordan-Dahlgren 1992).

To investigate and quantify if resheeting is a viable strategy for recolonization, experiments in Grape Tree Bay on Little Cayman Island were set up during summer of 2016 to measure both growth rates of currently resheeted colonies and success of our novel scrubbing method to promote recruitment on long dead colonies. After one year, the primary objective was to revisit these 37 marked colonies.

Progress/Methods:

In 2016, colonies were separated into two groups: unscrubbed and scrubbed. Twenty two randomly selected, partially resheeted colonies were selected for the unscrubbed group to evaluate whether live coral tissue was advancing or if existing macro-algae was inhibiting further tissue growth. The tissue/macro-algae line was marked with a stainless steel pin and neon zip tie pointing in the direction of growth.

Twenty of these colonies were successfully relocated using GPS coordinates and snorkeling.

Each colony was then photographed, and the tissue extension was measured three times: perpendicular to the growth margin and at 15° angles from the perpendicular. These values were averaged to account for the variation in tissue morphology. Our findings revealed an overall retraction of tissue growth on these colonies, suggesting that macro-algae may have the upper hand and an intervention may be necessary.

The experimental, scrubbed group included fifteen entirely dead *A. palmata* colonies with near total macro-algae cover. Each randomly selected colony was physically scrubbed with a wire brush during summer of 2016 to remove all organic material and detritus from the skeletal surface. All fifteen colonies were successfully relocated. During the day, photos were taken and each colony was thoroughly inspected for new recruits. A second revisit at night using UV torches was completed to check for smaller recruits, which fluoresce and are easily observed in the dark. Despite the long dead colonies being nearly free from new macro-algae cover, no new *A. palmata* recruits were observed. This suggests that other factors may be inhibiting larval settlement.

In addition to the expected work, I was also able to complete an additional 150 meter survey of a second reef, Mary's Bay, on Little Cayman. This survey catalogued over 250 additional live and dead colonies, and included data on sizes, presence of macro-algae, resheeting, and substrate. This data is currently being analyzed and added to the 2016 data cataloging all colonies in Grape Tree Bay. It will be used to explore relationships between substrate preference and colony success.

Future Work:

Our findings suggest that scrubbing may not be advantageous on long dead colonies, but could be used to remove inhibiting macro-algae on previously resheeted colonies. In the future, a pilot study to scrub live colonies would require additional permitting and more careful preparation to avoid damaging live tissue. Determining how close to scrub to the tissue line will be the biggest hurdle.

Using the additional data collected from Mary's Bay, a secondary objective is to establish where *A. palmata* prefer to settle. This can lead to better reef management, as corals grown in nurseries need to be out planted to places on the reef most beneficial to the specific species. Using these large data sets of colony information could help shed light into potential reasons for *A. palmata*'s failure to recover on a basin wide scale.

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Name: John Hunt

Major: Biomedical Engineering

Faculty Mentor, Department: Dr. Nicholas Fitzkee, Chemistry

Title: *NMR-Based Investigation of Biochar and Its Metabolic Effect on Native Soil Species*

Abstract

Biochar is an alternative carbon source that is often used as a soil additive in agriculture, due to its relative ease of production and low cost.¹ Its adsorptive properties make it ideal for removing various free chemicals from soil, including phosphates, pesticides, and organic dyes.² Other studies have shown that biochar can accelerate inorganic nitrogen transformations when added to soil.³ It is therefore interesting to know about the effect this has on the bacterial species which commonly inhabit the soil. One way of examining this is through the microbial metabolome, or the set of chemical pathways the bacteria uses to process available nutrients (metabolites). Our experiments use media that has been treated with biochar to grow *Escherichia coli* (*E. coli*), a species commonly found in the soil. These samples are compared against activated carbon-treated media and untreated media. The relative concentrations of specific compounds in the media and intracellular activity are measured using Nuclear Magnetic Resonance (NMR) spectroscopy. NMR is a non-destructive, non-targeted technique that essentially produces a snapshot of intramolecular processes. The chemical shift associated for each compound is unique so that the compound can be identified by the proton (¹H) NMR spectrum.

