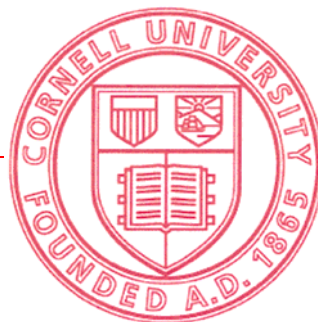


College of Agriculture and Life Sciences

2009—2010

Research Honors Program Abstracts



The College of Agriculture and Life Sciences is considered the best college of its kind in the nation, if not the world. Our mission is to discover, integrate, disseminate, and apply knowledge about agriculture and food sciences, applied social sciences, environmental sciences and the life sciences as a basis for sustainable improvement in the lives of people throughout New York State, the nation, and the world.

Nothing is more critical to the success of the college's mission than an engaged and inspired student body, as exemplified by the students who earn a bachelor's degree with honors. The 2010 honors thesis projects described in this booklet demonstrate an impressive capacity for personal dedication, mature scholarship and intellectual growth. The original research contained in this booklet examines some of the most pressing and relevant questions of our time.

Many students consider the research they undertake as undergraduates in CALS to be the most challenging, enduring, and valuable experiences of their time at Cornell. As a faculty member, I have witnessed this first-hand with my own advisees. As a new dean, I will continue to foster the college's unwavering commitment to undergraduate research.

I am extremely proud of our undergraduate students and their achievements, and I wish them the very best in their future endeavors. I am also proud of the dedicated faculty who supervised these honors research projects and mentored these students to their fullest potential. As you can see from reading the following abstracts, these new graduates will soon take their place among tomorrow's thought leaders.

Kathryn J. Boor, Ph.D.
*The Ronald P. Lynch Dean of
Agriculture and Life Sciences*

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Polymorphism Identification and Association Analysis of *MC4R* and *POMC* Genes

CAITLIN D. ARMSTRONG

Under the supervision of Dr. Samantha Brooks
Department of Animal Science

Identification of horses at high risk for developing laminitis, such as those predisposed to Equine Metabolic Syndrome (EMS), is an essential component of any equine management strategy. Pro-opiomelanocortin (*POMC*) and melanocortin 4-receptor (*MC4R*) are two genes expressed in neurons of the hypothalamus that are involved in the regulation of energy homeostasis in mammalian species. Re-sequencing of these two genes revealed a total of five synonymous SNPS; one in *MC4R* and four in *POMC*. The *MC4R* SNP showed an association with body condition score (BCS) and a significant association with light and dark shades of coat color. Three of the *POMC* SNPs were located in coding regions. All three were synonymous. The last *POMC* SNP was located upstream of the coding region of the gene, and is potentially regulatory. Horses were genotyped for the *MC4R* SNP using Fluorescence Resonance Energy Transfer (FRET) technology and melting curve analysis. New sequence data was generated for *POMC* and four distinct haplotypes were identified within the gene. Comparisons between the protein sequences of the two equine genes and other mammalian species show a high amount of evolutionary conservation. Additional work should focus on elucidating the exact nature of the link between the *MC4R* SNP and coat color, gathering data on more horses to determine if there is statistical significance between the *MC4R* SNP and BCS, as well as work to determine if the regulatory mutation in *POMC* affects transcript copy number in the hypothalamus. Either gene could affect adiposity in the horse, which is a known risk factor for both EMS and laminitis.

Cryopreservation of Bull Sperm in Egg Yolk-Tris Extender: Effect of Low-Density Lipoprotein and Elevated Yolk Cholesterol on Post-Thaw Sperm Motility and Viability

ALLISON M. BAILEY

Under the supervision of Dr. John Parks
Department of Animal Science

Semen cryopreservation has important implications for the propagation of domestic and wild animal populations. Since egg yolk and its lipid components were first discovered to be effective additives for freezing semen, research has focused on understanding the mechanism by which they impart their protective effects. This study evaluated the effectiveness of egg yolk and its low-density lipoprotein (LDL) fraction as bull semen extender components with and without elevation of unesterified (free) yolk cholesterol. The LDL fraction was extracted by ammonium sulfate precipitation. Free cholesterol was elevated within egg yolk by including cholesterol as 1% (w/w) of the laying hen diet. Protein content of whole yolk and LDL was determined using a modified Lowry procedure and assessed further by SDS-PAGE. Phospholipid content was measured colorimetrically and total lipids were fractionated by TLC. The extenders were used to process and freeze semen in 0.5 ml straws in a laboratory trial, which was

replicated with 6 ejaculates. Total sperm motility, progressive motility, path velocity, and lateral head displacement were evaluated post-thaw using an HTM-IVOS semen analysis system. Sperm were also evaluated post-thaw for viability and mitochondrial membrane potential by flow cytometry. Sperm motility parameters and sperm viability were higher in LDL fraction extenders. However, percent polarized mitochondria was not improved with the LDL fraction. Sperm parameters did not differ between extenders with basal or elevated cholesterol content. These results confirm the effectiveness of yolk LDL as an extender component. While elevated cholesterol did not affect the sperm parameters measured in this study, it may still affect the capacitation state of sperm in ways that could positively impact sperm fertility.

Investigating the Role of Soluble Adenylyl Cyclase and Protein Kinase A in Acrosomal Exocytosis in Equine Spermatozoa

MICHELE A. BATISTA

Under the supervision of Dr. Sylvia Bedford-Guaus
Department of Clinical Sciences

Capacitation involves the molecular changes that ejaculated sperm undergo within the female oviduct to become fertilization-competent, and can be achieved *in vitro* by incubating sperm in a defined medium. During this process, sperm gain the ability to undergo acrosomal exocytosis whereby the release of proteolytic enzymes from the acrosome facilitates penetration of the oocyte vestments at fertilization; this is often used as a marker of capacitation. This study aims to investigate the signal transduction pathway leading to acrosomal exocytosis in stallion spermatozoa, particularly the role of soluble adenylyl cyclase (SACY) and protein kinase A (PKA). In order to clarify their function in supporting this event in stallion sperm, we use the SACY-specific inhibitor KH7, and the PKA-specific activator 3'-5' cyclic adenosine monophosphate (cAMP) analog SP6. We add these agents to sperm incubated in capacitating conditions and compare rates of acrosomal exocytosis with those achieved after the addition of the agonists calcium ionophore (CaI) or progesterone, or control dimethyl sulfoxide (DMSO). First, it was determined that inhibiting SACY has no effect on rates of acrosomal exocytosis when the inducer is CaI, but partially reduces rates when the inducer is progesterone, albeit not to control levels. The results suggest that some cAMP production by SACY is required for acrosomal exocytosis under physiological conditions, but there may be multiple pathways involved. Next, it was found that stimulation of PKA by a cAMP analog resulted in rates of acrosomal exocytosis sperm higher than rates achieved with DMSO, suggesting that it is a PKA-dependent process.

Identification and Culture of Primordial Germ Cells and Somatic Cells from Undifferentiated Embryonic Chick Gonads and Formation of Presumptive Embryoid Body Precursors

ADRIENNE M. CHAN

Under the supervision of Dr. John Parks
Department of Animal Sciences

Primordial germ cells (PGCs) are pluripotent stem cells and exist as embryonic precursors to germ cells in vivo. PGCs have been shown to differentiate into embryonic germ (EG) cells which can aggregate to form embryoid bodies (EBs) in vitro. EGs within EBs are capable of differentiating into a variety of cell types; thus EBs can be useful for generating large numbers of stem cells for regenerative medicine. The objectives of this study were to harvest and culture primordial germ cells from indifferent gonads of the embryonic domestic chick and assess factors affecting survival, proliferation, and development of gonadal cells (somatic and germ) in vitro. PGCs were identified based on size and staining with pluripotent stem cell markers. Formation of cell aggregates, presumptive EB precursors, was observed throughout all gonadal cultures in the presence of PGCs. Gonadal cultures treated with busulfan to eliminate PGCs had only limited aggregate formation. Cultures supplemented with fibroblast growth factor showed increased aggregate formation. Co-culture with embryonic testes or ovaries seemed to influence somatic cells surrounding aggregates. PGC-derived EGs were identified immunocytochemically within aggregates using pluripotent stem cell and germ cell markers (anti-SSEA1, anti-SSEA4, and anti-EMA1). In vitro culture conditions for dissociated embryonic gonad cells in this study may provide a basis for expanding embryonic germ cells and directing their development for germ stem cell development, in vitro gamete production, and other stem cell applications.

A Candidate Gene Scan for Protein-losing Enteropathy in Yorkshire Terriers

VICTORIA S. HOOKER

Under the supervision of Dr. Nathan Sutter
Department of Clinical Sciences

Protein Losing Enteropathy (PLE) is a syndrome in which vital plasma protein is lost through crypts in the intestinal epithelium. It is often a fatal disease in dogs, and the clinical presentation of the disease in dogs is very similar to that in humans. There is believed to be a genetic predisposition, as PLE is most commonly seen in a few particular dog breeds, especially in the Yorkshire Terrier. Heparan sulfate proteoglycans (HSPGs) are a major contributor to the integrity of the intestinal epithelium, and the core protein of these macromolecules is encoded by the gene *syndecan-1* (*Sdc1*). Individuals with PLE lack HSPG in their intestinal epithelium. We collected DNA samples from affected and unaffected individuals by soliciting owners and breeders for blood samples, detailed pedigree and disease information. The information was compiled into a database. Polymerase chain reaction (PCR) was used to amplify eight amplicons, spanning five exons and the promoter of *Sdc1*,

in an attempt to discover markers and their respective allele frequency. Sixteen single nucleotide polymorphisms (SNPs) and one insertion/deletion segregated within the Yorkshire Terrier breed population. The genotypes of 11 affected and 46 unaffected Yorkshire Terriers were sequenced. Only affected dogs and unaffected ones over the age of 8 were included in the analysis. None of the markers had a significant correlation with disease susceptibility ($P \geq .21$ or higher). Therefore, it is unlikely that any of the markers detected are involved in a mutation that predisposes Yorkshire Terriers to PLE.

Investigating Insulin-like Peptide Signaling-Dependent Stress Resistance in *Caenorhabditis Elegans*: Possible Modulation Through an Imp-L2-like Binding Protein

SARAH M. KHATIBZADEH

Under the supervision of Drs. Yves Boisclair and Siu Sylvia Lee
Department of Molecular Biology and Genetics

Insulin-like signaling (ILS) regulates metabolism, growth, development and lifespan in both vertebrates and invertebrates. In vertebrates, ILS is triggered not only by insulin but also by insulin-like growth factors (IGFs.) IGF-specific modulation of ILS is partially conferred through IGF-binding proteins (IGFBPs). In *Drosophila*, ILS is initiated by insulin-like peptides (ILPs) and is also modulated by an IGFBP homolog known as Imp-L2. Specifically, Imp-L2 is upregulated when *Drosophila* larvae are starved and segregates the ILP in non-signaling complexes. This mechanism prevents ILS-dependent nutrient utilization and prolongs the lifespan of larvae during starvation. Interestingly, the nematode *Caenorhabditis elegans*, which possesses ILP and ILS, also prolongs its lifespan through decreased metabolism during periods of starvation or other chronic stresses (heat, crowding, etc.). However, it is not known whether ILS in the worm is modulated by an Imp-L2-like protein. To resolve this issue, studies were performed to determine whether an Imp-L2-like protein exists in *C. elegans*, and whether it prolongs lifespan during periods of stress. Using the Imp-L2 amino acid sequence as a template, the *zig-4*, *zig-3*, and *zig-2* genes were identified as possible Imp-L2 homologs in *C. elegans*. Next, RNAi techniques were used to assess the possible roles of the candidate gene products in dauer arrest, lifespan determination, and fat deposition. RNAi against *zig-4* significantly lowered dauer arrest frequency in *daf-2* mutants compared to the control RNAi ($P < 0.05$), while RNAi against *zig-3* and *zig-2* had no significant effects on dauer arrest. RNAi against *zig-4* also significantly shortened lifespan in wild-type and *daf-2* mutants compared to the empty vector control RNAi ($P < 0.05$), but these results were not consistent over several trials. These data are consistent with *zig-4* attenuating ILP-dependent ILS and with *zig-4* possibly encoding an Imp-L2 homolog in *C. elegans*.

The Effects of Environmental Temperature and Exercise on Serum Leptin Levels with Implications for Bone Quality

BARBARA K. LINNEHAN

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Leptin regulates energy intake and expenditure via its interaction with the hypothalamus and the sympathetic nervous system. More recently, it has been found to act as a paracrine mediator on bone and a skeletal growth factor during development, with a greater impact on long bones during fetal and postnatal development than in the mature skeleton, through direct angiogenic and osteogenic effects on bone marrow stromal precursor cells. Environmental variables such as cold temperature and exercise can have significant effects on bone length and quality. In response to cold exposure, the sympathetic nervous system decreases circulating leptin concentrations. While cold environmental temperature has been shown to stunt long bone growth, weight-bearing exercise increases bone mass, length, diameter, and bone mineral density in both humans and animals. The purpose of the current study is to examine the effects of temperature and exercise on serum leptin concentration in growing mice, with the long-term goal of determining the impacts on bone quality. The data showed that exercise had a significant negative effect on serum leptin concentration ($\alpha=0.05$) and warm, non-exercised mice exhibited higher concentrations than cold non-exercised mice, although non-significant. Differential effects on bone length were seen between the radius and femur, with the radius having a significant negative temperature effect and the femur having a significant positive exercise effect. Establishing this relationship was an important first step, and the next step is to determine the effects on bone quality via microCT scans and three-point bending tests to assess the whole bone biomechanical properties.

