College of Agriculture and Life Sciences

2017 – 2018

Research Honors Program Abstracts
The College of Agriculture and Life Sciences (CALS) is a pioneering practitioner of purpose-driven science and Cornell University’s second largest college. We work across disciplines to tackle the challenges of our time through world-renowned research, education and outreach. Since our founding, we have been evolving to meet the changing needs of our world. As our areas of study have diversified, we have established top-ranked programs and over 20 majors in community and rural development, environment and natural resources, food and nutrition, applied economics, agriculture, international programs and life sciences. CALS is fundamentally invested in improving the lives of people, their environments and their communities both in New York state and around the world.

An engaged and inspired student body is critical to CALS’ success. The 2016-2017 honors thesis projects described in this booklet demonstrate an impressive capacity for personal dedication, mature scholarship and intellectual growth. The original research contained herein examines some of the most pressing and relevant questions of our time.

Many students consider the research projects they undertake as undergraduates in CALS to be among the most challenging, enduring, and rewarding of their Cornell experiences. As a faculty member, I have witnessed first-hand among my own advisees the formative impact that undergraduate research can have on budding young scientists. As dean, I am dedicated to fostering the college’s unwavering commitment to providing our undergraduates with these life-changing research opportunities.

I am extremely proud of our undergraduate students and their achievements, and I wish them the very best in their future endeavors. I also appreciate the dedicated faculty who supervised these honors research projects and mentored these students to achieve their fullest potential. On behalf of the CALS community, we welcome them as the next generation of scientific leaders and innovators.

Kathryn J. Boor, Ph.D.
The Ronald P. Lynch Dean of Agriculture and Life Sciences
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Passive and Active Sensors for Yield Predictions and Precision Nitrogen Management in New York

LINDSAY A. CHAMBERLAIN

Under the supervision of Dr. Quirine M. Ketterings
Department of Animal Science

Normalized Difference Vegetation Index (NDVI), a ratio of reflected red and near infrared light, quantifies greenness and biomass of a crop canopy. Previous work has shown that accurate predictions of end-of-season yield can be made for corn (Zea mays L.) grain, corn silage, and forage sorghum (Sorghum bicolor L.) using midseason NDVI measurements from active sensors in New York (NY). Active sensors, such as the GreenSeeker crop sensor, emit their own light and measure reflectance in close proximity to the crop canopy (< 1 m). The NDVI can also be measured with passive sensors, including cameras mounted on unmanned aerial systems (UAS). Passive sensors (cameras) rely on sunlight for illumination and reflectance measurements are therefore affected by atmospheric conditions. In this study, NDVI was measured at 6 time points throughout the day using both active (GreenSeeker) and passive (UAS mounted cameras) sensors on one day each for corn and sorghum N rate studies. Drought in NY in 2016 impacted the physical features of both crops (rolling of leaves mid-day) and reduced the reliability of end-of-season yield predictions using midseason NDVI measurements. As a result of the drought, time of sensing during the day impacted NDVI measured with both active and passive sensors, but NDVI varied more for the passive sensor. Additional studies are needed to evaluate the impact of variations in sunlight intensity or sun angle in a non-drought year.

The Impact of Selection on the Siberian Husky Breed

KAROLYNN M. ELLIS

Under the supervision of Heather J. Huson
Department of Animal Science

The Siberian Husky (SH) was originally bred for its strength and endurance for semi-nomadic arctic tribes. Modern SH remain proficient in sledding but are also bred as show and companion animals. Racing SH are selected for endurance and hardiness, while show dogs undergo more rigid selection for their appearance and stature. Companion dogs may not meet sledding or show requirements. While there is overlap in selection criteria among groups, each group prioritizes selection criteria differently. In this study, we sought to explore the performance and conformation variation within the breed in comparison to genomic variation. We collected 19 physical body measurements, DNA, health and usage information, and pedigrees from 182 dogs. Principal component analysis on body size identified four body patterns distinguishing subpopulations including segregating sledding dogs based on ratio of wither height to leg length. We genotyped 155 dogs on the Illumina Canine BeadChip. Quality control filtering provided 108,047 single nucleotide polymorphisms (SNPs) for analysis. Genetic analysis of 45 sled, 43
show-sled, 32 show, and 18 companion SH identified three genetic subpopulations within the breed. Principal component 1 held two distinct clusters of show dogs from sled dogs. Principal component 2 separated companion dogs from the other subpopulations. Both measures of heterozygosity (Genome Wide Association Study and Fixation Index) and homozygosity (Runs of Homozygosity) highlighted genetic differences among these groups. Candidate genes in which SNPs reside indicate there has been selection based on protein and lipid metabolism, bone formation and skeletal development, and response to physical and mental stress.

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**Evaluation of Housefly Larvae Meal as a Fishmeal Alternative in Aquaculture Feeds**

**JOSHUA M. GODDARD**

Under the supervision of Dr. Eugene Won
Department of Animal Science

The global aquaculture industry has grown rapidly in recent decades to now produce half of the world’s seafood. However, sourcing protein to grow fish at current volumes has become a challenge, resulting in high feed costs and the overfishing of baitfish to make fishmeal. Finding more sustainable and cheaper feed ingredients is one of the aquaculture industry’s top priorities, and various alternative sources of nutrients are being explored, including plant meals, animal processing and industrial byproducts, and insects. In the current study, we evaluated the efficacy of housefly (*Musca domestica*) larvae meal as an alternative protein source to fishmeal for aquaculture production. The fishmeal component of isonitrogenous, isocaloric experimental feeds was replaced at rates of 50 and 100% by fly larva meal and evaluated for growth performance in juvenile rainbow trout (*Oncorhynchus mykiss*) for 16 weeks. Growth, body composition, and energy storage between groups of fish fed 100% fishmeal and 50% fly larva meal were comparable at the end of the trial, suggesting that larva meal is a potential alternative to commercial fishmeal when used in a balanced aquaculture diet. No negative health impacts to the fish, such as mortality or disease, were associated with dietary fly larvae meal. We conclude that fly larvae may therefore be able to supplant a substantial fraction of the fishmeal component of feeds for piscivorous fish, which could reduce aquaculture production costs and environmental impacts.

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**Soil Health Indicators in a Long-Term Manure-Based Corn/Alfalfa Rotation**

**SARAH E. HETRICK**

Under the supervision of Dr. Quirine Ketterings
Department of Animal Science

As climate change continues to impact agricultural production, it is imperative to manage soils for long-term production stability and soil health. Reliable soil health indicators must reflect
changes in soil health induced by long-term management practices. This study analyzed soil health indicators for their efficacy in identifying soil health changes after 15 years of a corn and alfalfa rotation. Corn silage was grown and harvested for 5 years, followed by alfalfa and corn grain (5 years each). Soil health tests were measured for plots amended, during corn years, with low versus high rates of composted dairy-solids or liquid dairy manure compared to plots managed with inorganic fertilizer in five replications. Tests included organic matter by loss-on-ignition, Illinois soil nitrogen test, aggregate size distribution, wet aggregate stability, in-field carbon dioxide emissions, and permanganate oxidizable carbon. Aggregate size distribution was not impacted by compost or manure management and therefore not a suitable soil health indicator. Other indicators showed trends (varying levels of significance) that included increased aggregate stability, higher organic matter by loss-on-ignition, greater Illinois soil nitrogen test nitrogen and permanganate oxidizable carbon, and elevated carbon dioxide emissions with compost addition compared to other treatments. Soil organic matter determined by loss-on-ignition (typically reported on a farmer’s soil test) and permanganate oxidizable carbon are the most practical soil health indicators for farmers. Commercial laboratories differ in methodology for the loss-on-ignition method and this makes results less comparable across farms. The permanganate oxidizable carbon is more standardized across laboratories and hence a better choice.

Balancing Diets for Intestinal Protein Digestibility in Lactating Dairy Cattle

COURTNEY K. HOFF

Under the supervision of Michael E. Van Amburgh
Department of Animal Sciences

To improve efficiency and lower the environmental impact of milk production, lower crude protein diets can be fed to cattle however, the intestinal digestibility (ID) of feed N should be known. An assay (Ross et al. 2013) that predicts the ID of feeds has been developed. The objective of this study was to determine if the assay of Ross et al. (2013) will allow us to accurately formulate for ID in lactating dairy cattle using different animal protein sources. Dairy cattle (n=96) were assigned to two treatments and the study conducted for 63 days. Two diets were formulated for high and low ID using a blend of blood meal (BM) and feather meal (FM) analyzed with the Ross assay. The BM was 74.6% ID whereas the FM was 54.6% ID, thus the high ID diet was formulated with 1.18 kg BM, and the low ID diet was formulated with 1.3 kg of a blend of 82.8% FM and 17.2% BM. The metabolizable energy allowable milk was 46.9 kg/d for both diets. Using data from the Ross assay, the metabolizable protein allowable milk was 46.0 kg/d and 42.5 kg/d, for high ID and low ID treatments, respectively. Observed milk yield was 44.5 kg/d for high ID diet and 43.1 kg/d for low ID diet and energy corrected milk yield was 49.5 and 46.2 kg (P = 0.04). These results indicate that the Ross ID assay can predict ID in cattle and improve predictions of the Cornell Net Carbohydrate and Protein System.
A Comparison of Methods to Assess Unavailable Nitrogen in Ruminant Feeds

HAOWEN (TOM) HU

Under the supervision of Dr. Michael Van Amburgh
Department of Animal Science

Intestinal digestibility of cattle diets is not routinely analyzed as part of diet formulation. The unavailable nitrogen (uN) assay of Ross (uNRoss) was developed to predict the uN of non-forage feeds, and questions have been raised about the applicability to forages. The rumen residency time of forages is about 30 h, whereas the current uN assay uses 16 h to represent the residency time of non-forage feeds. The objective was to evaluate the ability of the uNRoss assay to measure the uN of forages when adopting a longer in vitro digestion period. A total of 12 feeds were analyzed and for all feeds both 16 h and 30 h in vitro fermentations were conducted prior to the uN analysis for comparison. All samples were then evaluated using both acid detergent insoluble nitrogen (ADIN) assay and uNRoss assay to determine uN. Comparisons were made among the results from ADIN assay, uN-16h assay and uN-30h assay. Most feeds had a lower or equal uN after 30 h of incubation with rumen fluid compared to the standard 16 h. The 30 h of fermentation with rumen fluid apparently did not allow for adequate carbohydrate degradation to provide adequate surface area to digest the proteins integrated in the fiber and this might be related to some enzymes present in cattle that are not currently used in the uN assay. For non-forage feeds 16 h of in vitro ruminal exposure was adequate to allow the intestinal enzymes to function appropriately. Future research should focus on the addition of other enzymes to evaluate the ability to digest the fiber matrix to predict protein digestibility.

Exploration of Antibacterial Activity in Musca Domestica Larvae

SAMANTHA J. MALOY

Under the supervision of Dr. Vimal Selvaraj
Department of Animal Science

Chronic overuse of antibiotics has led to a worldwide antimicrobial resistance crisis. To mitigate the effects of this issue, steps must be taken to reduce the use of antibiotics and to develop alternative treatment options for bacterial infections. Insect host-defense mechanisms present a potential opportunity for novel drug therapy. The common housefly (Musca domestica) larvae exhibit antibacterial activity; however, there are differences in the reported inhibitory capabilities. In this study, we conducted a comparative analysis of various bioassays to determine the most effective method for detecting antimicrobial activity of the larvae. We determined that homogenization of larvae in a 90:9:1 (methanol:water:acetic acid) solution, followed by a turbidometric assay of bacterial growth was the most reliable method for screening microbial growth inhibition. Additionally, we explored the antibacterial activity of larvae reared in microbe-rich versus clean environments. Fresh dairy cattle manure was used for the microbe-rich environment, while clean larvae were reared on a standard lab mixture of wheat bran, calf
manna, wood chips, and Baker’s yeast. Our results demonstrated that the *M. domestica* third instar larvae from both environments exhibited potent antibacterial properties against *Escherichia coli*. These findings may contribute to the effort in developing a novel drug candidate to combat the spread of antimicrobial resistance.

