



AUBURN
MONTGOMERY

2018

College of Arts and Sciences

UNDERGRADUATE SYMPOSIUM

**Auburn University at Montgomery
College of Arts and Sciences
Undergraduate Research Symposium**

April 13, 2018

Presented by:
The Auburn University at Montgomery College of Arts and Sciences

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The Auburn Montgomery College of Arts and Sciences

Presents

The 2018 Undergraduate Research Symposium

On behalf of the faculty, staff and students of the College of Arts and Sciences, welcome to the annual Undergraduate Research Symposium! Our aim as a College is to engage students at a high level in their fields: to get them out of the classroom and producing their own knowledge or creative work. That challenge is hard for students (not to mention their professors). But like mountain climbing, achieving this goal exhilarates; there is nothing like it. I hope you will join me in congratulating these students and that you enjoy what they have produced.

Matthew Ragland
Acting Dean of the College of Arts & Sciences

Undergraduate Research Committee

Ann Marie O'Neill – Biology

John Hutchison – Chemistry

Eunyoung Kim – Communication & Theatre

Shannon Howard – English & Philosophy

Timothy Henderson – History & World Languages & Cultures

Jerome Goddard II – Mathematics & Computer Science

Bridgette Harper – Psychology

Schedule of Events

12:00 pm – 12:30 pm	Registration Goodwyn Hall Lobby
12:30 pm – 12:45 pm	Opening Remarks Goodwyn Hall 109
12:45 pm – 1:00 pm	Lunch (provided) Goodwyn Hall Lobby
1:00 pm – 2:00 pm	Oral Presentation Session I (lunch continued) Goodwyn Hall 109
2:00 pm – 3:00 pm	Poster Session Goodwyn Hall Lobby
3:00 pm – 4:30 pm	Oral Presentation Session II Goodwyn Hall 109
5:00 pm	Awards Ceremony and Closing Remarks Goodwyn Hall 109

Oral Presentation Session I

1:00 pm Obesity results in altered expression of genes associated with inflammation and oxidation

Safa Kazi & Omar Brito-Estrada

Mentor: Ann Marie O'Neill
Department: Biology

1:20 pm Effects of interaction-mediated dispersal on the persistence of a population

Emily Cosgrove & Eddie Lindsey

Mentor: Jerome Goddard II
Department: Mathematics and
Computer Science

1:40 pm Development of microbial enzyme and whole-cell cleaning products: An overview and initial studies

Felix Toussaint

Mentor: Ben Okeke
Department: Biology

Poster Session

1. Molecular characterization of proteolytic, amylolytic and lipolytic bacteria

**Ghadeer Jan, Danielle Warren, &
Felix Toussaint**

Mentor: Ben Okeke
Department: Biology

2. Screening of thermo-tolerant soil bacteria for production of protease, amylase and lipase

**Felix Toussaint, Danielle Warren,
Ghadeer Jan, Thinh Truong, &
Ashley Middleton**

Mentor: Ben Okeke
Department: Biology

3. Syntheses of divalent metal-organic frameworks: Ni-BTC and Cu-BTC

Mary White

Mentor: Daniel Kim
Department: Chemistry

Oral Presentation Session II

- 3:00 pm** The Rocco Interior
Tayler Allen-Galusha Mentor: Naomi Slipp
Department: Fine Arts
- 3:20 pm** Insulin resistant adipocyte exosome increases the proliferation of canine cancer cells
Martin Eastwold Mentor: Ann Marie O'Neill
Department: Biology
- 3:40 pm** The *C. elegans* spe-49 gene is required for fertilization and encodes a sperm-specific transmembrane protein homologous to SPE-42
Omoyemwen Obakpolor & Autumn Jones Mentor: Tim Croft
Department: Biology
- 4:00 pm** MRSA and *C. Diff*
Cheiuda Nguyen & Kiuana Crawford Mentor: Anita All
Department: School of Nursing

Abstracts

The Rococo Interior

Lead Presenter: Tayler Allen-Galusha

Other Authors/Presenters: None

Mentor: Naomi Slipp

Department: Fine Arts

The Rococo interior, typified by inlay and intricate designs, was a direct product of the popularized Baroque Bel Composto, a complete unification of the established visual arts. Through a consideration of the decorative motifs of gilding, relief work, stucco, and painting, along with mirrors and lighting within the interior of the Salon de la Princesse, constructed inside the Hotel de Soubise in Paris, France, this paper will establish the Rococo interior as a direct descendent and extension of the Baroque Bel Composto.