A Survey of the Northeastern United States for the Presence of *Angiostrongylus vasorum*

MISTY S. POCWIERZ

Under the supervision of Dr. Dwight Bowman
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Angiostrongylus vasorum is a metastrongyloid parasite of the pulmonary arteries and right ventricle of canids. While first described in France in 1866, it has spread to and is considered endemic in Ireland, Switzerland, Uganda and Brazil. Recently Newfoundland, Canada, has been considered a newly endemic area. It has become very clear that the parasite is continuing to expand its range, possibly due to climactic changes coupled with the increased occurrence of people traveling internationally with their dogs. Concern has been raised that this parasite that can cause severe disease in dogs may now be present in the United States. The parasite's presence in areas of close geographic proximity to the United States and in wildlife hosts not restricted to Canada alone, make this a possibility. Thus, this project was designed to survey the Northeastern United States for the

presence of *A. vasorum*. Gastropod intermediate hosts of the parasite were collected and analyzed to determine their level of infection. Fox carcasses collected from New Hampshire were dissected in order to recover adult worms. A serosurvey has begun of domestic dogs in areas where the parasite is first likely to appear. Lastly, a PCR method was developed to differentiate between *A. vasorum* and other metastrongyloid nematodes present in gastropods and canids.

The Effect of Dietary β -Cyclodextrin, a Cholesterol-Binding Agent, on Egg Production, Egg Hatchability and Yolk Cholesterol in Laying Hens

JENNIFER L. RUBY

Under the supervision of Dr. Richard Austic
Department of Animal Science

The objective of this study was to determine the effects of dietary β -cyclodextrin (β -CD) on egg yolk cholesterol levels and egg production in white leghorn laying hens. Twenty-seven 61-wk-old individually caged Babcock B-300 laying hens were randomly assigned into three treatments with triplicate groups of three hens each. Treatment 1 birds were fed a corn and soybean diet with 6% α -cellulose and a basal level of vitamins and minerals that satisfies the nutrient requirements set by the National Research Council (NRC) for poultry (1994). Treatment 2 birds consumed the same diet, except that 6% cellulose was replaced with 6% β -CD. Treatment 3 birds received the same β -CD diet as treatment 2, but had an enhanced vitamin and mineral premix. Over a period of 6 weeks there were no differences ($P>0.05$) between treatments in rate of egg production, change in egg weight, yolk as a percentage of egg weight, change in hen weight, and hatchability of eggs. There were increases ($P\leq 0.05$) in yolk egg cholesterol concentrations during week 3 of the experiment in hens on both treatments 2 and 3. By week 6, eggs from hens on treatment 2 remained higher ($P\leq 0.05$) in yolk cholesterol levels than eggs from treatments 1 and 3, which no longer differed ($P>0.05$). It was concluded that β -CD in the diets of laying hens had no positive effects on performance and may either not affect or increase the concentration of yolk cholesterol.

The Effect of Rumensin and Ruminant Nitrogen and Metabolizable Protein Balance on the Efficiency of Use of Protein in Lactating Dairy Cattle

CHAD J. WALL

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

The objective of this study was to investigate the efficiency of use of nitrogen (N) in lactating dairy cattle fed diets differing in ruminant N balance with Rumensin. Seventy-five lactating dairy cattle were used in a randomized complete block design. The study included three treatments in which ten primiparous and fifteen multiparous cattle were assigned to each. Treatments included Control (C), Control plus Rumensin (C+R), and Treatment plus Rumensin (T+R). The diets were formulated with CNCPSv 6.1 to be similar for metabolizable energy and protein supply but differ in rumen available

N. Diets C and C+R were formulated to contain 15% crude protein (CP), 8.84% rumen degradable protein (RDP), and have a rumen NH₃ balance of 140%. Diet T+R was formulated to contain 15% CP, 7.29% RDP and have a rumen NH₃ balance of approximately 100%. Rumensin was included in C+R and T+R diets at 400 mg/d per cow. Treatments were conducted for 100 d post adjustment. Cows were fed once a day and milked three times a day. Overall, diet formulation had no significant effect on any of the production parameters monitored. Feed efficiency and N efficiency were high among all the treatments averaging 1.88 and 0.36, respectively. Milk protein yield was significantly less for cattle fed diet C+R due to statistically non significant differences in milk yield and the protein content of milk. Rumensin had a significant effect on plasma and milk urea N where values increased by nearly 2 mg/dl indicating that Rumensin was altering the rate of hepatic urea production and the plasma pool of urea N. Overall, Rumensin did not affect the efficiency of N use but did alter N metabolism, an area which requires further investigation.

Alteration of Intersubunit Acid-base Pair Interactions at the Quasi-threefold Axis of Symmetry of Cucumber Mosaic Virus Disrupts Aphid Vector Transmission

CHRISTINE A. BRICAULT

Under the supervision of Dr. Keith Perry
Department of Plant Pathology and Plant-Microbe Biology

In the atomic model of Cucumber mosaic virus (CMV), six amino acid residues form stabilizing salt bridges between subunits of the asymmetric unit at the quasi-threefold axis of symmetry. To evaluate the effects of these positions on virion stability and aphid vector transmissibility, six charged amino acid residues were individually mutated to alanine. All of the six engineered viruses, mutants D100A, K101A, K127A, D176A, D179A, and K182A, were viable and able to systemically infect *Nicotiana tabacum* and to locally infect *Chenopodium quinoa*. In order to assess the physical stability of mutants, virions were purified from plants and tested in a urea disruption assay. Of the six mutant viruses, only mutant K101A had variable stability during purification in the presence of 1.5 M sodium citrate and chloroform. Virions of the remaining five mutants were purified and exhibited wild type levels of virion stability in the presence of urea. Aphid vector transmissibility was nearly or completely eliminated in the case of mutants D100A, K101A, K127A, and D176A. The two remaining mutants were intermediate (mutant D179A) or unaffected (mutant K182A) in their aphid transmission phenotypes. For the majority of the engineered mutants, second-site mutations were observed following aphid transmission and/or following mechanical passaging. In mutant K127A, a spontaneous second-site mutation, E98V, restored transmission rates to that of the wild type. A model is discussed in which the presumptive role of acid-base pairing involved in the dynamic properties of virions in turn affects aphid vector transmission.

Elucidating the Etiology of Preeclampsia through Investigation of *Thbs2* and *Gcm1*

SERENA PING HUA CHIANG

Under the supervision of Dr. Robin Davisson
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Preeclampsia is a pregnancy-specific disorder that is characterized clinically by the sudden onset of hypertension, proteinuria, and edema after 20 weeks of gestation. It is the most frequently encountered medical complication during pregnancy and affects upwards of 3-5% of pregnant women worldwide. The etiology of preeclampsia is unknown, but abnormal placentation observed in preeclampsia suggests that the placenta plays a central role. In normal placenta development, fetal extravillous cytotrophoblasts invade the maternal myometrium and decidua, transforming small vessels in the endothelial layer into larger vessels that will provide the required placental perfusion. In preeclampsia, cytotrophoblast invasion is restricted to the decidua. It has been hypothesized that development of the vasculature is regulated by angiogenic factors. Thus, an imbalance of these factors may contribute to the pathogenesis of preeclampsia. *Thrombospondin-2* (*Thbs2*) is one such factor and has been shown to be a potent, endogenous inhibitor of angiogenesis capable of inducing

cell death in endothelial cells. In addition, a protein essential to formation of the labyrinth in placental development is the transcription factor encoded by *Glial cells missing (Gcm)*. *Gcm1*, the mammalian homologue, regulates the differentiation of syncytiotrophoblast cells and the expression of its placental target gene, *Syncytin A*. *Syncytin A* encodes a fusogenic membrane glycoprotein that is fundamental for trophoblast cell fusion and differentiation and syncytiotrophoblast morphogenesis during placental development. In human preeclampsia, syncytin gene expression is significantly reduced. In this study, increased expression of *Thbs2* and decreased expression of *Gcm1* and *Syncytin A* in the feto-placental units of a mouse model of preeclampsia (BPH/5) are observed. This suggests that altered expressions of *Gcm1* and *Thbs2*, and subsequently altered expression of *Syncytin A* may help to explain the etiology of preeclampsia.

Skeletal Size and Shape Diversity in the Horse: Quantification of Skeletal Phenotype and a Candidate Gene Screen for Skeletal Trait Variation in *Equus Caballus*

ERIN T. CHU

Under the supervision of Dr. Nathan Sutter
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The domestic horse, *Equus caballus*, presents a wide range of skeletal variation. This variation provides a strong model to investigate the genetics of skeletal growth, as well as the genetic events that drive the process of domestication. The genetics of skeletal variation also have a direct application to the horse industry since first, body size and conformation directly affect the value of a horse; and second, specific skeletal proportions have been implicated in increasing susceptibility to orthopedic injury. Here we have identified and quantified the total skeletal variation present in the horse population. Using a set of 35 measurements, we have compared skeletal size and shape across 1215 horses representing 65 breeds. Principal component analysis of these measurements has identified two primary axes of variation in the horse: PC1, which defines overall skeletal size, and PC2, which defines overall body thickness. We have also conducted a candidate gene screen in 36 unrelated horses of extreme PC1 value, and have identified six polymorphisms that, through statistical testing, are suggested to associate with body size. Further studies will aim to analyze our candidate genes in a higher resolution and a larger sample size. Ultimately, we aim to use our quantified PC phenotypes in a genome wide association scan and map genes associated with body size variation in the domestic horse. Genes identified in such studies could then be applied to the treatment of athletic skeletal injury and disease in horses, as well as humans.

Interactions between Iron and Folate Metabolism using Fth and cSHMT Knockout Mouse Models

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Common variations in genes implicated in folate metabolism are linked to many adverse outcomes that compromise human health. Many studies using various models (cell cultures, animals, humans) have found that disruptions in iron metabolism lead to impairments in folate metabolism. The close interaction between these two systems is widely acknowledged, however, to date, no mechanism for how these systems interact has been found.

In this study, a murine knockout model of cytoplasmic serine hydroxymethyltransferase (cSHMT) was used to determine the effects of impaired folate metabolism on iron metabolism. cSHMT is an enzyme that functions as a metabolic switch to provide one-carbon units for folate metabolism, and it has been found to be differentially expressed in tissues implicated in folate-related pathologies. cSHMT^{+/+}, cSHMT^{+/-}, and cSHMT^{-/-} mice were fed either a control or folate and choline deficient diet. Levels of heavy chain ferritin (Fth), an iron storage protein that also affects folate metabolism, and transferrin receptor (TfR), which binds plasma iron for transport into the cell, were measured using Western Blotting techniques. Observations in liver tissue of differences in Fth and TfR levels between experimental groups were inconclusive, and neither Fth nor TfR expression varied with cSHMT level. Thymidylate synthase (TS), the enzyme responsible for synthesis of thymidylate, traverses into the nucleus with cSHMT during the S-phase of the cell cycle and may play a role in cSHMT regulation. TS levels were measured in cSHMT-deficient mice in liver and kidney tissue and did not seem to be affected by diet or genotype, however, when measured in colon tissue, mice showed a diet-independent genotype effect, with increased TS expression in cSHMT^{+/-} mice compared to cSHMT^{+/+} or cSHMT^{-/-} mice.

A second murine knockout model for the Fth gene was used to observe the effects of impairments in iron metabolism on folate metabolism. Fth^{+/+} and Fth^{+/-} mice (Fth^{-/-} was lethal) were fed either a control or folate and choline deficient diet. Using Western Blotting techniques, levels of cSHMT and TfR were measured along the four genotype and diet groups in liver, kidney, and spleen tissue. In each tissue, different effects on TfR and cSHMT expression were observed. TfR expression was affected by both diet (liver, increased expression in folate deficiency) and genotype (spleen, decreased expression in Fth^{+/-} mice). cSHMT expression was also affected by both diet (kidney, increased expression in folate deficiency) and genotype (spleen, decreased expression in Fth^{+/-} mice).

Hydrological and Climatic Controls on Watershed Export in an Aggrading New Hampshire Forest

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Stream chemistry of a 36 ha watershed in the Hubbard Brook Experimental Forest (Watershed 4) displays higher nitrate export than expected for an early successional forest in this region. Within Watershed 4, a small tributary (stream A, 300 m in length) has a chemical signature far different from the main channel (stream B, 1000 m in length). Previous monitoring has shown that the pH of the side tributary was significantly higher than that of the main channel and contains detectable levels of nitrate whereas the main channel had no detectable nitrate, and it is suspected that this side tributary significantly contributes to watershed export under base flow conditions. It was expected that Watershed 4's dominant water and chemical sources would vary with flow conditions, especially during summer thunderstorms. What are the sources of nitrate and other solutes under summer baseflow conditions? How does the relative dominance of these source contributions change with the onset of high flow events? The main hypothesis was that the side tributary is the dominant source area under the normal base flow conditions of the summer (usually under 1 L/s) and that the main stem exerts dominance under the high flow conditions brought on by events. Daily water samples were taken throughout summer 2008 with three ISCO automated samplers: one ISCO was placed at the main stem of the stream, a second at the small internal tributary, and a third was placed at the weir. The samples were analyzed for pH, specific conductivity, and major anions and cations. The chemical data were compared to precipitation and rate of watershed flow calculated at each sampling hour to detect associations between chemical dominance and hydrological conditions. Under the base flow conditions of the summer, much of the chemistry of watershed outflow was dominated by that of the short side tributary, with lower acidity and higher nitrate levels than the longer main channel, but with notable contributions from the main channel. During each of the three high flow events that occurred over the summer, flow in the main channel increased dramatically and flow at the weir corresponded to temporarily increased acidity and decreased acid neutralizing capacity (ANC). Nitrate data show that a dilution response was associated with these events since there were significant declines in nitrate concentrations of both the side tributaries and at the base of the watershed during high flow conditions.

Understanding the Effects of Agriculture on Stream Food Webs Based on Stable Isotope Analysis

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Land use practices within stream catchments greatly influence fundamental stream ecosystem properties such as light and nutrient availability as well as the resource base of aquatic systems. We used stable isotope analyses to investigate the effects of agriculture vs. forest land use on stream food web structure in the Finger Lakes region of New York State. We compared the $\delta^{15}\text{N}$, $\delta^{13}\text{C}$ and $\delta^2\text{H}$ signatures of samples of common food web compartments from two agricultural and two forested streams, and constructed isotopic food webs based on $\delta^{15}\text{N}$ vs. $\delta^{13}\text{C}$ isotopic signatures for each stream. We predicted increased abundance of algal biomass in agricultural versus forested streams, and consequently increased incorporation of autochthonous primary productivity into the tissues of consumers in agricultural streams. Furthermore, we expected that increased algal productivity would support larger herbivore populations, enabling potential predator species to rely more on animal than plant tissue, resulting in a greater range of trophic positions and a greater maximum $\delta^{15}\text{N}$ in agricultural food webs. We predicted that the greater range in $\delta^{15}\text{N}$, as well as increased incorporation of algal derived carbon, would lead to a larger trophic web, possibly indicating an increase in available trophic niches within agricultural streams.