### The Genetic Diversity in Body Size of African Goats

**JOHN C. NYSTROM**

Under the supervision of Heather J. Huson, AAS, BS, PhD
Department of Animal Science

Small-holder farmers in Africa rely heavily on goats because of their hardiness and ability to survive on sparse diets. The African Goat Improvement Network (AGIN) is a USAID collaboration with over 20 countries representing agricultural research institutions and universities, primarily African. One aim of AGIN is to phenotypically and genetically characterize body size, an attribute affecting goat income potential. Multiple genome-wide association studies (GWAS) were conducted to explore the genetic regulation of body size in African goats. The project utilized 968 goats from 13 African countries reflecting 58 populations. Goats were genotyped on the Illumina Caprine 50K beadchip using 51,005 single nucleotide polymorphisms (SNPs). Data collected included 5 body size measures, sex, breed, owner, and location. Principal Component Analysis (PCA) of body measurements produced principal component one (PC1) reflecting overall body size. The impact of weight for GWAS was also explored. Principal component one was used as the quantitative variable in an optimized mixed model linear genome-wide association analysis with covariates of sex and breed in a comparison of all goats and then applied to different subsets based on country of origin or breed. Weight was found to have minimal impact, and the GWAS on body size highlighted 34 quantitative trait loci (QTL) across the genome, with 12 genes having significantly associated SNPs within a gene itself. Furthermore, the two candidate genes, *Somatostatin* (*SST*), related to growth hormone, and *Succinate-CoA Ligase GDP-Forming Beta Subunit* (*SUCLG2*), related to bone growth, potentially contributing to body size, were highlighted by the identified QTL.

### Expression of the Micro RNA 302/367 Cluster and Pluripotency in Cattle

**SHANNON E. REDDY**

Under the supervision of Vimal Selvaraj, B.V.Sc., M.S., Ph.D.
Department of Animal Science

Attempts to estimate an authentic pluripotent cell line from cows has proved to be unsuccessful and this might be attributed to the limited knowledge of mechanisms regulating pluripotency. MicroRNAs (miRNAs), by their ability to simultaneously modulate multiple target genes serve
as attractive candidates to dissect such complex mechanisms. The highly conserved miR302/367 cluster, consisting of miRs 302b,c,a,d and miR367, is involved in the induction and maintenance of pluripotency in humans and mice. However, the effects of these miRNAs on bovine pluripotency or their target genes remain largely unknown. Using a bioinformatics algorithm, we predicted the genes targeted by the bovine miR302/367 cluster. Despite being highly conserved, a comparative analysis of the number of predicted target genes of these miRNAs showed a very low overlap between the cow (Bos taurus) and either human or mouse. In silico analysis of the bovine miR302/367 sequence identified the presence of a polyadenylation (polyA) signal downstream of miR302b, which we hypothesized would interfere with efficient processing and expression of other members of this cluster, accounting for the differences in predicted target genes. However, small-RNA sequencing after lentiviral overexpression of the miRNA cluster with or without the polyA signal revealed no difference among the cluster in expression levels downstream of this signal. Our results point to the possibility that despite conserved elements, pluripotency pathways between species might vary and this might contribute to the difficulty in establishing authentic stem cells from cattle.

The Effects of Age and Probiotics on the Lamb Immune System

Haley M. Scott

Under the supervision of Dr. Jerrie Gavalchin and Dr. Michael Thonney
Department of Animal Science

Lambs rely on maternal colostrum for immune protection since they are born immunodeficient. Research indicates that immunodeficiency at birth is required for the development of immune tolerance of commensal microbiota. Furthermore, the role between commensal microorganisms and host interaction supports that commensals play a role in immune training, but work regarding the role of commensal microbiota in immune development in ruminants is minimal. Even with support from maternal immunoglobulin, lambs exhibit high mortality rates, so implementing early and effective vaccination schedules for disease prevention is important. Unfortunately, this has not been well-studied.

In this experiment, we investigated whether treatment with probiotics could enhance immune response in lambs. Lambs received probiotics weekly beginning at two days old, and then were vaccinated with keyhole limpet hemocyanin (KLH) at either 2, 16, or 30 days after birth, followed by a booster 2 weeks later. Blood samples were collected immediately prior to vaccination on sample day (SmplD 0), at booster two weeks later (SmplD 14), and two weeks after the booster vaccination (SmplD 28). Serum was isolated and anti-KLH specific IgG and IgM production was assayed by ELISA.

Statistical analyses indicated significant differences for vaccination age and sample time. Levels of anti-KLH specific IgG increased with age, supporting that older animals can generate stronger IgG specific immune responses. Additionally, significant differences in sample time showed increased levels of IgM production after the primary vaccination and further increased IgM
levels after the booster vaccination. Although not statistically significant, general trends indicated that probiotics might enhance immune response in 30-day old lambs.

Estimating the Age of the Endogenous Viral Element in *Rattus Norvegicus*

CHRISTIAN URBINA

Under the supervision of Dr. Colin Parrish
Department of Microbiology and Immunology, College of Veterinary Medicine

As genomes have been sequenced for many plants and animals, they have often been observed to contain sequences derived from different viruses. In many cases, these viral elements are either excised or subject to mutations during the replication of the host DNA. However, there are also many examples of endogenous viral elements (EVEs) persisting and their sequences remaining highly conserved within the genome of their hosts for many generations and possibly, even after speciation. One such example of an integrated viral sequence is a parvovirus-derived sequence found in the brown rat, *Rattus norvegicus*. This region is conserved throughout the species and has the genomic characteristics of a parvovirus. To determine the possible age of the *R. norvegicus* EVE, multiple rat species were screened for the presence of the sequence. This was done using primers specific for the EVE sequence in PCR amplification. The results showed EVE sequences in two different branches of the *Rattus* genus, thus showing the age of the viral insertion to be at least 5 million years old. Phylogenetic analyses of the EVE sequences in rats, along with those of extant viruses and of EVEs from two mouse species, confirmed that the integrated virus in rats was most closely related to canine parvovirus and was not closely related to the EVEs discovered in the genomes of the different mouse species suggesting cross species transmission of the ancient parvoviruses.

Adding Sulfur to the Cornell Nutrient Mass Balance Software

JORDI J.M. VERHOEVEN

Under the supervision of Quirine M. Ketterings
Department of Animal Science

A nutrient mass balance (NMB) is an indicator of whole-farm long-term sustainability. It is defined as the difference between nutrient imports onto, and exports from the farm. Cornell University’s NMB assessment tool can be used to derive NMBs for nitrogen (N), phosphorus (P), and potassium (K). Trend analyses show that farms that use this tool annually tend to improve their farms’ NMBs over time. Sulfur (S) is a macronutrient of growing importance to farmers, as wet and dry deposition rates of S have been gradually declining over the past decades. Deriving a farm’s NMB for S may be a useful step in the decision-making on S fertilizer use. Here, the feasibility and practicality of adding S to the NMB assessment tool were evaluated. Specifically, availability of information on S contents of input and exports on dairy
farms was determined. Additionally, a calculator was developed based on the existing NMB assessment tool to determine S balances. Five years of farm records were used to derive N, P, K, and S balances for a case study dairy farm in Ohio. Results show that (1) it is feasible to add a S balance to the NMB assessments; and (2) the farm’s S balances follow a trend similar to its N and P balances. Additional research with more farms is needed to determine feasible balances for S for dairy farms and to determine if S deficiencies are likely to occur on dairy farms.

Effect of Sex on In Vitro Bovine Embryo Development

SARAH C. WRIGHT

Under the supervision of Dr. Soon Hon Cheong
Department of Clinical Science, Section of Theriogenology, College of Veterinary Medicine

In vitro fertilization has become a fairly standard practice for human infertility treatments and for the production of genetically superior dairy cattle. However, there is no consensus on the effect this method has on the sex ratio of the offspring. Some reports showed a tendency of higher male offspring production when embryo selection for transfer was performed at the blastocyst stage, while other studies failed to detect a difference in the offspring sex ratio. This study sought to determine whether there is a differential growth rate between embryos of different sexes and to determine if male embryos are more likely to reach the blastocyst stage than females. In vitro oocyte maturation, fertilization, and embryo culture were observed by time lapse video to determine the growth rates of male and female embryos. A fluorescent probe against the Y chromosome was used to determine sex. There was no difference in the growth rates of male and female embryos during any part of the developmental sequence to the hatched blastocyst stage (p>0.05). Based on these results, the culture conditions used in this study do not favor a selective growth advantage of one sex over the other. However, this study was limited by sample size (n=15 embryos analyzed under both time lapse and fluorescence microscopy), so further studies are needed to determine if these results hold true for larger sample sizes.

γH2AX as a Biological Indicator of Chemoresistance in Feline Injection Site Sarcomas

ZACHARIE J. WUND

Under the supervision of Dr. Kelly Hume
Department of Clinical Sciences, College of Veterinary Medicine

Feline injection-site sarcomas are uncommon but when they do occur they are clinically problematic tumors because of their high recurrence rates and the difficulty in achieving clean margins during surgical excision. Aggressive surgery and adjuvant radiation therapy are the current predominant treatment options. The efficacy of chemotherapy remains to be fully understood due to inconsistent response rates. A biomarker of chemoresistance would be useful
in identifying cats that would benefit from chemotherapy. Our objective is to evaluate the use of γH2AX as a biomarker for chemoresistance. We hypothesized that tumors that have higher levels of DNA damage, marked by expression of phosphorylated H2AX (γH2AX) at the site of DNA double strand breaks, are more resistant to carboplatin chemotherapy. To evaluate this association, 14 cell lines derived from feline injection-site sarcoma biopsies were treated with 2 μg/ml or 4 μg/ml of carboplatin and allowed to grow as colonies. The resistance of the cells to carboplatin was compared to γH2AX expression in the original tumors determined previously by immunohistochemistry. We found a statistically significant (p=0.0096) positive association between γH2AX expression and colony survival. Cells from tumors with high γH2AX expression are more resistant to carboplatin, and therefore γH2AX has potential as a biomarker for chemoresistance in feline injection-site sarcomas.
SMOC-2 Suppression in Diffuse Large B-Cell Lymphoma May Confer Resistance to Rituximab

Dhanesh Bindia

Under the supervision of Kristy L. Richards
Department of Biomedical Sciences

Rituximab is a genetically constructed chimeric mouse-human monoclonal IgG1 kappa antibody that recognizes the CD20 antigen. It has been the top selling oncology drug for nearly a decade. Rituximab was approved for medical use in 1997 and since then, it has improved outcomes in all B-cell malignancies. However, about 40% of patients relapse after initially responding to rituximab combined with cyclophosphamide, doxorubicin, vincristine, and prednisone (R-CHOP). It is therefore important to understand any potential mechanisms of resistance in order to improve patient survival through better therapeutic choices. Since rituximab’s mechanisms of action are challenging to study in non-human models, our group used in vitro studies linking genotype to phenotype via Genome-Wide Association study (GWAS) and identified a Single Nucleotide Polymorphism (SNP) in SMOC-2, which encodes an extracellular matrix protein that might be involved in rituximab sensitivity. In order to determine whether the expression of SMOC-2 affects rituximab sensitivity, malignant B cells with a SMOC-2 knockdown were tested in an in vitro Complement Dependent Cytotoxicity (CDC) rituximab killing assay. After performing CDC assays on several Diffuse Large B-Cell Lymphoma (DLBCL) SMOC-2 knockdown cell lines, the HBL-1 cell line exhibited resistance to rituximab. However, western blot analysis yielded inconclusive evidence about the knockdown of SMOC-2, since the SMOC-2 band could not be confidently identified. Understanding the mechanisms of intrinsic and acquired resistance to drugs in cancer therapy may enable the use of patient genotypes to determine which anti-CD20 would be most effective or allow interventions to restore rituximab sensitivity in patients.

