

2003–2004
Research Honors
Program Abstracts

The College of Agriculture and Life Sciences at Cornell University is an internationally recognized leader in many fields of research. Our reputation has been established by students and faculty who partner to make innovative leaps of intellect and scholarship in exploratory settings. Faculty at the college offer undergraduate students many opportunities to pursue their research interests. More important, the faculty mentor and guide the students in the process.

The abstracts in this book reflect the depth of scholarship and intellectual ability that exists in our college among undergraduates who have chosen to pursue a research project and graduate with honors. The students represented here have taken advantage of a wealth of academic resources and research facilities to conduct original research and grapple with important issues.

We live in an increasingly global community where many are faced with significant issues involving food security, environmental health and safety, communication, political unrest, and economic hardship. In this, the one hundredth anniversary of our designation as the New York State College of Agriculture, students and faculty at the college are working to find solutions in the new life sciences, the environment, the social sciences, and our land grant mission.

I am extremely proud of the undergraduate students and their achievements, and wish them the very best in their future endeavors. I am also proud of our dedicated faculty for supervising the student honors research projects and for nurturing and guiding our students to their fullest potential.

The College of Agriculture and Life Sciences is committed to developing leaders who are capable of addressing the global challenges of the twenty-first century and inspiring a better future for us all. Research like that exemplified in this booklet gives youthful legs and unbounded energy to that vision and helps make an important difference to the people in New York State, the nation, and the world.

Susan A. Henry, Ph.D.
*The Ronald P. Lynch Dean of
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Quantitative PCR Analysis of Antigen Shedding Patterns and Antibody Titers of *Coxiella burnetii* along with Somatic Cell Counts in Bovine Blood and Milk Samples

AMY E. CASSANO

Under the supervision of Sung G. Kim
Department of Molecular Diagnostics

A local bovine herd was surveyed for the presence of *Coxiella burnetii* for the purpose of determining patterns in antigen shedding and antigen's relationship to the presence of antibody and somatic cell counts. Smaller projects examined ovine and caprine milk samples along with equine, canine, and bovine placental samples to compare different species and sample types. Optimization of PCR techniques was also examined by comparing the house master mix versus the Invitrogen™ master mix and a comparison between the Cepheid Smart Cyclor and the ABI Prism 7000 Sequence Detection System.

The quarters study surveyed five cows once weekly for six weeks to examine shedding patterns among quarters. Somatic cell counts were also examined during the last two weeks of the survey. It was observed that not all quarters shed similar levels of antigen and that antigen levels remain relatively constant over time; some inconsistencies, however, were observed. This study was extended into an entire herd analysis in which milk and blood samples were analyzed in the months of September, December, and February. In September 25 percent (13/51) of the animals in the herd were positive, 20 percent (10/49) were positive in December, and 15 percent (8/52) were positive in February. No strong correlation was found between antigen shedding and somatic cell count.

The house master mix and the Smart Cyclor were used because they were cost-effective and efficient. Assays of the caprine milk samples and the placental samples were unsuccessful. Assays of the ovine milk samples were successful, but more testing is required to determine any relationship.

Are the Effects of the Eastern House Finch Bottleneck Evident Today? An Investigation Through the Use of Allelic Diversity and Heterozygosity Comparisons

DANIEL HANLEY

Under the supervision of Irby Lovette
Department of Ornithology

House finches (*Carpodacus mexicanus*), although now common across all of North America, are relatively new arrivals to the East Coast. This native western species was introduced in Long Island, N.Y., in the early 1940s after being released by a pet store owner who realized they were a protected species. The eastern population of house finches expanded quickly, and the house finch now represents one of the most common winter birds in many parts of the East. Since the founding population of eastern house finches was small, it was likely that there was a significant population bottleneck, which may have reduced levels of genetic variation. To date, however, no one has provided genetic evidence of a

significant bottleneck in this species. I attempt to provide this evidence through comparisons of allelic diversity and levels of heterozygosity across and within six native western and introduced eastern populations (three introduced, three native). Allelic diversity and richness were significantly lower in the introduced eastern populations than the native western populations. However, heterozygosity levels and F_{is} , the inbreeding coefficient, did not differ between eastern and western house finches. These results are consistent with a recent demographic bottleneck and support theoretical predictions that allelic diversity provides a more robust detector of population bottlenecks than population heterozygosity. The genetic bottleneck experienced by eastern house finches may have important implications for population viability, including susceptibility to disease. Reduced allelic diversity in the East may explain why eastern house finches have been readily colonized by a pathogenic bacterium, *Mycoplasma gallisepticum*, which has substantially reduced the growing eastern population.

Variation in Quarter Milk Somatic Cell Counts in Postpartum and Late Lactation Holstein Dairy Cattle Over Five Consecutive Days

KAREN L. JAMES

Under the supervision of Thomas R. Overton
Department of Animal Science

Holstein cows ($n = 34$) from a single commercial dairy herd were studied daily for five consecutive days to determine changes in somatic cell counts (SCC) in infected and uninfected quarters in cows both in the immediate postpartal period ($n = 16$) and in late lactation ($n = 18$). Infection status was determined by duplicate bacteriological culture testing. It was found that quarter milk SCC decreased in the first five days after calving, whereas it remained relatively level in late lactation cows. The decrease of SCC in fresh cows was more rapid in quarters that were culture negative. Negative quarter SCC for late lactation cows followed a relatively level trend. Particularly in late lactation cows, quarters infected with coagulase-negative staphylococci (CNS) showed an important increase in SCC. Based on this research, it is now possible to determine reference parameters for SCC level in the first few days after parturition to give an indication of intramammary infection status.

Ectoparasites of the Deer Mouse (*Peromyscus maniculatus*) and the White-Footed Mouse (*Peromyscus leucopus*) from the New York City Watershed

JENNIFER L. JOHNSON

Under the supervision of Susan E. Wade
New York State Animal Health Diagnostic Laboratory—Parasitology Section

Arthropod samples were collected from 184 *Peromyscus* species of mice (113 *P. leucopus* and 71 *P. maniculatus*). Two species of lice (*Hoplopleura hesperomydis* and *Polyplax auricularis*), four species of fleas (*Ctenophthalmus p. pseudagyrtis*, *Eptedia w. wenmanni*, *Orchopeas leucopus*, and *Peromyscopsylla h. hesperomys*),

one species of tick (*Ixodes angustus*), and 12 taxa of mites (*Androlaelaps fahrenheitzi*, *Dermacarus hypudaei*, *Eulaelaps stabularis*, *Euschoengastia* sp., *Hirstionyssus utahensis*, *Hirstionyssus* sp., *Laelaps alaskensis*, *L. kochi*, *Parasitus* sp., *Pergamasus* sp., *Poecilochirus* sp., and *Orycteroxenus soricis*) were recovered from these mice. A 76.3 percent prevalence of flea infestation, 32.2 percent prevalence of sucking louse infestation, and 34.2 percent prevalence of mite infestation was reported from these mice. *Peromyscus* spp. represents a new host record for the mite *Orycteroxenus soricis*. Prevalence rates were compared for the three groups of parasites between the two species of *Peromyscus*, age, sex, habitat (forested and municipal), and land use (agricultural, municipal, and pristine).

The Effects of Mexiletine and Sotalol in Combination and Alone on the Suppression of Inherited Ventricular Arrhythmias in German Shepherd Dogs

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Under the supervision of Anna R. Gelzer
Veterinary Clinical Sciences

Inherited ventricular arrhythmias seen within a colony of German shepherd dogs are the cause of sudden death at an early age. No current treatment has been discovered that proves effective in suppressing the overall amount of arrhythmia. Severely affected dogs can suffer ventricular fibrillation and die as a result of this disease. Sotalol, a class II and III β -adrenoceptor blocker, is commonly prescribed as an antiarrhythmic treatment for arrhythmias in client-owned dogs. Because of the morphology and underlying cause of the arrhythmia in the colony dogs, sotalol may provoke arrhythmias and cause sudden death. Lidocaine has been found to decrease arrhythmias. Mexiletine, which is functionally similar to lidocaine and orally active, should decrease arrhythmias but is not effective in doing so. Recent in vitro studies have shown that, when the two drugs are administered together, sotalol increases the antiarrhythmic properties of mexiletine. To test the effect of the drugs in co-administration in vivo, nine German shepherd dogs from the colony were selected for the study based on their overall amount of arrhythmia. Dogs were given three different drug regimes: (1) 8 mg/kg of mexiletine alone, (2) 2.5 mg/kg of sotalol, and (3) 8 mg/kg of mexiletine with 2.5 mg/kg of sotalol. The percentage of arrhythmia was measured before each drug regime using a 24-hour ambulatory electrocardiogram. Drugs were given for five days. Dogs were without medication for three days before starting a regime again. The combination of mexiletine and sotalol significantly reduced the amount of arrhythmia in dogs ($p = 0.001$) and was more effective than either mexiletine or sotalol administered alone. Neither mexiletine nor sotalol alone proved effective in decreasing arrhythmic levels. Sotalol increased the blood levels of mexiletine, which may be the underlying reason the combination proved so effective. Mexiletine blood levels were negatively correlated with the amount of ventricular arrhythmia found in a dog (Pearson Correlation = -0.516, $p = 0.034$).

Effect of Intramammary Lipopolysaccharide Infusion on Glucose Kinetics in Periparturient Dairy Cattle

AMY E. KULICK

Under the supervision of Thomas R. Overton
Department of Animal Science

We hypothesized that immune activation of early lactation dairy cows would result in metabolic changes, including alterations in glucose kinetics, that may have important implications for periparturient metabolic health. A pilot study using four multiparous dairy cattle was conducted to assess total body glucose production and utilization and body reserve mobilization following immune activation by intramammary administration of lipopolysaccharide (LPS). Two cows were infused with 100 μg of LPS in each of two right quarters. Controls infused with sterile saline were pair-fed with treatment cows to remove the potential confounding effect of dry matter intake (DMI) on glucose kinetics. To measure glucose kinetics, [6,6-D₂]glucose was infused via primed continuous infusion. To assess rates of appearance and disappearance accurately throughout the experiment, it was essential to ensure that isotopic steady state was reached before treatments (LPS or saline control) were infused. Plasma glucose concentrations and enrichments of plasma glucose with [6,6-D₂]glucose were measured throughout the treatment period. No significant changes in glucose concentration or enrichment, or plasma nonesterified fatty acids (NEFA) concentration attributable to treatment can be discerned from the four pilot cows. Fortunately, it was determined that isotopic steady state was reached by 180 min., indicating that sampling and infusion protocols were appropriate for continuation of the experiment.

Analyzing Visual-Field Information in the Face Perception of the Common Chimpanzees (*Pan Troglodytes*)

JOSHUA M. PLOTNIK

Under the supervision of:
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Peter A. Nelson, Scripps Institution, UCSD
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This study investigated whether chimpanzees exhibit a visual-field advantage (VFA) in face perception. Testing was conducted using a modified free-vision task. Six of six chimpanzee subjects were found to distinguish successfully between photographic images of chimera neutral faces consisting of two left sides (LL) or right sides (RR) of the face. Four of the subjects were also able to distinguish between artificially created abstract images consisting of two left sides (LL) or right sides (RR) of an asymmetrical image. All of the tested chimpanzees were previously trained on a computer joystick match-to-sample paradigm. This type of testing is specifically important in establishing the significance of information present in the utilized test images, although such tests are unlikely to be applicable in the separate VFA tests. Further testing on the chimpanzees' choice of the LL versus RR chimera of the neutral faces as a

match to the true, neutral image was performed, as were tests on their choice of the LL versus RR chimera of the abstract images as a match to the original image. A bias for either the LL or the RR chimera would indicate a hemispatial visual-field advantage. Results in both tests suggest that chimpanzees, unlike human beings, do not exhibit a left visual-field advantage. Although these results are not conclusive, they do have important implications for current and future studies on brain laterality and asymmetry in facial signals and their perception in primates.

A Proteomic Analysis of Mgrn1 Signaling

JENNIFER L. ROKHSAR

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Mahogunin Ring Finger 1 (*Mgrn1*, formerly *mahaganoid*) is a mouse mutant that was identified about three decades ago. Mice that receive one copy of the mutant gene (*Mgrn1^{md-nc/md+}*) are phenotypically normal, while mice that receive two copies of the mutant gene (*Mgrn1^{md-nc/md-nc}*) suffer from spongiform encephalopathy, hypomyelination, and body tremor. The mutation results in a lack of Mgrn1, a protein that has ubiquitin ligase (E3) activity. If this protein is absent, protein accumulations occur in the brain. Such accumulations have proven to be cytotoxic to cells and result in neuronal cell death. A proteomic analysis, specifically two-dimensional gel electrophoresis (2DGE), was used to observe the changes in protein expression between animals. As a pilot project, the goal of this study was to find ways to improve technique for proteomic analysis to allow for greater accuracy when examining protein expression levels. With a reliable protocol, protein spots that differ between mutant and control animals can be accurately identified and subsequently subjected to analysis.