Effects of interaction-mediated dispersal on the persistence of a population

Lead Presenters: Emily Cosgrove & Eddie Lindsey

Other Authors/Presenters: None

Mentor: Jerome Goddard II

Department: Mathematics & Computer Science

Dispersal of an organism plays an important role in its individual fitness, population dynamics, and species distribution. In the literature, dispersal is loosely applied to movement over different spatial scales, e.g. movement between habitat patches separated in space from other areas. Recently, ecologists have found that interacting organisms can affect one another's dispersal, a phenomenon known as interaction-mediated dispersal. Little is known regarding the patch-level consequences of habitat fragmentation of interacting species in the presence of interaction-mediated dispersal. In this talk, we will explore effects of habitat fragmentation and interaction-mediated dispersal on patch-level population dynamics through development and study of a model built on the reaction diffusion framework. The focal point of our results will be concerned with a one-dimensional patch and relies upon adaptation of methods from nonlinear analysis such as time map analysis (quadrature method). In particular, we will elaborate on the biological importance of these results.

Insulin resistant adipocyte exosome increases the proliferation of canine cancer cells

Lead Presenter: Martin Eastwold

Other Authors/Presenters: None

Mentor: Ann Marie O'Neill

Department: Biology

Obesity has been linked to a number of adverse health conditions, including increased growth of a number of cancers. Insulin resistance is a condition that often accompanies obesity. In this study, we sought to further investigate the effects of conditioned media obtained from insulin resistant adipocytes on the growth of cancer cells.

The cell line 3T3-L1 was differentiated and rendered insulin resistant by the addition of TNF alpha and subjecting the cells to hypoxic conditions and media collected after 24 hours. Canine melanoma and mammary tumor cell lines were used for cell growth and proliferation studies. To assess the effects of insulin resistance on cancer cell growth, cells were incubated in the presence of conditioned media obtained from normal adipocyte cultures and insulin resistant adipocyte cultures. After 24 hours, cell viability was assessed and quantitative PCR performed to determine expression of Ki67 and PCNA as markers of proliferation. As fatty acid oxidation has been implicated in increased tumor growth in a number tumors, we also assessed the expression of Acox1 and CPT1.

In the presence of CM from insulin resistant adipocytes, proliferation and upregulation of PCNA, Ki67, Acox1 and CPT1 was observed in CMT28 cells. These results suggest that the insulin resistant adipocyte exosome may contribute to increased tumor cell proliferation in canine breast cancer, and this may in part be due to increased fatty acid oxidation.

Molecular characterization of proteolytic, amylolytic and lipolytic bacteria

Lead Presenters: Ghadeer Jan, Danielle Warren, & Felix Toussaint

Other Authors/Presenters: Ashley Middleton, Thinh Truong, Rakia Butler, & Mary White

Mentor: Ben Okeke

Department: Biology

Modern nucleic acid technologies have advanced methods of microbial identification. Traditional methods were based on cultural characteristics, microscopic morphology, biochemical tests and immunological methods. DNA based microbial identification provides more sensitive, accurate, reliable and rapid identification of microorganisms. With advancement of DNA sequencing technology, ribosomal RNA gene sequence analysis has played a major role in identification and classification of organisms; and their selection for different applications. Regions of the 16S rRNA gene sequence are conserved; but are flanked by hyper-variable regions (HVR) unique to most microbial species. Hence, differences in DNA sequences in the HVR can be efficiently deployed in identification of microorganisms. Proteolytic, amylolytic and lipolytic bacteria have various industrial applications. This study employed ribosomal RNA gene sequence analyses to identify nine proteolytic, amylolytic and lipolytic bacteria to facilitate selection of candidate organisms for production of proteases, amylases and lipases. Genomic DNA was isolated from nine proteolytic, amylolytic and lipolytic bacteria. Their 16S rRNA genes were amplified by 35-cycle polymerase chain reaction (PCR) using universal bacterial primers 27F and 1492R. Purified PCR amplicons were sequenced using primer 27F and 519R in separate cycle sequencing reactions. Nucleotide BLAST was then used for identification of the organisms.