Methods

Our primary method for determining the concentrations of metabolites is NMR spectroscopy. We do this by observing differences in peak intensity from a media that was actively growing *E. coli*. This can help us to see which compounds the bacteria neglected, used, or excreted.

Samples of RPMI media are treated with either biochar or activated carbon, or are left untreated as a control. Then, the samples are inoculated with *E. coli*, and the OD₆₀₀ is measured every 0.5 hour until the 3-hour mark. 6, 9, 12, and 24-hour timepoints are also collected. The samples are centrifuged and the cell waste is removed as a pellet. The supernatant is collected and analyzed in NMR experiments. The metabolites remaining in the media are identified, and using AMIX Profiler we quantify each compound's characteristic chemical shifts. Statistical approaches, including principal component analysis, is used to identify meaningful differences between the three different conditions.⁴

Results

The results from this summer have allowed us to begin preparation of a manuscript that we hope will be in print by next year. We have also expanded the scope of our experiments to include different flavors of media treatment and growth conditions that will more closely simulate the actual soil environment.

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Name: Marisa Laudadio

Majors: Political Science and Communication

Faculty Mentor, Department: Holli Seitz, MPH, PhD, Communication

Title: *Ascertaining Public Opinion of International Adoption via User-Generated Comments on News Sites' Facebook Posts*

Background:

My research this summer focused on two things: determining whether or not public opinion can be ascertained via social media and identifying what current public opinion is regarding international adoption. To do this, I analyzed online user-generated comments on stories about international adoption posted on news sites' Facebook pages. The goal of my research was to use my results to advise advocacy groups and policy makers on what issues regarding international adoption are of primary concern to the public. My research questions were as follows:

RQ1: What are common perceptions of international adoption and how do these compare to perceptions of domestic adoption?

RQ2: What language is used to discuss these perceptions?

RQ3: What issues are most commonly talked about/can be identified as contributing to these perceptions?

Method:

In order to get a well-rounded group of news platforms, I looked at Pew Research Center's list of top twenty-five news providers with the highest U.S. traffic and chose five newspapers from that list that were representative of different geographic regions (*The New York Times*, *Washington Post*, *USA Today*, *Chicago Tribune*, and *LA Times*), and five of the most trafficked broadcast network television or cable news sites (ABC, CNN, Fox News, CBS, and MSNBC) (Olmstead, Mitchell, & Rosenstiel, 2011). In addition to these ten

sources, I also chose NPR since it has over 26 million radio listeners each week and has a significant presence on all the main social media platforms (Facebook, Twitter, Instagram, Pinterest, YouTube, and Snapchat) (“NPR Sees,” 2016). I gathered over 6,500 comments from 11 different news stories directly pertaining to international adoption that had been posted on these news sources’ public Facebook pages over the past year.

Inspired by the research conducted by Zhang and Counts (2015, 2016), I analyzed my data set using two different methods: content analysis and thematic analysis (Braun & Clark, 2006). First, I cleaned the data to remove any comments that did not pertain to international adoption and uploaded the resulting 350 comments to NVivo, a qualitative data analysis software. I then sorted the comments into different groups based on their comment valence and various recurring themes I identified.

Results and Conclusions:

The result of my research showed that public opinion toward international adoption is split basically in half between those who support international adoption and those who oppose it. Through thematic analysis, I was able to identify 10 different themes and 15 subthemes. I also identified 14 different strong adjectives used to describe people’s perceptions of parents who adopt internationally. Four distinct perceptions held by the public relating to international adoption were revealed and four issues that contribute to these perceptions were also identified. There also appeared to be a correlation between story content and comment quality. While stories that used emotional appeal had many comments, the comments were mostly of poor quality. In contrast, stories that were fact-based had fewer comments, but the quality of these comments was much higher and far more productive to discourse directly pertaining to international adoption.

After analyzing all the data, I concluded that public opinion toward international adoption, and different perceptions and concerns about international adoption, can be obtained by studying user generated comments on social media sites. The different themes and perceptions I identified can also be used to inform advocacy groups and

legislators about needs for additional public education or policy reform related to international adoption.