Comparing the Contributions of Intracellular and Extracellular Calcium in Hyperactivation of Bull Sperm

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Hyperactivation refers to a change from a symmetrical to an asymmetrical, frenzied swimming pattern that occurs in sperm around the time of ovulation. This swimming pattern is essential for fertilization to occur. The exact mechanism by which hyperactivation is turned on, however, is unknown, but it is known that calcium is one of the key components necessary for the initiation and maintenance of hyperactivation. It has already been discovered that an intracellular calcium store is involved in regulating hyperactivation. The calcium ionophore, ionomycin, and the calcium store-releasing agent, thimerosal, were used in this experiment to determine whether full development of hyperactivation requires extracellular calcium in addition to the calcium provided by intracellular stores. Hyperactivation was induced by both agents when they were added to sperm separately or together. Ionomycin induced

the highest percentage of hyperactivation in sperm, followed by ionomycin plus thimerosal together. These findings indicate that extracellular calcium is required to induce fully developed hyperactivation in bull sperm.

Forkhead Transcription Factor FOXO3a mRNA Levels in the Bovine Preovulatory Follicle

PETER J. SEPP JR.

Under the supervision of Susan M. Quirk
Department of Animal Science

After the luteinizing hormone (LH) surge, granulosa cells of bovine preovulatory follicles cease to proliferate and become quiescent. They also become resistant to apoptosis induced by serum withdrawal or treatment with Fas Ligand (FasL). A family of transcription factors known as forkheads is involved in the regulation of apoptosis and cell cycle progression. In quiescent cells, FOXO3a increases protein and mRNA levels of manganese superoxide dismutase (MnSOD), which is an enzyme that reduces oxidative stress and prevents apoptosis.

Experiments were performed to test the hypothesis that increases in FOXO3a and MnSOD mRNA after the LH surge are involved in withdrawal of granulosa cells from the cell cycle and development of resistance to apoptosis. Semi-quantitative reverse transcriptase-polymerase chain reaction (RT-PCR) assays were performed to assess levels of FOXO3a and MnSOD mRNA in granulosa cells of preovulatory follicles isolated before and after the LH surge. Primers for use in RT-PCR were designed based on a search of bovine expressed sequence tags (EST) for FOXO3a and sequences in GenBank for bovine MnSOD. We attempted to clone several fragments of the bovine FOXO3a cDNA produced by RT-PCR, although this was not successful. No major qualitative differences were observed between FOXO3a or MnSOD mRNA levels before and after the LH surge. To confirm that mRNA levels of FOXO3a do not change after the LH surge, the laboratory plans to develop a quantitative real-time RT-PCR assay.

The Role of Heavy Chain Ferritin and Ferroxidase Activity on the Regulation of Intracellular Folate Concentrations

PAUL D. ARIDGIDES

Under the supervision of Patrick J. Stover
Division of Nutritional Sciences

Increasing evidence indicates that folate catabolism, the oxidative degradation of folate cofactors, is a regulated, enzyme-mediated process. Recent studies have identified ferritin, an iron-storage protein, to be capable of catabolizing folate *in vitro* and increasing rates of folate turnover in cell culture models. Expression of cDNA encoding the heavy chain ferritin (HCF) subunit in mammalian cells results in increased levels of the enzyme cytoplasmic serine hydroxymethyltransferase (cSHMT), and upregulation occurs at the level of translation. The role of ferritin in the cell is to sequester free iron and store it in a mineral core composed of up to 4,000 iron atoms. Essential to the storage process is the ferroxidation of free Fe^{2+} to the Fe^{3+} mineralized form. Ferritin catalyzes this reaction at a ferroxidase site present on the HCF subunit; a mutant form of rat HCF (mrHCF) in which the ferroxidase site has been altered to replace key metal-site ligands has a greatly reduced capacity to mineralize iron.

In this study mrHCF was expressed in MCF-7 cells to determine if HCF with significantly reduced ferroxidase activity affects both intracellular folate concentrations and cSHMT translation. Expression of both rat HCF (rHCF) and mrHCF in mammalian cells resulted in a significant decrease in accumulation of intracellular folate, suggesting that ferroxidase activity is not essential for folate catabolism. The mutant form is also capable of increasing cSHMT levels, suggesting that the ferroxidase site is also not required for the upregulation of cSHMT.

The majority of cellular folate is bound to folate binding-proteins, but the role of folate binding-proteins in folate catabolism is unknown. In this study, cells treated with puromycin, an inhibitor of translation, exhibit a decreased rate of intracellular folate accumulation. When folate cofactors and degradation products were quantified using HPLC, puromycin treatment resulted in decreased folate uptake accompanied by an increase in catabolites. The observed increase in catabolism is not significant enough to suggest a protective effect of folate binding-proteins on folate catabolism.

Intraguild Predation and Cannibalism in a Size-Structured Community of Marine Amphipods

MICHELLE L. ARMSBY

Under the supervision of Myra J. Shulman
Department of Ecology and Evolutionary Biology

Body size differences can affect the strength and type of interaction among and within species. This study examines the effect of body size differences on intraguild predation (IGP), cannibalism, and competition in regulating the relative abundance of two species of temperate marine amphipods throughout

a season. Intraguild predation was asymmetrical, with only *Jassa marmorata* preying on *Apocorophium acutum* (but no predation by *A. acutum* on *J. marmorata*). Intraguild predation increased significantly as body size difference increased. Cannibalism in *J. marmorata* was significant only among individuals of different body sizes. Tube building (an indirect measure of competition) was similar among *A. acutum* and small- and medium-sized *J. marmorata*. Only large *J. marmorata* built significantly fewer tubes. Tubes were also found to be effective in protecting *A. acutum* against IGP, especially in the presence of large *J. marmorata*. Experimental results suggest that an ontogenetic niche shift occurs in *J. marmorata*, which may provide a potential explanation for observed patterns of abundance in a natural population.

Dynamic Mechanism for Stimulus-Induced Ventricular Fibrillation in Beagle Dogs

CARLO RENATO G. BARTOLI

Under the supervision of Robert F. Gilmour
Veterinary Biomedical Sciences

Recent research has shown that stimulation of ventricular muscle from a single point-source may be sufficient to produce spatial heterogeneity of voltage repolarization. In this atypical electrical environment, alternating waves of electrical excitation may develop. This alternans may lead to the block of a stimulus, an obstacle around which planar waves of excitation break and subsequently deteriorate into the chaotic electrical activity characteristic of ventricular fibrillation (VF). Using a stimulus protocol predicted by a one-dimensional computer model to maximize the development of action potential duration (APD) alternans and thereby block a stimulus, I investigated the efficacy of these pacing protocols for inducing wave break before VF.

Monophasic action potential (MAP) catheters were advanced into the apex of both the right (RV) and left ventricles (LV) to record the duration of LV activation during stimulation from the RV in anesthetized, closed-chest beagle dogs ($n = 8$). Using two pacing protocols, a standard (SX-SY) and a separate dynamic (SX-SX) protocol, the standard and dynamic beagle restitution relations were constructed by plotting APD as a function of diastolic interval (DI) and incorporated into a computer model. The computer model generated four appropriately timed premature stimuli (VFs2-s5) that were predicted to induce VF. As a control, the incidence of VF induction using the VFs2-s5 protocol was compared with that of a different stimulation protocol used routinely in human patients that was predicted by the computer model not to induce VF.

In all dogs, administration of VF s1-s5 triggered the onset of VF, whereas the standard stimulation protocol, as predicted by the model, did not trigger VF in any dogs. Similar to the results of the computer model, APD measurements showed a progression from concordant to discordant alternans between the RV and LV before the onset of VF.

In accordance with the predictions of the model, stimuli prematurely administered to maximize spatial dispersion of electrical repolarization reliably triggered VF in anesthetized, closed-chest beagle dogs. These results may have significant implications regarding mechanisms for sudden cardiac death.

The Rab Proteins of *Saccharomyces cerevisiae*

BENJAMIN J. BRIGGS

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The Rab family of small GTPases constitutes the largest group of the Ras superfamily of proteins. Rabs have been shown to be involved in membrane trafficking within the cell and have been suggested to be the “controllers” of intracellular membrane trafficking. Rab proteins have specific areas within the cellular architecture in which they localize. Each Rab, or subfamily of Rabs, seems to be involved with trafficking of membrane vesicles from one area to another or within a specific area. In this study we have investigated the physiological localization of all 11 members of the Rab family in yeast at physiological expression levels. Our results demonstrate the value of a joint proteomic and genomic approach to protein investigations and underscore a need for further investigation in Rab function, especially in higher eukaryotes.

In Vitro Chondrogenesis of Genetically Modified Equine Mesenchymal Stem Cells Expressing Transforming Growth Factor- β 1

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Veterinary Clinical Sciences

Osteoarthritis is the common cause of joint pain affecting the quality of life among an ever-aging population. It occurs when articular cartilage becomes destroyed and loses its ability to self-repair. One possible treatment that is currently being studied involves the transplantation of chondrogenic mesenchymal stem cells (MSC) in cartilage lesions. To induce chondrogenesis in MSC, however, certain growth factors and growth conditions are necessary.

Transforming Growth Factor- β 1 (TGF- β 1) has previously been shown to promote the differentiation of bone marrow-derived MSC along the cartilage lineage. Based on this knowledge, we hypothesized that an adenovirus (Ad) vector-encoding equine TGF- β 1 could be used to transfect equine bone marrow-derived MSC and that the transfected MSC grown in aggregate cultures would undergo chondrogenesis. An E1⁻ and E3⁻ adenovirus vector encoding equine TGF- β 1 (AdTGF- β 1) was constructed and was used to transfect MSC at 100 multiplicities of infection.

Results from quantitative real-time PCR indicated that AdTGF- β 1 transfected MSCs induced expression of TGF- β 1 RNA, and markers of chondrogenic function such as aggrecan, collagen type I, collagen type IIA and collagen type IIB. Toluidine blue and hematoxylin and eosin staining indicated the production of proteoglycan as early as day 2, and a compact circular morphology in MSC aggregates by day 21, respectively. Immunohistochemical analysis detected collagen type II as early as two days after beginning aggregate cultures. This phenomenon continued through day 21. Similar trends were seen in collagen type I immunohistochemical analysis. These results provide molecular, histo-

logical, and immunohistochemical evidence for partial *in vitro* chondrogenic differentiation of equine bone marrow–derived MSCs. Based on these results, AdTGF- β 1 treated MSCs may be used in cartilage repair and as a possible treatment for osteoarthritis.

Genes and Secondary Metabolites Putatively Involved in Pathogenicity of *Mycosphaerella fijiensis*

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Mycosphaerella fijiensis is the causative agent of black Sigatoka (or black leaf streak disease), the most destructive disease of bananas and plantains worldwide. Fungal secondary metabolites, including shunt metabolites of the dihydroxynaphthalene (DHN)-melanin biosynthetic pathway, have been predicted to serve as phytotoxins in the disease process. A polyketide synthase (PKS) gene encodes the first enzymatic step in fungal melanin biosynthesis. In addition to PKSs, peptide synthetases (PSs) and ATP-binding cassette transporters (ABCTs) have been shown to play roles in the production and transport of fungal phytotoxins. I attempted to identify genes from the PKS, PS, and ABCT families by performing PCR on genomic DNA of a virulent *M. fijiensis* isolate using degenerate primers designed to amplify conserved regions of these genes. Thirty gene fragments with significant similarities to genes in the GenBank database were cloned, including one PS gene and four ABCT genes. I compared transcription of a subset of genes from cultures grown *in vitro* and *in planta* to identify conditions in which the genes were expressed. Most genes were expressed both *in vivo* during early and late infection stages and *in vitro* on low and high glucose medium. Expression of the genes in banana suggests they may contribute to pathogenicity, and their expression *in vitro* indicates the possibility of isolating and characterizing the natural products they synthesize or transport.

Additionally, I characterized the accumulation of secondary metabolites in cultures of *M. fijiensis* (1) treated with tricyclazole (a biochemical inhibitor of reductase enzymes of the melanin biosynthetic pathway), and (2) genetically modified by targeted disruption or RNA-silencing of the PKS1 gene that encodes the first enzymatic step in the melanin biosynthetic pathway. We found that culture filtrates of virulent strain Mf301 treated with tricyclazole were enriched in several unknown compounds, as well as the melanin intermediate 1,3,8-trihydroxynaphthalene. These compounds were undetectable or present only in trace amounts in the untreated strain. Culture filtrates of a highly virulent strain, Mf743, and genetically altered PKS1 mutants of Mf743 yielded unexpected results. None of the metabolites detected from these cultures could be identified in comparison with known standards, with one exception: juglone was produced in small amounts in the wild type strain only. All Mf743 strains produced an unknown compound in a minimal medium, AMM, which eluted at ca. 6 min. All strains also produced a compound that eluted at ca. 13 min. In strains in which *PKS1* was disrupted or RNA-silenced, UV fingerprints of each 13-min. peak indicated that the compound was distinct from a second compound that eluted at the same time from extracts of the wild type strain, a spontaneous

melanin-deficient pink mutant, and the gene disruption (“ectopic”) and silencing (“nonsilenced”) control strains. Identification of these natural products in future studies may help elucidate the mechanisms of virulence of *M. fijiensis*. Several compounds detected by HPLC have been isolated by fractionation and await further analyses and identification via mass spectrometry and NMR. Studies of genetic and chemical contributors to the virulence of *M. fijiensis* will facilitate the development of alternative methods of controlling the disease by targeting the disruption or inhibition of such genes in the wild fungus.

