Natalie Abright

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. John Faaborg
Mentor Department: Biological Sciences
Funded by: Missouri Ozark Forest Ecosystem Project

Effect of clearcutting on the habitat within the clearcut and the surrounding forest and its relationship to the presence of wood thrush (*Hylocichla mustelina*) in the Current River Conservation Area

Natalie Abright, John Faaborg and Paul Porneluzi

Wood thrush were one of the few species of forest birds that increased in density on sites that received even-aged management as part of the Missouri Ozark Forest Ecosystem Project (MOFEP). One hypothesis is that this may be caused by shifts in vegetation structure, leaf litter production, and relative moisture level between regenerating clearcuts and the surrounding forest. I compared these habitat characteristics for five clearcuts in the Current River Conservation Area. Three clearcuts had adjacent wood thrush territories and two did not. For each clearcut, 5-meter radius vegetation plots were established at six randomly selected points—two within the clearcut, two at a distance of 30 meters from the clearcut's edge, and two at a distance of 60 meters. Habitat characteristics tested at each plot include average leaf litter depth, stem size distributions, horizontal foliar density, percent coverage by five types of ground cover, and relative soil moisture. These parameters serve as a basis of comparison between the clearcuts with and without wood thrushes to indicate what kind of habitat is preferred by these birds when breeding.

Christian Alvarez

Major: Mechanical Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. Tushar K. Gosh
Mentor Department: Nuclear Engineering
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Doping of natural diamond powder with boron to increase its hydrogen storage capacity

Christian Alvarez and Tushar K. Gosh

Have you asked yourself what will happen when we run out of fossil fuels, where will our electric power come from, how would we be able to transport ourselves over long distances? Think about what will happen to our economy and our way of life. The answer may be hydrogen. In a recent visit to a hydrogen fueling station in Washington D.C. [http://www.whitehouse.gov/news/releases/2005/05/20050525-1.html], President Bush said that “hydrogen is the wave of the future” and he further stated that “We're spending about $1.2 billion on hydrogen research”. The purpose of this research was to dope natural diamond powder with Boron to improve the hydrogen storage capabilities of diamond. Previous studies by the researchers from Nuclear Science & Engineering Institute, University of Missouri-Columbia have shown that diamond powder can store about 2% by weight hydrogen. It is hypothesized that the hydrogen storage capacity can be further enhanced by creating more micro-pores in diamond. In this study, we doped diamond with boron first at high temperature and then irradiated at MURR in a neutron flux to create more micro-pores. It is expected that this treatment will increase the storage capability of hydrogen, hopefully enough to meet the requirements of the US Department of Energy (DOE)’s goal of 6% weight percent hydrogen.

Jared Austin

Major: Chemistry
University: Southern University at New Orleans
Faculty Mentor: Dr. Susan Z. Lever
Mentor Department: Chemistry
Funded by: NSF-REU/NIH Program in Radiochemistry

Progress in the synthesis of a Technetium-labeled complex as a potential Sigma receptor binding ligand

Jared Austin, Rong Xu and Susan Z. Lever

The sigma receptors have been known to affect several physiological functions such as psychosis, depression and uncontrolled cell proliferation. But what makes the sigma receptors so great is the fact that they bind a variety of ligands. The phenylpiperazine and phenylpiperidine chemical classes of ligands have been identified to bind at sigma1 receptor sites and a pharmacological model has been proposed. On the other hand, due to the scarcity of sigma2 selective ligands, less is understood about this subtype. Non-invasive imaging of the sigma receptor in vivo would lead to a better understanding of the role that sigma receptors play in health and disease. Technetium-99m (Tc-99m) is the most commonly employed imaging radionuclide. This research project is focused on the preparation of a Tc-99m labeled complex designed to retain high affinity to the sigma1 receptor subtype. The design of the ligand is based upon 1-(3', 4'-dimethoxyphenethyl)-4-(3''-phenylpropyl) piperazine (1), a sigma1 agonist developed by Santen Pharmaceutical Co. Through a three-step synthesis, we have replaced one of the methyl groups with a diaminedithiol (DADT) chelating moiety attached through an alkyl chain (2). The first step, alkylation with dibromoethane, has been optimized to an excellent yield (82.5%). Steps two and three have not been optimized but have been shown to be feasible. Details of these reactions and progress toward complexation will be described.

Mona-Lisa Banks

Major: Agriculture
University: Lincoln University
Faculty Mentor: Dr. Galen Suppes
Mentor Department: Chemical Engineering
Funded by: NSF Program Alliance for Collaborative Research in Alternative Fuel Technology and Louis Stokes Missouri Alliance for Minority Participation

Conversion of waste corncob to activated carbon for use of methane storage

Mona-Lisa Banks, Galen Suppes, Peter Pfeifer, Rusty Sutterlin and Parag Shah

Missouri being one of the leading states in corn production has a large quantity of corn cobs. Corn cob can be used to produce activated carbon because its organic origin is similar to coconut and peach pits which have been previously used to make activated carbons. In this project, researchers at the University of Missouri Columbia are using adsorbents produced from corn cobs to store natural gas. Results have shown that a BET surface area of 800m2/g-1600m2/g can be obtained. Scanning Electron Microscope (SEM) images confirms that micro porous nature of the carbon. The main objective of this research is to develop flat low pressure high capacity natural gas tank holding no greater than 500psi of methane, allowing for more trunk space in cars. It is anticipated that the new Absorbed Natural Gas (ANG) will be the competitor with Compressed Natural Gas (CNG) which is currently stored in heavy tanks at high pressures of about 3600psi. Activated carbons obtained from the corn cob that has been through chemical activation process are used to make monoliths, in order to achieve the maximum density. The powdered form of the activated carbon is combined with a binding agent and pressed using a hydraulic press and die. By this process corn cobs can be converted into monolithic carbon and having methane uptake of 150v/v or more.

Roderick Bautista

Major: Biological Sciences
University: University of Maryland-Baltimore County
Faculty Mentor: Dr. Habib Zaghouani
Mentor Department: Molecular Microbiology and Immunology
Funded by: Life Sciences Fellowships/Meyerhoff Scholars Program

Construction of a knockout targeting vector to generate an Interleukin-13 Receptor α1 deficient Balb/c mouse

Roderick Bautista, John Hardaway and Habib Zaghouani

A recent publication from our lab has provided evidence for the involvement of the α1 chain of the Interleukin-13 cytokine receptor (IL-13Rα1) in the development of the neonatal immune system. Specifically, we have shown that cell death of T helper type 1 (Th1) effector cells can be prevented by antibody-mediated blockade of IL-13Rα1. Currently, a knockout mouse deficient in expression of IL-13Rα1 is not available and the development of an IL-13Rα1 knockout mouse will provide new insights on the relationship between IL-13Rα1 signaling and neonatal immunity. In this effort we have begun construction of a targeting vector that will bear sufficient homology to the IL-13Rα1 wild-type locus to allow for deletion of exons 7, 8, and 9 via homologous recombination, thereby rendering that allele non-functional. After construction of the targeting vector, a collaborative effort between the Transgenic Animal Core facility here at the University of Missouri will continue throughout the remainder of the cell culture, embryonic manipulation, and screening processes.