An Effort to Create a Bag of Marbles Gene Hypomorph in Drosophila simulans using CRISPR/Cas9 Gene Editing

Maya Biswas

Under the supervision of Charles Aquadro
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Although essential in early gametogenesis in the Drosophila genus, the bag of marbles (bam) gene has rapidly accumulated amino acid changes and has shown signs of positive selection within the melanogaster group of Drosophila. Here I describe the design and attempt of creation of a D. simulans bam hypomorph marked with DsRed, a red fluorescent protein, created using CRISPR/Cas9 gene editing techniques. A successful CRISPR/Cas9 edited bam mutant was created in D. simulans, but after phenotypic analysis, it was discovered that a bam null rather than a bam hypomorph had been created. The null phenotype is likely due to the disruption of
bam from the insertion of DsRed in the second intron. I also describe the design of a bam null in D. pseudoobscura, which ultimately failed to assemble due to cloning complications.

Mutational and Proteomics Approaches to Investigate the Regulatory Mechanisms of Golgi Trafficking

YI FAN CHEN

Under the supervision of Chris Fromme
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The Golgi apparatus is a dynamic organelle that regulates cellular trafficking events with high precision by integrating a diverse array of biochemical, temporal, and spatial signals. Guanine nucleotide exchange factors of the Sec7 family function as molecular master switches to effect vesicle formation and trafficking through specific interactions with small GTPases of the Arf and Rab families. Even though some of the biochemical signals recognized by these master regulators are well characterized, they represent only a small subset of the complex ensemble of potential interactions and limits an accurate understanding of the mechanism by which signals are integrated. The current study uses mutational and proteomics approaches in Saccharomyces cerevisiae to enhance the current understanding of regulatory mechanisms at the Golgi apparatus. My results have revealed important autoregulatory functions in the individual domains of the guanine nucleotide exchange factors that are crucial for appropriate localization and interactions with membrane surfaces. These results also reveal that mutant phenotypes may be rescued by overexpression of Ypt1. Furthermore, a platform is being developed to probe the global interactome of the master regulators to gain insight into the mechanism by which myriad signals are integrated. These results provide important insights into equivalent processes in mammalian systems to improve the current understanding of cellular trafficking and disease phenotypes.

The Different Effects of Cholinergic Neuromodulation via Muscarinic and Nicotinic Receptors on Olfactory Discrimination Learning

CHRISTINA CHO

Under the supervision of Christiane Linster
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Cholinergic neuromodulation has long been associated with various neural functions, such as learning and memory. In particular, cholinergic modulation in the olfactory bulb has been shown to affect olfactory discrimination learning, and there are two different types of cholinergic receptors, muscarinic and nicotinic. The effects of cholinergic input into the olfactory bulb via muscarinic receptors differ from those via nicotinic receptors. The present study tests to what extent behavioral conditioning and the activation of muscarinic and nicotinic receptors interact
and compensate for each other in modulating the strength and specificity of an odor reward association. In the study, the mice were infused with either a muscarinic antagonist, a nicotinic antagonist, or a saline vehicle control directly into the olfactory bulb, and then were trained over either 4, 8, or 12 trials to associate a given odor with a reward by digging for a reward in scented sand. Digging times measured in the test trials showed that blocking muscarinic receptors slowed down learning across all test odors while blocking nicotinic receptors impaired discrimination between perceptually similar odors by affecting their odor representations, independently of learning. Moreover, extended periods of learning allowed mice to compensate for lack of muscarinic, but not nicotinic, receptor activation.

Elucidating the Function of MSH5 c-terminus in Mammalian Meiosis

YIMENG FANG

Under the supervisor of Paula Cohen
Department of Biomedical Science

Meiosis is the essential process used by eukaryotes to produce haploid gametes. Accurate homologous chromosomal segregation in meiosis is dependent on crossover formation, or the exchange of genetic material between homologous chromosomes, and loss of crossovers leads to infertility across many species. MSH5 is a critical protein involved in crossover formation, during meiosis I. In this paper, I discuss the role of a highly conserved and mammalian specific c-terminal domain within MSH5. The high conservation of the c-terminus domain in mammalian indicates its importance; thus, I hypothesized that Msh5 c-terminus is related to homologous chromosomal synapsis in mammalian meiosis. We generated three genotyping mouse lines (Msh5+/+, Msh5+/AC and Msh5AC/AC) and based on the comparison of mice fertility, found that MSH5 c-terminus is necessary for normal mouse testis function and loss of the c-terminus results in loss of sperm production as well as homologous chromosomal pairing in prophase I of meiosis. I also found the impacted phenotype was more severe in homozygous mutant mice than in heterozygous mutant mice.

Equine Mesenchymal Stromal Cell Secreted Tenascin-C and PAI-1 Promote Fibroblast Migration \textit{in vitro}

MEGAN K. HE

Under the supervision of Gerlinde Van de Walle
Department of Microbiology and Immunology

The high prevalence of hard-to-treat cutaneous wounds has resulted in medical and financial incentives to develop novel therapeutics. Studies in the equine model are translatable to human medicine due to similarities between the wound healing processes. Equine mesenchymal stromal
cell (MSC) secreted factors have been shown to promote migration of equine dermal fibroblasts (NBL6), a critical step in wound healing.

My study aimed to determine the nature and activity of two of these MSC secreted factors. I subjected equine MSCs to RNA interference (RNAi) to knockdown tenascin-C and PAI-1, candidate proteins identified through mass spectrometry analysis. I collected the secretomes of siRNA transfected MSCs as conditioned media (MSC-CM) for assays to determine differences in NBL6 migration mediated by the different treatments and for use in actin staining and adhesion assay experiments.

Tenascin-C and PAI-1 knockdown, independently and in combination, significantly reduced the ability of MSC-CM to promote fibroblast migration, indicating that these proteins play an active role in the process. NBL6 cells treated with tenascin-C and PAI-1 knockdown MSC-CM showed greater adhesion in cell culture plates, and NBL6 cells treated with tenascin-C knockdown MSC-CM also displayed an increased anisotropy score. These results suggest that MSC secreted tenascin-C and PAI-1 decrease adhesion of fibroblasts and that tenascin-C also mediates rearrangement of the actin cytoskeleton, processes corresponding to an increased migratory phenotype.

The identification of equine MSC secreted bioactive factors increases our understanding of the secretome and enhances the therapeutic value of MSCs as a therapy for cutaneous skin wounds.

Adaptation of the Cre-loxP Recombinase System for Modification of the Germinal Micronucleus in the Bi-nucleated Ciliate, *Tetrahymena Thermophila*.

**KARUNA R. KATARIWALA**

Under the supervision of Donna Cassidy-Hanley
Department of Microbiology and Immunology

Cre-loxP recombinase system has been utilized to generate site specific recombination in a variety of organisms. The use of the Cre-loxP system in the bi-nucleated ciliate *Tetrahymena thermophila* (*T. thermophila*) has been successful when both Cre-recombinase and the recognition loxP sites are localized to the transcriptionally active somatic macronucleus. The implementation of the Cre-loxP system in the transcriptionally silent germline micronucleus presents unique obstacles due to the micronucleus’ tight regulation and relative impermeability. For Cre-recombinase to work in the micronucleus, it must transport across the micronuclear membrane and recognize loxP sites which must be introduced into the micronucleus. To assist in transporting the Cre recombinase protein into the micronucleus, two nuclear localization signals derived from a micronuclear specific histone were fused to the Cre gene; the resulting vector was transformed into *T. thermophila* cells via biolistic transformation. Initial Western blots and immunofluorescent imaging indicated Cre fused to both nuclear localization signals and is expressed, but no detectable localization in the micronucleus was assessed by immunofluorescence. The localization of the loxP sites to the micronucleus would allow for a
functional assay to determine whether Cre localized to the micronucleus at cytologically undetectable, but functional, levels. However, after several modifications with the standard biolistic transformation protocol, no viable, micronuclear loxP transformants were produced. Future work includes the use of the nuclear localization signals to target larger endogenous proteins to the micronucleus of *T. thermophila* and further modifications of the micronuclear transformation protocol to facilitate the migration of Cre to the micronucleus.

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**Brain Stains: Optimization of Immunohistochemical Methods for Cleared Thick Neural Tissue**

**Mackenzie E. Lemieux**

Under the supervision of Melissa Warden  
Department of Neurobiology and Behavior

Populations of GABAergic interneurons in the prefrontal cortex have been implicated in control and coordination of complex behaviors such as motivation and decision-making. Although the functions of each of the main GABAergic subtypes, SST, PV, and VIP, have been extensively investigated independently, a lack of techniques allowing simultaneous recording has precluded the ability to characterize the interactions between these cell types. Staining for markers of GABA cell types in thick tissue, and relating identities back to in vivo recordings, will allow explicit and direct characterization of how activity covaries in these populations. However, there has been minimal success when staining for GABAergic subtypes in thick tissue. I interrogated the different factors that might be affecting successful thick tissue staining using the Cuboid Method which enables controlled and efficient thick tissue preparation, staining, and experimental testing. Fixation, with both paraformaldehyde and glutaraldehyde, was observed to be a major factor influencing the ability of different SST, PV, and VIP antibodies to label their epitopes in thick tissue. Additionally, fixation appeared to affect SST and VIP staining differently than PV staining. SDS treatment prior to staining was shown to be compatible with GABAergic subtype staining while SDS treatment after staining was shown to dramatically decrease staining signal. Like others’ findings, blocking was shown to be unnecessary for better PV and SST staining. Lastly, relative proportions of SST, PV, and VIP in the PFC and their staining patterns in thick tissue matched results from previous work in thin tissue to support that staining was successful and also accurate. This research provides the knowledge necessary to successfully stain for SST, PV, and VIP in thick tissue in addition to showing the efficacy of the Cuboid Method for testing factors affecting staining in thick tissue.
Identification of the Pseudoautosomal Region 1 Length Polymorphism in Human Populations

XUEYAN ROSA MA

Under the supervision of Alon Keinan
Department of Biological Statistics and Computational Biology

The pseudoautosomal region 1 (PAR1) is a short region of homology on the otherwise dimorphic human sex chromosomes. The size of PAR1 was thought to be invariable. Recent evidence suggests that there may be a PAR1 length polymorphism in the human population. In particular, an extension of the PAR has been identified in males from 6 families of Belgian or French origin. This extension was caused by a recurrent insertional translocation from the X chromosome to the Y chromosome. I attempted to investigate whether such extension of PAR1 by the insertion exists in other populations, and if so, whether they have any phenotypic effects.

From the 1000 Genomes Projects, UK10K project, GAIN study, and nonGAIN study, I was able to identify individuals who were likely to be carriers of the insertion. However, due to the small number of such individuals, the statistical power was not strong enough for me to make an inference about the phenotypic effects of the insertion. Overall, despite that I was not able to elucidate the X and Y chromosomal structures of these carriers, my findings suggest that the PAR1 polymorphism may exist in other populations. Since PAR1 is associated with risks for several mental and developmental disorders, the size variations of this less studied euchromatic regions may provide a new perspective on these diseases.