Future Work:

I am currently in the process of writing a paper to be submitted to a political communication journal sharing the results and implications of my work. Further research needs to be done in the future to test if the correlation between story content and comment quality is consistent across other issues and stories or was merely a coincidence in this instance. More research needs to be done comparing articles that utilize a fact-based narrative style with articles that use an emotional-appeal narrative style to see if there is a correlation between narrative style, comment quantity, and comment quality.

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Name: Max Moseley

Majors: Industrial Engineering and Communication

Faculty Mentor, Department: Dr. Philip Poe, Communication

Title: *Distinguishing the Internet's True and False*

For summer 2017 I worked under the guidance of Dr. Philip Poe in the Department of Communication. Our initial project aimed to study residents in the Mississippi Delta and their ability to determine the legitimacy of information encountered online. First, agents from the MSU Extension Service would conduct a survey to record participants' current digital media literacy. Following this initial survey, agents would teach these survey takers from a curriculum designed to increase digital media literacy and then implement a post-survey to measure any changes in the participants' ability to discern the truthfulness of online news sources. While the curriculum was refined over the summer, I underwent training from the Institutional Review Board in order to gain access to the eventual survey results. Dr. Poe and I had a meeting with the Extension agents in September to determine the next steps for the project, and Dr. Poe and I have plans to implement the surveys and curriculum in one of his Communication classes this fall.

In the meantime, Dr. Poe and I have tackled a variety of other research projects. We updated a paper we wrote together, ""She's a Little Different": Autism-Spectrum Disorders in Primetime Television Dramas," based on feedback we received from reviewers at an academic journal, and we plan to submit the paper to a new journal soon. I also assisted Neely Tucker, a reporter from The Washington Post and a guest instructor at MSU this fall, with a promotional video for the New Narrative Festival, hosted at MSU in April 2018, to attract potential sponsors and donors for the conference.

Additionally, Dr. Poe and I have begun working on a project with the Department of Geosciences to examine hazard communication during natural disasters, inspired by Hurricane Irma's recent devastation in Florida. We have gathered over 663,000 Tweets from Twitter to study how news stations and meteorologists from major cities in Florida

interact with people on social media during an average, non-disaster week and during a week with a significant weather event or natural disaster. With these Tweets, we aim to quantitatively and qualitative analyze users' interactions and engagement with meteorologists.

Our main project this semester has been an analysis of the new Netflix television series *Atypical* and its depiction of autism spectrum disorder (ASD). Building on our previous research of TV portrayals of ASDs, I have written a literature review and have chosen the Parasocial Contact Hypothesis for the theoretical framework of our study. I have watched the show once through and taken notes, and now Dr. Poe and I will use a codebook to count and measure different aspects of the show's treatment and depiction of neuroatypical individuals as we watch the show again. Our plan is to have the study and paper finished by the time I graduate this December.

With the funding from the Honors Undergraduate Research Fellowship, I have been able to help Dr. Poe on a number of projects across several stages of development, which has given me a greater exposure to the research process as a whole. While we have not yet made much progress on our funded study, we have used the Shackouls Honors College's funding to advance multiple projects that will spawn future journal and conference submissions. Dr. Poe and I are grateful to the Shackouls Honors College for allowing us this opportunity.

Name: Jenna Mosier

Major: Biological Engineering; Biomedical Concentration

Faculty Mentor, Department: C. LaShan Simpson, PhD, Agricultural & Biological Engineering

Title: *The Effect of Fetuin-A as Therapy for the Calcification of Vascular Smooth Muscle Cells*

Introduction:

In end stage renal disease (ESRD) patients, increased calcium and phosphate levels in the serum are associated with mineral deposition in an atypical manner that results in vascular calcification. This leads to a phenotypic switch of smooth muscle cells in the intimal and medial layers of the artery into bone-like cells, and is the leading cause of mortality in kidney disease patients¹. Fetuin-A, also known as Alpha-2-Heremans Schmid Glycoprotein, is a circulating protein in the body that reportedly acts as an inhibitor of calcification by binding to free particles in the serum and preventing them from building up in the vessel². Dialysis patients are reported to have lower circulating levels of this protein, which could be associated with plaque buildup³. The goal of this project is to determine the efficiency of the protein to inhibit further calcification in smooth muscle cells and potentially reverse the calcification that occurs.