Robyn Beatty

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Mark D. Kirk
Mentor Department: Biological Sciences
Funded by: Arts & Sciences Undergraduate Research Mentorship Program

Camgaroo-2 as an indicator of function in embryonic and neuralized stem cells

Robyn Beatty, Christopher Pierret, Kathleen Spears and Mark D. Kirk

The transplantation of stem cells to replace cells that have been lost or damaged due to disease or injury is quickly becoming a conceivable treatment method. Embryonic stem (ES) cells have the capacity to become any cell in the body, so the therapeutic possibilities are vast. The ultimate goal of our research on ES cells is to induce them to differentiate into functioning neurons to replace those that are lost in patients suffering from neurodegenerative disorders. However, it is important that the differentiated cells possess the appropriate phenotype and are able to perform the correct function after transplantation. In the past, it was common to accept a differentiated cell's fate based solely on its morphology and the presence of specific membrane markers. Now, it is becoming increasingly important to determine a donor stem cell's fate based on its function, especially if the cell is to be transplanted into a subject as a means of therapy. This study used the calcium-sensitive protein Camgaroo-2 to test the function of embryonic stem cells and cells directed toward a neural lineage. Camgaroo-2 is a fusion protein that consists of calmodulin in between two halves of yellow fluorescent protein. When calcium is present, it binds to the calmodulin portion of the Camgaroo-2, inducing a conformational change that results in increased fluorescence. After mouse embryonic stem cells were transfected with Camgaroo-2, we used reagents such as potassium chloride and ionomycin, known to elevate intracellular calcium, to confirm that the ES cells were stably transfected with the plasmid, and that Camgaroo-2 was functioning correctly. Potassium chloride causes the cell to depolarize while ionomycin (a calcium ionophore) creates large pores in the cell membrane. Both reagents allow for an influx of calcium into the cell, leading to increased fluorescence. The Camgaroo-2 transfected ES cells showed the appropriate responses to KCl and ionomycin by depolarizing and showing visible increases in fluorescence. This confirms that our Camgaroo-2 construct is functioning in the ES cells. We are in the process of testing the responses of neuralized ES cells using appropriate neurotransmitters, the presence of which should induce unique fluorescent signatures in a cell specific manner. Confirming neuronal function from differentiated Camgaroo-2 ES cells is an important step toward neuron transplantation in a neurodegenerative disease model.

Holly Boedefeld

Major: Microbiology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Karen Bennett
Mentor Department: Molecular Microbiology and Immunology
Funded by: Life Sciences Undergraduate Research Opportunity Program

Hitting the greens: Backcrossing the *csn-5* mutant, par for the course, a CSN-5 protein null

Holly Boedefeld, Erica Racen and Karen L. Bennett

Germline development is crucial to all eukaryotic organisms and the survival of their species. The Bennett laboratory utilizes *Caenorhabditis elegans*, the free-living soil worm, to study cytoplasmic granules called P granules. P granules contain both protein and RNA and are specifically associated with the germ cells. The germline RNA-helicase proteins (GLHs) are necessary components of the P granules; they are essential for fertility in the nematode. Several protein interactors with the GLHs were previously identified in a yeast-two hybrid screen. One of these GLH binding partners is CSN-5, a known component of the COP 9 signalosome, a complex involved in protein stability that is conserved from plants to worms to humans. Recently, a deletion mutant strain, *csn-5(vc861)*, has been isolated by the *C. elegans* Knockout Consortium. This summer's project involves backcrossing (also called outcrossing) the green GFP balanced *csn-5(vc861)* strain against wild-type worms to remove other possible mutations arising from the original mutagenesis. The other objective is determining whether the homozygous non-green mutant is a CSN-5 protein null. To date, three backcrosses have been completed. In addition, immunocytochemistry and western blot analysis were done using an anti-CSN-5 antibody generated in our laboratory. Both of these assays show that *csn-5(vc861)* does not appear to make any CSN-5 protein.

Angela Bosier

Major: Agricultural Sciences
University: McNeese State University
Faculty Mentor: Dr. James R. Turk
Mentor Department: Biomedical Veterinary Sciences
Funded by: Louis Stokes Missouri Alliance for Minority Participation

L-NAME treatment in pigs

Angela Bosier and James R. Turk

Nω-nitro-L-arginine-methyl-ester (L-NAME) inhibits the enzyme nitric oxide synthase (NOS) which generates the physiologic messenger gas, nitric oxide (NO). In addition to its role as a vasodilator NO inhibits inflammation and vascular smooth muscle cell proliferation. It was shown recently that rats fed L-NAME contain evidence of inflammation and increased collagen in their coronary vasculature when compared with control rats. We hypothesized that L-NAME treatment will cause inflammation and an increase in collagen in the coronary vasculature of pigs compared with control pigs. To test this hypothesis we have four pigs, two received L-NAME in their drinking water and two did not. We have samples of the left ventricle (LV), right ventricle (RV), and left anterior descending (LAD), left circumflex (LCX), and right (RCA) coronary arteries of the heart. Similar to studies in the rat, we will stain these samples for monocyte chemoattractant protein-1 (MCP-1), a marker of inflammation; alpha smooth muscle actin (αSMA), a marker of vascular smooth muscle, and picrosirius red (PSR) a marker of collagen. We will photograph sections of the coronary vasculature stained with these markers and use a computer image analysis system to count the amount of MCP-1, vascular smooth muscle, and collagen. Preliminary results suggest that we have insufficient statistical power to show differences in the parameters measured and need to examined greater numbers of animals.

Joni Bramon

Major: Chemistry and Biology
University: Columbia College
Faculty Mentor: Dr. J. David Robertson
Mentor Department: Chemistry
Funded by: NSF-REU/NIH Program in Radiochemistry

Analyzing the effects of lactose on calcium absorption in premature infants using HR-ICP-Mass Spectrometry

Joni Bramon, Joseph Kyger, James Guthrie, Barry Higgins, Laura Hillman and J. David Robertson

With advances in neonatal care, premature infants are surviving at increasing rates. During the third trimester of pregnancy, the bone mineral content of infants rapidly increases. It is therefore becoming essential to accurately mimic the womb environment to maintain growth and sustain the health of premature infants as if they were in utero. Regulating calcium absorption in premature infants is crucial primarily for bone formation, as 99% of the calcium in the human body is found in the bones and the teeth. The effect of lactose containing formulas on calcium absorption in premature infants has not been well established. Concerns have been noted in the scientific community regarding lactose intolerance especially in premature infants, as lactase, the enzyme responsible for lactose digestion, is most readily detectible during the third trimester of pregnancy. In this study, in conjunction with Dr. Laura Hillman of the University of Missouri Hospital, each infant was fed lactose and maltose formulas during different weeks using a dual tracer method in which two calcium isotopes were administered, ^{44}Ca orally and ^{46}Ca intravenously. Urine samples were collected after 24 hours. Analysis related natural abundances of calcium isotopes to the measured values in the urine. Polyatomic ion interferences were differentiated from the calcium peaks by analyzing the samples at a resolution of 4000. Mathematical corrections for interferences caused by titanium and doubly charged strontium were determined by measuring the specific isotopes ^{47}Ti and $^{87}Sr^{++}$ and using known natural abundances of the interfering isotopes to correct each calcium count rate. Mathematical calculations relate the enriched isotope ratio measurements of ^{44}Ca and ^{46}Ca to calcium absorption. Analysis regarding the effect of lactose on calcium absorption is ongoing. Our data precision on the ICP-MS was acceptable with percent relative standard deviations (%RSD) for external precision over the course of a week at 1.4, 2.2, 0.71, and 1.4 for isotope ratios ^{42}Ca: ^{43}Ca, ^{42}Ca: ^{44}Ca, ^{42}Ca: ^{46}Ca, and ^{42}Ca: ^{48}Ca respectively. Daily internal precision (%RSD) values were .37, 1.3, .69, and 1.5. The precision shows the viability of utilizing HR-ICP-MS analysis for calcium isotope ratios.