Quantitative Measurement of SMAD 1-8 and SMURF 1 and 2 Expression in Osteochondritis Dissecans Cartilage by Real-Time Polymerase Chain Reaction

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Osteochondritis dissecans (OCD) remains a poorly characterized disorder of cartilage differentiation and endochondral ossification. Investigation of the etiopathogenesis has yielded no definitive cause, though several factors have been implicated. The purpose of this investigation was to determine gene expression of a number of signaling molecules associated with induction or inhibition of chondrocyte differentiation. Of specific interest are two groups of molecules commonly referred to as SMADs and SMURFs. The objective of this study was to determine the sequences of equine SMAD 1-8 and SMURF 1 and 2 and, using the newly obtained sequences, determine if a difference existed between control and OCD cartilage in the expression of SMAD 1-8 and SMURF 1 and 2. The hypothesis was that there would be a decrease in the level of expression of the R-SMADs (1,5, and 8), and the CO-SMAD (4) in the OCD samples and an increase in the level of expression of SMURF 1 in OCD samples. If this hypothesis was proven correct, it would show that differential expression of these nuclear regulatory proteins is a possible cause of the failure in endochondral ossification that ultimately led to the development of an articular cartilage lesion manifested as OCD.

Cartilage was harvested from OCD-affected stifle joints from 16 immature horses and 16 age-matched normal control horses. Specimens were snap frozen in liquid nitrogen. Frozen cartilage samples were processed for total RNA isolation. PCR primers were designed from published human sequences for SMURF 1 and 2 and published human and equine sequences for SMAD 1-8. The gene fragments were PCR amplified and were cloned into the pCR@II-TOPO vector. The clones were validated and sequenced. Primers and fluorogenic dual-labeled probes were designed for each of the cloned genes for quantitative Real Time PCR analysis of RNA from normal versus OCD cartilage. Quantitative Real Time PCR was performed to assess the relative levels of expression of these molecules.

All results were statistically insignificant ($p > 0.05$), although there were some notable differences in levels of expression with a P-value ≤ 0.10 between the RNA samples from the control horses and the RNA samples from the horses with osteochondritis dissecans. SMAD 1 ($p = 0.0825$) was overexpressed in the

OCD samples, and, as expected, SMAD 4 ($p = 0.0512$) and SMAD 5 ($p = 0.0717$) were both underexpressed in the OCD samples.

Selective Feeding by a Stem-Boring Beetle: Implications for the Biological Control of Invasive Weeds

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This study examined aspects of the biological control of the invasive Eurasian weed species *Linaria vulgaris* (Scrophulariaceae) by the stem-boring beetle *Brachypterolus pulicarius* (Nitidulidae). Using field censuses of the performance of *L. vulgaris* plants naturally damaged and undamaged by *B. pulicarius*, I examined growth, mortality, flowering, seed set, and clonal propagation over two growing seasons. Data indicated that foraging *B. pulicarius* have a strong inclination to feed selectively on the most vigorous *L. vulgaris* plants within a population. Plants that were initially taller early in the season were more likely to be damaged and were also more likely to flower. Selective feeding on vigorous plants could have impacts on the fitness of weed populations distinct from the impacts that would be expected from a generally feeding, indiscriminate herbivore. In this paper, I present two hypotheses about the potential long-term impacts of selective feeding. I propose that when combined with knowledge of the weed species' tolerance characteristics, the foraging behavior of herbivores may provide a useful criterion for choosing among candidate control agents. Data from my field censuses imply that tolerance of *L. vulgaris* to *B. pulicarius* feeding varies across sites, suggesting that the impact of this herbivore is context specific. Interactions between the foraging behaviors of control insects and the tolerance patterns of plant populations may help to explain the varying rates of success observed in this and other biocontrol systems.

A Genealogy of European Corn Borer for the $\Delta 11$ Desaturase Gene

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For recently diverged taxa, gene genealogies are often incongruent. Sequence comparisons for some gene regions will sort individuals into reciprocally monophyletic clades with respect to species or population boundaries, while other gene regions may not form similarly exclusive groups. In such cases, it is possible that not enough time has passed for genetic drift to eliminate shared ancestral polymorphism. Additionally, hybridization and subsequent introgression can contribute to genealogical discordance. For loci that have experienced directional selection, it is more likely that the effects of shared ancestral polymorphism and gene introgression will be reduced and that genealogies will reflect the evolutionary history of species or population divergence. A compari-

son of multiple gene genealogies for diverged populations may provide insight into the role of selection in speciation and yield information on the genomic regions involved in the formation of barriers to gene exchange. Here I focus on two reproductively isolated pheromone races (E and Z) of the European corn borer (*Ostrinia nubilalis*) for which preliminary evidence supports the view that differentiation varies with gene region. I present a genealogy for a gene encoding $\Delta 11$ desaturase, an enzyme that is involved in the pheromone production pathway, but not expected to be responsible for differentiation of the pheromone races. A genealogy of the $\Delta 11$ desaturase gene for European corn borer does not reveal the Z and E strains to be exclusive groups. These findings add to the accumulating data, suggesting that the Z and E races are differentiated for a relatively small portion of the genome. The genealogy also indicates that individuals segregate (without respect to E or Z) into two major clades separated by 3 to 4 percent sequence divergence. Analysis of the variation between clades provides information specific to the history of the $\Delta 11$ desaturase gene.

Pigment Pattern Development in *Danio albolineatus* and *Danio pathirana*

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Vertebrate pigmentation patterns are likely under strong selective pressures due to their roles in advertisement and crypsis. Within the genus *Danio* (Teleostei: Cyprinidae), larvae share a common pigment pattern before developing into different adult patterns during the juvenile growth period. The mechanisms of pattern formation are still unclear; some genes controlling some aspects of pigmentation have been identified, but it is not yet known how gene products interact to produce specific patterns. Theoretical models suggest that size, shape, and growth rate can profoundly affect gene product interactions, but their relative contributions remain unknown. This study describes pigment pattern development in *Danio pathirana* and *D. albolineatus*, relates pigment pattern development to changes in body size and shape, and quantifies differences in melanophore proliferation between the two species. *D. pathirana* develops three larval blotches of melanophores at 48 hours after fertilization, as has been documented previously only in *D. browni*. The pigment patterns in the two study species then converge at four to five days, sharing a nearly identical larval melanophore pattern. After the larval stage, however, formation of the adult patterns is fundamentally different. Pigment pattern formation in *D. pathirana* appears to be delayed compared to *D. albolineatus*; comparable stages in pattern formation are reached at a later age and greater body size. The vertical bars on the flank of *D. pathirana* are derived from melanophores dorsal to the swim bladder, and develop from anterior to posterior. Of the seven danios whose pigment pattern development has been characterized, *D. pathirana* is the first whose flank melanophores are derived from the cell population dorsal to the swim bladder. *D. pathirana*'s adult pattern is established by day 54 of development. In *D. albolineatus* the population of cells dorsal to the swim bladder does not migrate, and flank melanophores are instead derived from the

larval lines; the adult pattern is established by day 40 of development. In both species, pigment pattern formation coincides with the period of rapid growth and shape change, consistent with one prediction of models linking variation in pigment pattern to differential growth.

Functional Role of Mcm10 in *Drosophila melanogaster*

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In this study, three major experiments were done to clarify the role of Mcm10 in *Drosophila melanogaster*. The first experiment was aimed at understanding which regions of Mcm10 interact with the six known interactors of Mcm10: Mcm2, Mcm10, Cdc45, Orc2, Orc5, and Hp1. These regions were identified for each of these partners. The second aim was the generation of a transgenic stock of *D. melanogaster* capable of synthesizing Mcm10-CFP fusion protein. This strain was generated, and it was shown that Mcm10 localizes in the nuclei of the third-instar larva of *D. melanogaster*. The third experiment consisted in generating a fly line that would code for a shRNA (“hairpin”) that silences Mcm10. A putative line has been generated and effects of shRNA will be determined.

Vitamin E as a Transcriptional Regulator

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Vitamin E, the principal lipid-soluble antioxidant in mammalian tissues, represents a family of eight structurally related tocopherol and tocotrienol vitamers. In recent years α -tocopherol (α -TOH) has been shown to exhibit several non-antioxidant molecular functions that have yet to be fully characterized. Several studies implicate a role for α -TOH as a specific regulator of gene expression; however, the distinction between α -TOH’s antioxidant and nonantioxidant transcriptional activities is unclear, and the ability of other tocopherol forms to regulate transcription remains largely unexplored. The goal of this study was to identify genes whose transcription is regulated by α -tocopherol in a specific manner, and to evaluate whether α -TOH’s genomic effects stem from a specific transcriptional response or from a general response to redox/antioxidant status. The following was performed in triplicate: HepG2 C3A cells received control media or treatment media containing 100 μ M α - or β -TOH, total RNA was isolated after 48 hours, and DNA micro arrays (Affymetrix) were used to interrogate these samples. Because of its comparable free-radical scavenging ability and similarity in structure to α -TOH, β -TOH was used as a separate treatment group. From this experiment we obtained a list of genes significantly regulated by both vitamers and determined that α -tocopherol is a more potent transcriptional regulator than β -tocopherol in vitro. This gene list represented several functional categories, including lipid metabolism, signal transduction, and cell proliferation, and included a number of transcription factors that may be responsible for directly regulating the expression of significant genes. To

confirm transcriptional regulation observed on the arrays, real-time RT-PCR was performed on four differentially expressed genes. In addition, dose response and time course experiments with α - and β -tocopherol treatment were carried out to further characterize the nature of transcriptional regulation; both vitamers were able to regulate gene expression in a time-dependent manner but only β -TOH exhibited dose-dependent transcriptional regulation and was able to effect greater changes in transcript levels compared to α -TOH. These results suggest that both tocopherol forms can act as transcriptional regulators in vitro, and the difference in their regulatory effects provides further insight into tocopherol-dependent mechanisms that regulate gene expression in the body.

Rescue of Function in Non-Channel Forming KA2 and Chimeric Kainate/NMDA Subunits by Co-Expression in HEK 293 Cells

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Ionotropic glutamate receptors are divided into three groups: N-methyl-D-aspartate (NMDA), α -amino-3-hydroxy-5-methyl-4-isoxazole propionate (AMPA), and kainate receptors based on their pharmacological profile. While functional NMDA receptor-channels are formed by the heteromeric combination of NR1 and NR2 subunits, functional kainate receptor channels can be formed by homomeric expression of GluR5-7 subunits. In the kainate receptor family, KA1 and KA2 subunits do not form functional channels, but they do co-assemble with the GluR5-7 subunits in heteromeric kainate receptor-channels with altered function. Distinct contributions of the individual NR1 and NR2 pore domains were studied by creating kainate/NMDA chimeras in which the M1-M3 region of the GluR6 subunit was replaced by the corresponding region from NR1 or NR2B subunits. The earlier studies found that a GluR6/NR1 chimeric subunit formed functional channels by homomeric expression in human embryonic kidney (HEK) cells. The analogous GluR6/NR2B subunit did not form functional homomeric channels, but it did combine in heteromeric assembly with the GluR6/NR1 subunit to yield heteromeric GluR6/NR1-GluR6/NR2B channels. Homomeric function of GluR6/NR2B subunits was also achieved by replacing five pore-loop amino acids with the homologous ones from the NR1 subunit. Thus, it was hypothesized that the pore domain of the NR2B subunit does not form an effective ion permeation pathway. In this context, I examined whether co-expression of wildtype KA2 subunits with the chimeric GluR6/NR2B subunits would produce functional channels. To achieve this, I introduced a blasticidin resistance gene into the pRK5/KA2 plasmid and co-transfected HEK 293 cells with the modified vector and a pEF/GR6NR2B vector that contains the geneticin resistance gene. I established stable cell lines using a double drug selection strategy and confirmed the co-expression of GluR6/NR2B and KA2 by Western/immunoblot. The hypothesis that a KA2 subunit would be able to rescue a GluR6/NR2B and form functional channels was confirmed by whole cell recording responses in one cell line that co-expressed both KA2 and GluR6/NR2B. My studies extend the data supporting the hypothesis in our laboratory that the ineffective GluR6/NR2B pore domain can be rescued

by forming heteromeric channels with another subunit that contains a functional pore domain.

Aggression Around Oviposition in *P. dominulus*: Testing Models of Within-Group Conflict and Reproductive Skew

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Models of within-group conflict predict how aggression within a group should relate to reproductive division (or skew) between members of the group. The most significant difference between the transactional and tug-of-war models of conflict is the assumed function of aggression within the group. Under the tug-of-war framework, individuals obtain reproduction through aggressive competition. In the transactional model, subordinate individuals obtain reproduction as concessions from the dominant individual, so conflict occurs only over the portion of reproduction between the minimum reproduction a subordinate requires to be favored to stay within the group and the maximum reproduction that the dominant will allow before it pays to eject the subordinate from the group. Aggression outside of this allowable “window of selfishness” results in the collapse of the group. The function of aggression in reproductive division was tested in a field experiment in the social wasp, *Polistes dominulus*. Removal of the reproductive-destined eggs before worker emergence in multiple foundress colonies significantly decreased dominant aggression immediately before the dominant’s oviposition and subordinate aggression during the dominant’s oviposition. These results support the transactional model of within-group conflict and suggest that peaceful concession of reproduction does occur in groups to prevent group destabilization.