Because many consumer species displayed $\delta^{13}\text{C}$ values outside the range of either tree leaf or algal end-member, we were unable to ascertain whether autochthonous carbon contributed more to food webs in agricultural than forested streams. However, the $\delta^2\text{H}$ of nearly every consumer was between the expected algal and detrital end members, suggesting that $\delta^2\text{H}$ may be more reliable than $\delta^{13}\text{C}$ for indicating the origin of basal carbon resources within stream food webs. $\delta^{15}\text{N}$ analysis revealed that all trophic compartments collected from agricultural sites were enriched in ^{15}N compared to their forest derived counterparts. The results of this study suggest that stable isotope analysis holds promise as a useful method for comparing trophic niches for stream consumers, and that comparisons of species' trophic niches and community trophic niche space across streams or across time may provide insights into the impact of environmental change on stream food webs.

Characterization of an RNA Associated with Paramutation in Mice

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Methylation of the gene *Rasgrf1*, a paternally imprinted gene, is important for maintaining proper imprinting patterns and gene expression in mice. An important characteristic of *Rasgrf1* is the differentially methylated domain (DMD). The paternal allele is methylated and expressed while the

maternal allele is unmethylated and silent. Another important element of *Rasgrf1* is a set of 41 nucleotides repeated 40 times that is located immediately downstream of the DMD. The repeats have shown to be necessary for proper regulation of methylation within the DMD. Mouse *Igf2r*, a maternally imprinted gene in mice, has a region known as Intron 2 or Region 2 (R2) that controls methylation and imprinting. Mutant mice called Lu mice were designed with R2 in place of the repeats seen at *Rasgrf1*. R2 was partially effective in taking the place of the repeats allowing the methylation and expression of the paternal *Rasgrf1* allele. For the most part, Lu mice had proper methylation of the paternal allele as seen in wild type mice, but the normally unmethylated, unexpressed maternal allele was activated in trans and aberrantly expressed. This phenomenon is similar to paramutation in corn that is mediated by RNA. In fact, an aberrant RNA was being produced in the mutated *Rasgrf1* allele containing R2 and a recent study has data implicating that a piRNA pathway and DMD spanning RNAs may be controlling methylation. Whether or not the aberrant RNA is truly regulating methylation is unknown, but here in this study we sought to characterize the RNA to gain further clues. The technique of PCR using overlapping primers was used to determine the 3' end of the aberrant RNA formed in Lu mice.

Analysis of Male Agonistic Interactions in the Weakly Electric Fish, *Brienomyrus brachyistius* (Mormyridae) using a New Technique for Separating Electric Discharges

KEVIN F. GARDNER

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Department of Neurobiology and Behavior

The weakly electric mormyrid fish *Brienomyrus brachyistius* employs its electrosensory modality for the dual purposes of electrolocation and communication. The dominance relationship in mormyrids such as *B. brachyistius* can be described by two distinct phases: the initial phase of status determination and the ensuing phase of status maintenance. Much is known about the motor and electrical behavior of mormyrids in the initial phase of dominance, but much less is known about the second phase. This is due in large part to the technical difficulties associated with efficiently and accurately isolating the electric organ discharges (EODs) from individual fish. Through the use of a new EOD separation technique, G-PRIME, this study has been able to examine agonistic interactions during the second phase of dominance, status maintenance. This study describes G-PRIME and examines its accuracy, speed, and the volume of data it is able to handle. We also examined territoriality in this species and observed that territoriality was not present under these experimental conditions; rather a stable dominance hierarchy was in place. Additionally, the previously described sequence of pulse intervals (SPIs) "long cessation," "short cessation," and "pulse pairs" were observed and expanded upon by quantitative analysis, and a novel SPI termed the "long repeated acceleration-deceleration" (LRAD) was observed and analyzed. Adaptive functions of described SPIs are discussed as well as a possible neuronal mechanism of production of pulse pairs.

Air-assisted Intranasal Viral Delivery to the Olfactory Epithelium and Lung: An Enhancement for Studying Neurodegeneration in the Mouse Olfactory Epithelium

PHILIA GAU

Under the supervision of Dr. David Lin
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Neurodegenerative diseases affect millions of people, but the etiology of these diseases. One poorly understood aspect of neurodegenerative diseases is the role of glia. Sustentacular glial cells in the mouse olfactory epithelium support neuronal survival. Earlier work in the lab has shown that *Notch2* plays a neuroprotective role in adult sustentacular cells. In *Notch2* knock-out mutants, sustentacular cells produce lower levels of antioxidants. This is correlated with increased cell death of olfactory sensory neurons. These results suggest that *Notch2* acts in glia to regulate glial response to oxidative stress. One way to test this hypothesis is to manipulate *Notch2* signaling in sustentacular cells. We hypothesize that this will affect neurodegeneration in response to oxidative stress. However, *in vivo* methods to manipulate gene expression are often laborious and slow. Here, we have developed an intranasal viral delivery approach to manipulate gene expression to study *Notch2* in the olfactory epithelium. Intranasal instillation can deliver agents to the olfactory epithelium and lung. Despite the promise of intranasal methods, consistent delivery has not been achieved due to the complex structure of the olfactory epithelium and the lung. Many alternatives to intranasal instillation have been tried, but have generally made no significant improvement in virus distribution or involved complicated techniques. We use air-assisted intranasal viral delivery to greatly improve virus distribution to the olfactory epithelium and lung. This method can be used to further study the role of *Notch2* signaling in sustentacular cells.

Characterization of Polymorphic Microsatellite Loci in the B-genome Group of *Glycine* subgenus *Glycine*: Implications for Population Structure

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The B-genome group of *Glycine* subgenus *Glycine* (Fabaceae) consists of four named species *G. latifolia*, *G. microphylla*, *G. stenophita*, *G. tabacina* and several informally recognized entities. These species are interfertile with each other and can produce fertile hybrids thus classifying them as a genome group. The taxonomy of the B-genome group is complex making identification of the relationships between species and between accessions within a species main priorities. Multilocus genotype data from nine microsatellite markers were used to conduct a population structure analysis, leading to the conclusion that most of the accessions in each species group together resulting in four populations each corresponding to a specific species. There are a couple of *G. latifolia* and *G. microphylla* accessions that do not group with their species, but instead group with *G. tabacina* and those accessions unassigned to a recognized species. Each population is highly inbred with little

heterozygosity and significant differentiation from the other populations. The accessions in *G. microphylla* that group with *G. tabacina* compromise one of two detected groups when the population structure of *G. microphylla* is analyzed separate from the rest of the B-genome group. These populations have different inbreeding coefficients, different observed and expected heterozygosities, and different geographic ranges. Studying the population structure of the B-genome group of *Glycine* subgenus *Glycine* has clarified many of the relationships between species but has resulted in further questions pertaining to specific accessions and their unusual grouping.

The Effects of Partial Hus1 Impairment on Tumorigenesis

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The Atr checkpoint pathway responds to a broad array of DNA lesions and stalled replication forks. Hus1, a component of this pathway, is a member of the heterotrimeric 9-1-1 complex, which recruits other checkpoint and repair proteins to DNA damage sites. Because Hus1 and the other components of the Atr pathway are essential for viability, many of the physiological roles for this genome maintenance mechanism remain unknown. The objective of my research is to determine how Hus1 defects affect cell transformation and tumorigenesis. In order to bypass the severe effects of complete Hus1 deletion, we used a Hus1 allelic series in which mice express incrementally less Hus1. Mice with reduced Hus1 expression appear grossly normal and are not prone to spontaneous cancers but do show genotoxin hypersensitivity and increased genomic instability. To test how Hus1 function affects oncogene-induced cell transformation, we transfected Hus1 impaired MEFs with activated oncogenes. We then measured loss of contact inhibition and anchorage independent growth and found that reduced Hus1 expression hindered cell transformation. We next used a chemical skin carcinogenesis assay to test cancer susceptibility in vivo and observed significantly reduced skin tumorigenesis in mice with a partial Hus1 defect. Measurements of apoptosis and proliferation in skin indicated that Hus1 impairment was not associated with acute carcinogen sensitivity, suggesting that Hus1 dysfunction instead inhibits tumorigenesis by interfering with the ability of tumor cells to cope with the genomic stresses associated with neoplastic proliferation. Overall, this work reveals a Hus1 dosage dependence on transformation capability and highlights the potential value of targeting this checkpoint pathway as a therapeutic strategy.

The Antibiotic Pyrazinamide as a New Antileishmanial Drug

PATRICIA C. GREEN

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Leishmaniasis, a complex set of diseases caused by the intracellular parasite *Leishmania*, is a growing burden throughout the world. With no vaccine and current first line treatments that are

suboptimal there is a call for the development of new treatments for this disease that has a current at risk population of 350 million people with 12 million people already infected and 2 million new cases a year. Pyrazinamide (PZA), a drug currently used in tuberculosis treatment has properties that make it a potential new therapeutic agent for leishmaniasis treatment. It has already been demonstrated to be toxic to *Leishmania major* (*Lm*) as well as having immunostimulatory effects that are key in treating this disease. I further studied the effects of PZA treatment on *Lm* infections in an *in vitro* model as well as murine models of two forms of leishmaniasis, cutaneous and the fatal visceral form. I found that PZA increased the activation of cells important for the immune response to *Leishmania in vitro* as well as decreased disease pathology *in vivo*. These data suggest that PZA is a promising candidate for the treatment of this devastating disease.

The Frequencies of *Vssc* and *CYP6D1* Alleles in House Fly Populations from Florida, North Carolina, New York and Kansas

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House flies were collected in 2009 from dairies in Florida, North Carolina, New York and Kansas, and the frequencies of *Vssc* and *CYP6D1* alleles that confer resistance to pyrethroid insecticides were determined for each collection site. These frequencies were then compared to bioassay data and to previous studies. The *kdr* allele was found at the highest frequency in New York at 0.57, while Kansas had the lowest frequency at 0.13. The *kdr-his* allele was found in every state surveyed and frequencies ranged from 0.23 in Kansas to 0.81 in North Carolina. The *super-kdr* allele was identified in Kansas for the first time. It was found at a much higher frequency than previously determined in New York. This suggested that the *super-kdr* point of origin was most likely not New York. Combinations of at least one *CYP6D1v1* allele and one resistant *Vssc* allele accounted for the majority of all individuals, suggesting that a single resistant allele did not confer sufficient resistance to survive in the field. Florida was found to have the highest number of both *Vssc* and *CYP6D1* susceptible alleles. This is consistent with Florida flies having the lowest level of resistance to pyrethrins + PBO and cyfluthrin, although the percent survival of Florida flies was not significantly lower than the other states over time. There has been no discernable trend over time in Florida and New York for *Vssc* resistance alleles between years, although variation has been observed. There has been little change in the frequency of *CYP6D1* alleles between the years 2002 and 2009 in Florida, New York and North Carolina.

Runx1 Function in Mouse Skin Tumor Formation

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Adult stem cells, which are characterized by their slow-cycling, multi-potent and self-renewing nature, are crucial in maintaining tissue homeostasis and responding to wound-stimuli. In addition to these classical roles, one current hypothesis posits that deregulated adult stem cells may in fact be the origin of cancer-initiating cells. Within the epidermis, hair follicle stem cells (HFSCs) give rise to and maintain the hair follicle structure through a series of remodeling phases known as ‘hair cycles’. The transcription factor Runx1, also known as AML1, plays a role in the activation of HFSCs by prolonging the quiescent phase of the hair cycle when ablated. Coincidentally, Runx1 is also translocated in 20-30% of patients afflicted with the blood-related disease acute myeloid leukemia. In this study, we explore the role that Runx1 may have in skin tumorigenesis by using a mutagen (9,10-Dimethyl-1,2-benzanthracene, DMBA) and a phorbol ester mitogen (12-O-tetradecanoylphorbol-13-acetate, TPA) in a two-step, oncogenic protocol. First, we observe that epithelial-specific Runx1-mutant mice show decreased levels of phosphorylated Stat3 and acquire significantly fewer papillomas than their wild-type littermates in response to carcinogenic drug treatment, a phenotype which is reversed when the cell cycle regulator p21 is simultaneously knocked-out. Second, cells initially expressing Runx1 contribute to tumor formation. Lastly, induced removal of functional *Runx1*, which is up-regulated in tumors, following tumor formation actually resulted in a reduction in overall tumor volume. Taken all together, these results suggest that *Runx1* functions upstream of p21 and is involved in not only the initiation of tumors, but also their proliferation and progression, possibly via the Jak/Stat pathway

The Salicylic Acid Pathway is Involved in *Arabidopsis thaliana* Non-host Resistance to *Phytophthora capsici*

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Different defense pathways are activated in response to different pathogens. Resistance to pathogens that maintain a long-term feeding relationship with their hosts, i.e., biotrophs, is mediated by the salicylic acid (SA) pathway. However, resistance to pathogens that kill their host and feed on the dead cells, i.e., necrotrophs, is mediated by the jasmonic acid (JA) pathway. RNA interference (RNAi) is also involved in plant-pathogen interaction. And in some cases, pre-invasion responses mediated by the PEN family of genes restrict pathogens from penetrating the plant’s cell wall. The goal of our study was to determine the defense pathway involved in *Arabidopsis thaliana* non-host resistance to the hemibiotrophic (which has the potential to be biotrophic and necrotrophic) fungus-like pathogen, *Phytophthora capsici*. We tested the susceptibility of detached leaves and intact plants

from a variety of *Arabidopsis* mutant and transgenic lines affected in the SA, JA and RNAi pathways, and in cell wall penetration. Our results showed that resistance to *P. capsici* is primarily mediated by the SA pathway. *NahG* transgenic plants, which degrade SA into catechol, were most susceptible to *P. capsici* in detached-leaf assays. Also, using *Arabidopsis* leaves from transgenic lines expressing pathogen responsive promoters fused to a GUS reporter, we demonstrated that SA-responsive *PR-1* and *PR-2* genes, rather than the JA-responsive *PDF1.2* gene, were induced after the leaves were inoculated with *P. capsici*. Mutations in genes involved in RNAi, such as *argonaute* (*AGO*) and *silencing defective* (*SDE*) loci, did not hinder *Arabidopsis*'s defense against the pathogen. Taken together, these results suggest that SA accumulation and the activation of the SA pathway are necessary for basal defense against *P. capsici*.