Matthew Bratkowski

Major: Biology and Chemistry
University: University of Missouri--Columbia
Faculty Mentor: Dr. Miriam Golomb
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Recent lateral gene transfer from *Pasteurella multocida* into *Haemophilus influenzae*

Matthew Bratkowski, Miriam Golomb and Cole Linville

Haemophilus influenzae is a gram-negative bacterium that exclusively colonizes humans. Nonencapsulated strains of the bacterium are found in the upper respiratory tract of healthy humans, but can also cause the respiratory diseases otitis media, bronchitis, and pneumonia. Many of the chromosomal genes of *H. influenzae* were acquired by lateral transfer from other bacterial genera. Recently, we investigated a cluster of unusually virulent nonencapsulated *H. influenzae* implicated in human invasive disease. An island between *aspA* and *groES* in which a urease gene cluster present in *H. influenzae* had been replaced by a homolog *of Neisseria meningitides mtrF* was discovered (Erwin *et al.*, 2005). We compared the *aspA-groES* region with that of *Pasteurella multocida*, a member of the same family of bacteria. The two genomes have scattered synteny and share about 83% of their DNA. Both species have natural genetic transformation and use the same recognition site for DNA uptake. The *mtrF* gene is found between *aspA* and *groES* in *P. multocida*, within a somewhat larger island that includes a homolog of *fsxA*. The *H. influenzae mtrF* island is 95-100% identical to the region in *P. multocida*, as compared to 80% similarity in flanking genes. The direction of transfer is indicated by the presence of pseudogene fragments of *fsxA* persisting in *H. influenzae*. Because MtrF contributes to erythromycin resistance in *Neisseria*, we hypothesized that the gene transfer event occurred during the antibiotic era. To test this hypotheisis, we collaborated with Dr. Vivek Kapur (University of Minnesota) to test isolates of *P. multocida* from domestic poultry and wild fowl for the presence of *mtrF*. Long and inverse PCR was used to identify genes between *aspA* and *groES* in six wild-type *Pasteurella* genomes. This is the first report of gene exchange between *H. influenzae* and a pathogen of our domestic species.

Fallon Brice

Major: Animal Science
University: University of Missouri-Columbia
Faculty Mentor: Dr. David Ledoux
Mentor Department: Animal Science
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Evaluation of the efficacy of test products to ameliorate the toxic effects of aflatoxin present in broiler chick diets

Fallon Brice and David R. Ledoux

An *in vivo* study was conducted to evaluate the efficacy of several adsorbent test products to ameliorate the toxic effects of aflatoxin B1 (AFB1) in chicks. Ninety day-old straight run chicks were purchased from a commercial hatchery, weighed, wing-banded, and assigned to floor pens. A completely randomized design was used with 10 chicks (chick was experimental unit) assigned to each of 9 dietary treatments from hatch to 28 days. The aflatoxin used for this study was supplied by Aspergillus parasiticus (NRRL-2999) culture material (815 mg AFB1/kg). The dietary treatments included: 1) basal diet containing no AFB1); 2) basal diet supplemented with 1.5 mg AFB1 /kg diet; 3) As diet 2 plus Product 1; 4) As diet 2 plus Product 2; 5) As diet 2 plus Product 3; 6) As diet 2 plus Product 4; 7) As diet 2 plus Product 5; 8) As diet 2 plus Product 6; and 9) As diet 2 plus Product 7. The addition of Products 1, 2, 3, 4, 5, and 6 to AF diets did not prevent the reduction in body weight gain (BWG) due to AFB1. Chicks fed diets containing Products 1 thru 6 all had lower BWG (P >.05) compared with control chicks. Body weight gain of birds fed Product 7 was not significantly different (P > .05) from the birds fed the positive control; however, it was also not significantly different (P >.05) from birds fed AF B1 alone. Relative liver weights were not affected by dietary treatments (P > .05) and averaged 3.06 g/100g body weight across all treatments. Results of this study indicate that none of these products were effective in ameliorating the toxic effects of AFB1.

Elizabeth Brockman

Major: Biology
University: United States Air Force Academy and Denver University
Faculty Mentor: Dr. Paul Duval
Mentor Department: Chemistry
Funded by: NSF-REU/NIH Program in Radiochemistry

The effect of aryl substituted triamidoamine ligands on the structure of dioxo-molybdenum (VI) complexes

Beth Brockman and Paul Duval

Molybdenum is a known transition metal recognized for its crucial role as an active center for oxygen transfer in enzymes and has also been known to split dinitrogen. Experiments conducted during the internship period included the use of stabilizing multidentate ligands synthesized from tris aminoethyl amine (TREN) with aromatic aldehydes including binapthalene, benzene, and pyridine with synthesized molybdenum (VI) complexes MoO2Cl2(Me3PO)2, MoO2Cl2(MePh2PO)2, and MoO2Cl2(Ph3PO)2. Preliminary findings at the conclusion of the summer research phase indicate that pyridine-based TREN ligands are readily sterically adaptable to the octahedral molybdenum (VI) geometry and produce viable TREN ligand-molybdenum (VI) complexes for analysis by cyclic voltammetry. Future experimentation will seek to further knowledge of energy changes and interactions within the 5d orbitals during the formation of the TREN ligand-molybdenum complex, as well as redox chemistry of high oxidative oxomolybdenum derivatives to fully comprehend the role of this metal in relation to oxygen transfer.

Ashley Bush

Major: Biology
University: Southwest Missouri State University
Faculty Mentor: Dr. Lesa Beamer
Mentor Department: Biochemistry
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Expression and purification of AlgX in *Pseudomonas aeruginosa*

Ashley R. Bush, Catherine A. Regni, Lesa J. Beamer, Aniruddha Raychaudhuri and Peter A. Tipton

Pseudomonas aeruginosa is a Gram-negative bacterium that is the leading cause of hospital acquired infections. While this bacteria is present in water and soil, this bacteria only severely affects severely ill patients, such as those with cystic fibrosis. In cystic fibrosis patients, the bacteria will lodge in the lungs and form a coating, called a biofilm, around itself to protect it from the natural defenses of the body and antibiotics. This biofilm is formed by exopolysacchride sugar, known as alginate. The goal of this project is to, by isolating some of the proteins that help produce the biofilm, find the three-dimensional structure of those proteins. This will make it easier for various pharmaceutical research companies to create a drug to inhibit the specific active site in the proteins, preventing biofilm formation and allowing the infection to be treated with traditional antibiotics. The proteins encoded by two genes were picked for this study, algK and algX. Both are believed good targets because they have been shown in previously written papers to be critical to formation of the biofilm in *P. aeruginosa*. (1, 2) The cloned genes (in the form of a plasmid) previously obtained were used in the transformation step into E. coli. The lab protocol for general transformations was followed. To show that the bacteria were actually producing the protein we needed, the growth tubes were harvested; the cells lysed, and run on a 10% acrylamide gel to check for protein expression in the experimental versus control sample. The algK gel was inconclusive, however algX clearly overexpresses in large quantities. While most of the protein is insoluble, enough is soluble to warrant complete purification of the protein to set up crystallization trays. The current problem is how to optimize purification, because it co-elutes from a nickel column with contaminating proteins. A slow concentration bump of the buffers used to purify is being tested to see if it helps with this problem.
References 1. Antonette Robles-Price, Thiang Yian Wong, Havard Sletta, Svein Valla, Neal L. Schiller. 2004. AlgX Is a Periplasmic Protein Required for Alginate Biosynthesis in Pseudomonas aeruginosa. J. of Bacteriology. 186:7369-7377. 2. Jain, Sumita, Franklin, Michael J., Ertesvag, Helga, Valla, Svein, Ohman, Dennis E. 2003. The dual roles of AlgG in C-5-epimerization and secretion of alginate polymers in Pseudomonas aeruginosa. Molecular Microbiology. 47. 1123-1133