Evolution of Body Size and Sexual Size Dimorphism in Tortoises

SEAN W. MCHugh

Under the supervision of Kelly Zamudio
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Sexual size dimorphism (SSD) varies in terrestrial vertebrates from male-biased to female biased. In tortoises, SSD and body size vary widely across the family while following Rensch’s rule, an allometric trend in which the intensity of male-biased SSD increases and female-biased SSD decreases as average body size increases. The ubiquitous male combat found within the family may favor large male body size and explain a progressive male-biased trend in SSD in the family from a female-biased ancestor. Here, phylogenetic comparative methods reveal that while tortoises as a whole follow Rensch’s rule, individual clades within the family do not. South African tortoises followed nondirectional isometry, and tortoises of the genera Manouria and Gopherus exhibited a reverse Rensch’s rule. Furthermore, evolutionary rates for male and female body size evolution varied from clade to clade, ranging from higher rates of male change in three clades, higher rates of female change in one clade, and similarities for both sexes in other clades. The evolution of body size followed a similar pattern in males and females and only diverged near the tips, with males becoming larger than females in some lineages. The present study
suggests that the evolution of SSD in tortoises is not uniform, and that current distribution of
SSD biases is the result of recent divergences in body size driven by multiple selective
mechanisms.

The N-terminal Domain of *Staphylothermus marinus* McrB Shares Structural
Homology with Eukaryotic RNA Binding Proteins

YIMING NIU

Under the supervision of Joshua Chappie
Department of Molecular Medicine, College of Veterinary Medicine

McrBC is a conserved modification-dependent restriction system that in *Escherichia coli*
specifically targets foreign DNA containing methylated cytosines. Recent crystallographic data
show that the N-terminal domain of *Escherichia coli* McrB binds via a base flipping mechanism.
This region is poorly conserved among the plethora of McrB homologs, suggesting that other
species may use alternative binding strategies and/or recognize different targets. Here we present
the crystal structure of the N-terminal domain from *Staphylothermus marinus* McrB at 2.10 Å,
which adopts a YTH/EVE-like fold that is prevalent among eukaryotic RNA binding proteins.
Structural comparison and molecular docking experiments support the hypothesis that this
domain is specific for RNA recognition. Together these data suggest a broader biological
versatility for the McrBC family than previously described.

Na+/K+ ATPase α Subunit is a Promising Protein Partner of Epilepsy-causing
Protein, Julius Seizure, in *Drosophila*

SARAH H. PARK

Under the supervision of David Deitcher
Department of Neurobiology and Behavior

Epilepsy is a common chronic and debilitating condition, but the mechanisms of epileptogenesis
are not well understood. This study uses a *Drosophila* model of epilepsy in order to further
investigate the potential pathways that underlie epileptogenesis. *Julius seizure* (*jus*), previously
characterized as the gene responsible for bang sensitivity in *slamdance* flies, was utilized in a co-
immunoprecipitation experiment in order to identify proteins that interact with it on a molecular
level, and therefore may play a role in the epileptogenetic pathway. The expression of these
interacting proteins was perturbed, and the resulting adult flies were subjected to initial vortex
testing experiments. The perturbation of Squid and the alpha subunit of Na+/K+ ATPase
produced more significant effects on bang sensitivity in these initial experiments, and therefore
were selected for further study. Behavioral experiments were supplemented with imaging
techniques to observe of the distribution of protein hits in the *Drosophila* central nervous system.
Squid and Zasp, in particular, showed defined regions of expression that are similar to that of
Jus. Though the role of squid is less clear, it is possible that Na\(^+/K^+\) ATPase, which is vital for the regulation of electrical activity in the nervous system, is localized by Jus; thus, a lack of the latter would cause mis-localization of ATPase in such a way as to cause bang sensitivity.

Monosynaptic Tracing of Ventral Tegmental Area-Projecting Infralimbic Cortex Neurons Using G-Deleted Rabies Virus

KYLE PELLEGRINO

Under the supervision of Melissa R. Warden
Department of Neurobiology and Behavior

The advent of optogenetic technology has allowed for precise testing of modulatory effects that specific brain regions have on each other. This technology has been used to parse out potential neural circuits involved in depressive states. Depending on the circuit involved, various depressive symptoms can arise (Perry, 1996; Papakostas et. al, 2006), making it important to more fully understand these circuits to create more effective treatments for depression. The prefrontal cortex (PFC) is thought to play a key role in the integration of sensory information to plan out and execute complex behaviors (McGuire & Botvinick, 2010). In terms of depressive neurocircuitry, the PFC has been shown to project and modulate several midbrain regions, including the dorsal raphe nucleus (DRN) and ventral tegmental area (VTA) (Warden et. al, 2012; Post, unpublished results). It is also known that the PFC receives inputs from a number of cortical and thalamic areas (Goldman-Rakic, 1988). With this knowledge, the present study used newly developed rabies monosynaptic tracer technology (Callaway & Luo, 2012) to define the inputs to a specific neural circuit involved in expression of the depressive phenotype, VTA-projecting infralimbic cortex (ilPFC) neurons. Preliminary results support the idea that this circuit receives cortical inputs (n = 32), specifically from motor and somatosensory cortices. The results also revealed relatively few thalamic inputs to this circuit.

Functional Characterization of *Laccase 2* in *Vanessa cardui* Pigmentation and Cuticle Sclerotization

CEILI PENG

Under the supervision of Robert Reed
Department of Ecology and Evolutionary Biology

Species of the insect order Lepidoptera are defined by the presence of scales on their wings. These scales and the color patterns that they compose have important roles in flight, thermodynamics, mating, and predator deterrence, among others. Despite the crucial functions of these scales and patterns, there are gaps in our knowledge as to the genetic mechanisms responsible for their patterning, development, and coloration. *laccase 2* is a gene that has been previously identified as part of the melanin pigmentation pathway, but whose function is still
poorly characterized in Lepidoptera. Here, I knock out the laccase 2 gene in Vanessa cardui butterflies using CRISPR/Cas9 gene editing technology to assess its role in wing scale development. I hypothesized that there would be a reduction in melanin pigmentation, which I did observe in some mutant clones. However, I was surprised to also observe more dramatic mutant phenotypes, including scale loss and wing malformation. Our results therefore support roles for laccase 2 in both the melanin pigmentation pathway and in cuticle sclerotization. This work provides further support for the growing list of genes which play dual roles in melanin and cuticle formation and provides new insight into the evolution of lepidopteran wing coloration.

2D and 3D Ultrasonographic Methods versus the 2D Grid Method for the Evaluation of Ovarian Morphology

ADRIENNE J. PISCH

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Division of Nutritional Sciences

Introduction. Polycystic ovarian morphology (PCOM) is defined by a follicle number per ovary (FNPO) of ≥ 25 and assessed through non-invasive ultrasound imaging. The Grid Method represents the gold standard approach for evaluating ovarian morphology due to highly reliable estimates of FNPO, which can be challenging to obtain in polycystic ovaries. Other 2D and 3D techniques can be utilized to assess FNPO. However, their utility against the gold standard has not been evaluated, so may be inappropriate to diagnose PCOM. The study was conducted to determine the agreement in obtaining follicle counts using various 2D (Real-Time) and 3D methods (Multiplanar View, Tomographic Ultrasound Imaging and SonoAVC) versus the 2D Grid Method.

Methods. 32 ovaries were analyzed using each method for follicle number, follicle diameter, and PCOM-status. Bland Altman agreement statistics and Passing Bablok regression analyses evaluated the degree of agreement and proportional bias in follicle counts.

Results. 2D Real-Time showed positive systematic bias across all ovaries (+3.2 follicles; p=0.045) and within the non-PCOM population (+6.0 follicles; p=0.003). By contrast, SonoAVC showed negative systematic bias across all ovaries (-2.9 follicles; p=0.0012) and within the PCOM population (-4.1 follicles; p=0.0043). 2D Real-Time was the only approach that failed to identify PCOM from non-PCOM ovaries defined by the 2D Grid Method.

Conclusion. Of the approaches available to assess follicle populations on ultrasonography, Multiplanar View had the best agreement to the gold standard. 3D methods differentiated between PCOM and non-PCOM ovaries, but systematic bias and high variability infer they cannot be used instead of the 2D Grid Method.
To Sit or Not to Sit: Latitudinal Shifts in Incubation Behavior of a Widespread Songbird Indicate Importance of Male Contribution and Both Proximate and Ultimate Factors

JAMES R. PURCELL

Under the supervision of Vanya G. Rohwer
Department of Ecology and Evolutionary Biology

Incubating birds must trade-off leaving the nest to forage with staying on the nest to maintain optimal temperatures for developing embryos. This trade-off is expressed through different incubation behaviors, which can be heavily influenced by proximate factors such as climate, food availability, and nest predation risk. Comparatives studies across species have shown that incubation behaviors vary widely across latitudes, but few studies have explored variation in behaviors within a species. I explored how incubation behaviors differ geographically using a widespread songbird, the Yellow Warbler (Setophaga petechia), between a temperate and subarctic site that differ in biotic and abiotic challenges to breeding warblers. I quantified four incubation behaviors: male feeding rate, female off-bout duration, female off-bout frequency, and the proportion of time incubating females spent on the nest. My between-site comparisons revealed that, at the subarctic site, male feeding rates were higher, female off-bout durations were shorter, and the proportion of time females spent on the nest tended to be greater compared to the temperate site, whereas temperate and subarctic females showed no differences in the frequency of off-bouts. My within-site comparisons revealed that, as temperatures warmed, males fed females less often, and as male feeding rates increased, off-bout durations and frequencies decreased while the proportion of time on the nest increased. These results indicate that certain incubation behaviors are flexible and vary in response to ecological challenges associated with different breeding sites, and highlight the importance of male contributions in influencing female behavior.

The Effects of Red Fox (Vulpes vulpes) Predator Scent on Winter Burrow Use by Eastern Cottontail Rabbits (Sylvilagus floridanus)

JEREMY D. PUSTILNIK

Under the supervision of:
Jeremy B. Searle, Department of Ecology and Evolutionary Biology
Paul D. Curtis, Department of Natural Resources

During the winter months, the Eastern cottontail (Sylvilagus floridanus) must simultaneously cope with freezing temperatures that impose physiological stress, while remaining vigilant for a variety of predators. Because of this, rabbits frequently use burrows around man-made structures to escape the cold and predation. To enhance their detection of predators, Eastern cottontails are also sensitive to a variety of olfactory cues. However, despite the importance of Eastern
cottontails in red fox (*Vulpes vulpes*) diets, little is known about scent cues that rabbits use to detect red foxes. As such, I designed an experiment to determine whether winter burrow use by Eastern cottontails is affected by the application of red fox urine near burrows. After identifying active rabbit burrows near abandoned buildings in Ithaca, New York during winter 2017-2018, camera traps were installed to monitor their use before and after setting up scent wicks dipped in red fox urine or a water control near burrow entrances. Although no statistically significant effect was observed between burrow use before and after treatment, a variety of mammalian and avian species were seen in and around burrows over the course of the winter, including striped skunks, bobcats, deer, opossums, mice, house cats, and sparrows. This indicates that burrows may be important to a range of North American mammals and birds, knowledge which may be helpful in creating future conservation management plans for these species. This project has also provided continued evidence for the usefulness of camera traps in documenting predator-prey behavior and studying wildlife ecology.