The Importance of Initial Conditions on Amphibian Development in Experimental Ponds

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Wetland creation is currently used to restore ecological services, with a focus on providing amphibian habitat. The suitability of new ponds for amphibians may strongly influence the later success of these animals, but little is known. Using six created woodland ponds at the Arnot Teaching and Research Forest in Van Etten, N.Y., during summer 2003, we examined how the presence of plants affects the growth and development of introduced amphibians. Nine replicates of cylindrical mesocosms, 40 centimeters in diameter and 60 centimeters tall, were placed in each pond at the beginning of the summer. One-third of the mesocosms contained a plug of a live plant (*Eleocharis obtusa*), another third had a plastic plant added, and the remaining mesocosms had no plants added. Thirty replicate *Rana clamitans* tadpoles were then released into

each mesocosm. Weekly sampling measured the snout-vent length of 15 to 20 percent of the initial population from each mesocosm. A multiple ANOVA analysis found that tadpoles from the real and plastic plant treatments were significantly larger than the animals from the no-plant mesocosms ($F = 9.8217$, $Pr(F) = 0.000097$). There were no significant differences in tadpole growth patterns when compared among ponds. The varying physical pond parameters and the final mean tadpole size also yielded only weak correlations. The effect of initial conditions in the mesocosms was therefore rapid and considerable, with animals in real and plastic plant treatments growing significantly larger. These treatments contained more physical structure than the no-plant treatment, and this difference may have caused the observed growth patterns by providing surface area where algae could accumulate or additional basking sites for the tadpoles. This evidence suggests that with thoughtful planning and consideration of the initial conditions, goals for wetland creation can be accomplished more successfully.

Agonistic Interactions of Two Invasive Shore Crab Species, *Carcinus maenas* and *Hemigrapsus sanguineus*, in Northern New England

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The Japanese shore crab, *Hemigrapsus sanguineus*, also known as the Asian crab, has spread south to North Carolina (McDermott 1998a) and north to mid-coast Maine (Seeley and McDonald, in prep.) since it was first found on the New Jersey coast in 1988 (Williams and McDermott 1990). In both its native range and along the U.S. Atlantic coast, *H. sanguineus* shows a strong preference for rocky intertidal habitats (Takada 1999, Lohrer et al. 2000, Ledesma and O'Connor 2001). In the United States, the long-established invasive European shore crab, *Carcinus maenas*, commonly called the green crab, also occupies these habitats. Since *Hemigrapsus*'s invasion, there has been a dramatic change in the relative abundances of these two crab species in the rocky intertidal of southern New England: *Carcinus* is now virtually extinct on the rocky shores. Two mechanisms have been suggested for the change in relative abundance: (1) *Hemigrapsus* predation on *Carcinus* recruits (Lohrer and Whitlatch 2002a) and (2) *Hemigrapsus* outcompeting *Carcinus* for food and shelter (Jensen et al. 2002).

Field observations in summer 2002 indicated that *Hemigrapsus* often behave more aggressively than *Carcinus*, suggesting that this aggressive behavior may be a mechanism by which *Hemigrapsus* outcompete *Carcinus* for shelter or food. Jensen et al. (2002) noted differences in *Carcinus* behavior toward *Hemigrapsus*, dependent on *Carcinus*'s experience level with *Hemigrapsus*. The goals of my research were to examine and describe fighting behavior and aggression levels in the two crab species; quantify any differences in aggressive behavior and aggression levels; and quantify any differences in aggressive behavior of "experienced" and "naive" *Carcinus* toward *Hemigrapsus*. I used frequency of striking behavior (hitting with claws) as a measure of aggression. I found that: (1) in intraspecific fights, *Hemigrapsus* strike less frequently than *Carcinus*, (2)

Hemigrapsus strike conspecifics and *Carcinus* opponents with equal frequencies, (3) “naive” and “experienced” *Carcinus* strike conspecifics with equal frequencies, and (4) an experienced *Carcinus* decreases its striking frequency when fighting a *Hemigrapsus* (relative to fights with conspecifics), but a naive *Carcinus* strikes conspecifics and *Hemigrapsus* with equal frequency. My two main findings are that, in the laboratory, *Hemigrapsus* were less aggressive than *Carcinus* and constant in striking frequency regardless of opponent; and “naive” *Carcinus* were more aggressive than “experienced” *Carcinus* toward *Hemigrapsus*.

The Biochemical and Biological Characterization of an Apoptotic-Inducing Isoform of Tissue Transglutaminase

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Tissue transglutaminase (TGase) is a dual-function, Ca²⁺-dependent protein, which couples GTP binding and hydrolysis capability with a transamidation activity. Full-length (FL) TGase has been implicated in cellular processes such as apoptosis, cellular differentiation, cell adhesion, and survival. A naturally occurring truncated isoform of TGase was recently cloned from a human erythroleukemia cell. This truncated isoform of TGase (65 TGase) is identical to FL TGase in the amino terminal end, containing the GTP binding and transamidation domains, but lacking FL TGase’s carboxyl terminal tail. Biochemical analysis shows that 65 TGase has lost the ability to bind GTP and nearly all of the enzymatic transamidation activity of FL TGase. When exogenously expressed in NIH3T3 cells, 65 TGase induced apoptosis in 64 percent of the cells, while FL TGase-expressing cells did not undergo apoptosis. The ability of 65 TGase to induce apoptosis was not limited to NIH3T3 cells, as transfection of the breast tumor cell line, SKBR3, with 65 TGase also resulted in an apoptotic response. When FL and 65 TGases were coexpressed in NIH3T3 cells, the percentage of cells undergoing apoptosis increased to 82 percent, indicating that FL TGase expression could not inhibit the cell death caused by 65 TGase. Mutations in the GTP binding site of FL TGase, which eliminates transamidation ability, and mutations in the transamidation active site of 65 TGase, were used to study the importance of the small amount of transamidation activity detected in 65 TGase. The transamidation-defective FL TGase did not induce cell death, whereas the transamidation-defective 65 TGase did not reduce the apoptotic response. It therefore seems that the loss of carboxyl tail is responsible for the apoptosis-promoting effect. Overall, these results indicate that the 65 TGase isoform is a pro-apoptotic factor in cells, with its unique apoptotic activity resulting from deletion of the carboxyl-terminal tail of TGase and not because of the loss of transamidation activity.

Physiological and Morphological Synaptic Plasticity in Shaker; Activity-Dependent Effects at the *Drosophila* Neuromuscular Junction

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Changes in synaptic structure often accompany memory formation and long-term synaptic plasticity. Previous studies have conflicted on whether altering synaptic morphology affects neurotransmission at the *Drosophila* neuromuscular junction (NMJ). The ability for the *Drosophila* NMJ to be used as a memory model depends in part on determining whether altered morphology affects physiology at the NMJ. This study uses transgenic expression of the cell adhesion molecule Fasciclin II (Fas II) to rescue the increased NMJ structure of the hyperexcitable double mutant, *eag Sh*. This causes a rescue of the synaptic strength and short-term functional plasticity phenotypes of the double mutant. Results are compared to the effects of reduced NMJ structure in the extreme Fas II hypomorph, *FasII^{e76}*. While previous studies did not find altered physiology in the hypomorph, at the calcium concentrations used here, altered physiology is apparent. I conclude that interactions between synaptic area and vesicle depletion must be considered when predicting the effects of altered synaptic morphology. These interactions ultimately imply a self-regulating model of synaptic morphology, whereby increased synaptic strength correlates with a decreased ability to augment synaptic structure.

A Look into Some Interactions of Stem Spot Fungus (*Dothideales* spp.) with Native *Phragmites australis*

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Department of Natural Resources

Plants and fungi have interacted as long as both have been living on land. Interactions make up a broad spectrum from positive to negative with regard to the effects the fungi have on the plants. An even more complex web of interactions is formed when the plant's herbivores are taken into account. The system used for this project was that of native *Phragmites australis*, a common wetland grass, and an unstudied species of fungus in the order Dothideales that is ever-present on the native stems. To investigate possible effects of this stem spot fungus (as we call it) on the plants, we harvested stems from the Northern Montezuma Wetland Complex and measured factors such as stem height, internode diameter, number of spots per internode, and stem toughness (which is the amount of weight applied by a penetrometer it took to crush or penetrate the stem). Spatial analysis was also used to determine if there are any distribution patterns between the fungus and insect herbivores. I found that the stem spot fungus is not affecting the stem toughness or the stem height either in a positive or negative way. There also does not seem to be any effect of high fungal presence on herbivore presence in the stem. These findings support a neutral interaction. There is a spatial correlation of the stem

spot fungus up to about 41 meters. This could indicate that there are factors influencing distribution of the fungus, such as methods of spore dispersal or environmental factors.

The Relationship between the Lunar Cycle and Reproductive Patterns in Female Luminescent Ostracod Crustaceans

ZEENAT PATRAWALA

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For organisms that depend on visual systems, ambient light levels significantly influence biological responses such as dispersal, feeding, and reproduction. Male grassbed *Photeros* (Crustacea: Ostracoda), aquatic crustaceans found in the grassbeds around South Water Caye, Belize, use levels of solar and lunar light as cues to begin complex bioluminescent displays for attracting potential mates. Although research has focused on male courtship displays, little is known about female reproductive response and breeding activity. This study focuses on the relationship between female receptivity and the lunar cycle for which two hypothetical extremes were proposed. The first, or Null Model, suggests that females do not rely on a circalunar trigger to determine their receptivity. In the second, or Full Moon Model, females have a circalunar cycle in terms of their receptivity, and cue off the phase of the moon, thus having synchronized reproductive cycles. I collected 374 female grassbed *Photeros* and observed brooding, embryo development stages, and release of crawl-away juveniles. The maximum time for mating to the first appearance of embryos in the marsupium (mate to brood time) is 16 days according to field samples. The average brooding time in the marsupium before release of crawl-away juveniles is 19.2 ± 2.37 days (range of 14–27 days). Estimated gestation time (mate to release) is approximately 35.2 days and does not conform to the 29.5-day lunar cycle. There is no apparent relationship between female receptivity and the lunar cycle, and therefore this study rejects the Full Moon Hypothesis and supports the Null Hypothesis.

Is High Rate of Unequal Crossing-Over Driving Concerted Evolution of the PIGSFEAST Tandem Repeats in *Dumpy*?

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The *dumpy* gene product in *Drosophila melanogaster* is a unique 2.5-megadalton membrane protein that acts as a cell adhesion molecule and a cuticle organizer. It is largely an extracellular moiety composed primarily of EGF repeats. The extracellular domain contains 30–40 repeats of 102 amino acids in size called PIGSFEAST (PF). In this region there is an unusual amount of variability in the number of repeats among different *D. melanogaster* strains. Within- and

between-species sequence comparisons of *D. simulans*, *D. melanogaster*, *D. yakuba*, and *D. mauritiana* of the PF region show different repeat sequences and suggest this region is evolving by concerted evolution. By performing strategic crosses and restriction fragment analysis of flies with flanking markers, we attempted to show that variation in the PIGSFEAST region was coupled with a crossing-over event. The lack of observable variation suggests that, although the rate of recombination in PF may be high, it is most likely lower than our original expectations.

Substrate-Induced CH₄ Production Assay for Peat Soils

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Under the supervision of Joseph B. Yavitt
Department of Natural Resources

Anaerobic bacteria and methanogens inhabit most peat soils, but their biomass is highly uncertain. I applied the substrate-induced respiration technique to estimate anaerobic microbial biomass in four peat soils. Two soils were from *Sphagnum* (bog moss)-dominated bogs with acidic soil. One soil was from a mixed conifer-red maple forest, and one soil was from *Carex* (sedge) peatland, both with near-neutral pH soil. Soil samples were incubated in vitro under anoxic conditions, and I estimated microbial biomass following additions of glucose, ethanol, or H₂/CO₂. Basal respiration ranged from 1.1 to 12.1 $\mu\text{g C g}^{-1}$ hour⁻¹. The SIR microbial biomass ranged from 280 to 1,910 $\mu\text{g C g}^{-1}$, or 0.1 to 0.4 percent of peat organic C. Biomass levels were greater in peat collected in June than in September. Acidic pH conditions did not curb microbial biomass as expected. Basal rates of CH₄ production ranged from 0.16 to 1.5 $\mu\text{g C g}^{-1}$ hour⁻¹. Peat from one bog showed more CH₄ production with added H₂/CO₂ than the other substrates, suggesting a dominant population of methanogens that reduced CO₂ to CH₄. The other peat soils showed more CH₄ production from ethanol or glucose, suggesting acetotrophic methanogens or, possibly, ones that used ethanol directly. Applying SIR to CH₄ production resulted in methanogen biomass of 15.6 to 150 $\mu\text{g C g}^{-1}$, or about 5 percent of the microbial biomass. I found a relatively poor relationship between methanogen biomass and microbial biomass (Pearson correlation $r = 0.52$), suggesting different controls on methanogens versus microbial biomass in general in peat soils.