Clayton Butcher

Major: Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Thomas Quinn
Mentor Department: Biochemistry
Funded by: Molecular Imaging Program

Optimization of metal-cyclization of alpha-MSH peptide analogs used in the treatment and detection of melanoma

Clayton Butcher, Fabio Gallazzi and Thomas Quinn

Over the past few years Dr. Quinn and his lab have made significant progress in the development of a melanoma treatment drug. Based upon peptide analogs of the alpha-melanocyte stimulating hormone, A-MSH, Dr. Quinn has developed a metal cyclized drug that shows very promising results in therapy as well as early detection/imaging of melanoma tumors. The cyclization of the peptide around a metal core was shown to greatly increase the affinity of the peptide for its target. There are slight problems with the cyclization process that needed to be resolved or limited in order to make the synthesis of the drug as efficient as possible. The primary problem with the cyclization of the peptide is the fact that two main products are produced. One of these products is caused by the histidine residue swinging down and binding with the metal core. Histidine is one of the four amino acids directly involved with receptor recognition and thus this product's tumor uptake is at least 50% lower.

Three variables were explored in hopes of reducing this second unwanted product. A new and simpler process developed by Fridkin *et. al.* [1] was first considered. HPLC was used to purify the two major products and their identities were confirmed using mass spectrometry. The new procedure proved to be slightly more effective as the old procedure. With the old procedure roughly 32.3% of the two major products were of the undesired compound, however, using this new procedure this was reduced to 23.4%. A variation of the new procedure was then tried. Instead of dissolving the linear peptide in water, as the procedure called to do, the peptide was dissolved using DMF. This modification showed a significant change in the percentage of the two products. Of the two major products only 12.8% of the total was of the unwanted product thus producing 87.2% of the desired cyclized peptide. Finally an addition of an extra amino acid residue near the beginning of the sequence was tried in hopes of moving the histidine residue far enough away from the metal core in order to limit their interaction. Current tests are still being performed to determine whether or not this will be successful.

(1) Fridkin, G., Bonsera, T.A., Litman, P., and Gilon, C. Nucl. Med Biol 32, 39-50, 2005.

Pierre-Etienne Cagniart

Major: Biomedical Engineering
University: University of Texas-Austin
Faculty Mentor: Dr. Gabor Forgacs
Mentor Department: Physics and Astronomy

Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Epithelial-mesenchymal transition of brain tumor cells is differentially regulated in response to dexamethasone

Pierre-Etienne Cagniart, Francoise Marga and Gabor Forgacs

In the epithelial-mesenchymal transition of tumors, the loss of cohesivity and the migratory capability of cells determine the invasiveness and therefore the malignancy of the cancer. Understanding these biophysical mechanisms of cancer propagation will help control the disease thereby facilitating its treatment. In this study, cohesivity and invasiveness were characterized using three-dimensional aggregates constructed from human glioblastoma multiforme cells (HB cells). First, we showed that cohesivity was affected by the physical environment during incubation. Shear stress, simulated microgravity and normal 1g gravity conditions were produced respectively by incubation in a gyrotary shaker, in NASA's High Aspect Ratio Vessel (HARV) and in statically kept 24 well-plates. The surface morphology of the aggregates observed by field-emission scanning electron microscopy became rougher (indicative of a lower intercellular binding) as the forces acting upon it were reduced. Interestingly, the effects due to the environmental conditions were canceled by addition of an anti-cancer drug: dexamethasone (DEX), a corticosteroid often used as an anti-inflammatory agent. In a second experiment, the effect of DEX on the invasive pattern of HB-cells in three-dimensional collagen matrices was studied. We found that DEX slows down cell migration from the aggregate indicating that it modifies the interplay between cell-cell adhesion and cell-extracellular matrix interaction. One possible mechanism of DEX action is increase in intercellular binding due to higher N-cadherin expression, the predominant cell-adhesion molecule in brain cells. The quantity of N-cadherin proteins was assessed by immunolabelling and flow cytometry after HB cells were exposed for 24 hours to various doses of DEX (0 to 10-6M). Preliminary data indicate that cells treated with 10-9 to 10-6M DEX express 5 to 60% more N-cadherin than non treated cells. Further investigations are needed to determine the effect of DEX on other factors involved in cell motility such as cytoskeleton, integrins, metalloproteinases. Exploring the molecular bases that control the bulk physical properties of tumor tissues (modeled here by the multicellular aggregates) may create new means to control cancer metastasis.

Michelle Carter

Major: Biology
University: Truman State University
Faculty Mentor: Dr. Mark D. Kirk
Mentor Department: Biological Sciences
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Determining an efficient protocol for production of neural stem cells

Michelle Carter, Jessica Struckhoff and Mark Kirk

Mouse embryonic stem (ES) cells are pluripotent cells derived from the inner cell mass of the developing blastocyst. When cultured in non-adherent dishes, ES cells form free-floating embryoid bodies (EBs). Cells within the EBs can then be induced to form neural stem and progenitor cells. These 'neuralized' mouse ES cells have been used for therapeutic transplantation experiments in mouse models of human neurodegenerative diseases, including neuronal ceroid-lipofuscinoses (NCLs). This study focused on developing a more homogenous population of neural stem cells from ES cells for use in transplantation experiments. A homogenous population of neural stem cells could provide a renewable source of neural stem cells and thus a more consistent fate outcome for transplanted cells. We tested selected protocols for neural induction of mouse ES cells and compared their efficiencies in creating neural stem cells in vitro. Three previously developed protocols were tested in this study. The first induction protocol was specifically used to generate spheres of neural precursor cells, or neurospheres. It used a retinoic acid induction protocol followed by seeding dissociated EBs into neurosphere media. The second protocol involved growing neural stem cell colonies in astrocyte-conditioned media. The third protocol consisted of growing ES cells in flasks in neurosphere media (including FGF) without EGF for four days and then four days in neurosphere media plus EGF. Four variations on the last protocol were also tested. Preliminary results suggest that to produce a larger yield of neurospheres, the first protocol would need to be altered. The second protocol was time consuming and produced a small population of neural stem cells. The third protocol produced promising results with a larger yield of neurospheres than the first two protocols. Future studies will focus on the third protocol and define the optimal conditions whereby it will produce more neural stem cells.

Rachel Castleberry

Major: Chemistry and Mathematics
University: Austin Peay State University
Faculty Mentor: Dr. John E. Adams
Mentor Department: Chemistry
Funded by: Stevens' Chemistry Program

If it won't explode, hit it with a hammer: Facilitating chemical reactions at a liquid surface

Rachel Castleberry, Tamas Szabo, Carol Deakyne and John E. Adams

Collisional energy transfer at a gas-liquid interface may play an important role in the initial decomposition of multiphase combustibles. The energy feedback of hot, energetic, gaseous atoms, in this case Ar, striking the liquid surface can potentially impart enough energy to break one of the liquid's bonds in a homolytic fashion thus creating radicals necessary for a resulting explosive chain reaction. Liquid nitromethane (CH_3NO_2) is a prototypical explosive and is modeled here as a simple diatomic consisting of one methyl (CH_3) and one nitro (NO_2) groups. The methyl and nitro groups are shown through MP2 6-311+G (2d, 2p) calculations to be the most likely resulting decomposition fragments; as such, focus is placed on the breaking of the C-N bond. For this study, the attractive term of the gas-liquid interaction potential is assumed to be zero to find the limit of Ar-nitromethane interaction. The energy transfer is studied by running simulations, using the DL_Poly_2 program, of Ar impinging the liquid nitromethane from zero degrees to the surface normal and over multiple incident energies. The results are then analyzed for energy transfer and C-N bond breakage.