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**Exploring Color-Physiology Relationships Across Two Populations of Tree Swallows, *Tachycineta bicolor***

**Alyssa Rodriguez**

Under the supervision of Maren Vitousek  
Department of Ecology and Evolutionary Biology

Signal traits often evolve to communicate information about individual differences in physiological state, especially those important for fitness. As the ability to cope with stressors is an essential aspect of an animal’s fitness, it may be beneficial to advertise to conspecifics. When facing stressors, vertebrates mount a glucocorticoid stress response. However, mounting a stress response is energetically demanding and can be especially costly when breeding. Because regulation of the stress response is important to fitness, and because glucocorticoids (CORT) shares biochemical pathways with many condition-dependent ornaments, I investigated whether ventral plumage color in tree swallows—an apparent social signal—predicts CORT regulation across populations of tree swallows, *Tachycineta bicolor*. Specifically, I examined whether the brightness of white ventral plumage predicts three aspects of CORT regulation: baseline levels, the CORT response to a standardized stressor, and the ability to down-regulate the CORT response through negative feedback. For a population in Alaska (AK), facing harsher breeding conditions than one in New York (NY), I expected brighter ventral plumage to positively correlate with negative feedback efficacy. My results showed that in NY, birds with brighter breast feathers had significantly stronger negative feedback, but that in AK, there was no relationship between feedback efficacy and breast brightness. Neither baseline nor stress-induced CORT levels predicted color in either population. Mean negative feedback strength was weaker in NY for the favorable year of 2016 than in 2017, despite both populations facing challenging environmental conditions that year. These results suggest that bright white breast plumage in tree swallows could serve as signal trait to communicate strong negative feedback to potential mates or aggressors.
A Capillary Paper Biofluid Viscometer

NATHAN J. SARKAR

Under the supervision of Saurabh Mehta
Division of Nutritional Sciences

Viscosity is an important property of biofluids, and measurements of biofluid viscosity can yield important medical information. I present a novel method for cheaply and easily determining biofluid viscosity. I allow a sample fluid to flow through capillary paper and determine the flow rate by detecting an electrical current passed through the fluid at two points along the capillary paper. I found that the flow rate can be reliably correlated with the viscosity of the liquid with a simple linear model. This thesis describes the methods and techniques used in the production and optimization of this device. It also includes an analysis of the device’s consistency between sensor panels and temperature sensitivity. I found that the two sensor panels did not yield statistically different readings, and that the temperature sensitivity of the flow rate became more pronounced at higher viscosity levels. Given this device’s portability, size, low cost, and ease of use, it may be suited for use in resource-limited settings. Future work with this device includes testing its medical applications and its applications in the LAL gel-clot test.

Search for Novel Factors Affecting Nuclear Structure and Function in Arabidopsis thaliana

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Under the supervision of Eric Richards
Department of Molecular Biology and Genetics, Boyce Thompson Institute

The nuclear lamina is of critical importance to the cell as it has a multitude of roles. Its various functions include nuclear transport, involvement in signaling pathways, and chromatin organization. The structure of the nuclear lamina impacts its function, so an in depth understanding of the proteins composing the nuclear lamina is imperative. The animal nuclear lamina is composed of lamin, yet plants lack lamin orthologs. However, the plant nuclear lamina contains analogous proteins that are structurally and functionally similar. One of these proteins, CRWN4 is encoded by a member of a family of genes required to maintain the structure of the plant nucleus. This project utilizes a suppressor screen of the crwn4-2 mutation to find genes that could play a role in the structure and function of the plant nuclear lamina. The crwn4-2 allele is a missense mutation that reduces the abundance of the protein in the nucleus. I identified a mutation that suppressed the crwn4-2 allele and restored normal protein levels in the nucleus. A series of genetic experiments were conducted to characterize the suppressor mutation and lay a foundation for its molecular identification. Through these genetic crosses, it was found that the suppressor allele is inherited in a semi-dominant manner and exhibits allele-specificity. Whole Genome Sequencing is currently being undertaken to locate the allele’s position within the...
genome and identify a candidate gene. The findings of this thesis provide evidence that genetic suppressor screens can be used to identify novel genes and interactions affecting plant nuclear architecture.

Applications of a Mineral-Containing 3D Scaffolds to Study Characteristics of Ductal Carcinoma in situ

SONALI SRIVASTAVA

Under the supervision of Claudia Fischbach-Teschl
Department of Biomedical Engineering

Engineered three-dimensional microenvironments prove advantageous for studying the cellular mechanisms behind the micro-environmental regulators involved in breast cancer metastasis to the bone. Hydroxyapatite (HA), a calcium-phosphate mineral, is a primary inorganic nano-structural component of the bone, and the micro-calcifications of breast tissue. While HA has been prevalent in the microenvironment of breast tumors, its specific role in cancer pathogenesis is yet to be explicitly distinguished. This study demonstrates that DCIS cells when cultured on 3D HA mineral containing scaffolds, exhibit greater proliferation, adhesion, and of particular interest, increased IL-8 secretion.

Il-8’s ability to promote metastasis to secondary sites was suggested through treating hMSCs with tumor-conditioned media collected from DCIS cells cultured on HA-containing scaffolds. Specifically, it was found that stromal-derived factor-1 (SDF-1) expression increased, as did the expression of alkaline phosphatase, an osteogenic differentiation marker typically associated with invasive disease.

To better understand the unique factors contributing to invasive pathologies in HA mineralized scaffolds, cellular properties in repose to calcium oxalate (CO), a mineral typically associated with benign pathologies was studied. Common cellular characteristics typically indicative of aggressive tumors such as cellular adhesion, cellular proliferation, and IL-8 secretion were studied. While, cell adhesion, proliferation, and IL-8 secretion were all higher in the CO condition compared to the non-mineral condition, these parameters were not significantly different when compared to the HA condition. Suggesting, that downstream signaling differences triggered during interaction with the mineral may be responsible for the differences in disease phenotype observed in the clinic.
Mineralization and Crystal Structure in the Proximal Sesamoid Bone of Thoroughbred Racehorses

CAROLINE WOLLMAN

Under the supervision of Heidi Reesink
Department of Clinical Sciences

Catastrophic proximal sesamoid bone (PSB) fracture is a frequent injury sustained during racing and training in Thoroughbreds and is associated with increased PSB volume fraction. To determine whether increased bone volume fraction was associated with changes in bone mineral content and crystal structure, ash fraction and x-ray diffraction (XRD) measurements were performed on PSBs obtained from Thoroughbred racehorses. The fracture group (n=8) consisted of horses that had sustained a fracture of one or both PSBs in only one forelimb. The control group (n=8) PSBs were obtained from racehorses that were euthanized for reasons unrelated to the fetlock. I hypothesized that bones from fracture horses would be more mineralized and; therefore, more brittle as compared to controls. Objectives of this study were to (1) determine the mineral content of PSBs via ash fraction, and (2) analyze crystalline size and percent crystallinity via X-ray diffraction in fracture and control PSBs.

Percent mineral was increased in controls compared to fracture horses in the basilar and midbody regions. The basilar region had increased percent mineral compared to the apical region. PSBs from horses sustaining fracture had less mineral, which suggests that PSBs from these horses are not more brittle but may be weaker. XRD produced similar results between fracture and control groups for percent crystallinity and crystal size. My results motivate future studies to investigate whether decreased bone mineralization is associated with weaker bones and whether alterations in collagen structure and alignment of PSBs are affecting bone tissue quality in racehorses.
The Consequences of Intraspecific Diversity in Defense Traits on the Performance of an Important Agricultural Pest, *Trichoplusia ni*

**Nana Yaa B. Britwum**

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Insect herbivory can be detrimental to the production of agricultural crops. A key component of sustainable pest management programs is plant breeding and the use of crop varieties that are resistant to attacks by herbivorous insects. Typically, research on crop resistance to insects focuses on average resistance levels in monocultures, but it overlooks the effects of plant trait diversity on insects. This study investigated the consequences of intraspecific trait diversity in juvenile and reproductive tomatoes (*Solanum lycopersicum*) for the performance of an important agricultural pest, the cabbage looper, *Trichoplusia ni*. We hypothesized that exposing larvae to a diet with intraspecific plant diversity would decrease insect growth and survival. *Solanum pennellii* x *S. lycopersicum* (cv. M82) introgression lines (ILs) were used to test larval performance. In trials, we grew caterpillars on constant diets of one or two genotypes or forced caterpillars to switch between genotypes and recorded larval mass. All larvae were moved to fresh leaves every 48 hours regardless of the treatment. Experiment 1 on IL 8-1-1 and IL 2-2 resulted in adequate performance on each line in monoculture, but the caterpillars had low performance when they were forced to switch from one line to the other. Since larvae are often forced to move host plants in response to predator activity and weather events, the switching treatment mimics what happens when larvae move to a neighboring host plant in a field with intraspecific crop diversity. Conclusions from Experiment 2 on IL1-3 and M82 indicated that when given the choice larvae are able to capitalize on behavioral plasticity. Results from Experiment 3 suggests that ILs lose defensive effects based on ontogeny. These results suggest that intraspecific crop diversity could be useful for reducing pest damage. Focusing plant breeding efforts on diversity relevant to insect pests through incorporating intraspecific diversity holds potential for increasing the sustainability of agroecosystems.

The Buzz about Fungi: Factors Influencing Fungal Pathogen Dynamics in a Solitary Bee *Osmia cornifrons*

**Erin Krichilsky**

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Declines in managed and wild bees threaten both ecosystem function and agricultural productivity. Bee declines are thought to be caused by multiple interacting factors including loss of floral resources, pesticides, and pathogens. Yet, few studies have explored these factors with respect to solitary bee species or their interactions with fungal pathogens. Here we explore the impact of landscape composition and pesticide exposure on the prevalence of the bee-associated
fungi *Ascosphaera* in nests of the managed solitary mason bee *Osmia cornifrons*. The aim of this study is to shed light on the factors that possibly interact to influence host-pathogen dynamics in a solitary bee. We hypothesize that synergistic effects of landscape and pesticides will have a larger effect on pathogen prevalence than either factor individually. To test our hypotheses *O. cornifrons* nests were collected from 17 apple orchards, which varied in surrounding landscape composition and pesticide use. Phylogenetic analyses of *Ascosphaera* sequences amplified from both healthy adults and infected larval cadavers revealed the presence of both pathogenic and saprophytic *Ascosphaera* species. Of five different surrounding landscapes at four different radii, open natural habitat at 500 meters was the only type found to have an impact on *Ascosphaera* prevalence. Of four different pesticide classes, orchards with the highest measures of fungicide toxicity were positively associated with larval mortality due to *Ascosphaera* infection. In addition, fungicide toxicity was negatively associated with *Ascosphaera* prevalence among adult bees. We also found evidence of an interaction between landscape and fungicides whereby *Ascosphaera* prevalence in adults decreased most in orchards with high amounts of surrounding urban habitat. We further explored the potential for fungicides to increase *Ascosphaera* mortality by rearing larvae in the lab and feeding them varying diets. Our experimental study revealed an additive effect of fungicides on *Ascosphaera* infection rates. Our results underscore the importance of studying interactions among factors associated with bee decline and improve our ability to predict outcomes for bee health leading to more sustainable delivery of ecosystem services.


KRISTIANNA M. LEA

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The white-eyed assassin bug, *Platymeris biguttatus* (Hemiptera:Reduviidae), injects a potent toxin into its prey. I performed a series of behavioral and neuropharmacological tests to characterize the effects of the saliva’s neurotoxic components, after previous work in our lab established a stereotypic bite pattern of prothorax, head, then abdomen. Biting the pleural membrane of T1, the prey is rapidly immobilized within 30sec. There is a spatio-temporal sequence of paralysis of thoracic legs and mouthparts, supporting the hypothesis that the bug injects saliva into the hemocoel. After the T1 bite, the bug bites and feeds from the cockroach’s head. “Milking” the bug to collect saliva and reconstituting it to known concentrations allowed production of a dose-response curve (LD50 306 mg/kg). Injection of milked saliva and contents of the posterior lobe of the principal salivary gland reproduced the same paralytic and time-course effects as natural bites. Proteinase K-digested saliva had little effect, revealing that the neurotoxin is likely a protein or peptide. After a natural bite, or injection to T1, the legs and mandibles were paralysed in tonus; the cockroach no longer responded to cercal air-puffs. However, the giant fibers of the abdominal ventral nerve cord still responded briskly as recorded
electrophysiologically, dying after many minutes when the venom percolated to the abdomen. Activity ceased more rapidly with direct application to the abdomen. Recording spiking activity of the anterior leg nerve in T1 with salivary application revealed increased firing followed by nerve death, similarly timed to the paralysis of the legs measured behaviorally.