Cellular Interactions between a Pathogenic Fungus and a Gorgonian Coral Host

ANDREA V. SHAW

Under the supervision of Catherine Drew Harvell
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One hypothesis for the recent increase in coral disease is a result of compromised host immunity resulting from increasing environmental stress. Little is known about coral immunity, except that it is largely based on innate, nonadaptive cellular responses. In this study, I developed methods for primary in vitro cell culture of the sea fan, *Gorgonia ventalina*, used to examine its resistance to

thermal stress and infection by a fungal pathogen, *Aspergillus sydowii*. Primary cell cultures are prepared with basal liquid medium, serum supplements to stimulate cell growth, antibiotics and antimycotics to control microbial contamination, and cryopreservation techniques for long-term storage. Cell proliferation is quantified with live cell counts using trypan blue exclusion.

This is the first use of marine invertebrate cell culture methods to study defense response to temperature and disease. Gorgonian cell densities were the same, and the rate of zooxanthellae mortality increased when cultured at natural bleaching temperatures for sea fans (30° C and 35° C) compared to 25° C. This was counter to my hypothesis that cell densities would decrease at bleaching temperatures. Both nonpathogenic (terrestrial reference strain) and pathogenic strains (isolated from infected sea fans) of *A. sydowii* reduced gorgonian cell growth rates in culture. This was counter to my original hypothesis that a pathogenic fungal strain would more severely affect gorgonian cell proliferation than a nonpathogenic strain. Host-pathogen reciprocal density experiments showed that live gorgonian cells decreased in the presence of increasing fungal concentrations, while fungal growth appeared to increase with increasing gorgonian cell concentrations in culture. The increase in fungal growth was counter to my original prediction that cells would inhibit fungal growth, but is not surprising since it is a pathogen capable of killing corals. Significantly higher chitinase (antifungal) activity was induced in culture wells with gorgonian cells and increasing concentrations of fungus. Increasing fungal concentrations without gorgonian cells expressed chitinase activity at our lowest detectable limits, rejecting the hypothesis that the fungus produces chitinase. Further experimentation with this system has the potential to enhance our understanding of gorgonian immunity and response to external stresses.

Characterization of the Lia Cell Wall Stress Response Locus in *B. subtilis*

TERRY ANN SMITH

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The bacterial cell wall is a very important and unique structure. It gives the cell its shape and counteracts the inner pressure within the cell. Since many bacteria are pathogens, from a medical perspective the cell wall and its biosynthesis are good targets for antibiotics.

For bacterial cells to survive, they must have some mechanism to counteract the attack of antibiotics. The reaction of a bacterial cell to the presence of antibiotics that interfere with cell wall biosynthesis has been termed the cell wall stress response. Cell wall stress response systems generally consist of a sensor protein in the membrane that detects the presence of antibiotics and activates a cognate regulator protein in the cytoplasm. The regulator protein then binds to DNA resulting in the expression of the genes that help the cell to counteract the effect of the antibiotic.

In *Bacillus subtilis*, six of these regulatory systems have been identified so far, one of which is the LiaSR (formerly YvqEC) two-component system, the focus

of this manuscript. This system leads to expression of the *liaIH* (*GFEC*) locus when bacitracin and vancomycin are present. The biological function of *liaIH* is unknown. The goal of my project was to define the range of inducers for *liaIH* and characterize its biological function.

To define the range of inducers for the locus, cell wall antibiotics, organic solvents, surfactants, and other antibiotics were tested using the β -galactosidase assay. From the antibiotics tested, only ramoplanin and nisin, two cell wall antibiotics, were identified in addition to bacitracin and vancomycin as strong inducers of *liaIH* expression. All four of these antibiotics interact with Lipid II, the carrier molecule in the cell membrane that transports the cell wall building blocks from the cytoplasm to the extracytoplasmic side for incorporation into the cell wall. Ramoplanin and nisin were tested as inducers of other cell wall stress response signaling systems. It could be shown that these two antibiotics induce only the LiaSR system but none of the other five systems. The analysis of a *liaIH* deletion mutant shows that the gene products of this locus do not confer resistance to bacitracin, vancomycin, ramoplanin, and nisin.

Signals from Hxk2p and Rgt1p Inhibit Transcription of *INO1*, Independently of Opi1p, in the Bakers' Yeast, *Saccharomyces cerevisiae*

JARED C. TALBOT

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INO1 is the most highly regulated of the structural genes encoding proteins involved in phospholipid synthesis in yeast. *INO1* is co-regulated with many other genes encoding proteins involved in lipid metabolism. The primary negative regulator of *INO1* expression is Opi1p. Transcription of *INO1* is highly sensitive to changes in lipid precursors and general nutrient availability. As a result of this sensitivity, the regulation of *INO1* has been used to study the regulation of lipid metabolism. The glucose response signal transduction pathway is a mechanism by which cells sense the availability of glucose, and alter gene expression accordingly. Several studies have implicated members of the glucose response signal transduction pathway, specifically the G1c7p/Reg1p protein phosphatase complex and the Snf1p/Snf4p protein kinase complex, in the regulation of phospholipid synthesis. However, the role that the glucose response pathway as a whole plays in the regulation of phospholipid synthesis remains elusive. Furthermore, the relationship between the glucose response pathway and Opi1p is in need of investigation. Hxk2p converts glucose into glucose-6-phosphate, and also is a protein acting upstream of G1c7p/Reg1p in the glucose response pathway. Here, it is shown that Hxk2p represses the transcription of *INO1* through a mechanism that is independent of Opi1p. Thus, it appears that the upstream components of the glucose response pathway may have a role in the regulation of *INO1*. However, it appears that downstream of the Snf1p kinase, the glucose response pathway does not regulate lipid metabolism in the same way that it regulates classical glucose-controlled genes such as the hexotransporters. A model for the role of the glucose response pathway in the regulation of *INO1* is presented.

Dopamine D2 Receptor Modulation Parallels the Effects of Changes in Odor Intensity on Rat Odor Discrimination

CATHERINE J. WEI

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Evidence for the dopaminergic modulation of cortical activity, including motor control and initiation as well as affective behavior and reward associations, is abundant. While several studies have examined the role of dopamine in modulating olfactory bulb activity through changes in odor detection thresholds, the manner in which dopaminergic modulation affects odor discrimination capabilities remains unclear. Previous findings from our laboratory suggested the involvement of dopamine D2 receptors and odorant intensity in altering the ability of adult rats to simultaneously discriminate two perceptually similar odorants. To determine whether these changes in performance are the direct result of dopamine-related changes in sensitivity to olfactory stimuli or otherwise, the present study tested the rats' abilities to discriminate between similar odor pairs at three concentrations (0.001, 0.1, 10 Pa) and with the administration of either a selective D2 agonist quinpirole or a selective D2 antagonist spiperone. Injection of the D2 antagonist spiperone (0.5 mg/kg) significantly increased odor discrimination performance at the lower odor concentrations of 0.001 and 0.01 Pa. On the other hand, injection of increasing concentrations of D2 agonist quinpirole produced a dose-dependent decrease in performance that paralleled the changes in discrimination ability observed in controls performing the same task at decreasing odor concentrations. Thus, dopamine D2 receptor modulation affects odor discrimination in a manner similar to changes in odor concentration. These results suggest that dopamine D2 receptor activity is not only important in modulating odor perception, but is also involved in adapting to changes in olfactory sensitivity when learning to discriminate similar odors.

Lipids and Pulmonary Function: Is There a Role for HDL?

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Division of Nutritional Sciences

This study investigated the association of serum lipids with pulmonary function using data from a 1989 cross-sectional study of 69 rural counties in the People's Republic of China. Using a three-stage random clustering procedure, 60 males and 60 females aged 35 to 64 were selected from each county. Pulmonary function testing followed standard methods, and individual blood samples were assayed for apolipoproteins B (apo B, a component of low-density lipoprotein, LDL) and A-1 (apo A-1, a component of high-density lipoprotein, HDL). Of 7,404 participants, 5,794 had complete data. Regression analyses used hierarchical linear models adjusted for age, height, sex, adiposity, smoking, alcohol intake, and physical activity. Apo A-1 was positively associated with the mid-maximal expiratory flow rate (MMEF): a one standard deviation increase in apo A-1 was

associated with a 31 ml increase in MMEF (95 percent confidence interval 6.5, 56.4). There was little or no association between apo B and pulmonary function. In models further adjusted for socioeconomic status, antioxidants, and indoor air pollution there was little or no change in the findings. This study extends prior studies by considering a population with lower mean total cholesterol relative to Western populations. The findings support a small, positive association of HDL with pulmonary function.

Keywords: Apolipoprotein A-1; Apolipoprotein B; forced expiratory volume; mid-maximal expiratory flow; cholesterol; lipoproteins, HDL; lipoproteins, LDL

Identification of the Binding Interface between the Dbl Proto-oncogene and the Chaperone Hsc70

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The *dbl* oncogene product is the defining member of a family of onco-proteins known as Dbl guanine nucleotide exchange factors (GEFs). Members of the Dbl family regulate proliferative signaling pathways by their ability to facilitate activation of the small GTP-binding proteins Cdc42, Rac and Rho. Oncogenic activation of proto-Dbl occurs through loss of the amino-terminal 497 residues, rendering the protein constitutively active. Because both onco- and proto-Dbl contain the structural elements required for GEF activity (i.e., the DH-PH domain), it is thought that the amino terminus of proto-Dbl somehow inhibits the biochemical activity of the catalytic domain. Our lab has recently identified the chaperone heat shock cognate protein 70 (Hsc70) as a preferential binding partner of the proto-oncogenic form of Dbl. In this honors thesis, I used a targeted deletion approach to identify the domains in Dbl that mediate Hsc70 association. I report two regions in Dbl that mediate Hsc70 binding: the amino terminal spectrin homology domain (residues 286–348), and the carboxy terminal pleckstrin homology (PH) domain (residues 711–808). Interestingly, binding of Hsc70 to Dbl's PH domain occurs only in the context of the proto-oncogenic form of the protein. These observations suggest that an *intermolecular* interaction involving Hsc70 provides critical means for modulating the biochemical activity of the Dbl proto-oncogene.

The Effect of Spotted Salamanders on Mosquito Larvae in Small Woodland Pools

NICHOLAS R. WOLFER

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Mosquito control in areas of human habitation has always been an important topic in the United States, but the recent emergence of West Nile Virus, a potentially deadly, mosquito-transmitted disease, has led to a dramatic rise in public concern regarding this insect. In response, some people have begun to question whether pond creation and wetland restoration might contribute to

an increase in mosquito populations by providing breeding habitat for these insects. Our study addressed this issue by monitoring spotted salamander (*Ambystoma maculatum*) consumption rates of mosquito larvae in both laboratory and natural environments. Twenty larval salamanders were collected on July 9, 2003, kept in separate containers in a laboratory setting, and fed only mosquito larvae until they were released on August 8. The growth of these animals (snout-vent length) and the number of mosquitoes eaten per salamander per day was recorded during this time period. Laboratory salamanders grew from a mean of 1.66 cm (s.d. = 0.10 cm) to 2.57 cm (s.d. = 0.08 cm), and consumption averaged 44 mosquito larvae per salamander per day during the experiment. We also compared growth and feeding rates to those of wild-caught salamanders, which were sampled periodically from three ponds within Cornell University's Arnot Forest in Van Etten, N.Y. Results from wild-caught and laboratory salamanders were very similar, indicating that laboratory data can be used to extrapolate to a natural setting. To examine this issue on a landscape scale, we estimated larval spotted salamander populations in 11 ponds throughout the Arnot Forest using egg counts conducted in April and mark-recapture data from early August. Total populations in two small ponds were approximated using a Lincoln-Peterson Index. Survivorship from egg to late-stage larvae was approximately 26 percent, indicating that the 11 ponds contained over 14,000 spotted salamanders during the period of the study. Based on laboratory data, this many animals could consume more than 17 million mosquito larvae in a single month. We therefore propose that salamander larvae may be important to the regulation of mosquito populations in the natural environment. Moreover, introduction of spotted salamanders could be an effective means of controlling mosquitoes in restored wetlands and newly created ponds.

Emergence Cues of a Mayfly in a High-Altitude Stream Ecosystem: Implications for Consequences of Climate Change

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Over the past four years there has been a severe drought in western USA, and concurrently, the high-altitude stream mayfly *Baetis bicaudatus* has been metamorphosing to the adult stage earlier in the summer. Long-term patterns of early emergence during low-water years suggest that mayflies could use either declining stream flow or increasing water temperature as proximate cues for metamorphosis. A long-term database from the upper East River in western Colorado showed that the magnitude and date of peak stream flow, and degree-days per day predicted peak emergence date of this mayfly. However, a two-year survey of multiple streams in the drainage basin showed that water temperatures but not stream flow predicted emergence phenology of this mayfly. To decouple definitively flow and temperature as potential cues for metamorphosis, we reared *Baetis* larvae in circular flow-through artificial streams under four treatments: high or low flow, warm or cold (ambient) water temperatures. Mayflies emerged sooner in the warm-water than the cold-water treatment, but low flow alone did not cause mayflies to metamorphose early. Nonetheless, using warming temperatures to trigger metamorphosis synchronizes emergence with the descending limb of the hydrograph when oviposition sites become available. We speculate that large-scale climate changes involving warming could have profound effects on populations with life histories sensitive to the thermal regime.