Kinetics of RSV Gag Budding in an Inducible Cell Line

ALICE Y. LU

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Rous Sarcoma Virus (RSV) is a chicken retrovirus used as a model system for Human Immunodeficiency Virus (HIV). An inducible DF1 chicken cell line was used to explore the kinetics of retroviral Gag budding. Upon treatment of the cells with doxycycline (dox), RSV Gag-GFP is synthesized. RSV Gag-GFP exhibits a diffuse cytoplasmic distribution in uninduced cells. Induction with dox results in the multimerization of RSV Gag-GFP at the plasma membrane to form nascent virus-like particles (VLPs), appearing as punctuate clusters. RSV Gag-GFP incorporation and release into VLPs reaches steady-state approximately 21 hours after dox treatment, regardless of the concentration of dox applied in the range initially tested. Maximum dox induction results in a ten-fold increase in intracellular Gag-GFP levels at steady-state, although the magnitude of this value likely underestimates the actual increase in Gag-GFP synthesis in response to dox treatment. The effects of induction are not all-or-nothing; instead, cell populations exhibit gradual shifts in fluorescence distributions with varying concentrations of dox treatment. The amount of Gag detected both within the cell and released into VLPs increases with increasing concentrations of dox treatment. Generally, the fluorescence curves of fully induced and uninduced cells exhibited a more narrow distribution compared to cells treated with an intermediate level of dox, indicating a high degree of heterogeneity. A considerable amount of residual Gag can be detected intracellularly 20 hours post-induction, suggesting newly synthesized Gag molecules are outcompeting a subpopulation of endogenous Gag in budding. Although these studies reveal some basic insights into aspects of RSV Gag budding previously unexplored, they only begin to address the potential kinetic effects of Gag levels on budding.

Host-parasite Specificity and Local Host Adaptation Help to Favor Dispersal as a Mechanism for Anciently Asexual Bdelloid Rotifers to Avoid Extinction by Fungal Parasites

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Bdelloid rotifers are an obligately asexual class of invertebrates that appears to contradict evolutionary theories of sex, including the well-supported Red Queen hypothesis, which posits that organisms need novel genomes (i.e., sex) each generation to escape extinction by rapidly co-evolving parasites. The "hide-and-see" hypothesis attempts to explain how bdelloids could have existed for millions of years amidst numerous parasites. Bdelloids have been shown to disperse over great distances in a parasite-free desiccated state, potentially migrating to habitats with parasites not as well co-adapted and 'escaping' the Red Queen. A critical prediction of this hypothesis is that bdelloid parasites should not be indiscriminate generalists, so this study investigated host-parasite specificity of common fungal parasites. Furthermore, dispersal would be a more effective strategy if parasites in distant habitats are less pathogenic, displaying local host adaptation, so we also examined differences between sympatric and allopatric parasite pathogenicities. We paired parasites and bdelloids from two distant locations, New York (U.S.A.) and Japan, to observe pathogenicity differences, and found that parasites do display significant specificity, as well as some evidence for local host adaptation trends. We conclude that parasites do not infect bdelloids indiscriminately, and that bdelloids may indeed be "safer" following dispersal, with potential for added protection in more distant habitats.

Cloning and Characterization of slo Family Potassium Channel Isoforms in the Lobster Nervous System

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In the nervous system, potassium channels help maintain the neuron's resting potential, decrease a neuron's overall excitability, and shape neuronal firing patterns. One particular subfamily of potassium channels, the big K (BK) calcium-dependent potassium channels, contributes significantly to the total potassium conductance of many neurons. We examined the molecular basis for these important channels in nervous tissue from the lobster *Panulirus interruptus*. Calcium-activated potassium currents play critical roles, for example, in spike termination and plateau potential termination in neurons from the lobster stomatogastric ganglion (STG). In many species, a large family of BK channels with variable properties is derived from the *slo1* gene as a result of abundant alternative splicing of its RNA, modification by regulatory β -subunits, and/or metabolic regulation. We used *slo1* sequences from other species, degenerate PCR, and 5' and 3'

Rapid Amplification of cDNA ends (RACE) methods to clone the *slo1* sequence from lobster nervous tissue. We also identified and further examined seven alternate splicing sites with PCR. Finally, we prepared and injected RNA from select cloned sequences into *Xenopus* oocytes and used standard two-electrode voltage clamp methods to attempt to characterize the channel properties. We obtained 13 unique and viable full-length sequences ranging from 1107 to 1164 total amino acids in length, with 96.6%, 82.5%, and 82.9% homology to crab, *Drosophila*, and cockroach nucleotide sequences respectively. Alignment of the full-length sequences showed in-frame differences at seven identified locations, which featured multiple variants, and were thus defined as alternate splicing sites X1-X7. Finally, our voltage clamp experiments have helped progress towards defining the properties of the slo alpha subunit.

What's in a Wail? The Presence of Individual Characteristics in Common Loon, *Gavia immer*, Vocalizations

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Common loons, *Gavia immer*, are large diving birds that rely on several vocalizations for territorial and social interactions. One such call, the wail, is given by both males and females. It ranges in function from calling to a mate or chicks, to a warning call for threats such as eagles or unknown intruder loons. We examined the wail to see if individual loons expressed measurable variation in their calls and if specific loons could be identified by a set of characteristics of both frequency and duration in their wails. Measurements from 13 different loons were found to be significantly different and using a discriminant analysis technique, we were able to classify individual wails to specific loons with a high rate of success. We discuss these results and suggest how the presence of individuality in the wail call is pertinent to loon behavior.

Sperm Usage Patterns in the Dengue vector mosquito, *Aedes aegypti*

LAURA F. SEEHOLZER

Under the supervision of Dr. Laura Harrington
Department of Entomology

This was the first study to report specific details on sperm transfer and movement. Though sperm degradation and loss occur in other insect species, its role in *Aedes aegypti* is not known. I explored the issue by quantifying: (1) the dynamics of sperm movement after full and interrupted copulations, (2) the occurrence of sperm loss or damage over time and (3) the effect of genotype on sperm capacity. Sperm were detected in the spermathecae shortly after transfer. Short term (10 sec - 10 min), the proportion of sperm in the bursa decreased due to both transfer to spermathecae and sperm loss. Mid-term (10 min - 6 h), there was no decrease in the proportion of sperm. Long-term (6 h - 48 h), the decreased proportion was due to sperm loss. Over time there was a decreasing amount of

sperm in the reproductive tract; only 25% of transferred sperm was stored. Interrupted copulation reduced numbers of sperm transferred to females to only one third of the uninterrupted total, yet there was no effect on the amount of sperm stored in the spermathecae. In addition to sperm loss, I found that sperm head detachment occurred over time, as has been documented for other insects. Lastly, transgenic mosquitoes (RILD) and wild-type (GDLS) mosquitoes did not differ, overall, in sperm quantity. One approach for mosquito population control is releasing transgenic mosquitoes. The success of most genetic control strategies relies on understanding reproductive fitness factors like sperm production, transfer, movement, loss and damage.

Ancient DNA Reveals a Mitochondrial Cline across a Classic Avian Hybrid Zone

LINDSAY G. SERENE

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Studies of genetic variation across hybrid zones have demonstrated that the evolutionary dynamics within these zones are often complicated. An ornithologically classic hybrid zone occurs in North America between the Bullock's (*Icertus bullockii*) and Baltimore (*I. galbula*) Orioles (Sutton 1938). Sibley and Short (1964) provided the first in-depth investigation of this zone via their collection and scoring of the phenotypes of hundreds of specimens. I examined mtDNA introgression across this same hybrid zone using ancient DNA methods applied to this large series of museum skin specimens, by developing a method to score each bird using a species-specific restriction cut site in the ND2 gene. I compared Bullock's mtDNA haplotype distributions with the plumage hybrid index scores from Sibley and Short (1964), finding that each type of marker had narrow and highly concordant clines. This concordant pattern indicates that the maternally inherited mtDNA marker shows the same relationship as (presumably) the autosomal plumage markers, and the narrowness of the clines further suggest that some form of selection is acting against hybrids, at least outside of the zone.

Alzheimer's Disease, Mild Cognitive Impairment, and ApoE: What Does $\epsilon 4$ Really Predict?

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Alzheimer's disease (AD), a common form of dementia among elderly adults, may be preceded by mild cognitive impairment (MCI). Receiving an MCI diagnosis is correlated with receiving an AD diagnosis later. Having the $\epsilon 4$ allele of the Apolipoprotein E (ApoE) gene is also correlated with receiving an AD diagnosis. However, previous research suggests that receiving an MCI diagnosis is not correlated with having the $\epsilon 4$ allele. Using diagnostic and genetic information from the Aging, Demographics, and Memory Study (ADAMS), the present study shows that MCI and the $\epsilon 4$ allele

are, in fact, correlated when subjects with other forms of cognitive impairment are eliminated from analysis and when subject age is properly controlled. More accurate prognoses for MCI patients can help them to make appropriate medical decisions, and can help doctors to begin potential AD interventions as soon as possible.

The Role of Female Proteins in the Proteolytic Processing of Ovulin in *Drosophila melanogaster*

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Drosophila melanogaster seminal fluid proteins are made in male reproductive tissues and transferred to females during mating. One such protein, Ovulin, increases ovulation rate. Ovulin is interesting because, although it is made in the male and proteolytically processed in the female, it appears to require both male and female contributions for its processing. Two male proteases necessary for ovulin processing are known, but little is known about female contributions. I investigated the role of female proteins in ovulin processing. Three proteins made in the female, CG10363, a predicted protease inhibitor, and CG13318 and CG9897, predicted inactive proteases, were chosen because their sequences show signs of rapid evolution, like ovulin's does. While results of interrupted mating experiments have been variable for CG10363 and CG9897, CG13318 appears to have an effect on ovulin processing at 15 minutes after the start of mating (ASM). An important part of this study was determining what may cause the variability found in ovulin processing studies. I found that female age does not have an effect on ovulin processing at 30 minutes ASM, but may have an effect for one day old versus two day old females at 15 minutes ASM. Similarly, it appears that male age can affect the efficiency of ovulin processing. In addition, ambient temperature was not found to not affect ovulin processing. Together, my results show that some female-derived proteins affect ovulin processing and that the rate of ovulin processing can be quite variable.

Adding to the Repertoire of Genetically-Encoded Calcium Indicators: Construction and Characterization of RCaMP2

JUSTIN L. TOROK

Under the supervision of Dr. Holger Sondermann
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Of the many uses of fluorescent proteins as tracking molecules *in vivo*, one of the most exciting areas of study involves its use in artificial calcium sensor proteins. While GCaMP2 is one of the most sensitive genetically-encoded calcium indicators (GECIs) to date and exhibits a 7-fold change in fluorescence upon calcium binding under physiological conditions, it has several limitations that make this construct non-ideal for studying all calcium-signaling processes. Here we describe the construction and characterization of a novel GECI using GCaMP2 as a template and the recently

discovered far-red fluorescent protein mKate, a collaborative effort between the Kotlikoff and Sondermann labs. Our construct, RCaMP2, undergoes a more than 3-fold change in quantum yield upon calcium release at physiological pH, making it a promising candidate for future optimization through site-directed mutagenesis. Though the exact molecular details underlying the reason for this calcium sensitivity in RCaMP2 remain elusive, analysis of our crystal structure of this construct in tandem with analysis of the crystal structure of mKate at various pH's provides some clues as to how this protein may function and highlights key residues that could be prime targets for mutagenesis.

Molecular Identification of the Equine Major Histocompatibility Complex and an Investigation of its Role in Reproduction

CHIA T. TSENG

Under the supervision of Dr. Douglas Antczak
Baker Institute for Animal Health

Five microsatellites spanning the Major Histocompatibility Complex (MHC) class I and class II regions were tested on a panel of 273 horses that were either unrelated or members of family trios. A total of 40 haplotypes were identified and 15 of these were linked to 9 serologically identified Equine Lymphocyte Antigen (ELA) types. The molecular signature of each MHC haplotype was determined based on a particular constellation of microsatellite alleles, and subhaplotypes of 4 serologically defined haplotypes were detected. Microsatellite haplotypes associated with Thoroughbreds and Standardbreds were identified. When comparing frequency of MHC microsatellite haplotypes in Thoroughbreds to the serological patterns determined previously, 90% of the chromosomes were comprised of well-defined serological ELA haplotypes, and the majority of these chromosomes carried ELA-A2 and ELA-A3 types. Using microsatellite analysis to supplement serology and confirm homozygosity in the Equine Genetics Center herd, I investigated the role of the MHC in equine pregnancy from fertilization to Day 30 among 5 MHC homozygous stallions and 74 mares of various MHC types in a retrospective study from 1986 to 2008. The outcome of a total of 978 mated estrus cycles and 673 conceptions was analyzed, and the average pregnancy rates were not significantly different between compatible (68.25%) and incompatible (69.08%) matings ($p > 0.05$). The compatible mating group was further sorted into two subcategories based on the MHC genotypes of the mare and the embryo. It was further hypothesized that matings producing only MHC homozygous embryos (A x A) would be less successful than those that had an equal probability of producing MHC homozygous or heterozygous embryos (A x A/B). Again, no difference in the pregnancy rates was found between these two groups. We concluded that the MHC did not operate in the period from fertilization to Day 30 in equine pregnancy to influence reproductive success.