Materials and Methods:

Human vascular muscle cells (HVSMCs) were cultured on 6-well plates and chamber slides in varying conditions to determine whether the protein, Fetuin-A, had any effect of calcification. The study consisted of 7 different groups:

1. 7 day control in normal media
2. 14 day control in normal media
3. 7 day in calcifying media

4. 14 day in calcifying media
5. Low Fetuin Treatment (9 μM)
6. Mid Fetuin Treatment (12 μM)
7. High Fetuin Treatment (15 μM)

For calcifying media, we used normal media (Dulbecco's Modified Eagle Medium+10% FBS+ 1% pen/strep antibiotics) with 3mM dibasic phosphate, with treatment groups being supplemented with differing concentrations of lyophilized bovine fetuin. Cells were analyzed at the two time points (day 7 and 14) with a calcification kit, PCR, western blots, and staining to determine calcification levels, protein levels, and gene expression. The goal is to determine which concentration produces the lowest calcification.

Results and Discussion:

By day 14, the high fetuin treatment (15 μM) resulted in significantly lower calcium/protein (μg , mg) content, with a p-value < 0.05. A calcification kit was used to determine mineral content, and a BCA assay was used to look at protein. As shown in Figure 1, all treatments of fetuin resulted in lower calcium content, though the highest concentration was the only significant value. There was a significant difference between the 7 and 14 day control and calcified groups, showing that calcification was successfully induced in cells. Staining was used to confirm these results, with xylenol orange for calcification and DAPI counterstain for nuclei. Fetuin-treated groups showed reduced calcification. Preliminary western blots results indicated that under calcifying conditions, SMCs lose their native α -SMA phenotypic marker. This indicates a change from the smooth muscle cell phenotype to that of bone-forming osteoblasts. In contrast the fetuin normal group still expressed that marker, revealing that fetuin is able to shield that phenotype. In PCR results, the groups that lost α -SMA markers in western blots expressed RUNX2, a gene typically only found in bone cells. These results confirmed the osteoblastic switch seen in VSMCs during calcification, as bone morphogenic markers were present in calcified groups versus controls. These results agreed with literature sources stating

healthy patients typically have circulating levels of Fetuin-A over 14 μM , the point at which our results showed a significant decrease in calcium levels.

Conclusions:

Our study showed potential for fetuin as a novel calcification inhibitor, decreasing calcium content in smooth muscle cells overtime. Further testing with higher fetuin concentrations is required, and a way to administer this protein still needs to be studied. The next step in designing these studies would be to create an *in vivo* model under uremic conditions to observe and manipulate the effects of fetuin and to determine an adequate delivery mechanism.

Acknowledgements:

Thank you to Bobby & Judy Shackouls, the National Strategic Planning & Analysis Research Center (NSPARC), and the Office of Research and Economic Development at Mississippi State University for generous funding, MSU IGBB center and Dr. Hsu for PCR analysis, and special thanks to Dr. Simpson for amazing guidance and support.

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Name: Troy Viger

Major: Biological Engineering

Faculty Mentor, Department: Dr. Hyeona Lim, Mathematics and Statistics

Title: *Image Segmentation methods for bio-inspired materials design*

Goal:

The main goal of this research project is to develop efficient and robust segmentation algorithms and apply them to various kinds of bio-materials images. These numerical algorithms will be performed with the ImageJ software and compared to manually masked images from Parker Berthelson as well as the algorithms developed by Dr. Myungjoo Kang and Dr. Jihoon Kwak at Seoul National University (SNU), Korea.