Keywords: *Baetis bicaudatus*, climate change, drought, emergence cues, stream invertebrates

Applying a Phenomenological Method to the Design Process

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A phenomenological method is used to reveal the mechanics of a design project, “Garden of Lights,” which was developed for the World Trade Center Memorial Competition. The “Garden of Lights” case study investigates the application of a phenomenological method for informing the design process. Phenomenological description is used as a way of editing and refining design elements based on the experiences perceiving them. A phenomenological method is developed based on Edmund Husserl’s philosophy of phenomenology. Husserl’s work provides a referential structure for accurately describing experiences of the designed objects and spaces in “Garden of Lights.” Phenomenological description focuses on two elements of the design—a path through a meadow, and the representation of names in a large below-ground space. Two different versions of each element are described phenomenologically, and a design analysis is developed based on these descriptions. In the path element, one version is chosen based on the experiential issues of the meadow made explicit through description and analysis. A study of the representation of names reveals problematic issues within the experiences of each version. Analysis based on the phenomenological description is used to develop guiding principles for redesigning the space. By applying a phenomenological method to the design process, experiential structures are created on which more specific design work can be based.

Visual Ecology: An Exploration in Ecology as Art—The Everson Museum, Syracuse, New York

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The city is a diverse environment and a cultural landscape system with its own specific water systems, topography, flora and fauna, soils, air, interactions, and phenomena. This ecological view within the design process considers the artwork within larger contexts of how people, plants, and animals are interconnected with each other, the site, and ultimately, the Earth. As an aesthetic intervention, visual ecology deals with the visibility and invisibility of natural environment as a cultural awareness strategy.

The Everson Museum has been a major cultural center of the city of Syracuse, N.Y., for 30 years and is now upgrading and expanding in response to the museum’s objectives for the new millennium. In addition to the proposed highly contrasting extension to the west of the current building, the museum is seeking design proposals for the surrounding plaza space and outdoor viewing of contemporary art, allowing for a transparent, neutral, and inclusive museum space. The redesign of the Everson’s landscape offers an opportunity to reconsider the landscape’s role in making ecology visible. It looks to reveal the elements of phenomena and energy, time and flux, and the interactions

between human and nonhuman species through a public art form. The museum landscape intervention becomes a mediator between the interior museum and the surrounding context. Most important, it becomes a mediator between ecology and urban society that seeks to entwine nature and culture.

The initial design was completed in May 2003. This past year was spent conducting research on ecological and environmental artists and discovering new interpretations within the original site design. This exploration led to the realization of how conceived forms can offer a multiplicity of functions and derivations. Issues of ephemerality, in terms of time and natural processes, combined with intended user interaction, posed challenging and complex questions. In terms of nature and culture, the design investigation and research seeks a method to begin dealing with the complex issues that face contemporary society.

Arboreal Structures: Architectonic Art in the Landscape

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Arboreal structures can be viewed as the confluence of landscape architecture, land art, and architecture, the theoretical basis of the phenomenon known as a treehouse. The definition of an arboreal structure, a term created for the purpose of this thesis, is one that includes the treehouse along with any structure lacking the habitability associated with the treehouse. Outdoor sculpture that is categorized as land art thus becomes germane to this discussion. The works of Mary Miss, Alice Aycock, Andy Goldsworthy, and Hannsjorg Voth are studied in the creation of land artwork that ties into Jay Appleton's theories on landscape aesthetics and the evaluation of landscapes. His book *The Experience of Landscape* (1979) extensively outlines the *prospect-refuge* theory where the landscape is composed of symbols representing prospect and/or refuge. The background research and investigation on historical and contemporary treehouses and their building methods delve into the architecture of treehouses concerning how to build a structurally stable treehouse.

This thesis culminates in the design of an arboreal structure on a site close to Cornell University. The design is a hypothetical exploration of the *prospect-refuge theory* and an example of an arboreal structure. The process and proposal of my original design was an exercise in the creation of a theory and its application to a site. The difficulty comes in adapting to the conditions of that site. From ideation to fruition, the *prospect-refuge form* and *arboreal structures* are interconnected via symbolic and visual cues that propel movement through the site and upward into the trees.

Geographic Distributions of Dragonflies (Suborder: Anisoptera) in New York State: An Analysis of Ecozones

MICHAEL J. ANDERSEN

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County-level distribution data of the 129 species of dragonflies (suborder Anisoptera) in New York State were analyzed with the state's 11 major ecoregional (ecozone) boundaries using a geographic information system (GIS). A measure of ubiquity, defined as the proportion of counties in a species' distribution, was established for each species. In addition, two descriptive statistics were generated based on each species' distribution relative to ecozones. This research was done to determine whether dragonflies show patterns in their distribution relative to ecozones. Three broad geographic regions were defined in the state (northern New York, coastal plain, and the Great Lakes plain/Appalachian plateau) based on distinct dragonfly faunas. Northern New York has eight species that occur there, but nowhere else in the state, and the coastal plain has 15 species that occur only there in the state. The Great Lakes plain/Appalachian plateau is defined by the occurrence of species that are widespread throughout the eastern United States. Finally, the conservation implications of dragonflies and their wetland habitats are discussed, along with recommendations for future work in dragonfly biology and conservation.

Factors Influencing Survivorship of American Beech (*Fagus grandifolia*) Seedlings at Hubbard Brook Experimental Forest

MADELEINE P. FAIRBAIRN

Under the supervision of Timothy J. Fahey
Department of Natural Resources

I used a nested experimental design to examine the effects of light availability, nutrient availability, and insect herbivory on survivorship of beech seedlings in Hubbard Brook Experimental Forest (HBEF), N.H. The seedling stage of development is an important determinant of forest stand composition, but first-year beech seedling survivorship has received relatively little study. Nine pairs of plots were established, one of each pair being in a canopy gap and the other beneath the closed canopy. Nested within each plot were 1-m² treatment quadrats that received pesticide application, a trenching treatment, or both. Beech seedling densities in the quadrats were counted throughout the summer, and the leaves of 288 marked individual seedlings were traced monthly to determine leaf area. In addition, 32 marked individuals were located in the water addition (receives 50 percent extra rainfall) and water displacement (receives 50 percent less rainfall) areas of a throughfall displacement experiment conducted by the U.S. Forest Service. The results showed significantly greater survivorship in the gap plots than in the closed canopy plots ($p < 0.001$). Water addition resulted in increased survivorship (91 percent), whereas water displacement had no effect. There was a significant treatment effect on leaf area loss

($p < 0.001$), with greater herbivory on the individuals in the trenched quadrats, especially in the gap plots. The results suggest that water is a primary limiting factor to beech seedling survivorship at HBEF, even in relatively wet years. Beech seedlings also have higher survivorship in high light environments, despite their shade-tolerant status. Caterpillar herbivory appears not to be a major cause of beech seedling mortality at HBEF. Further research should examine in greater detail the effects of light and water co-limitation on beech seedling growth and survivorship.

Trophic Interactions between Native *Phragmites australis* and Its Associated Herbivores and Predators

RACHEL H. FARR

Under the supervision of Bernd Blossy
Department of Natural Resources

Phragmites australis is a widespread cosmopolitan perennial wetland grass. In the past few decades, *P. australis* populations have increased significantly in North America, which has resulted in the decline of numerous native wetland species. The potential implementation of biological control is currently being investigated but has been complicated until recently by the lack of knowledge about the status of *P. australis* as a native or introduced species. It has been determined that there is an introduced, prolific invasive strain that is likely threatening the native strain. Little is known about the life history and ecology of native *P. australis*, including the occurrence and abundance of specialized herbivores and their predators, which is required knowledge in developing an effective biological control program for introduced *P. australis*. This study examines the relationship of native *P. australis* with its herbivore community and their natural enemies (hymenopteran parasitoids) at a wetland site in upstate New York using spatial analysis. Over 1,000 stems were collected in December 2003 and dissected between January and March 2004. Insects found in stems were identified and tallied. Seven herbivore species and three host-specific parasitoids were found. The results indicated little or no spatial correlation among the *P. australis* stems and its associated herbivores. However, there was some spatial relationship between the *P. australis* stems and the parasitoids. The parasitoids had no spatial association with their insect hosts. Overall insect abundance at the site was low, and no evidence of competition was found between the herbivore species or parasitoids.

Effects of *Trapa natans* and Its Herbicide Treatment on Macrophytes, Zooplankton, and Benthic Macro-invertebrates

JOSHUA B. GRINATH

Under the supervision of Bernd Blossey
Department of Natural Resources

Water chestnut, *Trapa natans*, is an invasive aquatic macrophyte that has potential profound impacts on native ecosystems and requires management

efforts. I investigated the biotic responses of several components of the aquatic community to *T. natans* and its 2,4-D herbicide treatment at three sites in Ox Creek and Oneida Lake, N.Y., during the summer of 2003. The Ox Creek site comprises a continuous *T. natans* bed with treated and nontreated plots, while the Oneida Lake sites included a treated *T. natans* plot and a nontreated native vegetation plot. I found that 2,4-D had detrimental effects on nontarget *Potamogeton* spp. and *Ceratophyllum demersum*. A treated *T. natans* plot supported greater zooplankton biomass than a nontreated *T. natans* plot. Greater zooplankton biomass in the native vegetation site may indicate indirect adverse effects of 2,4-D or legacy effects of *T. natans*. Filter feeding zooplankton respond positively to decreased association with *T. natans*, while cyclopoid copepods show an opposite response. Treated and nontreated sites in both Ox Creek and Oneida Lake exhibited similar levels of benthic macroinvertebrate taxonomic richness, but the communities were different in composition, and many taxa were significantly more abundant in treated sites. The results showed that 2,4-D is an appropriate short-term tool for treating *T. natans* infestations, with few observed detrimental side effects.

Vesicular-Arbuscular Mycorrhizal Colonization and Morphology in *Acer saccharum* (Sugar Maple)

ELIZABETH A. HARTMAN

Under the supervision of Timothy J. Fahey
Department of Natural Resources

A number of species of fungi form mutually beneficial vesicular-arbuscular mycorrhizae in sugar maple roots, and there is believed to be a correlation between decline of sugar maple and mycorrhizal infection. I studied mycorrhizal infection and relative contributions of different mycorrhizal structures in sugar maple roots in relation to fertilization, land use history, and the presence or absence of a forest floor layer. I studied four different combinations of variables during two sampling periods, several months apart within each of three sites in central New York: Mount Pleasant, Ringwood Preserve, and Turkey Hill Plantations. After being cleared, bleached, and stained, roots were examined for mycorrhizal colonization using the magnified intersections method. I found that Mount Pleasant sugar maples had more arbuscules, vesicles, and coils in post-agricultural land than in old forests, with nonoverlapping standard errors. Ringwood Preserve also had greater total mycorrhizal colonization in post-agricultural land than old forest during the second sampling period. Mycorrhizal colonization at Ringwood exhibited seasonal variability. The effect of fertilizer treatments on mycorrhizal infection in Turkey Hill sugar maples depended on the presence or absence of a forest floor. Fertilization increased mycorrhizal colonization in the presence of a forest floor and decreased mycorrhizal colonization in the absence of a forest floor. At both Mount Pleasant and Ringwood, mycorrhizal colonization was greater in the forest floor layer than the mineral soil in plots with a forest floor. My results showed spatial variability among sites in addition to the effects of fertilization, land use history, and presence or absence of a forest floor layer.

Impact of Groundwater Sulfate Delivery on Anaerobic Respiration and Dissolved CO₂ Concentrations in a Rich Fen in Central New York

MELANIE K. HAYN

Under the supervision of Barbara L. Bedford
Department of Natural Resources

This study examines the interactions between groundwater flow and porewater chemical concentrations to elucidate controls on dissolved CO₂ concentration and the rate of anaerobic carbon mineralization along a transect in a wetland fed by groundwater, Junius Ponds Fen, in central New York. Three hypotheses were tested: (1) groundwater flow paths influence pool sizes of sulfate and nitrate in shallow peat, (2) supply of sulfate through groundwater flow is responsible for high dissolved CO₂ concentrations within the fen, and (3) response of anaerobic CO₂ production to sulfate addition in vitro will be correlated with rates of sulfate supply via groundwater, as indicated by sulfate pool sizes. Groundwater rich in sulfate is entering the fen both laterally from the adjacent upland, and through a deep plume that reaches the surface of the fen. Groundwater gradients in sulfate, nitrate, dissolved organic carbon, and dissolved inorganic carbon were found to follow paths of groundwater flow and to be spatially related to the dissolved carbon dioxide concentrations across the fen. Sulfate-amendment incubations did not show a significant increase in soil respiration rate as a result of sulfate addition, but did show a response to carbon addition in some cases. Incubations also failed to show a spatial response to sulfate addition. The high bulk density of peat at this site, in conjunction with the incubation data, suggest that labile carbon availability may be more important in controlling the rate of anaerobic carbon mineralization than sulfate pool size.