Patricia Catrow

Major: Biology, International Studies and German Studies
University: Westminster College
Faculty Mentor: Dr. Walter Gassmann
Mentor Department: Plant Sciences
Funded by: Plant Genomics Internship @ MU

Identifying plant resistance pathways in *Arabidopsis thaliana*

Patricia Catrow, Soon-Il Kwon and Walter Gassmann

The destruction of plants by a pathogen results in millions of dollars lost in crop yield annually. Identifying the plant response pathway to the presence of a pathogen is key to combating plant disease. The gene-for-gene hypothesis suggests that for every pathogen avirulence gene (*avr*), there is a corresponding specific plant resistance (*R*) gene that recognizes it and elicits a defense response. One method for discovering resistance pathways is through the use of a suppressor screen in which the deletion or mutation of a negative regulator can reactivate a signaling pathway. Our *srfr* (suppressor of rps4-RLD) mutants were discovered to provide resistance to the *Pseudomonas syringae* pv. tomato DC3000 expressing *avrRps4* and thus is possibly a regulatory gene. The *srfr* mutants reactivated resistance to *avrRps4* in plants that have a non-functional *RPS4* gene. We are studying to see if the *srfr* gene signaling pathway reactivates *avr* responses dependent on R genes other than *RPS4*. We chose the well-studied *RPM1* gene, which functions in detecting bacteria expressing *avrRpm1*. After crossing *srfr3* and *rpm1-3* mutants and harvesting F1 seeds, we grow these F1 seeds to get the F2 generation population. We isolated genomic DNA from F2 plants and then applied PCR based markers to find homozygous double mutants using 2 genetic markers linked to the *srfr3* and *rpm1-3* mutation, respectively. The F3 generation plants will be available to test disease symptoms in these double mutants. Based on the results of disease symptoms of the F3 population against bacteria expressing *avrRpm1*, we will propose whether or not the *srfr3* gene is involved in the *RPM1* defense signaling pathway. If the F3 generation is susceptible to *avrRpm1*, then *srfr3* is not involved in the *RPM1* defense signaling pathway.

Karla Claudio

Major: Chemical Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentors: Dr. Timothy Glass and Dr. Jerry Atwood
Mentor Department: Chemistry
Funded by: Stevens' Chemistry Program

Host-guest complexes to molecular encapsulation of hydrogen

Karla Claudio, Tim Glass and Jerry Atwood

Science has always been about man learning from and attempting to mimic nature. In supramolecular chemistry this possibility is evident due to particularly interesting architectures of natural shell-like containers such as viruses and ferritin. One class of compounds studied for this purpose are calixarenes. Their typical cone structure allows them to sequester a variety of other molecules making it useful to form host-guest complexes or supramolecules. In such complexes, the host is a large molecule, in our case a calixarene, possessing a sizeable central cavity and the guest can be a monoatomic cation, a simple inorganic anion or a more sophisticated molecule such as a hormone, pheromone or neuro transmitter. In today's supramolecular chemistry field these compounds can be used for catalysis, biocatalysis, stabilization of reactive intermediates, drug transport, and the now emerging field of storage, processing and release of gases. The synthesis of this molecular capsule able to incorporate a guest begins with the methylation of the phenols present on the lower rim of calix[4]arene, an aldehyde was introduced along the upper ring followed by an oxidation to a carboxylic acid yielding tetracarboxycalix[4]arene. The tetrasubstituted calix[4]arene was crystallized from methanol and water to yield pale yellow crystals that were analyzed by X-ray. In this particular case, the objective was to incorporate gaseous hydrogen as the guest, which will be studied in due course. Further applications of this host-guest system could be the purification and storage of hydrogen for use in fuel cell. The nanoscale systems are a leading development strategy in many research areas. General advantages are the ability of saving time, space, costs, and materials for that reason supramolecular chemistry open a door to a new source of inspiration in the science world.

Franklyn E. Colmenares Ochoa

Major: Mechanical Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. Mark Prelas
Mentor Department: Nuclear Engineering
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Storing hydrogen, by enhancing diamond powder properties with CaF_2 and KF for use in fuel cells

Franklyn Colmenares and Mark Prelas

Whaaaat!!!!!!!!! Hydrogen as a fuel? Yes just like you read it, hydrogen is becoming the best alternative to change our economical dependence on fossil fuels. Today fossil fuels are the main source of energy in the world, covering over 80% of these needs, and most of this fuel is used in transportation systems. Hydrogen covers about 75% of matter in the universe, being by far one of the most abundant elements; it is also a very simple atom that consists of an electron and proton. Since hydrogen can easily provide energy; a technology called fuel cells has been developed. A fuel cell is like a battery that instead of using electricity to recharge itself, it uses hydrogen. In the fuel cell industry, one of the main problems is storing hydrogen in a safe way and extracting it economically. Gaseous hydrogen requires high pressures which could be very dangerous in case of a collision. The success of hydrogen use depends largely on the development of an efficient storage and release method. In an effort to develop a better hydrogen storage system for fuel cells technology this research investigates the use of 99% pure diamond powder for storing hydrogen. Mixing this powder with a calcium fluoride and potassium fluoride compound in its solid form and treating the surface of the powder with hydrogen plasma, modifies the surface of the diamond. After some filtration through distilled water and drying, the modified diamond is treated with hydrogen. We expect hydrogen to be attracted to the diamond powder surface in higher quantities due to the CaF_2 and KF treatment. Due to the large surface area of diamond nanopowder and the electronegative terminal bonds of the fluorine particles on the structure’s surface, to the method shows promise in storing high densities of hydrogen.

Lissandra Comas

Major: Industrial Engineeering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. Luis Occeña
Mentor Department: Industrial and Manufacturing Systems Engineering
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Single component vs. whole furniture packing in virtual reverse manufacturing

Lissandra Comas Flores, Luis G. Occeña, Eknarin Santitrakul and Li-Hsiu Wang

Previous research studies have analyzed the issues associated with the computer integration of the various technologies now available for hardwood log sawmills. These new technologies were created to optimize the quantity and quality of wood extracted from the logs. The technology that I am working in my research consisted of a computerized tomography (CT) scans that were converted to solid model images of the internal structure of the log. The availability of such images offer the potential for more precise sawing decisions. The potential for improvement of log utilization and whole furniture yield are the two factors considered in this research. We conducted a nondestructive process simulation experiment using a specially-developed software that enables us to evaluate the process variation in the way wood is extracted for the production of furniture. Instead of packing all the components needed for a specific furniture as done in a previous study, only one component was packed in each log. So far we have found that when we mix the three logs from each grade, with only one log supplying each component, the number of whole tables completed was less than when we packed all components together. However when we combined all the nine logs without considering the grades, we found one combination that resulted in more tables. Log utilization, however, was improved in 55% of the logs when only one component was packed instead of the whole furniture.