Patterns of Ribosomal RNA Gene Evolution in Arbuscular Mycorrhizal Fungi

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Ribosomal RNA (rRNA) genes are widely used in phylogenetic studies under the assumption that the hundreds of rRNA gene repeats found within a typical eukaryotic genome are kept homogeneous by the mechanisms of concerted evolution. However, recent studies have shown that strict homogeneity is not always the case and that a different mechanism may govern multi-copy gene evolution, birth-and-death evolution. This study documents distinct rRNA gene repeats within the *Glomus etunicatum* lineage of arbuscular mycorrhizal (AM) fungi (phylum Glomeromycota). Amplification, cloning, and sequencing of 5.8S-ITS2-28S rRNA gene regions revealed that individual spores harbored multiple, distinct rRNA gene repeats. Strikingly, each spore contained two variant repeats differing by a roughly 100 bp deletion in the ITS2 region. Phylogenetic reconstruction showed that the two variant rRNA gene repeats arose before *G. etunicatum*, *G. claroideum*, and *G. luteum* diverged. Relative rates tests revealed that the rate of molecular evolution of the deletion-carrying variant was significantly accelerated relative to the that of the variant without the deletion. Yet transcript analysis showed that in *G. etunicatum* both rRNA gene variants are actively transcribed. Modeling of the ITS2 secondary structure revealed that, despite the large deletion, important pre-rRNA processing landmarks are retained in the deletion-carrying variant. These results exhibit elements consistent with the birth-and-death model, and show that AM fungi have clearly experienced a relaxation of concerted evolution. The presence of such distinct variants at appreciable frequencies highlights the hazards of using multi-copy genes for phylogenetic analyses for not only AM fungi, but eukaryotes in general.

Comparing Female Characteristics to Egg and Yolk Size in the Chilean Swallow (*Tachycineta meyeni*): Insights from Non-destructive Photographic Techniques

MITCHELL J. WALTERS

Under the supervision of Drs. Caren Cooper and David Winkler
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Variation in female and environmental characteristics can lead to variation in egg composition for a variety of bird species. I investigated the relationship between female attributes and egg size and yolk size in Chilean Swallows (*Tachycineta meyeni*) breeding in Ushuaia, Argentina. I examined whether egg volume, yolk volume, and relative yolk volume (the yolk-to-egg volume ratio) varied with three non-genetic factors: female mass, laying order, and lay date. All egg parameters showed no significant correlations with either female mass or laying order. Yolk volume and relative yolk volume decreased across the laying season, whereas egg volume showed no change at all. I carried out my investigations using egg measurements collected in the field as well as egg and yolk measurements extracted from digital photographs taken in the field with a standardized egg candler,

the ovolux. If egg dimensions extracted from photographs were comparable to field measures, then the ovolux could reduce egg handling and breakage in the field. However, there wasn't a significant correlation between field values and ovolux values. This suggests that some refinements to the ovolux methods may be needed to better assess egg quality.

Localization and Expression of a SLC4-like $\text{Cl}^-/\text{HCO}_3^-$ Exchanger in Renal Tubules of Adult Female Yellow Fever Mosquito *Aedes aegypti*

LI WANG

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In Malpighian tubules of the mosquito *Aedes aegypti*, an apical vacuolar-type (V-type) H^+ -ATPase in principal cells energizes transepithelial fluid secretion by translocating H^+ from the cytoplasm to the tubule lumen. However, the handling of intracellular HCO_3^- by principal cells is presently unknown. In this thesis, the hypothesis was tested that a solute-linked carrier 4 (SLC4) $\text{Cl}^-/\text{HCO}_3^-$ exchanger is expressed on the basal membrane of principal cells to mediate the absorption of intracellular HCO_3^- in a manner analogous to acid-secreting intercalated cells of the mammalian renal tubule. Using Western blotting, it was demonstrated that the expression of *AeAE* in adult female Malpighian tubules is enriched in the Malpighian tubules relative to that of the midgut. Moreover, using immunohistochemistry, expression of *AeAE* was shown to occur exclusively at the small stellate cells that intercalate between principal cells. Lastly, using Western blots, challenging female mosquitoes with an acid or base load to their sucrose diets did not directly influence the expression of *AeAE*. The finding is consistent with previous work by the Beyenbach laboratory indicating that *AeAE* is important for maintaining the diuretic rates of fluid secretion by Malpighian tubules after an initial stimulation by kinin and calcitonin-like diuretic peptides.

PARP-1 and SIRT1, but not NMNAT-1, Regulate Neuronal Differentiation of Neuroblastoma Cells

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NAD^+ (nicotinamide adenine dinucleotide)-related enzymes play important roles in fundamental molecular and biological processes like DNA repair, transcription, aging, and neuronal gene expression and differentiation. Key enzymes include the NAD^+ biosynthetic enzyme, NMNAT-1 (nicotinamide mononucleotide adenylyl transferase 1), and enzymes that catalyze the use of NAD^+ , PARP-1 (poly(ADP-ribose) polymerase 1) and SIRT1 (sirtuin 1). To study the role of PARP-1, SIRT1, and NMNAT-1 in neuronal differentiation, I used a short hairpin RNA (shRNA) approach to stably knock down these factors in SH-SY5Y neuroblastoma cells (the knockdown was confirmed by immunoblotting and real-time quantitative PCR analyses). Expression analyses showed that

PARP-1 and SIRT1 repressed expression of the neuronal differentiation markers, NF-M and Tau. However, PARP-1 and SIRT1 knockdown reduced retinoic acid and brain-derived neurotrophic factor (RA+BDNF)-induced SH-SY5Y neuronal differentiation. Analysis of neurite formation (indicative of neuronal differentiation) also showed similar results. Unlike PARP-1 and SIRT1, NMNAT-1 knockdown did not have a significant effect on NF-M or Tau expression and neurite formation. These results thus suggest that PARP-1 and SIRT1, but not NMNAT-1, are involved in the regulation of neuronal differentiation.

Characterization of the Subcellular Localization of ZFP568, a Member of the Krüppel-associated Box Domain Zinc Finger Protein Family

VICTORIA A. WELLS

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During embryonic morphogenesis, the attainment of the correct body plan is dependent upon the precise regulation of cellular processes. Convergent extension is a morphogenetic process whereby cells intercalate towards the embryonic midline resulting in elongation of the anterior-posterior axis and concomitant narrowing of lateral tissues (Tam and Behringer, 1997; Wallingford et al., 2002; Yamanaka et al., 2007; Ybot- Gonzalez et al., 2007). *chato* mutants, isolated from an ENU mutagenesis screen, have embryonic malformations consistent with the disruption of convergent extension, including a shorter and wider body axis, open neural tube, and mediolaterally expanded somites (Garcia-Garcia et al., 2008). Positional cloning revealed that *chato* disrupts *Zfp568*, a member of the KRAB domain zinc finger protein family, causing a Leu to Pro change in the first KRAB-A of two highly conserved KRAB domains (Garcia-Garcia et al., 2008). Complementation tests revealed *chato* is a null allele of *Zfp568* (Garcia-Garcia et al., 2008). KRAB domain proteins are proposed to function as transcriptional regulators. Consistent with this hypothesis, previous experiments in the Garcia Lab showed that GFP-tagged ZFP568 localizes to the nucleus, the cytoplasm, or both subcellular compartments in NIH-3T3 cells. Transfections of ZFP568-GFP and ZFP-myc in ST0 cells reproduced these localization patterns. Truncations of ZFP568 fused to GFP were constructed to map protein domains responsible for subcellular localization. KRAB-GFP localized to the nucleus, the cytoplasm and to both the nucleus and cytoplasm albeit with different frequencies as compared to full length ZFP568 and zinc-finger-GFP localized primarily to the nucleus. The observed localization patterns suggest that specific domains within ZFP568 affect its subcellular localization. In particular, the observed higher frequency of nuclear localization of ZF-GFP fusions is consistent with the proposed DNA binding function of the zinc finger domains. This is also consistent with the observed decrease of KRAB-GFP fusion proteins localized in the nucleus.

PSPT04723 Controls the Production of the Coronamic Acid Moiety of Coronatine in *Pseudomonas syringae* pv. *tomato* DC3000

AARON G. WEXLER

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The disease symptoms of *Pseudomonas syringae* pv. *tomato* DC3000 are induced by the translocation of effector proteins via the type III secretion system, as well as by the production of various phytotoxins. These virulence factors contribute to the survival of *P. syringae* within the host apoplast. One phytotoxin in particular, coronatine (COR), is the major determinant of spreading chlorosis in several pathovars of *P. syringae*. COR is composed of two moieties, coronafacic acid (CFA) and coronamic acid (CMA), linked via an amide bond. CFA is a polyketide and CMA is an ethylcyclopropyl derivative of isoleucine. Phytotoxins and type III effectors may have overlapping functions in virulence, and disentangling these functions is complicated by redundancy and linkage of their genes in horizontally acquired gene clusters. Here, the production of COR, as well as the resulting chlorosis phenotype, was shown to occur independently of the type III effectors, and with minimal bacterial growth within the host apoplast. The small ORF, PSPT04723, located within effector-gene cluster IX of DC3000, was shown to be necessary for the synthesis of COR due to its control over the production of CMA, but not CFA. This chlorosis-promoting factor is a member of the DUF1330 family of hypothetical proteins and appears to play a role in the regulation of the CMA biosynthetic pathway.

Genetically-based Latitudinal Clines in the Growth and Defense of Common Milkweed, *Asclepias syriaca*

ELLEN C. WOODS

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Several climatic variables, most notably temperature, predictably vary latitudinally and have been hypothesized to be responsible for gradients in species diversity and the intensity of biotic interactions. This study focused on how ten degrees of latitudinal variation in climate (and potentially biotic interactions), encompassing latitudes between Quebec City, Quebec and Knoxville, Tennessee, impacted adaptation in growth and defense traits of common milkweed, *Asclepias syriaca*, across its native range. In particular, we established a large field common garden to examine genetically-based latitudinal clines from 22 populations of *A. syriaca* and used various multiple regression techniques to examine relationships within and between climatic variables, plant growth characteristics, and defense against herbivory (latex, cardenolides, trichomes, and resistance to a specialist insect herbivore). Our study did not support the notion of increased herbivore pressure, and hence greater investment in defense, in more southern latitudes. On the contrary, *A. syriaca* populations showed significant positive correlations between latitude and latex exudation, plant

height, seed mass, and root buds (a measure of asexual reproductive potential). A path analysis revealed that although several of these response variables were correlated, latitude predicted investment in seed mass, which subsequently influenced plant height; similarly, latitude drove genetically-based variation in latex exudation, which was the primary mechanism of plant resistance to specialist monarch, *Danaus plexippus*, caterpillars. Precipitation (independent of latitude) at the sites of the 22 populations had a modest impact on several plant traits. Our experiment suggests that selection within a species along a latitudinal gradient is driven by both clines in abiotic and biotic interactions. Common milkweed, which originated in northeastern North America, shows a pattern of clinal genetic differentiation with populations from higher latitudes being more vigorous and investing more in plant resistance to herbivores.

Functional Analysis of the Role of *Mai5*, *MAPKKK α* , and *MAPKKK ϵ* in Plant Innate Immunity

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Plants have evolved their own defense mechanisms against pathogen infections, and understanding such mechanisms may have agricultural and economical benefits. Tomato *MAPKKK α* (*SIMAPKKK α*) is currently one of the best characterized *MAPKKK* proteins, which are a superfamily of proteins involved in signaling cascades in response to both extra- and intracellular stimuli. Another member of this family, *SIMAPKKK ϵ* , was found in a microarray study and preliminary results suggested that *SIMAPKKK ϵ* is involved in PAMP (Pathogen-associated Molecular Patterns)-triggered immunity (PTI). Interestingly, a serine/threonine protein kinase, *SIMai5*, was found to interact with both *SIMAPKKK α* and *SIMAPKKK ϵ* in yeast. My objective was to characterize the role of *MAPKKK α* , *MAPKKK ϵ* and *Mai5* in plant immunity in *Nicotiana benthamiana*. Silencing of either *MAPKKK α* or *MAPKKK ϵ* in *N. benthamiana* does not compromise PTI in a cell death suppression assay, suggesting perhaps they are not involved in PTI. However, silencing of *Mai5* did compromise PTI similar to that seen in an *FLS2*-silenced control, indicating it plays a role in PTI. A possible explanation for these results is that *SIMai5* is able to utilize multiple *MAPKKK*s, thus *SIMAPKKK ϵ* is not required for the PTI pathway; instead, another "true" *MAPKKK* may be required. This explanation is consistent with research showing a possibility for multiple *MAPKKK* pathways associated with PTI.

Phase Boundaries between Macroscopic and Nanoscopic Domains in a 4-Component Bilayer Mixture, DOPC/POPC/DSPC/Cholesterol

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Quaternary phase diagram of the liquid order phase and liquid disordered phase (Lo+Ld) coexistence region was constructed from two previously known ternary phase diagrams of DOPC/DSPC/cholesterol and POPC/DSPC/cholesterol by visualizing giant unilamellar vesicles (GUVs) with fluorescent microscopy. The Lo+Ld coexistence regions of these two phase diagrams show visible domain size variation. The phase domains in the Lo+Ld coexistence region of the DOPC/DSPC/cholesterol system separate into large macroscopic domains in the order of microns that are clearly visible under the microscope. The phase domains in same region of POPC/DSPC/cholesterol system separate into very small nanoscopic domains that makes the GUVs appear uniform or single phase under the microscope. Trajectories between the two phase diagrams were constructed by replacing only DOPC by POPC at each given DSPC:cholesterol ratio until the boundary where macroscopic becomes nanoscopic domains can be identified. More POPC is required for transition at higher DSPC to DOPC and POPC ratios. Several modifications were made to the original gentle hydration method of GUV preparation that decreases impurity of negatively charged lipids and improves the yield of GWs. Imaging method was modified to reduce the length of fluorescent exposure, which has been previously observed to be one of the factors contributing to light induced phase separation.

Assessing the Comparative Efficacy of Humor- and Fear-based Public Health Messages

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With the majority of published research focusing on the separate persuasive abilities of humor and fear, little has been accomplished in the way of comparing the efficacy of these tactics. Given this gap in the literature, this research juxtaposed humor and fear appeals in order to assess participants' responses to health messages. Additionally, because health messages are directed at those individuals who currently engage in harmful health behaviors, it was expected that such behaviors would, in tandem with the inclusion of humor or fear, result in differing responses to health messages.