Health and Mycorrhizal Colonization Response of Sugar Maple (*Acer saccharum*) Seedlings to Calcium Addition at Hubbard Brook Experimental Forest

STEPHANIE M. JUICE

Under the supervision of Timothy J. Fahey
Department of Natural Resources

Acidic deposition and resultant leaching of soil base cations are known to affect overstory sugar maple health and contribute to the unusually high rates of current dieback. Canopy decline has also been correlated with decreased mycorrhizal colonization. Response by sugar maple seedlings to acidic deposition deserves further research because of its implications for future stand regeneration. We examined the health and mycorrhizal colonization rates of sugar maple germinants on a Ca-treated watershed at Hubbard Brook Experimental Forest and compared their status to the health of seedlings growing on control sites. We quantified general sugar maple germinant health by height, leaf area, specific leaf area, chlorophyll content, biomass, and nutrient analysis. To determine vesicular-arbuscular mycorrhizal colonization rates, we first cleared and stained germinant roots and then examined their structures microscopically. We found that sugar maple seedlings on the Ca-addition site

were taller, had larger leaves, more chlorophyll, more Ca and Mg in their tissues, and less foliar N content. These seedlings also had a significantly larger percentage of their roots colonized by mycorrhizal fungi. Our results indicate a correlation between soil Ca availability, mycorrhizal colonization rates, and seedling health that has three possible interpretations. Soil cation deficiency may restrict fungal infection rates, or alternately, reduced seedling health may restrict mycorrhizal colonization. There may also be an interaction between the inoculum potential and the rate of fungal colonization. Our results indicate that base cation deficiency does affect seedling status, which will therefore affect the future health and regeneration of sugar maple stands.

Analysis of Spatial and Temporal Variation in HIP Survey Response

LAURA D. KIERNAN

Under the supervision of Evan G. Cooch and Jody W. Enck
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Waterfowl management involves a network of federal and state agencies developing harvest regulations annually, with the goals of ensuring long-term sustainability of continental waterfowl populations and providing the greatest state-specific harvest opportunity. The U.S. Fish and Wildlife Service uses adaptive harvest management to identify an appropriate regulatory framework for each of the four Flyways, taking into account uncertainty in biological and harvest data. Annual harvest estimates are based on data collected through surveys of hunters, stratified by state and relative harvest from the previous year. Using data from the Mississippi Flyway for 1999–2002, I assessed annual overall response rates, specifically response rates by geographic cluster (region), by harvest strata in the previous year, and by response wave following the initial survey. To assess the degree of uncertainty in the harvest data, I determined mean hunter effort and harvest and examined whether these estimates differed by region or response wave. Annual overall response rates never exceeded 65 percent, which could contribute to uncertainty in the harvest data. Response rates declined from north to south among regions within the Flyway, with northern respondents replying earlier than southern respondents. Mean harvest and effort increased from north to south, along with the correlation between harvest number and effort days. These variations may exacerbate uncertainty from the low response to the survey. Due to variability in response time by hunters from previous sampling strata, the reminder notices are an important tool for including data from all hunter types in the regulation-setting decisions of adaptive harvest management.

Recent Patterns of Large Fire Events on Kaibab Plateau, Arizona, USA

GARRETT W. MEIGS

Under the supervision of Timothy J. Fahey
Department of Natural Resources

Humans have altered historic ranges of fire disturbance, dramatically changing forest ecosystems from local to global scales. To explore spatial and temporal trends and significance of recent large fire events on Kaibab Plateau, Ariz., I asked three questions regarding (1) recent patterns and effects, (2) causal factors, and (3) implications for altered fire ecology and research methods. I synthesized information from field observation, agency fire history records, fire weather and fuel databases, regional literature, and spatial databases. The Kaibab Plateau is located in north central Arizona within Kaibab National Forest and Grand Canyon National Park. Forest communities and fire patterns have changed significantly in the past century, and current conditions may be more susceptible to large, stand-replacing fire events. Between 1959 and 2003, 26 large fires (greater than 200 hectares) burned a total of 56,519 hectares (16 percent of the study area). Fire numbers and area burned increased significantly over the study period, with 15 fires burning 42,046 hectares since 1994. Large fire events occurred in all forest and management types but were not evenly distributed. Many causal factors contribute to ignition and development of fire events. Differing agency management appears to be the strongest influence on large fire patterns. High maximum winds are also important, particularly for the three largest fire events. I calculated a mean fire return interval of 275–300 years for all fires and about 83 years for fire events since 1994. Both of these estimates are outside historic ranges of variability for all forest types except high-elevation forests with stand-replacement fire regimes. Recent policy changes require increased burning and may allow a partial recovery of historic fire patterns and processes.

Spatial and Temporal Variability of Chlorophyll in Hawaiian Mesoscale Eddies

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Seasonal variations in prevailing northeasterly trade winds, in conjunction with island topography, create cyclonic eddies on the leeward side of the Hawaiian Islands. These westward propagating rings are areas of enhanced biological productivity, with increased phytoplankton concentrations and increased fish catch. The periodicity of occurrence of phytoplankton blooms was examined from 1997 to 2003 using the SeaWiFS satellite to analyze the chlorophyll concentrations in mesoscale eddies. Eight-day weekly chlorophyll averages were used to investigate the eddies. Weekly chlorophyll anomalies were analyzed using Empirical Orthogonal Function analysis. The first EOF mode likely represented seasonal variation and accounted for approximately 40 percent of the total variance. The second and third EOF modes represented upwelling features and explained 8 percent and 6 percent of the total variance, respectively. Eddies usually develop between June and September, with most forming at the end of August. These data also show that the formation, propagation, and eventual destruction of these blooms can last two to eight weeks. Weekly anomaly data were also analyzed using longitude versus time plots. Propagation rates were found to be approximately 3.75 km per day. Yearly analysis revealed strong eddy formation in 1999 and 2000 with an abrupt decrease in the frequency and intensity of eddy formation from 2001 to 2003. Comparison with Southern Oscillation Index values revealed a correlation between positive values (La Niña) and the presence of strong eddy formation. Years with negative values (El Niño) had less intense eddies, or none at all. This suggests a link between ENSO events and the frequency of eddy formation.

The Diversity of Oomycete Communities in Agricultural Soils

JESSICA M. ARCATE

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Department of Plant Pathology

Oomycetes are ecologically and phylogenetically distinct eukaryotic microorganisms that inhabit both aquatic and terrestrial ecosystems. Their presence within terrestrial ecosystems as both parasites and saprotrophs is believed to greatly affect degradation and nutrient cycling in soil ecosystems, and also disease development within agroecosystems. Very little is known about the structure and function of oomycete communities in terrestrial ecosystems, and no modern molecular ecological studies of oomycetes have been conducted. The ultimate goals of this project were to determine whether plant species influence the composition of rhizosphere oomycete communities, and whether communities described through traditional baiting methods represent a true assessment of rhizosphere communities. In this research, the diversity of oomycete communities was investigated in three different agricultural fields planted to different plant species (squash, tomato, and sorghum). Oomycetes were recovered from rhizosphere soils using traditional baiting techniques with hempseed baits. Additionally, DNA was extracted directly from soils and also from baits. Amplification of 28S rRNA gene sequences (rDNA) was accomplished using an oomycete specific primer set (Oom1f, Oom1r) in PCR reactions. Amplified 28S rDNA was cloned, sequenced, and subjected to Basic Local Alignment Search Tool (BLAST) searches and phylogenetic analyses. BLAST searches yielded significant matches to multiple *Pythium* spp. and *Peronospora parasitica*. Phylogenetic analysis using neighbor-joining methods revealed considerable species variation in both soil and baited oomycete communities. Visual assessments of phylogenetic tree topologies revealed greater diversity in soil communities than in baited communities. Lineage per time plots based on maximum likelihood trees supported a greater diversity of divergent lineages in the soil communities as compared with the baited communities, which contained more closely related lineages. A comparison of the genetic diversity within soil and baited communities suggests that soil communities harbor greater oomycete diversity than do the baited communities. Combined neighbor-joining analysis of both soil and baited communities indicated the presence of several distinct clusters unique to either baited or soil communities. However, these clusters were interspersed throughout the phylogenetic tree. These results provide a new approach to the study of oomycete communities and reveal a level of diversity not previously recognized.

The Genetic Mapping of Two Grain Size Mutants on Rice Chromosome 3

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Rice is an important world food crop, and in the future producing higher-yielding rice varieties will become essential as human populations increase. Grain size is a polygenic trait that is highly correlated with yield. Genes associated with grain size and shape can be mapped through the use of quantitative trait locus (QTL) analysis. The QTL *grain weight 3.1* (*gw3.1*) was recently fine-mapped to the genetically defined centromeric region of chromosome 3. Morphological mapping has shown that two grain size mutants, controlled by the genes *Minute* (*Mi*) and *Long Kernel Fusayoshi* (*Lkf*), which are found in *temperate japonica* backgrounds, also occur in this region. To better understand how genes on chromosome 3 control grain size, and to decipher the relationships between *Mi*, *Lkf*, and *gw3.1*, we mapped *Mi* and *Lkf* in crosses with the indica cultivar IR64, using microsatellite (SSR) markers and populations of approximately 120 F₂ individuals. Interval mapping of *Mi* positioned this gene in the 3.6 cM interval between markers JL8 and JL14, in the genetically defined centromere region on chromosome 3. Preliminary mapping results for *Lkf* failed to conclusively identify the location of this gene. The position of *Mi* corresponds closely to that of QTL *gw3.1* and suggests that mutations at the same locus may be responsible for *Mi* and *gw3.1*.

Transport of the Free Cyclitols D-*chiro*-Inositol, Myo-Inositol, or D-pinitol Fed to Buckwheat Explants and Analysis of Galactosyl Cyclitols in Seeds

JANET M. MA

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Food crop seeds accumulate soluble carbohydrates as part of their maturation process. In buckwheat (*Fagopyrum esculentum* Moench) seeds, cyclitols are accumulated as their galactosyl derivatives, mostly as fagopyritols that are galactosyl derivatives of D-*chiro*-inositol. This study was conducted to determine the effects on the levels of soluble carbohydrates in embryos of feeding free cyclitols D-*chiro*-inositol, myo-inositol, and D-pinitol to buckwheat stem-leaf-seed explants, and to characterize the transport and metabolism of these cyclitols in buckwheat. Buckwheat explants, consisting of leaves, flowers, and developing seeds attached to a stem segment, were used to study the transport of cyclitols, in particular, D-*chiro*-inositol, myo-inositol, and D-pinitol, from the stems to the maturing seed, and their incorporation into galactosyl cyclitols in maturing embryos. Feeding D-*chiro*-inositol to explants resulted in a threefold increase in the accumulation of fagopyritol B1 in embryos; however, feeding D-*chiro*-inositol resulted in 30 percent less embryo dry mass compared with the control treatment without cyclitols. Feeding myo-inositol to buckwheat explants increased accumulation of fagopyritol A1 and fagopyritol B1 fivefold, fagopyritol A2 and fagopyritol B2

threefold, and fagopyritol A3 twofold in mature embryos, with no reduction in accumulated embryo dry mass. Feeding free *myo*-inositol to buckwheat explants was more effective in increasing fagopyritol accumulation in embryos than feeding *D-chiro*-inositol. Feeding *D*-pinitol to buckwheat explants resulted in accumulation of free *D*-pinitol in mature embryos but only very small quantities of galactopinitol A (2.4 μ g/embryo) and galactopinitol B (1.2 μ g/embryo). Embryos from mature seeds on buckwheat explants fed the control treatment without cyclitols did not accumulate *D*-pinitol, galactopinitol A, or galactopinitol B. Feeding *D*-pinitol also resulted in reduced *D-chiro*-inositol transport to or uptake by buckwheat seeds. Increasing *myo*-inositol biosynthetic capacity through overexpression of a *myo*-inositol phosphate synthase gene (MIPS) in buckwheat leaves may be an effective means to enhance the accumulation of *D-chiro*-inositol and fagopyritols in seeds, compounds that are beneficial to producing hypoglycemic effects in patients with type II diabetes.

Modification of the PGO Assay for Use in Acylsugar Quantification

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Natural insect pest resistance mediated by the production of acylsugars in trichome exudates was transferred from the wild species *Lycopersicon pennellii* to breeding lines of the cultivated species of tomato, *L. esculentum*. Acylsugar quantification was successfully performed using an established acylsugar assay based on the Nelson reaction for reducing sugars. However, the high cost and labor required for this assay stimulated an interest in developing an alternative acylsugar assay protocol. The PGO (peroxidase/glucose oxidase) assay was chosen as a viable alternative to the Nelson reaction for quantification of reducing sugars. A series of experiments were performed to test methods for removing the acyl groups from the acylsugars to release the sugar components, to split sucrose into its component monosaccharides, and to measure the sugar released from the acylsugars in the samples. A new protocol for acylsugar measurement based on PGO quantification assay was created as a result of these experiments. This assay should be less laborious, faster, and less costly than the original acylsugar assay.