Charles Cooper

Major: Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Elizabeth Rogers
Mentor Department: Biochemistry
Funded by: MU Monsanto Undergraduate Research Fellowship

Characterization of a putative mutant for iron homeostasis

Charles B. Cooper, Dirk V. Charlson and Elizabeth E. Rogers

Little is known about the genetics of iron homeostasis in plants. A novel genetic screen was used to identify mutants with alterations in iron homeostasis. Because Ferritin (Fer1) mRNA expression is upregulated by intracellular iron concentration in leaves, this gene can be used to predict intercellular iron concentrations in leaves. To identify mutants that over- or under-accumulate leaf iron, Arabidopsis was transformed with the reporter gene Green Fluorescent Protein (GFP) driven by the Fer1 promoter. Seed from this transgenic plant were mutagenized with EMS. The resulting M2 seed were screened for high or low GFP fluorescence relative to transgenic controls grown on iron-sufficient medium. A putative Over-Accumulator of Fe, pOAF40, was identified that expressed high levels of GFP fluorescence. Our objective was to characterize this mutant for alterations in iron homeostasis. Seed of pOAF40 and the non-mutagenized transgenic control were germinated and plants grown on iron-sufficient medium for 14 days before transferring to iron-sufficient or -deficient media for four days. Fer1 mRNA levels, chlorophyll content, and ferric-chelate reductase activity (an enzyme whose activity increases during iron deficiency) were determined at the point of transfer and again four days after transfer. Fer1 mRNA expression was the same at the time of transfer, but greater relative to transgenic controls regardless of iron concentration 4 days later. The average concentration of chlorophyll in pOAF40 was less than the control regardless of sampling time or iron concentration. pOAF40 exhibited lower reductase activity than control on the day of transfer, however this difference in activity was not detected four days after transfer within iron-sufficient or -deficient treatments. Furthermore, ferric-chelatate reductase activity was greater in iron-deficient than -sufficient media for both mutant and control suggesting normal response to iron-deficiency by pOAF40. Further characterization of this mutant is being performed to determine whether the mutation deregulates ferritin expression or leads to over-accumulation of iron in leaves.

Amanda Corey

Major: Biomedical Engineering
University: North Carolina State University
Faculty Mentor: Dr. John K. Critser
Mentor Department: Veterinary Pathobiology
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Membrane permeability of Bovine Ooctyes to Propylene Glycol and the application to the improvement of Cryopreservation

Amanda M. Corey, Steven F. Mullen and John K. Critser

In this study, the goal was to determine the permeability parameters of bovine oocytes for water (Lp) and Propylene Glycol (PPG) at temperatures of 30, 20, 10, and 5°C. By determining permeability parameters, we can model cell volume changes during addition and removal of cryoprotectants to determine a method that will prevent osmotic damage to the cells. Individual oocytes were held stationary by a holding pipette in a Petri dish on a Nikon inverted microscope. The oocytes were initially equilibrated in propylene glycol (PG) and 0.1M Sucrose for 20 minutes and then a solution of TL-Hepes with 0.1M Sucrose was added to a drop of 1.5M PG containing the oocyte. The specific initial concentration of PG and volumes of added solutions were modified for each temperature. Then digital images were captured on a regular time scale using a Spot RT Cooled CCD Digital camera in order to record shrinking and swelling. Morphometrical analysis was then performed on each image using Adobe Photoshop to measure the radius of each oocyte at the various time points during the volume excursions. Using Microsoft Excel, we were able to fit the experimental data to a best fit curve of a theoretical model for volume change, which allowed the determination of the values of Lp and PPG. These values were used to model the cell volume changes using MLAB (Civilized Software, Inc., Bethesda, MD) to developing optimized addition and removal procedures for 3.0M CPA that would minimize potential damage of the oocyte due to shrinking and swelling, and toxicity effects of the CPA due to excessive exposure. Currently, our results for the mean values of the permeability parameters Lp and PPG at 20°C are 0.3 ± 0.03 μm-min.atm and 15 ± 7.2 μm/min, respectively (mean ± SD, n=2). Further data acquisition and analysis is in progress.

Michael Cressman

Major: Animal Sciences
University: Pennsylvania State University
Faculty Mentor: Dr. Monty S. Kerley
Mentor Department: Animal Sciences
Funded by: F.B. Miller Undergraduate Research Program in Animal Sciences

The measurement of residual feed intake to determine feed efficiency of pregnant Hereford heifers

M.D. Cressman, M.S. Kerley, W.H. Kolath and L.S. Miller

The large potential improvement in profitability is what makes feed efficiency such a studied and concerned topic in the beef industry today. Currently, no herd exists in the United States that has been selected solely for the purpose of measuring and improving feed efficiency. The objective of this study was to rank forty-two pregnant Hereford heifers based on their feed efficiencies, so that they may be mated to bulls of known efficiency. The long term goal of this project is to create both efficient and inefficient herds for future feed efficiency research. These heifers were acquired from various beef producers across the state to ensure genetic variation within the herd. The heifers were fed an alfalfa/grass hay to which they had ad libitum access. Their diet was 86% dry matter and contained 58% neutral detergent fiber, 38% acid detergent fiber, and 14% crude protein on a dry matter basis. The individual intake of each heifer was recorded by the GrowSafe® feed intake system. Expected feed intake was calculated as a regression of actual intake on average daily gain and metabolic mid-weight. Expected feed intake was subtracted from actual feed intake to calculate the residual feed intake value of each individual heifer. Residual feed intake was then used as a measure of feed efficiency. The average body weight at the start of the study was 488 kg. Heifers consumed on average 17.77 ± 5.24 kg/d, and the herd gained at a rate of 0.77 ± 0.32 kg/d. The most efficient heifer consumed 9.78 kg/d less than was expected, while the most inefficient heifer consumed 11.54 kg/d more than was expected. Calculating residual feed intake as a means of determining feed efficiency will enable us to establish both efficient and inefficient herds for further research.

Lauren Criss

Major: Psychology and Black Studies
University: University of Missouri-Columbia
Faculty Mentor: Dr. H. Colleen Sinclair
Mentor Department: Psychological Sciences
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Examining the consequences of stalking misconceptions

Lauren A. Criss and H. Colleen Sinclair

It has been proven through previous research that stalking is a form of intimate violence. It is possible that by researching other forms of intimate violence, such as rape, we can come to gain a better understanding of stalking, particularly in our legal system. By following the example of rape myth literature, and previous studies on rape myths, we produce a starting point and a guide by which to follow. It is first necessary to build a scale to assess the stereotypes that people have about stalking. Our first study did this by creating the Stalking Myth Scale, a reliable and valid scale that yielded a reliability of 0.80, and correlated, as expected, with five other measures of intimate violence. We then used this scale, along with four other measures to examine the extent to which stalking myths were an acceptable predictor of case severity, sentencing, victim blaming, and perpetrator responsibility. We hypothesized that the endorsement of stalking myths would result in a minimization of case severity, lower sentencing, more victim blaming, and reduced perceptions of perpetrator responsibility. A scenario experiment was run, varying the gender of perpetrator and victim, and the type of victim-perpetrator relationship (stranger or intimate). Through this study our hypothesis was proven. It was found that endorsement of stalking myths was a significant predictor of all four variables (case severity, sentencing, victim blaming, and perpetrator responsibility).