Participants were exposed to four common topics used in health messages, and each viewed two messages that incorporated humor appeals and two messages that included fear appeals. Participants then responded to a series of measures assessing their perception of threat and self-efficacy, as well as their depth of processing, message discounting, and ultimate intention to follow health recommendations for each type of appeal. Additionally, questions of perceived threat, efficacy, and future behavioral intention were revisited following a time delay in order to account for changes due to the sleeper effect.

Overall, humorous message appeals positively influenced viewers' evaluations of a message's recommendations. Exposure to humorous appeals resulted in greater intention to practice healthy behaviors following message exposure and was largely predicated on humor's positive associations with self-efficacy and negative associations with message discounting. The results of this study imply that persuasion towards a message's recommendations results from an individual's perceived ability to overcome a health threat, internalize a message's arguments, and positively evaluate the quality of the message, rather than from the inherent traits of a message's valence.

Positive Pressure: Anxiety Relief as a Function of Somatosensory Stimulus Therapy in Autistic Children

ALEX E. KELLER

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Despite a considerable amount of anecdotal evidence supporting the positive effects of somatosensory (deep pressure) therapy on anxiety in autism spectrum conditions (ASC), very little empirical evidence exists to substantiate this therapy. The present study measured galvanic skin response (GSR) in 5 children with ASC in response to various forms of pressure-based therapies. Subjects were engaged in a structured behavioral interaction with the experimenter, and GSR levels

were measured as a function of applied and withdrawn applications of therapy throughout the interaction. Our results indicate that there was a significant decrease in levels of skin conductance during only the first 30 seconds of applied pressure. These findings suggest that somatosensory therapy is effective during only the initial period of application, although results could also be an effect of procedural confounds, materials employed, or the small sample size and consequent lack of statistical power. Future research should specifically recruit participants who already adhere to forms of pressure therapy, and should employ additional physiological and behavioral markers of anxiety to complement GSR data.

Patterns of Prey Sharing in an Unusual Social Spider: Individual and Kin-related Benefits in *Delena cancerides*

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Under the supervision of Dr. Linda Rayor
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Although the benefits of group foraging likely drove the evolution of sociality in the social spiders, the factors that influence group-level and individual-level benefits of prey sharing in social spiders are still poorly understood. In the present study, the effects of kin relationships and familiarity on the amount of prey shared and the patterns of distribution of the shared prey biomass among individuals were examined in the unusual transitional social spider *Delena cancerides* (Sparassidae). To determine whether more prey was shared among kin groups, treatment groups containing spiderlings of varying relatedness and familiarity to each other were each fed a single prey item and the amount of weight gained by sharing and solitarily feeding individuals was measured. The levels of relatedness and familiarity were shown to have no effect on the amount of prey consumed by prey-sharing groups of *D. cancerides*, although the duration of sharing, number and age of the spiders involved, and the size of the prey item all had significant effects. This lack of differential sharing based on kin relationships and familiarity is thought to be a byproduct of the adaptive willingness to share prey in this species when prey abundance is high and influenced by the likelihood of prey sharing among unrelated individuals in this species. To determine whether prey is equally distributed in prey sharing events, colonies of *D. cancerides* were each given a single flesh fly, which turns abdomens of the spiders increasingly pink relative to the amount of prey biomass consumed. When multiple spiders share a prey item, the biomass of prey consumed by the group is not distributed evenly among all of the spiderlings. Greater color change reflects longer duration feeding and is most clearly demonstrated in the younger spiders. These results provide support for the hypothesis that there are significant foraging benefits to communal living in *D. cancerides* and this may be one of the factors that selected for social behavior in the species.

Identification of Possible Virulence Factors in the Broad-spectrum Pathogen *Serratia marcescens*

GABRIEL T. LAHUE

Under the supervision of Dr. Brian Lazzaro
Department of Entomology

The identification and characterization of bacterial virulence factors is important for effective treatment of bacterial infections, especially in the case of opportunistic human pathogens like *Serratia marcescens*. In this study I assess the virulence level of five *S. marcescens* strains by infecting *Drosophila melanogaster*, a natural host of the pathogen. I had the genomes of these strains sequenced using high-throughput Illumina-Solexa technology, and compared the whole genomes of a highly virulent *S. marcescens* strain and a non-virulent one to find genes or regions that were absent in the non-virulent strain. Forty-nine putative virulence genes were identified by sequence

homology to genes involved in virulence in other pathogens. These putative virulence genes were located in fourteen genetic regions that were missing in the non-virulent strain. These potential virulence factors may prove to be important in the pathogenicity of *Serratia marcescens* against a broad spectrum of natural hosts.

The Biodiversity of Bees in the Apple Orchards of New York State

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Department of Entomology

Bees are the most important pollinators in many agroecosystems, providing billions of dollars in revenue each year in the U.S. alone. Despite the existence of nearly twenty thousand bee species, past focus on pollination has been placed almost solely on the honey bee as a managed pollinator, with little research on unmanaged pollinators in agroecosystems such as apple orchards. In our study, we collected bees of all species in apple orchards to determine the biodiversity of bees present, while also investigating orchard size, pesticide usage, honey bee abundance, and edge effect as having a potential role in bee richness and non-honey bee abundance. A total of 75 species were found in the collections. We also found that while none of the examined parameters were correlated with observed species richness, non-honey bee abundance was negatively correlated with orchard size, which when combined with the finding that significantly more species are found at the edge of orchards suggests edge effect and distance from edge habitat play an important role in the pollination services provided to apple orchards by unmanaged bees. In the future, more work will be necessary to determine the magnitude of the role edge effect and distance from edge habitat play in apple orchards and other agroecosystems.

Why Are Native Ladybeetles Shrinking? A Case for Invasive Competition

JORDAN E. PERLMAN

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Since inception, the Lost Ladybug Project has collected six-thousand ladybeetle images, and its investigators have established sustainable colonies of rare coccinellids. In 2006, after a fourteen year absence from the eastern U.S., a nine-spotted ladybeetle (*Coccinella novemnotata*) was discovered in Washington, D.C. In June 2009, thirteen *C. novemnotata* specimens were collected from western Oregon. Entomologists are pondering the reasons for the disappearance of New York's State Insect, which was formerly common across the U.S., but is currently found solely in the west, and very rarely even in that region. One hypothesis is that *C. novemnotata* (and other native species) are being outcompeted for prey by introduced species. Since lowered prey levels may lead to smaller adults, this research examines two native (*C. novemnotata*, *Coccinella transversoguttata*) and one introduced coccinellid species (*Coccinella septempunctata*) and quantifies the size differences apparent between historical specimens (stored in the Cornell University Insect Collections), recent captures, and

individuals reared in the laboratory. The second component of this study varies prey availability to *C. novemnotata* larvae, and investigates the apparent differences in the resulting adult beetles. Results indicate that the average, natural volumes of these species have, in recent years, declined significantly. The data from the nine-spotted ladybeetle demonstrates several notable patterns; historical individuals are twice as large as recent captures, and specimens bred in captivity are four times the size of those in nature. Findings indicate that each examined species may have become deprived in its access to nutrition. The feeding study data suggest that *C. novemnotata* found in nature may be eating fewer than three aphids daily. Low fed larvae are significantly smaller than high fed larvae. Low fed larvae take longer to pupate and then eclose sooner. Ongoing research seeks further explanation of the variables responsible for the decline in *C. novemnotata* prevalence.

Investigating the Synergistic Effects of Carbon Dioxide and Human Skin Volatiles in Mosquito Attraction and Its Application in the Development of a Novel Mosquito Control Strategy

LAURA F. SEEHOLZER

Under the supervision of Dr. Laura Harrington
Department of Entomology

Host-seeking female mosquitoes are attracted to two major classes of compounds in the human odor plume: carbon dioxide and human skin volatiles. Although it is known that these kairomones (attractive compounds) are necessary for attraction, two aspects of their relationship were unknown; (1) if they were sufficient for attraction and (2) if the mechanism of attraction was synergistic or additive. To test this, I conducted a field behavioral assay in Ifakara, Tanzania comparing the number of mosquitoes caught when using a human volunteer, CO₂ alone, synthetic human kairomones (blend), or blend+CO₂ as the attractive lure. I found that the combination was sufficient for attraction and had a synergistic effect on *An. arabiensis* and *Mansonia* female attraction. The practical purpose in evaluating the relationship between kairomones is to use this knowledge to create maximally effective lures for use in both interception and sampling traps. The combination was, subsequently, used as the attractive lure in an interception trap. Mosquito interception, as a method of vector control, aims to divert mosquitoes into a trap so as to reduce the total amount that reach their intended destination. When the volatiles and CO₂ were used as the attractive compounds in the interception trap, the number of mosquitoes entering experimental huts significantly decreased without increasing the total number of mosquitoes responding to the cues. This showed the effectiveness of the OBS as an interception trap and the potential of interception traps as a viable method of mosquito control.

Greenhouse Gas Emissions from a Community Anaerobic Digester with Mixed Organic Wastes

CHRISTOPHER A. BENTLEY

Under the supervision of Dr. Louise Buck
Department of Natural Resources

Opportunities for reducing greenhouse gas (GHG) emissions through farm manure management systems and the implementation of anaerobic digestion are of growing interest to farmers, electric utilities, and environmentalists alike. There is a prevalent concern however, that, certain elements of centralized anaerobic digestion (e.g., transportation) constitute emissions additional to current manure management systems. This thesis attempts to shed light on this dilemma by developing a scenario modeling methodology to project potential GHG emissions from five potential anaerobic digestion systems that have been proposed by the Cornell University Department of Biological and Environmental Engineering and the Department of Applied Economics and Management in the context of an economic feasibility study completed for the Town of Lowville, New York, and the County of Lewis, New York. The proposed Lewis County community digester is presented as an example of community-based co-digestion of mixed organic wastes and its implications for GHG emission reductions accounting within an economic feasibility framework.

The research findings reinforce that anaerobic co-digestion of manure and food processing waste can considerably soften the carbon footprint of dairy production at the community scale. Expanding transportation networks do indeed lessen the net emission reductions of anaerobic digestion projects in which biomass transportation is considerable. However, on the scale of this analysis, emissions associated with transportation were relatively inconsequential to the overall balance of GHGs.

Assessing the Restoration Needs of the San Francisco Estuary Using a Target Fish Community Analysis

SYDNEY P. BLANKERS

Under the supervision of Dr. Mark Bain
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Historically, aquatic ecosystem restoration has attempted to return a region to past or pristine conditions, which is often unachievable. Here I examine a different approach using a target fish community analysis that efficiently reveals aspects of the ecosystem that are most important for site improvement. The target community is comprised of the relative proportions of fish species that should be at a location based on fish present in biologically similar reference sites considered to be ecologically acceptable. Comparison with the current proportions of species at the restoration site reveals specific objectives on which ecologists can focus in order to maximize restoration efforts. This study examines the effectiveness of target fish community analysis in the San Francisco Bay, the largest estuary on the Pacific coast, using four coastal estuaries: Columbia Estuary, WA/OR;

Tillamook Bay, OR; Morro Bay, CA; and Santa Monica Bay, CA. Trawl data from South San Francisco Bay conducted by the Marine Science Institute in Redwood City, CA from 1970 - present were used for the comparison. Data revealed no changes in species abundances through time, and benthic species were consistently underrepresented relative to the target. In addition, pelagic Northern Anchovy were overabundant even though they were the most prevalent species in the target. I propose that the dominant Northern Anchovy benefits from eutrophic conditions and increasing food availability, which lowers benthic oxygen and results in lower fish abundance. In addition, toxins such as mercury and polychlorinated bisphenols buried in sediment could contribute to low abundances of benthic species. The study showed that restoration efforts should focus on eutrophication and sediment toxicity as important aspects of the San Francisco Bay that impact fish communities and that the target community analysis has great potential for systems with appropriate reference sites.

Resource Selection and Home Range Size in a Suburban White-Tailed Deer Population

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Increased levels of human-wildlife conflict with white-tailed deer (*Odocoileus virginianus*) in suburban landscapes have forced many communities to manage these overabundant animals. In order to best allocate limited resources for deer management, deer ecology, including resource selection, must be thoroughly understood (Kilpatrick and Stober 2002). We conducted a telemetry study on 71 sterilized deer to determine habitat preference across seven different land types at two scales within and across eight seasons. Deer did not exhibit resource selection in this study. Different habitat types were used significantly differently than one another ($P < .0001$), due to the fact that they were available in varying proportions. Different habitat types were not selected for significantly differently than their availability ($P=.72$). This provides evidence that deer are habitat generalists. Deer selection was not affected by seasonality ($P=.89$) or maternal status ($P=.70$). Average core 50% KDE home ranges were in 11.2 ha in spring, 11.1 ha in summer, 13.5 ha in fall, and 18.5 ha in winter. Average 95% KDE home ranges were 51.6 ha spring, 50.3 ha in summer, 53.6 ha in fall, and 74.0 ha in winter. Further study of deer resource use and habitat preference may allow managers to devise strategies to discourage deer from causing conflicts in suburban areas.

Testing Microbial Home-Field Advantage in Native Versus Introduced *P. Australis* and Potential Impacts on Producer and Consumer Trophic Levels

INGA E. CONTI-JERPE

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Traditionally, microbial communities have been viewed as invariant across ecosystems; however recent research suggests that microbes have a “home-field advantage” in that they are adapted to decompose leaf litter from surrounding plants, indicating that evolutionary relationships play an integral role in ecosystem function. We investigated how the interactions between microbial communities and available leaf litter that result from introduced *Phragmites australis* invasions impact decomposition rates, primary productivity (algae growth), and primary consumer growth (*Daphnia sp.*). Our results did not support the theory of home-field advantage; microbial communities decomposed native *P. australis* litter faster than introduced *P. australis* litter regardless of where the microbial communities originated from. However, microbial communities did have a significant influence on decomposition rates, suggesting that there is variation among populations. Decomposition rates were negatively correlated with lignin content of litter, indicating that litter quality was the overall driver of decomposition rates. Decomposition rates were positively correlated with algal growth. *Daphnia* data is still preliminary, but there appears to be a significant influence of microbial source on *Daphnia* abundance that is unrelated to decomposition.