The Interplay of Fungal Species and Insect Herbivory on the Growth, Defense, and Mycorrhizal Colonization of Tomato Plants

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Arbuscular mycorrhizal fungi are widespread plant mutualists that can have impacts on many aspects of plant biology, including nutrition and defense. These fungi can be affected by stressors on their host plants, such as herbivory, which can lead to changes in root colonization levels of the fungus. Mycorrhizal fungi are diverse, and fungal species can differ in the benefits that they provide to their host plants, as well as their tolerance to host plant stress. In this study, we compare the benefits provided to plant growth and defense by three species of mycorrhizal fungi, and relate these benefits to the ability of each fungal species to withstand stressors on their host. We grew these fungi with Solanum lycopersicum plants under normal conditions and under conditions of simulated insect herbivory using jasmonic acid application, and measured plant growth and chemical defenses. Fungal root colonization was also measured across treatments. We found that Rhizophagus intraradices had higher colonization levels and produced plants with greater biomass than the other two fungal species, Acaulospora morrowiae and Claroideoglomus etunicatum. Fungal species did not differentially affect the level of defenses in the plant or the performance of insect herbivores. In addition, all fungal species experienced decreased colonization levels under simulated insect herbivory. The results of this study suggest that differences in benefits between mycorrhizal fungi species may be mainly nutritional in nature, and that different species of fungi may not differ in their effects on plant defenses or in their ability to tolerate host plant stress.

CYP6A17 Metabolizes Methyl Parathion in Drosophila melanogaster

LAURA TELFER

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Cytochrome P450-dependent monooxygenases (CYPs) are enzymes responsible for the metabolism of endogenous and xenobiotic compounds in virtually all living organisms. CYPs play an essential role in enabling insects to defend themselves against insecticides. The findings of a recent study suggest that CYP6A17 may play a role in the metabolism of deltamethrin, a
pyrethroid insecticide (Scott et al. unpublished). The objective of this study is to determine the role of this CYP in the metabolism of various insecticides in *Drosophila melanogaster*. Bioassays were used to determine the toxicity of eight insecticides. The results of this study indicate that CYP6A17 may detoxify methyl parathion. This CYP is capable of metabolizing an array of substrates with different structures. Thus, it is evident that CYP6A17 has a broad substrate specificity. These findings can be used to inform future studies about the substrate specificity of individual CYPs.
Internal and External Phosphorus Loading in Oneida Lake: Implications for Oneida Lake Algae Bloom

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Phosphorus (P) is a limiting nutrient in many lakes and an important factor determining water quality. In some lakes, internal phosphorus loading can contribute more P than external loading, and both external and internal loading may be pulsed in time. The timing of this P pulse can drive the timing of algal blooms. In contrast to stratified lakes where internal loading occurs during the fall mixing, internal loading can happen throughout the year in shallow, polymictic lakes. However, the timing and magnitude of internal P loading is difficult to measure. In this thesis, a mass balance approach is applied for calculating internal P load based on the difference between external P loading from input streams, P leaving the lake with the outflowing water, and accumulations of P in the water column over the period from June 1st to September 30th. This method requires accounting for the water budget, including evaporation and precipitation to the lake. I applied this method to Oneida Lake, a large polymictic lake in New York State, and an important resource for the local economy. External P loading was estimated using the USGS gauges available from the major discharge streams adding water input from ungauged streams based on the relative watershed area that were not gauged. Phosphorus concentration in the inflowing water was measured weekly at 4 in-stream sites close to the lake. Lake P content was measured at 4 sites in the lake. Outflowing water was also gauged by USGS and assumed to have the same P concentration as the average in the lake. Water budget showed that additional ungauged areas and/or groundwater was around 15% of the total inflow in 2017 summer. The P budget calculations indicated four major increases in internal P loading in the summer of 2017 (June 5th, July 24th, August 21th to August 28th). Internal P loading exceeded the external P loading during the summer of 2017x by a factor 2. The late summer increase in internal P loading was correlated to algae bloom formation although the first blue-green bloom of the year followed a pulse in external P loading.

Soil Microbial Enzyme Activities after Five Years of Annual Nitrogen and Sulfur Fertilization in a Temperate Mixed Deciduous Forest

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Atmospheric nitrogen added to natural ecosystems from anthropogenic activities may exceed background deposition. Because nitrogen is a key nutrient and can acidify forest soils, understanding the impacts of additional deposition is crucial. Here I examined shifts in microbial enzyme activity in response to five years of annual nitrogen and sulfur fertilization in a
temperate mixed deciduous forest in Ithaca, New York, USA. Prior research on deciduous forest soils suggested increased activity of glucose, phosphorus, and nitrogen-acquiring enzymes, whereas added nitrogen decreased activity of enzymes that break down low-quality lignin. Soils were extracted from the top 20 cm and analyzed using spectrophotometric and fluorometric enzyme assays. Results revealed that added nitrogen and sulfur did not influence enzyme activities. The results suggest that other factors influencing soil enzyme activities include plant-microbial interactions, the importance of other key nutrients such as phosphorus, shifts in microbial communities, and mineral interactions. An understanding of the multiple ways in which nitrogen deposition alters microbial enzyme activity, soil organic matter decomposition, and nutrient cycling will provide a more complete understanding of the anthropogenic impacts on forest soils and forest ecosystems.

The Potential for Nutrient Loading through Groundwater Seepage in Oneida Lake, New York

JACQUELINE M. DOERR

Under the supervision of Dr. Rebecca L. Schneider
Department of Natural Resources

A comprehensive understanding of a lake’s hydrology, including the often overlooked component of groundwater flux, is needed in order to understand sources for nutrient loading to aquatic systems. In particular, external nutrient inputs are hypothesized as key contributors to harmful algal blooms. Oneida Lake is a large, shallow, mesotrophic lake in upstate New York, an ideal system for studying lakeshore groundwater seepage. We investigated the potential for nutrient loading through groundwater to the overall nutrient budget of Oneida Lake using seepage meters and porewater samplers. We evaluated spatial and temporal patterns of seepage flux along a 550 m stretch of shoreline over five months, and explored the potential relationships between nitrogen and phosphorus concentrations, seepage flux rate, and dissolved oxygen concentrations. We also evaluated the potential for adjacent land use to influence groundwater nutrient loads by comparing seepage among three broad land class types: fields, forested wetlands, and residential sites. We found a clear, temporal correlation of seepage flux with precipitation events and an overall decrease in seepage throughout the study period. The highest concentrations of dissolved phosphorus occurred in seepage associated with the shoreline homes. There were significant correlations between ammonium, phosphate, and dissolved oxygen concentrations, providing insights into the underlying processes driving nutrient dynamics in groundwater. Extrapolating from the average phosphorus concentrations in this study, Oneida Lake’s entire 88 km long shoreline could potentially be contributing as much as 485 kg of phosphorus in a single year from groundwater seepage alone. Clearly, groundwater can be an important contributor to nutrient loading and management actions need to address not only surface flows entering Oneida Lake but also subsurface flows when considering how to reduce the magnitude and frequency of harmful algal blooms.
Investigating Blue-Green Algae in Oneida Lake: Methodological Strengths and Weaknesses

SOPHIE A. HEARN

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Department of Natural Resources

In freshwater bodies, harmful algal blooms (HABs) are caused by cyanobacteria or “blue- green algae.” In this study, I investigated the advantages and disadvantages of different algal enumeration methods, to improve our ability to monitor blue-green algae on Oneida Lake. I focused on particle counts, biovolume calculations, and measurements of chlorophyll-\(a\) as quantifying units. Data was collected at the Shackelton site on Oneida Lake from May through September 2017 and analyzed at the Cornell Biological Field Station. Particle counts by genus were performed using microscopy and a FlowCAM\textregistered. Chlorophyll-\(a\) was measured on filtered water using the acetone-extraction technique, and in-situ using a Hydrolab Datasonde 5 and a FluoroProbe\textregistered. Manual and FlowCAM counts were strongly correlated (R\(^2\) = 0.72) showing good data intercompatibility, but FlowCAM counts were consistently lower than manual counts. Particle counts also revealed that blooms over the summer period were dominated by the genera Anabaena, Aphanizomenon, and Microcystis. Biovolume calculations and FluoroProbe chlorophyll were weakly correlated (R\(^2\) = 0.15), but FluoroProbe and extracted chlorophyll measurements were strongly correlated (R\(^2\) = 0.92), with a slope not significantly different from a 1:1 line. The Hydrolab Datasonde 5 did not give reliable values and was not correlated with either the extracted chlorophyll (0.02) or the FluoroProbe (R\(^2\) = 0.05). This may be due to quenching. Overall, the particle counts allowed the identification of major genera in algal blooms across the 2017 summer season, while the chlorophyll-\(a\) data provided a picture of phytoplankton community composition (FluoroProbe) and density at the Shackelton site on Oneida Lake.

Response of Ecosystem Nitrogen Following the Removal of Ungulates in Tropical Dry Forest Ecosystem in Hawaii

YUNG-YI LAN

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Common management practices for restoration and conservation of degraded ecosystems often involve the removal of non-native ungulates. In the Pacific Regions of Hawaii, non-native ungulates have been introduced for centuries and they have a large impact on native biodiversity, structure and function of native ecosystems. Studies have shown that without proper management and population control, these non-native ungulates could extirpate native taxa and facilitate exotic plant invasions, yet the underlying ecosystem processes of the impacts exerted by these ungulates on soils and nutrient cycling and availability have not been discussed widely.
We evaluate the effects of non-native ungulate removal on sites in Tropical Dry Forest, found on Department of Defense (DoD) military installations at Pōhakuloa Training Area. The objective is to quantify changes in ecosystem Nitrogen (N) to better understand how ungulate removal affects key underlying ecological processes with respect to time, and the implications in terms of management strategy for promoting native plants. Although we observed some trends towards responses of soil and plant N to removal of ungulates, the only statistically significant result was a strong decrease in soil N2O emission with time since ungulate removal. We also observed an unexpected switch in plant 15N enrichment in a non-native herb “phytometer” between shrubland and woodland, suggesting inherently different N cycling processes in these two vegetation types.

The Correlated Respiratory Health Impacts of Exposure to PM2.5 – With Application to Diplomats Serving at the U.S. Missions to Beijing and Shanghai, China

OLIVIA A. MESZAROS

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Particulate Matter 2.5 has been connected to cardiorespiratory distress in studies conducted by the U.S. Environmental Protection Agency and independent research. This correlation has prompted the EPA to establish National Ambient Air Quality Standards as a public health safeguard for U.S. residents. American diplomats serving abroad are not under these protections and can be exposed to dangerous levels of particulate matter for the duration of their service. This exposure could result in lasting and negative health implications. This paper examines the correlated impacts of long and short-term exposure to PM2.5 and applies them in the form of recommendations to the U.S. State Department for posting Foreign Service Officers in Beijing and Shanghai, China.

The Effect of Round Goby invasion on Piscivory and Growth Rates of Young-Of-Year Largemouth and Smallmouth Bass in Oneida Lake

IMAN PAKZAD

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As a recent invasive species in the Laurentian Great Lakes region, the potential impacts of the round goby (Neogobius melanostomus) on young piscivores are still unclear. Since a high piscivory rate is strongly tied to growth and survival of young-of-year (YOY) piscivores, we examined the diets and growth of YOY largemouth bass (Micropterus salmoides) and smallmouth bass (M. dolomieu) before and after the arrival of goby in Oneida Lake, New York. Goby comprised 10% and 70% of identifiable fish consumed by largemouth bass and
smallmouth bass respectively. Growth of largemouth bass did not change in response to availability of gobies. For smallmouth, incorporation of gobies into YOY diets was correlated with significant increases in success in piscivory and increases in growth. Improved growth may lead to increased survival of YOY smallmouth bass and increases in the smallmouth bass population.