Obesity results in altered expression of genes associated with inflammation and oxidation

Lead Presenters: Safa Kazi & Omar Brito-Estrada

Other Authors/Presenters: None

Mentor: Ann Marie O'Neill

Department: Biology

Current figures estimate that over one third of the adult population of the United States is obese, and that figure is predicted to rise. Obesity has been linked to the worsened prognosis in a number of cancers. One of the characteristics of obesity is a chronic low grade state of inflammation in adipose tissue, including the presence of M1 macrophages. Recent interest has also focused on antioxidants and disease. In this study, we aimed to assess the differential expression of a little known marker of M1 macrophages, IFN-induced transmembrane protein (Ifitm6) and the glutathione peroxidase gene, Gpx6, between normal and obese adipose tissue. Using cDNA obtained from adipose tissue of lean mice that were fed a chow diet or mice rendered obese by a high fat plus sugar diet, we sought to verify initial data obtained by RNA sequencing. Using quantitative PCR, our initial data indicates that both Ifitm6 and Gpx6 expression is increased adipose tissue from obese mice compared to lean. Previous work has demonstrated that adipose tissue from obese mice displays an increase in the number of genes associated with M1 macrophages compared to that of lean mice. Our results suggest that Ifitm6 may be an additional maker for the presence of M1 macrophages in adipose tissue. In addition, Ifitm6 has been shown to be present on the surface of tumor infiltrating macrophages. Given the paucity of data on this marker, further studies will attempt to elucidate the usefulness of Ifitm6 as both a marker for inflammation and macrophage infiltration in both adipose tissue and tumors.

MRSA and *C. Diff*

Lead Presenters: Cheiuda Nguyen & Kiuana Crawford

Other Authors/Presenters: Mallory Shirah & Zach Vogel

Mentor: Anita All

Department: School of Nursing

Diagnoses of hospital acquired infections (HAIs) are on the rise, especially amongst large hospitals. Methicillin-resistant *Staphylococcus aureus* (MRSA) and *Clostridium difficile* (*C. diff*) are the most common causative agents of HAIs. *Staphylococcus aureus* is a part of the human body's normal flora, commonly found on the surface of the skin and the mucous membranes of the nose and throat. *S. aureus* is an opportunistic pathogen that commonly causes skin infections that are typically treated with antibiotics. Some strains of *S. aureus*, however, have become increasingly resistant to these treatments. These resistant strains, namely MRSA, are responsible for most cases of HAIs.

C. diff is another common human microbe found in the intestines. Antibiotics often kill large numbers of beneficial bacteria in the intestines, disrupting the natural balance of the gut flora. *C. diff* sporulates in stressful conditions, which allows it to survive in much larger numbers than other bacteria during antibiotic treatment. This relative increase in *C. diff* in the gut often leads to inflammation in the colon, known as colitis.

The staggering rise of MRSA and *C. diff* infections may be due to poor healthcare professional performance, on hand hygiene and use of antibiotics. Education on hand hygiene and antibiotic therapy must be improved to reduce the number of HAIs and ensure patient safety. This evidence review will focus on the effectiveness of hand hygiene and appropriate use of antibiotics.

The *C. elegans* spe-49 gene is required for fertilization and encodes a sperm-specific transmembrane protein homologous to SPE-42

Lead Presenters: Omoyemwen Obakpolor & Autumn Jones

Other Authors/Presenters: Luke Wilson, Abigail Richie, Bryce Mieczkowski, Gabriel Fall, Rosine Hall, & Jon Rumbley

Mentor: Tim Kroft

Department: Biology

New life begins at fertilization, the binding and fusion of a sperm and an egg to form a zygote. The nematode *Caenorhabditis elegans* serves as a model organism for the identification of specific molecular pathways and genes required for gametogenesis and fertilization. We identified a mutant allele of the spe-49 gene in an F2 mutagenesis screen for new spermatogenesis defective (spe) mutants that function during fertilization. Worms mutant for spe-49 produce sperm with normal morphology that can activate to form amoeboid spermatozoa and migrate to and maintain position in the hermaphrodite reproductive tract, but fail to fertilize oocytes. Cloning of the spe-49 gene through a combination of deficiency mapping, transgenic rescue, and genomic sequencing revealed that the cDNA encodes a predicted 772 amino acid six-pass transmembrane protein that is homologous to SPE-42, another spe gene that is required for fertilization. The presence of two SPE-42 homologs in animal genomes from worms to humans suggests that these proteins are highly conserved in the molecular apparatus required for sperm-oocyte recognition, binding, and fusion.