Arbuscular Mycorrhizal Response to Group Selection Management of *Sequoiadendron giganteum*

CATHERINE FAHEY

Under the supervision of Dr. Teresa Pawlowska
Department of Plant Pathology and Plant-Microbe Biology

Because of the threat of low regeneration success in giant sequoia (*Sequoiadendron giganteum*), group selection management is being studied as a tool for giant sequoia regeneration. Mycorrhizal associations are widely accepted as being highly beneficial in seedling growth and success; therefore there is interest in better understanding the role that mycorrhizal associations play in the regeneration of giant sequoia seedlings in group selection openings. This study quantified percent colonization of giant sequoia roots by arbuscular mycorrhizal fungi (AMF) in order to meet three objectives; 1) to determine the impact of gap size, 2) location within gaps, and 3) soil substrate on AMF colonization of giant sequoia roots. A new protocol was developed for the clearing and staining of giant sequoia roots. Our findings showed an average of 30% colonization by AM. The trends in our data suggest that there is higher colonization at the centers of gaps which suggests that the colonization is controlled by availability of assimilated carbon to the fungus rather than by the AMF supply of nutrients to the tree roots. Additionally, the mid-sized gaps had higher colonization than the large and small gaps, which supports that the light availability at the centers of gaps is not limiting in gap

sizes above 0.2 hectares. We also found a negative correlation between AM colonization and infection by non-AM hyphae suggesting a negative interaction between these species.

An Evaluation of Community-based Cloud Forest Restoration in Northwestern Ecuador

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Communities within the region of Intag (province Imbabura) in Northwestern Ecuador have implemented cloud forest restoration projects to assist in the reestablishment of Ecuador's threatened Tropical Montane Cloud Forests. The Andes of Ecuador are located in a biological diversity hotspot, but most reforestation projects have historically used exotic species because of the lacking basic ecological information for native species. Small restoration projects thus serve as valuable opportunities to acquire knowledge about reforesting with native trees. The objectives of this study were to evaluate the success of reforestation projects, specifically tree survivorship and growth, within 5 small community-owned reserves and to develop a set of recommendations for improving success of future community-based restoration efforts. The species, approximate age, height and diameter were recorded for 1424 trees. This included 46 different species of which 7 were non-native to the region. The most commonly measured trees were *Croton sp.*, *Delostoma sp.*, non-native *Alnus spp.*, *Clusia flaviflora*, and *Calliandra pittieri*. In general, among the 5 reserves survivorship and growth were high and results indicated significant differences in height among species. Species, tree age, and reserve were all significant in determining height. Recommendations include the further prioritization of reforesting with native species and obtaining accurate scientific names. It is also important to continue research identifying relevant factors that characterize sites within reserves and matching suitable species under differing conditions. Restoration incorporates both ecological and socio-economical factors, so a successful project must include ecological monitoring on a long term basis and ensuring communities remain interested and involved.

A Funnel into a Runnel, Problem or Solution? The Impacts of Roadside Ditches on Stream Geomorphology

JONATHAN M. KIMCHI

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

Increases in the extent of impervious surfaces throughout watersheds of the Northeastern U.S. have had significant impacts on downstream waters. Research studies have documented the impact of impervious surface on the hydrologic regime, water quality, and ecosystem health of associated streams. Roads are the first impervious surfaces constructed during new development and quickly affect their surroundings by increasing surface runoff and contributing toxic chemicals and heavy

metals to streams. Runoff directly from roads has contributed to increased peak flows and degradation of water quality. However, in nearly all studies examining the effects of roads on streams, researchers have failed to include the impacts caused by roadside ditches. This study examined the impacts of roadside ditches on in-stream geomorphology of five streams in the Doolittle Creek Watershed in Candor, N.Y. The objectives were to compare stream reaches upstream and downstream of the ditch confluence for longitudinal profile, cross-sectional profiles, bank scour and streambed grain size. Three of the five streams exhibited an incising of the downstream channel while two appeared to be broadening. Downstream bank scour demonstrated a greater proportion of steep cut, bare bank than was measured in the upstream scour profile. Evaluation of the streambed grain sizes indicated a fining of the overall grain size downstream of the ditch interface. The grain size was similar to that of the delta formed at the ditch-stream interface. All findings are limited by small sample size. However, overall, we conclude that the ditches have a significant impact on stream geomorphology, both through the sudden increase in large amounts of flow and through the input of gravel and finer grain sediments.

The Effects of Land Legalization on Economic Productivity in the Amazon Floodplain

APOLLONYA M. PORCELLI

Under the supervision of Dr. James Lassoie
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The Amazon estuary in northern Brazil has been marred by political inconsistency since its colonization. Due to the 2006 implementation of *Nossa Várzea*, a national initiative to privatize floodplain lands, the region has seen a rise in federally mandated organization. Instigating a triplicate approach to sustainable development, this research compares two communities, Bela Patria and Piriá in order to show the effect of land legalization on economic productivity. Bela Patria, as a completely privatized area, is contrasted with Piriá, which has yet to participate in the initiative. Socio-economic indicators gathered from quantitative and qualitative surveys yielded distinctively polarized results. Using a coupled human and natural systems lens for analysis, it was seen that the efficacy of land legalization on environmental, social and economic channels of development to promote overall economic productivity was greater in Bela Patria than in Piriá. Complemented by discussions of social capital, the need for multi-scaled governance as a precursor for continued sustainable development is demonstrated.

Nesting Density an Important Factor Affecting Chick Growth and Survival in the Herring Gull (*Larus argentatus*)

MATTHEW S. SAVOCA

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The Herring Gull (*Larus argentatus*) is one of the largest, most common, and most conspicuous gulls in North America. They are facultative, colonial nesters on Appledore Island, with pairs nesting both in dense colonies and in more isolated situations. Colonial pairs breed in mixed-species colonies with Great Black-backed Gulls (*L. marinus*) whereas the more isolated, solitary-nesting pairs are found around the buildings of the Shoals Marine Lab campus. As such, Appledore Island offers a unique opportunity to compare reproductive success between pairs nesting in both contexts on the same island. Chicks reared in dense colonies had a significantly higher growth rate than those reared in more isolated settings. A survival analysis in Program MARK determined that a chick's expected survival is dependent on several factors: hatch weight, hatch date, hatch order, and nesting context (dense colony vs. isolated). Additionally, C (third-hatched) chicks have a significantly higher chance of survival from hatching to fledging if they are born and reared in the dense colony than in the isolated nest setting. Differences in chick survival and growth rate could be due to differences in food quality, food delivery rates, proximity to nesting Great Black-backed Gulls, and agonistic interactions. Agonistic interactions were significantly higher in the dense subcolony, but most of these interactions were of low intensity, suggesting vigilance that has a positive impact on chick survival.

A Qualitative Study of the Ideal Meal

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This project aimed to understand the way people define and describe the ideal meal as well as the interaction of ideals with other influences on food choice. In depth qualitative interviews with 42 adults were conducted and analyzed using the constant comparative method. Analysis of participants' self-reported ideal meals revealed four prominent themes (*comfort/togetherness, role fulfillment, freedom from responsibility, and adventure and indulgence*) and two methods of defining ideals (*past and imagination*). The exploration of ideals provides insight into one of the influences on food choice. An increased understanding of ideals may lend insight and explanation to behaviors that influence dietary intake and may help marketers present their products to prospective consumers more effectively.

Investigation of the Role of Two Iron Exporters; Breast Cancer Resistance Protein 1 (BCRP1) and Feline Leukemia Virus Receptor, Subgroup C (FLVCR) in Placental Iron Transfer

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Mechanisms of placental heme iron transport are largely unknown. To address this area of research, expression of two heme transporters; Feline Leukemia Virus, Subgroup C, Receptor (FLVCR) and Breast Cancer Resistance Protein (BCRP) were measured in placental tissue from a cohort of pregnant adolescents (13-18 y of age). Iron status indicators, hemoglobin (Hb), serum ferritin (SF) and serum transferrin receptor (sTfR), were measured at mid-gestation (25.1 ± 3.5 wks) and in maternal/cord blood obtained at delivery (39.8 ± 1.2 wks). At delivery, 29% (N = 18/62) of teens were anemic (Hb < 11 g/dL), 30% (N = 26/87) had depleted iron stores (SF < 12 μ g/L), and 13% (N = 11/87) had tissue iron deficiency (sTfR > 8.5 mg/dL). Neonatal SF averaged 133.7 ± 81.0 μ g/L (N = 82). FLVCR and BCRP were detected in all placental tissue assayed, however, the expression of BCRP was much more variable. Maternal age, ethnicity, pre-pregnancy BMI, gestational age at delivery, placental weight, and neonate gender were not identified as determinants of either placental FLVCR or placental BCRP expression. A significant positive relationship was observed between placental FLVCR expression and the maternal: neonatal SF ratio at delivery ($p < 0.05$, N = 59). Placental FLVCR expression was significantly positively related to placental BCRP expression ($p < 0.05$, N = 77). However, unlike FLVCR, placental BCRP expression was not significantly related to maternal/fetal iron status. A significant positive relationship was observed between maternal mid-gestation estradiol and placental BCRP expression ($p < 0.05$, N = 66) which is consistent with the presence of an estrogen response element upstream of the BCRP gene. Further analysis is needed to

explore the functional roles of FLVCR and BCRP in the placental and their possible involvement in placental iron transport.

Investigation of the Climatic Impacts of Cloud Whitening Geoengineering using GFDL CM2.0G

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Projected increases in greenhouse gases have prompted serious discussion on geoengineering the climate system to counteract global climate change. Cloud albedo enhancement is an economically and technologically feasible geoengineering approach, but previous research suggests undesirable consequences of globally uniform cloud whitening. The present study uses GFDL's CM2.0G global coupled model to simulate cloud albedo enhancement via increases in cloud condensation nuclei (CCN) targeted at the marine stratus deck of the Pacific Ocean, where persistent low clouds offer a regional approach to cloud whitening. We investigate the impact of this regional geoengineering on global circulation and climate. In the first forty years after cloud whitening begins, surface temperatures returned to near Pre-Industrial over much of the globe. In the first 40 years and over the 160 year mean, significant cooling over the Equatorial Pacific, continued Arctic warming, and large precipitation changes over the western Pacific, and a westward compression and intensification of the Walker Circulation were simulated. The cloud whitening caused a persistent "La Nina" condition associated with an increase in annual hurricane max potential intensity in the tropical Atlantic, decreased annual vertical wind shear and decreased annual SST. Future investigation will focus on seasonal analysis to determine the relevance to the Atlantic hurricane season.

An Analysis on the Impacts of Ice Cover on Two Eastern Great Lakes Lake Effect Snow Events

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Analysis of lake effect snow events is important due to the economic effects lake effect events can have on a region, such as the replenishment of watersheds used in agricultural purposes. It is generally accepted that a number of factors play a role in the persistence and intensity of lake effect snow events, such as ice formation of the surface of the lake, but only recently has that relationship begun to be thoroughly examined. This observational study focuses on the impact of lake surface ice coverage on two lake effect storms that occurred downwind of both Lake Erie and Lake Ontario: "Jack Russell", which occurred from February 19-20 2008, and "Jararaca", which occurred from January 16-17, 2009. This study undertakes a graphical analysis of the lake surface conditions at the time as well as a mathematical study of the heat fluxes and total energy transfer interaction between the lakes and the atmosphere during the duration of the two lake effect events. The analysis identifies that Lake Erie, which is mostly ice covered, experiences a significant decrease in energy transfer as the event persists, while the relatively ice-free Lake Ontario experiences no significant

change in energy transfer for the duration of the two storms. Graphical analysis indicates that the areas of heaviest and most persistent snowfall were experiencing wind fetches off the lake that had traveled over lake surface areas with minimal ice coverage and thickness, highlighting the influence of ice coverage and thickness on the development of lake effect bands.

Chemical Constraints on the Origin of the Frailes Volcanic Complex in the Central Andean Altiplano Plateau, Bolivia

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The Frailes volcanic complex of the Bolivian Altiplano plateau is the largest and most prominent ignimbrite of the Andean Central Volcanic Zone. With 2000 km³ of exposed volcanic deposits dating from 25 Ma to the present, the complex supplies insight into the processes of large-volume silicic melt formation in a back-arc setting. However, the voluminous 0-10 Ma main body of the Frailes complex remains poorly studied, as the majority of the literature focuses on a small region of 12-14 Ma Sn-Ag mineralization at Cerro Rico – the world's largest silver deposit. Here, we present geochemical analyses of 25 representative samples from our fieldwork on the Frailes ignimbrite. Whole-rock major element analysis by X-ray fluorescence spectroscopy showed the ~7 Ma samples to be highly peraluminous, potassic (>5% K₂O) andesitic to rhyodacitic welded volcanic tuffs with an Al-rich, chemically reduced mineral assemblage including biotite, calcic feldspar, magmatic cordierite, and ilmenite. Trace element analysis by neutron activation revealed steep rare earth patterns with Sm/Yb > 5.0, requiring the presence of garnet in a deep-crustal, high-pressure restitic assemblage. In contrast, the presence of cordierite indicates crystallization at low pressure (< 450 MPa), at depths of less than 14 km. These ignimbrites are consequently best explained by mixing of a mantle-derived melt with a reduced, lower crustal component at great depths to produce hybrid magmas that ascended and evolved to form shallow crustal (<14 km) magma bodies before erupting in catastrophic, caldera-forming events.

Investigating the σ^B Stress Response System in Two Lineage IIIA Strains of *Listeria monocytogenes*

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Strains of *Listeria monocytogenes*, an intracellular foodborne pathogen, classify into three genetic lineages. Lineage III strains, associated most commonly with animal disease, have not been extensively studied. σ^B , a transcription factor encoded by *sigB*, has been shown to contribute to stress survival and virulence in *L. monocytogenes*. Recent studies have revealed that σ^B regulons have varied among strains, and that σ^B did not contribute to stress survival in one representative

lineage IIIA strain. The purpose of this study was to determine if σ^B significantly contributes to acid and oxidative stress survival in two additional lineage IIIA strains of different serotypes. Two lineage IIIA strains, FSL F2-695 and FSL F2-525, had isogenic $\Delta sigB$ mutants made using allelic exchange mutagenesis. Those strains and a control lineage II lab strain, 10403S, with its $\Delta sigB$ mutant were subjected to acid stress at pH 2.5 and oxidative stress with 13 mM cumene hydroperoxide for 15 minutes. All three isogenic $\Delta sigB$ mutants had significantly higher acid stress death rates ($p < 0.001$) and oxidative stress death ($p < 0.01$) than their corresponding wild-type strains. FSL F2-525 exhibited a significantly higher acid stress death rate than the other wild-type strains. 10403S had significantly higher oxidative stress death than FSL F2-695. Consistent with strains in other lineages, σ^B is a significant factor in acid and oxidative stress survival in most lineage IIIA strains of *L. monocytogenes*.