Performing the Environment: An Inquiry into Eco-Shakespeare

JACK PRESS

Under the supervision of Shorna Allred
Department of Natural Resources

Wrestling with the dilemma of anthropogenic climate change forces us as social scientists to work in an interdisciplinary manner and learn from other fields of study in order to identify methods for generating positive environmental behavioral change. This study aims to develop an understanding of how ecologically motivated Shakespeare productions can create opportunities for positive environmental attitude changes amongst audience members. Literature related to green theatrical practices and ecocritical readings of Shakespearean texts was reviewed in order to gain a better sense of current trends in eco-Shakespeare studies. Interviews with theatre artists and Shakespeare academics yielded a strong consensus that the challenges in mounting impactful eco-Shakespeare productions lie in effectively finding the environment within the human story and in demonstrating the human-environmental relationship in creative ways that do not take away from the emotional human-centered narrative. Currently, eco-Shakespeare productions are done in largely community-oriented settings. Two eco-Shakespeare productions, one at La Trobe University in Australia and the other at Montana State University in the United States, are critically analyzed for how they render ecological concepts on stage for effective audience engagement. The study defines a conceptual framework that lays a roadmap for a production company or theatre artist that seeks to produce a Shakespeare production that deals with ecological themes with the aim being to induce environmental attitude change amongst audience members. Ultimately, more research into the development of an eco-Shakespeare based pedagogy is necessary in order to develop a more robust set of norms for producing eco-Shakespeare productions.
Microplastics Consumption, Electivity Indices, and Coefficient of Condition of Fish in the Hudson River

M. GRAY RYAN

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There is growing concern surrounding microplastics in the aquatic environment and their effect on the health of organisms, especially since there is evidence that a variety of aquatic animals consume plastics. This is of particular concern for organisms whose main food source is zooplankton, many of which fit into similar size categories as microplastics. However, our understanding of whether fish consumption of microplastic is intentional or not is limited. There is also limited understanding on how intentional consumption of microplastics affects fitness. To answer these questions, the fitness and degree of selective feeding on various categories of microplastics were determined and compared for a sample of 108 fish collected from the Hudson River. Microplastics made up around 10% of the >335 micron portion of fish diets and around 20% of the same size category in the water sample from the Hudson. Our results revealed selective feeding on zooplankton and avoidance of all microplastic types and all microplastics colors, with the exception of tan. There was no correlation between degree of selectivity toward any particular food types and fitness.

Understanding Response of Peatland Vegetation to Atmospheric Pollution in Northern Ontario, Canada Using Paleoecological Techniques

VIOLA YU

Under the supervision of Joseph Yavitt
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The region around Sudbury, Ontario, Canada experienced a history of metallic pollution that demolished surrounding peatland ecosystems, but how their vegetation has responded has not been studied. I examined peat cores taken from impacted and not impacted (reference) sites around Sudbury to investigate pre- and post-pollution vegetation composition. Utilizing loss-on-ignition (LOI) and macrofossil analysis I determined the presence of vegetation regime shifts in two of the impacted sites (Garcon and Long Lake) but not in the third impacted site, Laurentian University. The sedge-dominated peatland at Garcon site transformed to a peatland dominated by Sphagnum and ligneous materials. The ligneous-dominated peatland at Long Lake site transformed to a Sphagnum-dominated vegetation and later to a brown moss-dominated vegetation recently. This suggests that air pollution has impacted the plant community dynamics.
Food Apartheid: A Radical Approach to Food Accessibility on the South Side of Chicago

DEJAH POWELL

Under the supervision of Rachel Bezner Kerr
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Much scholarly research has been conducted across the nation looking at the effects of food deserts on both rural and urban communities. Many solutions to the problem of food deserts and food insecurity seek to attract supermarkets, grocery stores and other outlets that increase residents accessibility to food. I sought to take another approach, looking at food accessibility in Chicago through a more radical lens. Drawing on interviews collected from residents of Chicago and historical text accounts, I examine the question of what is the underlying reason and motivation for the food apartheid conditions that exist on the South Side of Chicago? My findings suggest that the food environments and accessibility at present were not haphazard, or naturally occurring as suggested by the usage of the term “food deserts”. Rather, they rather were intentionally created and crafted and capitalism, racism and federal policy were main tools used to perpetuate such an environment. These findings, on the root causes behind food apartheid, a system that creates food opulence for some and food dearth for others, provide a roadmap for those changemakers in the future who are truly invested in radically solving issues of food accessibility not only in Chicago but also across the country.
ReOccupyng the Rubble: Typologies + Spaces of Resistance in the West Bank

JACOB L. KUHN

Under the supervision of Jamie Vanucchi
Department of Landscape Architecture

The central design questions of this project are: what can be done with the rubble from demolished structures in the West Bank, and what potential does this material have for the creation of new structures? Additionally, what design moves can be made using the rubble as the main material? Initial research began with mapping the West Bank and a spatially analyzing Palestinian and Israeli settlements using modeling and algorithmic software like Rhino and Grasshopper to study boundaries and calculate areas. Further research was done through photo collaging to understand the experience and materiality of the landscapes adjacent to the wall that separates Israel and the West Bank. The goal is to ultimately design typologies for rubble that can be implemented along the wall to create spaces of resistance for Palestinians. These spaces can be used for hiding from Israeli surveillance, seeking shade, setting up informal markets, or instigating conversation. These design investigations were supplemented with writings of historians, social geographers, and architects, including Lefebvre, Foucault, Edward Said, and Eyal Weizman, to understand the power inherently tied to the production of space. This project also draws connections across space and time to evaluate how power must always be considered and shared in the design process.

Entangled Landscapes: Designing with a Multi-Species Perspective in the Post-Industrial Syracuse Inner Harbor

TREVAN A. SIGNORELLI

Under the supervision of Jamie Vanucchi
Department of Landscape Architecture

Pollinator species are extremely important for food security and drive the agricultural economy, but are in decline primarily due to habitat fragmentation and the effects of climate change. Rust Belt cities like Syracuse have suffered from social and economic decline, and the primarily post-industrial landscapes lack pollinator habitat. By understanding the entanglements of economy, technology and species interactions, it’s possible to see cities like Syracuse playing a key role in developing a productive green economy. How can analyzing landscapes from pollinators’ perspective give insight into how to rethink the way landscape architects design for the benefit of multiple species? And how can this lead to the creation of landscapes that benefit both people, other species and the environment? Designers must move away from the typical anthropocentric design methods and explore new techniques for altering the landscape. This thesis is experimenting new methods of site analysis and design with the goal of embracing the entanglements and allowing for multi-species engagements to create a sustainable and productive landscape.
Changes in Spatial Extent of Extreme Rainfall Events Area in the Northeastern U.S. Using High Resolution Gridded Data Sets

THOMAS M. FAVATA

Under the supervision of Arthur DeGaetano
Department of Atmospheric Science

Using several high-resolution gridded daily precipitation datasets, the temporal change in the annual total geographic area (km²) receiving extreme precipitation is analyzed. Extreme precipitation events are defined by unique (separated by at least 10 km) closed 5.08 cm contours as defined by the contour function in Basemapper. The numpy convexhull procedure is used to compute the area enclosed by each contour. Analyses are repeated for three datasets, 1) simple nearest neighbor interpolation of station data, 2) PRISM and 3) the satellite-based PERSIANN-C DR.

There is significant increase in the extreme precipitation area, with quantile regression analysis showing strong positive trends across all quantiles using the station data based nearest neighbor interpolation. With PRISM, the inclusion of radar data after 2002 introduces a discrepancy in the data record that substantially increases the number of events in the lowest quantiles. Prior to this artificial break (1981-2001), trends in the central quantiles (events on the order of 10² kilometers squared) showed significant increases. The results indicate that the spatial extents of extreme precipitation events, particularly in mid-sized quartiles, are noticeably increasing temporally.

Cross-Cultural Examination of a Product of Differing Familiarity (Hard Cider) by American and Chinese Panelists Using Rapid Profiling Techniques

SIERRA MARI R. JAMIR

Under the supervision of Robin Dando, Ph.D.
Department of Food Science

This study investigated the cultural differences in characterization of craft and commercial hard ciders between American and Chinese consumers, two markets reporting notably different cultural experiences regarding hard cider. Two untrained panels assessed their perception of hard cider samples (two commercial, five craft hard ciders, one additional blind duplicate) through multiple free sorting (MFS), grouping samples based on similarities multiple times, and flash profiling (FP), ranking samples based on attributes generated during ballot creation. A multiple factor analysis (MFA) for MFS and General Procrustes Analysis (GPA) for FP showed that the sensory maps produced by the groups were fairly similar, except that more variability was noticed in the Chinese group. Additionally, the American group was better at differentiating cider samples, employing more sophisticated descriptors for aroma and flavor (e.g. nutty, onion, oxidized, robustness, yeasty) and describing complex mouthfeel attributes (e.g. carbonation, viscosity, and roughening). American panelists used 1.4 times more terms than Chinese
panelists, who used mostly basic flavors, tastes, hedonic terms, and comparisons to describe varying sensory experiences. A lack of exposure to hard ciders in the Chinese group, combined with a lack of standardized wording for ciders may explain why less discriminability was perceived between products, whereas the American group was more comfortable utilizing terms common to the wine, beer, and apple industry. Understanding these cultural differences and the methods used to conduct cross-cultural sensory research, therefore, may be of great importance to cider makers, as the industry moves towards developing a standardized vocabulary for hard cider evaluation.

Analysis of *Alicyclobacillus* Growth in Apple, Orange, and Grape Juice via Standard Plate Counting and Guaiacol Spectroscopy

**ETHYN K. LEONG**

Under the supervision of Randy W. Worobo
Department of Food Science

The *Alicyclobacillus* genus is comprised of non-pathogenic, gram positive, aerobic, spore forming bacilli species capable of growing in acidified beverage products. This organism’s acidophilic nature has made it a recent concern in the fruit juice industry, due to their ability to produce a pungent spoilage flavanoid, guaiacol. Originally colonized in soil, *Alicyclobacillus* enter the fruit juice production chain through fruit and sugar ingredients. Upon germination, *Alicyclobacillus* metabolize ferulic acid to guaiacol through various decarboxylation pathways. Shelf-stable fruit juices are of particular concern, as their lack of bacterial growth inhibitors create ideal conditions for *Alicyclobacillus*. The purpose of this study was to investigate the growth rates of *Alicyclobacillus* in apple, grape, and orange juices, along with resulting spoilages by guaiacol, to determine whether or not companies would be able to identify the level of juice spoilage based on *Alicyclobacillus* levels. Cell growth rate was measured by inoculating store-bought shelf stable grape and orange juice, and study-made shelf stable apple juice, and quantifying *Alicyclobacillus* levels. Guaiacol content was measured by inoculating Potato Dextrose Broth (PDB) acidified with malic, tartaric, and citric acids, and quantifying concentration by UV-vis spectroscopy calibrated to 470nm; acidified PDB was used because juice pigments may absorb at the same wavelength. After weekly measurements for five weeks, it was observed that guaiacol production steadily increased, despite cell population decrease, indicating an inverse relationship between the two variables. The initial *Alicyclobacillus* population in juice products appears to be more important than the growth kinetics, and should be used as a means to anticipate the extent of spoilage due to guaiacol production.
Changes in Extreme Precipitation Area Frequency in the Northeastern U.S. Using High Resolution Gridded Data Sets

GRIFFIN S. MOOERS

Under the supervision of Dr. Arthur T. DeGaetano
Department of Earth and Atmospheric Sciences

This study relied on several high resolution gridded daily precipitation data sets to analyze the number of extreme precipitation areas over the Northeastern U.S. An extreme precipitation area is defined by unique (separated by a minimum of ten kilometers) closed 5.08 centimeter contours as defined by the contour function in the Basemapper module from Matplotlib. The built in ‘get paths’ and ‘vertices’s’ functions were used to help define area enclosed by each contour. This analysis is performed on the PRISM dataset, the satellite derived PERSIANN-CDR dataset and simple nearest neighbor interpolation of station data. Station and grid point data are used for comparison and analysis.