Colin Cunningham

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Dennis Miller
Mentor Department: Psychological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Lobeline antagonizes the discriminative stimulus properties of cocaine

Colin S. Cunningham and Dennis Miller

Lobeline has high affinity for nicotinic acetylcholine receptors and inhibits the function of vesicular and plasmalemmal monoamine transporters. Moreover, lobeline has been shown to alter the neurochemical and behavioral effects of psychostimulants. In drug discrimination studies, lobeline generalized to cocaine and diminished the stimulus properties of methamphetamine. The present study determined the effect of lobeline, nicotine, mecamylamine and hexamethonium on the discriminative stimulus properties of low doses of cocaine (1.6 or 5.0 mg/kg) or d-amphetamine (0.3 mg/kg) in rats, using a standard two-lever drug discrimination procedure for food reinforcement. Nicotine partially generalized to amphetamine and fully generalized to cocaine, although the discriminative stimulus properties of cocaine and amphetamine were not altered by mecamylamine or hexamethonium. In contrast, lobeline fully generalized to cocaine, but did not generalize to amphetamine. In antagonism tests, lobeline doses that did not generalize to cocaine decreased responding on the cocaine-paired levers. Surprisingly, lobeline did not alter the discriminative stimulus properties of amphetamine. This research further supports the supposition that nicotine, cocaine and amphetamine produce similar, but distinct subjective states. Furthermore, the present findings suggest that lobeline has a complex mechanism of action to disrupt the behavioral effects of drugs of abuse.

Jonathan DeGraff

Major: Biology
University: Brigham Young University
Faculty Mentor: Dr. Kathleen J. Newton
Mentor Department: Biological Sciences
Funded by: Plant Genomics Internship @ MU

Comparison of regulatory regions in the mitochondrial genomes of grasses

Jonathan E. DeGraff, James O. Allen and Kathleen J. Newton

Regulation of transcription in plant mitochondria is not well understood. The recent sequencing of the mitochondrial genomes of 10 closely related grasses allowed a comparative analysis of regulatory regions. To look for conserved regions and potential “swapped” regulatory regions, we have performed a comparative analysis of the upstream and downstream regions of all of the protein-coding genes in the mitochondrial genomes of eleven grasses: five mitochondrial types of maize (two fertile and three cytoplasmic male sterile), three other taxa within the genus (*Zea mays ssp. parviglumis, Z. luxurians, Z. perennis*), two close relatives (*Tripsacum dactyloides, Sorghum bicolor*), and an outgroup, rice. These genomes contain an average of 35 protein-coding genes, composed of 40 transcriptional units. Our analyses examined 1000 base pairs (bp) upstream of the first exon of each transcriptional unit and 1000 bp downstream of its last exon. The reference genome was NB, the most common fertile maize mitochondrial genotype. Compared with the genes from NB, more than half of the mitochondrial genes in the other genomes contain sequences that flank different genes in NB; we refer to these as “swapped” regions. More than 25% of the translocated sequences are longer than 100 bp, and 21 are greater than 500 bp. The longer sequences are more likely to have a regulatory function. In addition, some of these regions were found multiple times: 12 of the translocated gene-flanking regions were found flanking five or more other genes; four had sequences that were flanking ten or more. Furthermore, in *Z. luxurians, Z. perennis and T. dactyloides*, the co-transcribed 18S and 5S ribosomal RNA genes have been translocated immediately upstream of the start of *cox*1, with the 5S rRNA 3’ end only 80 bp from the start of *cox*1 exon 1. This is a position that is difficult to rectify with the divergent transcriptional needs of the two types of genes.

Patrick Dell

Major: Music Education
University: University of Missouri-Columbia
Faculty Mentor: Dr. Michael J. Budds
Mentor Department: Music
Funded by: MU Undergraduate Research Scholars Program

Video game music beyond its original function: Practices, styles, and ends

Patrick Dell and Michael J. Budds

Rapidly growing in complexity of compositional practices, styles, and ends, video game music is an art form that surpasses its original function as “background music” as well as any utilitarian, stereotypical expectations of the general public. Many video game soundtracks have been issued separately from their original contexts and offered to the public as musical entertainment or art; these compositions communicating musical values transcending their initial function are conceived for the enjoyment of the listener outside of the in-game experience. Many scores have also been arranged for live performance by alternative media and occasionally published for amateur consumption. In my study I analyze selected video game scores from the past two decades and examine their nature and organization. These scores represent a wide variety of compositional traits and musical styles, from Wagnerian leitmotif techniques using a conventional orchestra to a series of unrelated cues of experimental harmonies and instrumentations. Some composers borrow ideas from recognizable sources, including the James Bond film scores or the works of classical masters such as Mozart and Rimsky-Korsakov. Many scores approximate the common Hollywood film practice by using either a live or synthesized orchestra, while others incorporate unique synthesized sounds or an entirely different sound ideal. I also examine the relationship of arrangements of video game music to their original sources: many games have corresponding albums of music that go beyond the original score’s intent. For instance, piano arrangement albums allow composers to explore the timbre of the piano, while the corresponding sheet music allows consumers to create their own role in the soundtrack. Orchestral arrangement albums, which are live or studio recordings, generally exist where the source material is synthesized, allowing composers to hear their music as it may have been originally conceived, possibly expanding on musical thoughts originally expressed in the scores.

Braden DeLoach

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Gary Stacey
Mentor Department: Plant Sciences
Funded by: MU Monsanto Undergraduate Research Fellowship

Analysis of *Arabidopsis thaliana* mutants defective in the oligopeptide transporter *OPT3*

Braden DeLoach, Minviluz G. Stacey and Gary Stacey

The transport of peptides across membranes is a phenomenon found in both prokaryotes and eukaryotes as a method of obtaining amino acids, nitrogen, and carbon. Peptides can be transported by ATP-dependent transporters, as well as proton-coupled transporters. Among the latter are members of the oligopeptide transport (OPT) family, which transport tetra- and pentapeptides. Sequence comparisons led to the identification of nine OPT genes in Arabidopsis and our laboratory is investigating the role of these transporters in plant growth and development. Previous studies showed that mutations in the *OPT3* gene resulted in embryo lethality. More recently, *OPT3* expression was shown to increase under conditions of iron limitation, suggesting a possible role for *OPT3* in transporting iron-chelates. The lethal nature of *OPT3* T-DNA insertion mutation makes them difficult to study in a homozygous condition. Therefore, we sought non-lethal mutations within the *OPT3* gene sequence, which can be maintained as homozygous plants. To create such mutations, we used the process of Targeted Induced Local Lesions IN Genomes (TILLING) to identify non-lethal, point mutations in the *OPT3* gene. Eight mutant alleles, *opt3*-1 to *opt3*-8, were identified by TILLING. These mutants were sequenced and aligned with the other members of the OPT family to determine whether the mutations occurred within conserved regions of the protein. The mutations *opt3*-5 (P628S) and *opt3*-8 (P547L) were the first homozygous mutants identified which occurred within a highly conserved region and, therefore, were the likely candidates to disturb *OPT3* function. These mutations were followed in segregating populations by CAPS (Cleaved Amplified Polymorphic Sequence) markers. Homozygous mutant lines and wild-type controls were grown on medium containing limited, moderate, or excess iron. The iron effects on the plant were determined by assaying the chlorophyll content in whole plants. These assays revealed no measurable effect of the *OPT3* mutations on chlorophyll content under the conditions tested. We are now examining other *opt3* alleles for a role in iron transport and other possible phenotypes displayed during plant growth and development.