Screening of thermo-tolerant soil bacteria for production of protease, amylase and lipase

Lead Presenters: Felix Toussaint, Danielle Warren, Ghadeer Jan, Thinh Truong, & Ashley Middleton

Other Authors/Presenters: Rakia Butler, Mary White, & Jasmine Walker

Mentor: Benedict Okeke

Department: Biology

Microorganisms are very important sources enzymes for industrial applications. Proteases are biocatalysts that breakdown proteins to peptides and amino acids. Proteases are useful in food processing, leather manufacture, disease therapy; and are used as additives in laundry detergents. Amylases catalyze starch conversion to saccharides and dextrin. Food, paper, textile, detergent and pharmaceutical industries use amylases in different applications. Lipases hydrolyze triglycerides (common lipids) to mixtures of glycerol, diglycerides, monoglycerides and fatty acids. Lipases have applications in bakery, cosmetics, dairy, detergent, food processing, beverages and pharmaceutical industries. Lipases also catalyze esterification and are useful in organic synthesis. Thermotolerant enzymes are attractive in that they are more resistant to temperature denaturation; and are more likely to be stable at room temperature. This study was undertaken to isolate, screen and select thermotolerant protease, amylase and lipase producing bacteria from soil. Over 50 bacterial isolates from soil were screened for production of protease, amylase and lipase; and nine isolates producing at least 2 enzymes were shortlisted for further studies.

Development of microbial enzyme and whole-cell cleaning products: An overview and initial studies

Lead Presenter: Felix Toussaint

Other Authors/Presenters: Ghadeer Jan, Danielle Warren, Rakia Butler, Thinh Truong, Mary White, & Ashley Middleton

Mentor: Ben Okeke

Department: Biology

Interest in use of biocatalysts in cleaning has been increasing since the last decade. There are numerous benefits of using biocatalysts over chemicals as cleaning products. Microbial biocatalysts are renewable, biodegradable, and environmentally benign; and when used as additives in chemical cleaning agents such as detergents, the quantity of chemicals can be reduced. Currently, microbial cleaning products are being used in domestic, commercial, industrial, and recreational settings. The active bio-ingredients are lipases, proteases, and amylases; which breakdown lipids (triglycerides), proteins and starch (amylase and amylopectin), respectively. Whole microbial cells capable of producing these enzymes are also deployed in formulation of cleaning products. Combination of enzymes can be used to formulate potent cleaning products for the removal of aggregates of fats, proteins, and starch in domestic waste that frequently clog sinks, sewer pipes and septic tanks. Moreover, such cleaning products can be used for muck removal from ponds and lakes. To select microbial isolates for production of cleaning products, nine microbial isolates shortlisted from over 50 soil isolates were examined for production of lipase, protease, and amylase in liquid submerged culture. Further studies will examine the influence of environmental parameters: temperature, pH and salt on whole cell and cell free microbial biocatalysts. Robust isolates will then be used for production of enzymes and whole-cells for formulation of bioactive cleaning products.

Syntheses of divalent metal-organic frameworks: Ni-BTC and Cu-BTC

Lead Presenter: Mary White

Other Authors/Presenters: Rakia Butler

Mentor: Daniel Kim

Department: Chemistry

Metal-organic frameworks (MOFs) are crystalline porous materials which are known for their various applications in the fields of gas adsorption/storage, separation, catalysis, adsorption of organic molecules, drug delivery, and environmental remediation. Synthesis of MOFs proceeds via the self-assembly of primary building units through a self-recognition process. The utilization of high intensity ultrasound offers a facile, versatile synthetic tool for the nano-structured materials that are often unavailable by conventional methods. Conventional methods to synthesize MOFs take long time (more than 12 hours) of reaction in high temperature conditions in pressure vessel. Divalent metals of Ni (II) and Cu (II) were used to be complexed with BTC (1,3,5-benzotricarboxylic acid) under ultrasonic irradiation. Time range needed for the formation of MOFs under ultrasonic irradiation was between 15-60 minutes at room temperature. Solvent effect was critical under ultrasonic syntheses of MOFs.



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