A distinct increase in the frequency of extreme precipitation areas at a given point location according to the gauge and gridded point data replicated the findings of previous studies. These increases were generally statistically significant, though there was variation in confidence levels between sub-regions and time frames. In terms of frequency of extreme precipitation areas over the whole Northeastern U.S., the high resolution gridded data show a steep decline over the time frame with the exception of the Parameter-elevation Regression on Independent Slope Model (PRISM) dataset. With PRISM, the inclusion of Radar data after 2002 cause an increase in the frequency of extreme precipitation areas detected in the data. The results show that while a given point in the Northeastern U.S. is more likely to see extreme precipitation, the absolute number of areas of extreme precipitation in the region is declining.

Exploring the Impacts of Electricity Generation Composition on the Future Climate

CLAYTON R. S. SASAKI

Under the supervision of Peter G. Hess
Department of Biological and Environmental Engineering/Earth and Atmospheric Sciences

Many studies have talked about natural gas "bridging" as a path to a more sustainable future. Increased interest in the use of natural gas as a "transition" fuel over the last decade or so has spurred many studies into the leak rate of natural gas when used as a source of electricity. This study aims to answer questions about the usefulness of natural gas "bridging" on varying time scales; namely, would a natural gas "bridge" really lead to a lower overall peak temperature? Would it lead to reduced rates of warming? And would it lead to lower long-term temperatures? Societal and economics questions are also discussed such as whether building these natural gas "transition" plants could backfire, slowing down the transition to renewables? With the aim of
answering these questions, a simplified atmospheric climate model was created using the Absolute Global Temperature Potential metric along with equations for life cycle emissions of coal and natural gas plants. Approximate carbon emissions and global temperature changes were simulated from IGSM future electricity production estimates as well as scenarios based upon projections of fully renewable years. Results show that assessing the use of natural gas bridging is very dependent on the metric chosen to minimize: peak temperature, rate of temperature change or long-term temperature. A transition to natural gas with a moderate-high leak rate would likely lead to increased rates of warming in the short-term, no matter the rate of change to renewable energy. While the benefits of natural gas bridging at lower leak rates appear minimal with conversion to renewables in this century, they are larger at longer time periods.

Quantification of Projected Future Changes in Stratosphere-Troposphere Exchange (STE) Ozone Fluxes

FRANK L. TIAN

Under the supervision of Peter Hess
Department of Earth and Atmospheric Sciences

In this study, three different model simulations—General Circulation Model (GCM), Community Atmospheric Model version 4 with chemistry (CAM4-Chem) under the Reference Simulation C2 (REF-C2) simulation protocol (referred to as REFC2 in this paper) and Whole Atmosphere Community Climate Model under the REF-C2 simulation protocol (referred to as WACCM)—were used to quantify the yearly global flux of O₃ into the troposphere via stratosphere-troposphere exchange (STE) for the present and future time periods. The GCM simulation assumes changing CO₂ concentrations under REF-C2 specifications with emissions of other greenhouse gases and ozone precursors held constant at the year 2000 levels specified in the CMIP5, while the REFC2 and WACCM simulations assume time-changing concentrations of CO₂ as well as other greenhouse gases. REFC2 and GCM are low-top model simulations with lower vertical resolution, while the WACCM is a high-top model simulation with higher vertical resolution and more comprehensive stratospheric chemistry. In all three models, the present-day STE is in agreement with the accepted range of STE O₃ values produced in previous studies. The GCM simulations showed the smallest increase in yearly global STE O₃ flux from present to future—a 8.62% increase from 383 ± 151 Tg yr⁻¹ to 416 ± 174 Tg yr⁻¹. In comparison, the REFC2 simulations saw a 34.13% increase in yearly global STE flux from 375 ± 139 Tg yr⁻¹ to 503 ± 175 Tg yr⁻¹. Similarly, the WACCM simulations showed an increase of 32.56% from 390 ± 137 Tg yr⁻¹ to 518 ±169 Tg yr⁻¹. The results show that future changes in CO₂ alone do not significantly increase the flux of global STE across all months. However, simulations with future changes in CO₂, emissions of other greenhouse gases and ozone precursors does show significant future increases in STE for every month. In general, the REFC2 and WACCM simulations showed a greater degree of agreement in future changes of the monthly distribution of global STE O₃ flux values than either had with the GCM simulations. However, more research is needed to elucidate the causes for significant difference between the simulations.
Summary: Three different model simulations were used to quantify the yearly global flux of ozone into the troposphere via stratosphere-troposphere exchange (STE) for the present and future time periods. The results show that future climate forcings due to changes in CO2 alone do not significantly increase the flux of global STE across all months but in simulations with future changes in CO2, emissions of other greenhouse gases and ozone precursors do show significant future increases in STE ozone flux for every month.
Role Elucidation of Terpene Synthase TPS2 in Maize-Aphid Defense

CAIRO M. ARCHER

Under the supervision of Dr. Georg Jander
Section of Plant Biology, School of Integrative Plant Science

*Zea mays* produces volatile compounds that contribute to a variety of biochemical defense mechanisms aimed to combat insect herbivory. A specific volatile-producing enzyme, a terpene synthase, TPS2, was found to exhibit a significant genetic up-regulation in maize inbred line B73 in response to *Rhopalosiphum maidis* (corn leaf aphid) feeding and chemically mimicked caterpillar herbivory. These findings indicated the potential involvement of TPS2 in maize-insect defense. Somewhat surprisingly, *R. maidis* grew less well on a *tps2/3::Ds* mutant line. Based on this observation, it was hypothesized that TPS2 primary products are not aphid deterrents, but aphid attractants. Subsequently, the suppression of these attractants with the knockdown of the TPS2 gene alters the preference feeding behavior of *Myzus persicae* (green peach aphid). Choice determined general preference between the TPS2 knockout line *tps2/3::Ds* and maize parental inbred line W22. Olfactory assays identified whether volatile primary products of TPS2 activity, linalool, (E)-nerolidol, and (E,E)-geranyllinalool, serve as attractants for *M. persicae*. Finally, electrical penetration graph (EPG) analysis highlight differences in *M. persicae* feeding patterns between wild type maize and *tps2* mutants. It was found that aphids exhibited a choice in favor of wild type W22 over *tps2/3::Ds* (p=0.08), and more data collection would increase the validity of these conclusions. Olfactory assays indicated that (E)-nerolidol acts as an aphid attractant (p=2.1*10^-7) with (E,E)-geranyllinalool potentially serving as an attractant as well (p=0.21). EPG analysis was somewhat inconclusive, indicating that the role of TPS2 in maize-aphid defense rooted in aphid attraction and less so in aphid feeding behavior.

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Plant and Pathogen Wars Outside the Cell: The exDNA/exDNase System

ZERAN LIN

Under the supervision of B. Gillian Turgeon
Section of Plant Pathology and Plant-Microbe Biology, School of Integrative Plant Science

DNA is considered as hereditary material that is normally found in nuclei and other cellular organelles. This view of DNA as intracellular was radically altered with the discovery that DNA can be secreted by mammalian neutrophils and by plant cells as a defense mechanism against invading pathogens. Secreted DNA, along with other molecules, forms extracellular DNA (exDNA) traps to confine pathogens. As counter-defense, pathogens can produce enzymes (exDNases) that degrade the trap. Pathogens are then released and can continue to infect the host. In previous studies, one exDNase (protein ID 144206), of seven that were tested, was proven to be a virulence factor of the maize pathogen, *Cochliobolus heterostrophus*. A genome survey indicated that additional candidate exDNase-encoding genes are present in this
In this study, we constructed mutants lacking another candidate (ID 197632) and screened them for alterations in virulence and for exDNase activity as compared to wild-type. Using the same approaches, we created mutants of the oat pathogen, *Cochliobolus victoriae*, lacking the ortholog (ID 113105) of *C. heterostrophus* protein 144206 and are currently examining whether the protein functions similarly in a different fungal species that is pathogenic on a different host. In addition to the exDNase experiments, we adapted the CRISPR/Cas9 system to *C. heterostrophus* to facilitate site-specific gene targeting in future research. A gene responsible for melanin synthesis, *PKS18*, in *C. heterostrophus* was selected as target because mutants are easily identified (albino) by visual inspection. Using CRISPR/Cas9, we successfully generated albino mutants using two individual protospacer sequences (protospacer-1 and protospacer-2). More mutants edited for protospacer-1 were obtained than for protospacer-2. Although there was some variation, the types of mutations were more consistent in mutants edited for protospacer-1 (mostly point insertions), than for protospacer-2, which caused large deletions of different size.

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**Phenotypic Variance and Disease Aggressiveness Caused by *Fusarium graminearum***

**JAMES WINANS**

Under the supervision of Gary Bergstrom
Section of Plant Pathology and Plant-Microbe Biology, School of Integrative Plant Science

*Fusarium graminearum* is a pathogenic fungus that is economically important to the production of wheat (*Triticum aestivum*) and barley (*Hordeum vulgare*), and colonizes wild grasses asymptptomatically. Thirty-eight isolates collected from either wheat or grass heads were assessed for several different phenotypes. Wheat-host isolates were significantly more successful than grass-host isolates in causing fusarium head blight (FHB) on wheat hosts in greenhouse trials (*P*<.05). The chemotype of an isolate had no significant effect on its mycelia growth, perithecia formation, or disease aggressiveness. Visual disease ratings in the greenhouse significantly correlated with fusarium damaged kernels (FDK) found after harvest. Spatial correlation tests among 19 isolates showed no significant correlation for any measured phenotypes. A trend was found that increased mycelia growth over five days correlated with decreased perithecia formation (*P*=.054) and warrants further research.
Assessing the Gendering of Food Journalism: A Critical Content Analysis of the New York Times

AMANDA M. WAHLSTEDT

Under the supervision of Brooke Erin Duffy
Department of Communication

This project seeks to probe the outwardly egalitarian genre of food journalism, taking the perspective that the intersection between gender, journalism, and food has significant implications for societal gender norms. Building upon a pilot study conducted in 2017, this study examined 100 food-driven articles drawn from The New York Times website that were published over a 20-year time period. Fifty articles were written by five male food journalists, and 50 were written by six female food journalists. After conducting a qualitative content analysis using a grounded theory approach, this study indicated that male and female food journalists both challenge and conform to gender norms. Contrary to previous literature, male food journalists wrote more about food shopping and health, whereas female food journalists stressed the historical and perspective of dishes while presenting themselves as experts. Yet, in terms of style and tone, male food journalists used stereotypically “stronger” language in their writing through frequent uses of humor and anecdotes, along with personal preferences and experimentation with dishes. Female food journalists, meanwhile, avoided such assertions and literary devices, writing from a more collective standpoint and following traditional recipes. These implications speak to the engrained gender stereotypes that food journalists are both challenging and fulfilling. While female food journalists seem to be advertently avoiding typical feminized content – such as health and diet – this study implies that a long history of oppression is reflected in the expressed confidence of female food journalists, resulting in a silencing of their preferences, experiences, and opinions in their writing. Further research is needed on the examination of how gender influences news, outside of content assigned, in order to fully understand the implications of our current gender constructions around journalism and food.
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