The Use of Sexual Imagery in Print Advertisements and Its Gender-Based Effects

JACOB R. BROWN

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Department of Communication

The use of sexual imagery in advertising has been a powerful and attention-grabbing tool for many years. More recently, however, its ubiquitous use has raised questions in areas concerning appropriateness, purchase intentions, recall, and overall effectiveness. In this study the differences in participant responses based on gender and the level of sexual imagery in printed advertisements were investigated. Subjects viewed a series of advertisements and evaluated them based on levels of model attractiveness, ad appeal, model use appropriateness, ad offensiveness, and purchase intentions. Results revealed no significant difference in recall based on levels of sexuality in the advertisement. Advertisements with sexual imagery did not create higher purchase intentions than ads without. Advertisements containing functional models were evaluated more positively by female subjects than by male participants. Results indicate that while most of the historic data still hold true, consideration should be paid to results that indicated an interaction effect between gender and the level of sexuality in the advertisements.

Baseball Statistics

STUART L. COHEN

Under the supervision of Martin T. Wells
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Baseball is a sport that has been studied for many years but has failed to be fully understood. For many years an incredible amount of what baseball has called statistics, but is more of an accounting ledger, has been collected. There is constant debate over which statistics have any meaning as well as how to decide the best player. I wrote a study that answers the question of which players are the best and which statistics are the most important. Using Java to create a computer simulation of many baseball games, I created my own statistic called "runs yielded does." This statistic attempts to be an unbiased estimate for the value that a player adds to his team while controlling for the differences across teams. Once this statistic was created, all known statistics were regressed to find the statistics of value that can be used to determine a player's value and estimate his runs yielded statistic. The same program that ranks players also has the ability to analyze several important managerial decisions. This program determines the best lineup for every baseball team by deciding on the nine best position players to use in the proper order. This program also serves to compare two or more teams by analyzing the distribution of runs scored by the two teams and looks at two decisions that must be made at every baseball game by the manager: when to walk a batter, and when to bunt.

On Lying and Being Lied To

LAUREN E. CURRY

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Department of Communication

Although lying involves both a sender and a receiver, the majority of previous research has focused primarily on the senders of deceptive messages. This study investigates changes in both the sender's and the target's linguistic style across truthful and deceptive dyadic communication. A computer-based analysis of 242 transcripts revealed that senders used more words overall, increased references to others, used more unique words, and used more sense-based descriptions (e.g., seeing, touching) when lying as compared to telling the truth. In addition, highly motivated senders employed more causal terms when lying than when telling the truth, while unmotivated senders used more negations during their lies. Receivers used more words and asked more questions when they were being lied to than when they were being told the truth, especially when the sender was not highly motivated. These findings are discussed in terms of their implications for linguistic style matching and interpersonal deception theory.

Unemployment in the United Kingdom: Is Gender a Factor?

ILANA M. GREENE

Under the supervision of David R. Just
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This paper discusses how, in the United Kingdom, men have substantially higher unemployment rates than women and that men are more likely to receive a higher level of education that would lead to a greater probability of undertaking higher skill-level jobs. These prestigious jobs, which are usually dominated by males, are also found to have a significantly higher rate of job turnover. There is also evidence that other jobs dominated by males require physical labor and men that occupy these jobs are likely to be made unemployed. Finally, males are more likely to become inactive in the workforce because they do not have an incentive to reenter.

A Case Study in Rural New York

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Under the supervision of Kai A. Schafft
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Regional and urban planners are using youth participation in community development projects to make policies and plans more reflective of youth needs. Successful youth participation involves youth in the community development process; and inclusive community development values the ideas of all participants, regardless of age. This study defined and assessed youth participation in a community and economic development project in Stewart, N.Y., from September 2003 to March 2004. Youth participation in the first phase of the

project included two community youth-evaluation projects, a photo project, and an interview film project. Observation and interview data evaluated the experiences of two discrete groups of youth participants, a group of African American youth, and a group of skateboarders and BMX bike riders. Although they participated in the same project, each group showed a distinct understanding of reasons for participating in the project. The two groups also had different experiences with adult community members during the project. Each group experienced distinct benefits and challenges of youth participation. The result of youth participation in Stewart was a development plan, which included the interests of young community members, and gave some youth in Stewart the opportunity to learn about effecting change in their community. However, youth participation methods used in Stewart did not address many of the race and class issues that construct the small but very diverse community.

A Study of Newspaper Readership Using the *Cornell Daily Sun* as a Framework

JULIA R. KORNBLATT

Under the supervision of Dietram A. Scheufele
Department of Communication

This study examines the newspaper readership habits of Cornell University students, alumni, and faculty. The *Cornell Daily Sun* was used as a framework in examining this topic. Data were collected from 294 Cornell students, 712 Cornell alumni, and 146 Cornell faculty.

An online survey asked the respondents questions about newspaper readership in general, as well as patterns of reading the *Cornell Daily Sun*, if at all. The respondents answered questions designed to measure what readers and nonreaders choose to read, or would choose, and why, in addition to how they use newspapers. This information was used to identify how readership could be increased, using the *Cornell Daily Sun* as an effective and real framework.

Findings from this study indicated that all three samples pay the most attention to national and international news when reading a newspaper, and all pay the most attention to campus information when reading the *Cornell Daily Sun*. Lack of interest and availability were the two most influential reasons given by student and alumni nonreaders as to why they do not read the *Cornell Daily Sun*, and the reasons most likely to be given by faculty were lack of interest, already reading other local daily newspapers, and lack of time. Students are dissatisfied with the amount of national and international news in the *Cornell Daily Sun*. Students and alumni most often go online when seeking national and international news, and faculty go online for these sections only second in frequency to reading national and state newspapers.

Presidential Rhetoric During Times of National Crisis

ALLISON D. KORNET

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Department of Communication

Presidential rhetoric plays an important role in modern American politics. This study examined presidential speeches before and after national crises with respect to rhetorical variance in presidential public addresses. The national emergencies chosen for this particular study included the September 11 attacks, the bombing of Pearl Harbor, and the Cuban Missile Crisis. Speeches from George W. Bush, Franklin D. Roosevelt, and John F. Kennedy were examined. In addition, newspaper coverage was analyzed to assess the degree of presidential media coverage following a national crisis and public address. Finally, public opinion polls were compared to assess the amount of support that surrounds a president following a crisis and/or speech. Based on communication theories including rally-around-the-flag, agenda building and setting, priming and framing, research questions and hypotheses focused on message content, audience behavior and the relationship between these variables. Using State of the Union addresses, nationally broadcast speeches, and formal news conferences, content analyses were conducted to assess presidential rhetoric during times of crisis. Using Diction, a specialized computer program, this study found that presidential rhetoric varied during national crises. However, the rhetorical changes were not consistent between presidents. With regard to media coverage, newspapers printed more articles related to the president and the crisis following an attack, or potential attack, on the United States. Finally, it was also found that presidential approval ratings increased following a presidential speech related to a national crisis.

Another Look at Social Identity and De-Individuation (SIDE): The Role of Visual and Personal Identifiability in Computer-Mediated Communication

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Under the supervision of Jeffrey T. Hancock
Department of Communication

Computer-mediated communications are by nature visually anonymous and often have an element of personal (name and location) anonymity as well. This study investigates the role of these types of anonymity on the production of abstract and stereotypical language. An examination of 64 messageboard communications made by participants assigned to four anonymity conditions (visually and personally anonymous, visually anonymous but personally identifiable, visually identifiable but personally anonymous, visually and personally identifiable) revealed that only participants who were visually identifiable exhibited the group norm to a significant degree. These results are inconsistent with predictions derived from SIDE theory. Possible limitations and alternative explanations are discussed.

Students' Attitudes and Behaviors Toward Downloading Music on the Internet: An Exploration with Cognitive Dissonance Theory

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Department of Communication

With the recent upsurge in music downloading on the Internet, most previous research in this area has focused on the legal history of the file-sharing/copyright debate. This study takes a social science approach and investigates the attitudes and behaviors of college students who download copyrighted music at a large northeastern university. An analysis of 10 interviews and 50 questionnaires revealed that participants (N = 50) experience cognitive dissonance and seek reassurance to reduce logical inconsistencies between their attitudes and behaviors. Participants who reported that their attitude changed after they learned their downloading behavior was illegal are more likely to feel stress because of that behavior. In addition, participants who sought information to reinforce their downloading behavior more frequently changed their attitude regarding their downloading behavior when they realized it was illegal. These findings are discussed because of their uniquely sociological and psychological implications in applying cognitive dissonance theory to the legal downloading debate in a university setting.

Student-Instructor Communication: Comparing Face-to-Face and Computer-Mediated Communication and Their Relationships with Academic Performance, Learning, and Instructor Immediacy

LINDE M. RICKERT

Under the supervision of Joseph B. Walther
Department of Communication

The two major objectives of the study were (1) to determine what observable relationship, if any, exists between student-instructor communication and student academic performance, student learning, and student perception of instructor immediacy, and (2) to determine whether the relationship observed between student-instructor communication and these outcomes differs depending on whether the communication is face-to-face or computer-mediated and how.

A sample of 176 undergraduate students at a large semi-public, semi-private university completed a questionnaire that took an audit of their communication with the instructor(s) of a course selected at random from their course schedule of the previous semester. The questionnaire also collected self-report data on academic performance, learning, perception of instructor likeability, SAT score, and general demographic information.

The study's results demonstrated that computer-mediated communication played a unique role in student learning and perception of professor immediacy. Face-to-face communication played a unique role in perception of teaching assistant immediacy. The study's findings indicate that large class size in and

of itself cannot be directly linked with low levels of academic performance, learning, or perception of instructor likeability.

This research may have important implications for educators as one more critical step toward unraveling the myths that guide our understanding of what constitutes an effective learning experience.

Everyday Lies and Everyday Technology in the Community: An Exploration of the Feature Based Deception Model in a Nonstudent Population

THOMPSON CAVAGE RITCHIE

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Department of Communication

Until recently, little research has been done to establish the roles of communication media in people's use of deception. Our research attempts to replicate the findings of Hancock, Thom-Santelli, and Ritchie (2004) to verify the Feature Based Deception Model (FBDM), which hypothesizes that three media factors play an important role in deception production: (1) simultaneity, or direct feedback between communication partners; (2) recordlessness, or the lack of a written record of the interaction; and (3) the co-presence of media, the idea of communication occurring in a shared location. We tested the FBDM on a group of nonstudent community members to see if the results reflect the FBDM, as they did in Hancock et al.'s (2004) student sample.

This study attempts to address the effects of technological interpersonal communication media on the deception patterns of a nonstudent population. Closely following in the footsteps of DePaulo et al. (1996) and Hancock et al. (2004), we hope to compare the daily deception and technology use of community members to those of students at a neighboring northeastern university. We discuss the implications of differing social and technology-use patterns between the two populations, and how these differences may affect deception habits.

Included in this research is the analysis not only of how technology affects deception, but how technology can aid in scientific research and data collection. We have designed an interactive program that can be used by participants to record data in a journal format. This program is run on a handheld Personal Data Assistant and was used by our participants to record their daily interactions instead of using the more traditional paper and pencil journal technique.

With the advent of computer-mediated communication (CMC) such as e-mail, instant messenger, chat rooms, blogs, and bulletin boards, comes questions about how these new media affect communication behavior. Researchers have long been interested in the different modes of communication but have only recently focused on the specific qualities of communication media. Early theoretical approaches, such as Shannon and Weaver's (1949) communication model, depicted interpersonal communication "channels" or media as nothing more than a source of "noise" in communication, while more contemporary theoretical approaches, such as Walther's (1996) Hyperpersonal Model, argue that not only are computer-mediated methods of interpersonal communication

as diverse and personal as the more traditional methods, such as face-to-face (FtF) and the telephone, but that the media themselves may play a complex role in a wide variety of interpersonal communication processes.

Studies about the use of media for communication have begun to explore an increasingly large array of interpersonal processes and phenomena. For example, recent research by Hancock et al. (2004) examined how e-mail, the transfer of letter-like text messages between computer users, and instant messenger, a more immediate form of text communication, affected the rate at which students lied in their everyday communication. The primary objective of the present study was to replicate and extend this initial research in deception and communication technology by examining deception rates in a nonstudent population. A secondary objective in the present research was to develop, implement, and examine a new handheld-based survey program that will be used by participants to record their social interactions and lies.

Social Structures, Social Movement Alliances, and Perspectives on Work: The Unemployed Workers Movement of Neuquén, Argentina

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Changes in Argentina's social structures, specifically the decline of organized labor's political power connected to neoliberal economic reforms, have influenced the Unemployed Workers Movement (MTD) of Neuquén to organize, in an alliance with employed workers, to promote a model of work that benefits the worker and the community.

Argentina's transition to a neoliberal economic system required a dismantling of the labor movement, which was then accelerated by the neoliberal reforms such as privatizations and deregulation of labor protections. To fill the working-class political power gap, the MTD has organized not only to win control over government workfare subsidies for its unemployed members, but also to protect and create "genuine work" for all workers.

The MTD's definition of "genuine work" is examined through an analysis of the MTD's daily discourses, its administration of work projects, and the work conditions in the worker-controlled factory Zanón endorsed by the MTD as a site of genuine work. Their definition of genuine work includes: living wages with medical and pension benefits, job security, democratic organization in the workplace, an orientation toward benefiting the community, and recognizing women's work in the home as valuable. This case study advances our understanding of work as seen from the workers' perspective, and the alliance organizing that produced it affords an opportunity to reconsider one version of social movement theory.

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