Biochar as an Amendment to Improve Soil Fertility

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Biochar, a soil amendment resulting from pyrolysis of biomass, can improve soil texture and increase nutrient and water retention. Biochar produced from various feedstocks, each under a range of temperatures was used to amend field soil at 0.2, 0.5, 2.0, and 7.0% (w/w) application rates (equivalent to 2.6, 6.5, 26, and 91 t biochar ha⁻¹) for growing maize in a greenhouse pot trial. Unamended controls were grown at 60, 80, 90, 100, and 140% of recommended fertilizer application rates to compare the effects of biochar against fertilizer effects. Feedstock, pyrolysis temperature, and application rate all had significant and interrelated effects on total maize biomass. In general, animal waste biochars increased biomass by up to 17%, while food waste biochar decreased biomass in relation to controls by 7 to 92%. Increasing the temperature from 300°C to 600°C decreased the negative effect of food waste biochar. The optimal application rate, regardless of feedstock or pyrolysis temperature, was 2.0% (w/w) (equivalent to about 26 t ha⁻¹), indicating that an increased application past that point did not necessarily lead to increased yield benefits. However, several of the biochar treatments, such as poultry with sawdust and high production temperature corn stover, did lead to greater total biomass than the 140% fertilization controls. Feedstock, pyrolysis temperature and application rate deserve consideration prior to field application, as certain feedstocks can have negative effects on yield. The initial soil environment will largely determine the interaction and impact of biochar due to varying chemical and physical qualities of biochar.

Evaluation of the K Saturation and Soil Test K Approaches for Their Effectiveness in Predicting a Yield Response to K Addition

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Potassium (K) is an important nutrient for alfalfa (*Medicago sativa* L.) in terms of yield, winter hardiness and forage quality. Due to recent increases in K fertilizer prices, farmers are interested in fine-tuning their K management. The objectives of this study were to evaluate two soil-test based K management strategies: (1) the sufficiency concept using the Cornell Morgan soil test and (2) the K saturation ratio according to the basic cation saturation ratio concept (BCSR); and to compare Morgan and SrCl₂ extraction based K saturation determination methodologies. Crop response to K fertilizer was measured in on-farm alfalfa trials (16 fields) and a greenhouse bioassay (12 soils) with annual ryegrass (*Lolium multiflorum* Lam.). Soil test K and K saturation prior to K application (0-20 cm) were linearly correlated with greater variability in calcareous soils ($r^2=0.88$, $n=22$) than acidic soils ($r^2=0.99$, $n=6$). Despite a trend toward higher yield with higher soil test K and K saturation, there was no consistent yield response to extra K in the bioassay while in the on-farm trials, a yield response was measured when soil test K levels exceeded 60 mg kg⁻¹ or SrCl₂ derived K saturation over 1.6%. We conclude that no yield response should be expected with soils testing over 60 mg kg⁻¹ Morgan K or 1.6% K saturation. Response studies need to be conducted on more soil types with both low Morgan soil test K and K saturation, in particular, to determine if the findings of this study can be extrapolated to other soils.

Regulatory Focus and Optimism-Pessimism in Persuasive Health Messages

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Under the supervision of Dr. Michael Shapiro
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Messages about health can take two forms according to regulatory focus theory (Higgins, 1998), that of approaching positive events or avoiding negative events. One possibility is that optimists respond better to promotion focused messages, and pessimists respond better to prevention focused messages. In the current study, participants filled out a standard measure of dispositional optimism. They were also exposed to 4 messages about health topics in either a promotion of health focused or a prevention of illness focused form. The experiment aims to investigate the hypothesis that when the health topic is consistent with promotion focused language, rather than prevention focused language, optimistic college students will think the practice being described is more effective, and will have greater intentions to behave according to the practice compared to more pessimistic college students. Additionally, it is hypothesized that when the health topic is consistent with prevention focused language, rather than promotion focused language, pessimistic college students will think the practice being described is more effective, and will have greater intentions to behave according to the practice compared to optimists. Although the results do not support the proposed hypotheses, this study proposes that the conceptual link between optimism-pessimism and regulatory focus is sound, and with different dependent variables may be demonstrated empirically.

The Effects of Framing Environmental Arguments and Motivating Citizen Action: How Should Environmental Arguments be Framed to Effectively Reach Different Target Audiences?

MICHAELA M. CULVER

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As the current state of the environment becomes a growing concern, people are increasingly interested in ways to protect the environment through motivating positive environmental choices. Currently there is little definitive research on environmental messages and motivating behavior. There is evidence that people will respond in different ways to differently framed arguments depending on their demographic characteristics. This study will investigate the association between people's location of residence (urban, rural or suburban) and responses to different environmental arguments. The degree to which individuals would be motivated to take action and the extent to which they see truth or relevance in the argument will be specifically explored. The effectiveness of framing an argument in a local (location-specific) or global (universally created or felt) sense will be measured, as well as the different types of environmentally conscious decisions or actions participants plan on making. This information will ideally be part of an overall construct guiding the creation of persuasive environmental messages.

From Superman to Supercrip: Media Framing and Perceptions of Disability

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People who are not disabled often have no contact with the disabled unless it is through media messages. These media messages about disabled people employ different lenses or frames of interpretation, which can change the way the message receiver thinks about the disabled exemplar. The “supercrip” is a media frame that portrays a disabled person who overcomes his disability to do something extraordinary. Supercrip frames usually occur within human-interest news stories. The “entitlement” frame, on the other hand, typically depicts a disabled person as taking advantage of a non-disabled person, often because the disabled person seeks revenge against the abled world or feels that the abled should repay him for a lifetime of suffering. Entitlement frames tend to be used in the entertainment context (i.e., Captain Hook). A randomized experiment compared how three media frames (entitlement/supercrip/control) impacted implicit and explicit stereotypes of the disabled. Findings indicate that the entitlement frame caused an increase in implicit prejudice as measured by the IAT compared to both the supercrip frame and the control. The mechanisms behind these implicit attitudes effects were more consistent with attribution and illusory correlation than theories of mere exposure. Explicit attitude effects were also found - the supercrip frame led to endorsement of equality while entitlement led to endorsement of positive discrimination, possibly as a way to compensate for the increased implicit prejudice. Conclusions and avenues for future research are discussed.

Technology, Patents, and Humanitarian Aid: A Comparative Study of Plumpy’nut, Golden Rice, and Oral Rehydration Therapy

EMILY C. GOLDSMITH

Under the supervision of Dr. Philip McMichael
Department of Development Sociology

This thesis explores the use of technological fixes by humanitarian aid and international development programs. Technological fixes are often promoted by international aid organizations, but they face several potential limitations. First, technological fixes can be controlled via international patents. Secondly, technological fixes are often foreign supplied and distributed. This thesis attempts to identify how these two characteristics impact the effectiveness of technologies used for international humanitarian aid. Specifically, this research was carried out through a qualitative comparative study of three representative technologies aimed at improving child health in the developing world. The three technologies chosen were: Plumpy’nut, Golden Rice, and Oral Rehydration Therapy. Plumpy’nut is patented and of simple design, Golden Rice is patented and scientifically complex, and Oral Rehydration Therapy has a simple structure and was never patented.

By comparing the cases of these three technologies, several preliminary conclusions were drawn. First, patents can slow the development, limit the supply, and increase the price of technological fixes and detract from their ability to effectively meet the health needs of children in the developing world. Secondly, technological fixes risk being band-aid solutions that only address the curative side of child health problems, without addressing their causes. Lastly, when technological fixes are developed and supplied by companies and organizations in the developed world, they often fail to create the local health knowledge and community-based capacity that is needed for long-term improvement in child health.

Should Emerging Markets Lessen Foreign Privatization of Natural Resources? : An In-Depth Look into the Grasberg Mine in Indonesia

MARY J. GONDOKUSUMO

Under the supervision of Drs. Garrick Blalock and David Lee
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Natural resources, particularly in emerging markets, that are under the control of foreign companies often bring controversies that lead the government to consider deprivatization of the sites. In this thesis, this question is explored through an in-depth analysis of the Grasberg Mine, the largest gold and third largest copper mine in the world located in West Papua, Indonesia that is controlled by US-based Freeport McMoran. The analysis is done by taking into account the human rights, environmental, and economic impacts of the mine. The human rights condition is controversial due to land rights issues and displacement of indigenous people. The environmental impact is also great due to the toxic wastes dumped in the region, which produces harsh chemicals such as copper, iron, zinc, lead, and mercury to be detected in the soil and water. This leads to death of indigenous species as well as the indigenous people to have an above-average amount of these chemicals in their body due to contaminated food and water consumption. The economic impact of the mine turns out to be a positive one for the country due to the large tax payments and royalties that the firm pays to the government. Furthermore, the comparison of the cost of capital of the firm and the country finds that the firm has a lower cost of capital. Thus, from an economic standpoint, it would be better for Indonesia to leave the mine under the control of Freeport-McMoran while, from a human and environmental standpoints, the decision becomes a more complicated one.

The Next Hollywood Sensation: The Synergistic Effect of Affect in Motion Picture Marketing

ROBERT T. GRUE

Under the supervision of Dr. Sahara Byrne
Department of Communication

This paper examines the effects of emotional convergence between theatrical trailers and the audience. The study analyzes the impact of the audience's emotions while watching movie trailers of certain emotional content, both similar and disparate from their own. Attraction hypotheses are primarily based on mood management theory. The goal is to complement previous research on full-length motion pictures, applying similar and novel variables to a medium of lesser scrutiny, but potentially high economic impact— movie trailers. An experiment was designed to test mood management theory's applicability to three types of movie trailers: sad, happy and uplifting. To test the effect of mood on an individual's preference and likelihood of watching a film, participants were randomly assigned into three conditions: sad, happy and control. Participants in the sad and happy conditions wrote about one of the saddest and happiest moments of their lives to ensure sufficient mood representation, respectively. The control group skipped this procedure. Participants in the sad condition were effectively induced into a sad mood while participants in the happy condition did not significantly elevate in mood.

Contrary to mood management theory, sad participants did not show significant preference for either sad or happy films. Rather, these individuals indicated a considerable preference for uplifting trailers. Similarly, participants in the happy condition showed no significant preference for either happy or sad trailers, but indicated a higher likelihood of watching the movies advertised in the uplifting trailers. Possible explanations of these findings are provided, along with areas of future potential study.

Understanding and Overcoming Agribusiness' Perceived Barriers to GM Technology Donations to Developing Countries

LAURA D. JOHNSON

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Plant biotechnology provides unprecedented opportunities for improvements in agricultural productivity in developing countries. Multinational agribusinesses hold intellectual property (IP) rights on much of this technology. Many developing country farmers lack the purchasing power to attract private sector innovation for their specific crops; humanitarian technology donations may provide a partial solution. This study interviewed three leading agribusinesses to document firsthand the private sector's perspective on technology donations and barriers for transfers. By recognizing

the barriers perceived by private sector donors, potential recipients will have a more thorough understanding of the necessary conditions and prerequisites for successful collaborations.

In most cases, corporate respondents indicated donations were justified as a moral imperative and to a lesser extent, long term new market development. While IP protection and legal liability were frequently cited valid concerns, the most pressing barriers are the lack of regulatory and stewardship infrastructure/capacity in the recipient countries, product development costs and negative international opinions towards genetically modified organisms (GMOs). If a country lacks functional regulatory and biosafety systems, it would be irresponsible for a donor agribusiness to introduce transgenics. Making donations to a consortium of organizations with external funding and a wide array of expertise is the preferred method, but may not indemnify the company from legal liability or provide IP protection.

The future success of technology donations will depend on countries' regulatory and stewardship capacity, a non-hostile climate for GMOs, financial support for product development, fair GMO import thresholds and communication between parties involved in agricultural development.

Estimating the Potential Supply of Biomass for Cofiring in Electricity Production in New York State

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In order to effectively integrate renewable energy sources such as biomass into New York State's electricity market, industry leaders and policymakers must have access to accurate information about the potential supplies of biomass. Particularly, they require information on biomass resources that are currently available so that these resources may be used efficiently in the production of electricity through cofiring in existing coal-fired power plants. This technology has the potential to utilize renewable energy sources and reduce greenhouse gas emissions in the near future. This project seeks to estimate and map the supply of different sources of biomass through New York State in order to remedy the current lack of information available on this topic. Herbaceous energy crops, represented by switchgrass, and short-rotation woody crops, represented by willow, are considered as potential alternative feedstocks. Supplies are estimated based on land potential, land constraints, economic factors, and power plant capacities. GIS is used to map these factors. Varied scenarios are analyzed and discussed to illustrate a range of potential outcomes. The least intensive production scenario predicts a potential supply greater than the cumulative capacities of all power plants for cofiring. All other scenarios predict that production can meet capacity in more concentrated areas near power plants. This study finds that New York State has the resources to cofire biomass at all of its coal-fired power plants in the short-term.

Political Deception: A Linguistic Analysis of Presidential Lies

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Current research on language and deception finds that word patterns are different across false and non-false communication. By applying the Newmann-Pennebaker (NP) model of deception to a multi-level linguistic analysis of five American Presidential Administrations – Clinton, Reagan, Nixon, Johnson, and Kennedy – the present research examined discrepancies between false and non-false political speech. Out of the thirteen linguistic dimensions that were studied, only four were accurately classified based on the NP model. However, separating Presidential deceptions into three categories of lies (War, Personal and State) revealed that different kinds of lies produce different language patterns. The results indicate that false, inaccurate, or deceptive language can be identified with above-chance accuracy based on language features in political discourse.

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