Introduction:

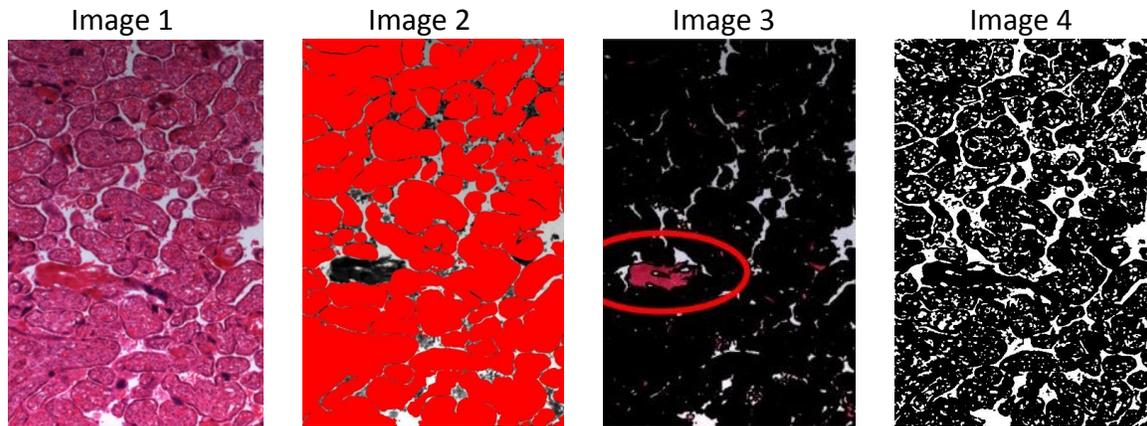
Bio-inspired materials design of protective gears (e.g., helmet, body armor, etc.) is at the forefront of state-of-the-art research. Unlocking the hierarchical design also involves a detailed study of microstructural feature and morphometry in diverse mechanical loads. However, image analysis in bio-inspired materials design is in a nascent stage; especially, in capturing the physics of the hierarchical-based design of bio-materials. Medical and bio-materials images can involve different types of noise and unclear edges. Therefore, their segmentation is often challenging, and images cannot be efficiently processed using the conventional segmentation methods. For this purpose, accurate segmentation algorithms for different types of cells are important primary tools to extract various information from bio-materials or medical images. Such information could be used to design better protective gears. We will develop efficient and robust segmentation algorithms and apply them to various kinds of bio-materials images. The new methods and algorithms will be compared to existing conventional segmentation methods.

Results and Findings:

Images of placenta tissue were analyzed in various ways to produce the best masked result for thresholding. Each image was converted to an 8-bit, binary image and then a threshold was applied under specific conditions best appropriate for the individual image. Techniques such as filling spaces, changing contrast, skeletonizing, subtract background, and many others were used to filter the picture for pieces of tissue rather than cells. After, a threshold was applied to the image to calculate the percent area fraction of the tissue in the image. The following results in Table 1 were obtained from ImageJ's analyzing procedures.

Table 1. ImageJ Results				
Name	Count	Total area	Average	% area
Tension-0.22 strain-image 1	11	1247776	113434.182	74.699
Tension-0.22 strain-image 2	85	835819	9833.165	77.829
Compression 0	478	1014636	2122.669	60.233
Compression 0.36	8	1289421	161177.625	78.394
Compression 0.92	2	1409714	704857	86.126
Shear 0.39	8	1311003	163875.375	77.888
Tension 0.41	37	925793	25021.432	56.286

Image 1 is the original image of the tissue placenta at normal compression conditions. Notice the difference in the pink tissue of the placenta compared to the darker blood cells in the background. The blood cells are not supposed to be included in the mask for calculating percent area of the tissue. Image 2 is the manually masked version of Image 1 and does not include the blood cells, however this method is very tedious and requires a lot of time to be worked on. Image 3 is the masked version of Image 1 by SNU's algorithm, which is the most proficient and time efficient method. Image 4 is the masked version of Image 1 by using ImageJ's software, which is also very efficient but the least accurate method of the three.



Conclusions and Future Research:

Medical and bio-materials images can involve different types of noise and unclear edges. Therefore, their segmentation is often challenging, and images cannot be efficiently processed using the conventional segmentation methods. For this purpose, accurate segmentation algorithms for different types of cells are important primary tools to extract various information from bio-materials or medical images. Such information could be used to design better protective gears. Dr. Kang and Dr. Kwak's algorithms for image segmentation prove to be the most efficient and accurate methods to use compared to the tedious manually masked version and ImageJ's poor thresholding and analyzation.