Jennifer Dine

Major: Nursing
University: Truman State University
Faculty Mentor: Dr. Jane Armer
Mentor Department: Sinclair School of Nursing
Funded by: NIH Grant to J. Armer

The psychosocial response to lymphedema

Jennifer Dine and Jane M. Armer

Lymphedema, a life-altering disease, affects many breast cancer survivors throughout the world. Manifested as either an acute or chronic illness, lymphedema can occur at any time during and following post-breast cancer treatment as the result of damaged lymph vessels. Resulting in the accumulation of protein-rich fluid in the affected limb, lymphedema inhibits the mobility of the limb and is both disabling and disfiguring. These factors ultimately result in a variety of psychosocial responses from both the patient and the family, including lowered self-esteem and depression in the patient and role modification of the family. Cultural and age factors also affect the patient's perception and understanding of the disease, further necessitating new approaches to health care practice. A preliminary content analysis of qualitative responses on impact of lymphedema following breast cancer treatment described by study participants will also be provided. [Funded by NIH R01 NR05432-03 to J. Armer.]

Laura Donnelly

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Jim Birchler
Mentor Department: Biological Sciences
Funded by: MU Monsanto Undergraduate Research Fellowship

Identification of chloroplast DNA insertions in nuclear chromosomes of maize B73 line using the FISH procedure

Laura Donnelly, Leah Westgate, Louis Meyer, Patrice Alberts, Kathy Newton and Jim Birchler

It is known that chloroplast DNA can incorporate itself into the nuclear genome of plants. However, the sites of chloroplast (ct) DNA integration into chromosomes of maize have not yet been analyzed. This project is the first attempt to find the location of the ctDNA on the maize chromosomes. Fluorescent *in situ* hybridization is a technique that has proved useful in karyotyping and chromosomal mapping in maize. The FISH procedure is being used in this study to discover the location of the ctDNA in the nuclear genome of the inbred line B37. In order to develop ctDNA "probes" for FISH analysis, we have used the polymerase chain reaction (PCR) to produce fragments of ctDNA. Primers were chosen to amplify fragments of 10 kb or larger. The amplified DNAs were purified and labeled with fluorescent dyes and these probes were subsequently hybridized to chromosomes. The probes recognize and bind to the corresponding DNA sequences within the chromosomes. Root tip cells were used to prepare the slides for hybridization. Because the cells are collected during the metaphase stage of division, the chromosomes are compact and more easily visible. Chromosomes that contain ctDNA can be detected using a compound microscope with fluorescent attachments. The location of the ctDNA on the chromosomes is made visible by the fluorescent labeling of the probe. Eight of eleven regions of the chloroplast genome of the B73 line have been specifically amplified and have been observed under the microscope for FISH analysis. This information will contribute to an understanding of the extent and mechanism of transfer of organellar genomes to the nucleus.

Stephen Eastman

Major: Mechanical Engineering
University: University of Missouri-Columbia
Faculty Mentors: Phil Buckley and Darren Radke
Mentor Department: Midwest Research Institute
Funded by: NSF Program Alliance for Collaborative Research in Alternative Fuel Technology and MU Access in Engineering

Fuel system design for an adsorbed natural gas vehicle

Stephen Eastman, Antonio Howard, Darren Radke and Phil Buckley

With energy and environmental concerns mounting as the global energy demand increases, alternative fuels are drawing more and more attention. Natural gas is one such alternative fuel. However, the major shortcoming of natural gas is that it must be highly compressed in order to store at a comparable energy density to liquid fuels. For this reason, The Alliance for Collaborative Research in Alternative Fuel Technology (ALL-CRAFT) aims to develop low-pressure, high-capacity storage technologies for natural gas (methane).

Midwest Research Institute (MRI), an ALL-CRAFT partner, is assigned the task of developing a fuel tank and fuel delivery system for a natural gas-powered vehicle modified to store natural gas using adsorbed natural gas (ANG) technology. The design work performed thus far has been creating a preliminary model and solving the logistics of modifying the vehicle's fuel delivery system to accommodate the use of the ANG tank in addition to the pre-existing compressed natural gas (CNG) tank.

The fuel system of a 2005 Honda Civic GX will be modified by installing an ANG fuel tank to serve as an auxiliary tank to the existing higher pressure CNG tank. The vehicle will have additional capabilities while maintaining all of its original functions. One such capability is running either from its CNG or the ANG tank, with emphasis on maximizing mileage from ANG tank use. Moreover, the CNG tank will be equipped to simultaneously fuel the engine and refill the ANG tank upon the latter's depletion. An on-board CPU will be installed to control this modified fuel delivery system and record data such as mileage accrued from each tank.

The MRI involvement in the ALL-CRAFT project is only at the end of the first of two stages towards completion, but this initial research should provide a solid foundation to complete and fabricate the design.

Marie Elorza

Major: Animal Science
University: California State University-Chico
Faculty Mentor: Dr. Matthew C. Lucy
Mentor Department: Animal Sciences
Funded by: F.B. Miller Undergraduate Research Program in Animal Sciences

Expression of ISG15, UBE1L and MX2 in white blood cells of early pregnant and bred-nonpregnant dairy cows

M.T. Elorza, J.F. Bader, T.L. Ott, J.P. Meyer and M.C. Lucy

Identifying pregnant and nonpregnant cows shortly after insemination can improve reproductive efficiency in dairy cows if resynchronization is practiced on nonpregnant cows. Bovine Interferon Stimulated Gene Product 15 (ISG15), Bovine Ubiquitin-Activating E1-Like (UBE1L) Enzyme and MX2 are produced in response to conceptus-dervied interferon-τ. The objective was to determine the level of these mRNA in pregnant and bred-nonpregnant Holstein cows (n=14). We hypothesized that the amount of ISG15, UBE1L and MX2 mRNA would increase between d 14 to 20 in pregnant cows but not increase in bred-nonpregnant cows. Cows were synchronized to estrus and inseminated (d 0). Blood samples were collected on d 14, 16, 18 and 20 following insemination. Pregnancy status was determined at approximately 30 and 60 d after insemination. RNA was isolated, reverse transcribed into cDNA and amplified using quantitative RTPCR. Six cows were nonpregnant (open) and eight cows were pregnant on d 30. On d 60, four of the pregnant cows remained pregnant (pregnant-pregnant) and four were found open (aborted; pregnant-open). mRNA data were expressed as fold increase above control and relative to cyclophilin. A status by day interaction was detected for ISG15 ($P<.001$) and MX2 ($P<.02$). The interaction was not significant for UBE1L. Mean ISG15 and mean MX2 remained low for open cows, but increased markedly on d 18 and 20 in pregnant-pregnant cows. Pregnant-open cows either had low levels of ISG15 and MX2 or underwent an increase in ISG15 and MX2 on d 18 and 20. We conclude that ISG15, UBE1L and MX2 are differentially regulated in dairy cows during pregnancy recognition. ISG15 and MX2 mRNA expression could be used as an indicator of early pregnancy. Cows that abort their pregnancy after d 28 (pregnant-open) have abnormal ISG15 and MX2 mRNA expression between d 14 to 20.

Michael Forney

Major: Physics
University: University of Missouri-Columbia
Faculty Mentor: Dr. Ioan Kosztin
Mentor Department: Physics and Astronomy
Funded by: Life Sciences Undergraduate Research Opportunity Program

Free energy profile of sugar transport through maltoporin of *Escherichia Coli*

Michael Forney and Ioan Kosztin

The purpose of my project is to investigate molecular (glucose and maltodextrin) transport in the sugar selective, highly asymmetric maltoporin (LamB) outer membrane channel from E. coli by employing all atom molecular dynamics (MD) simulations. The choice to study maltoporin is motivated by the following facts: (i) it is well characterized experimentally; (ii) it has a highly asymmetric structure as inferred from its high resolution crystal structure (PDB entry 1MPM); and (iii) this is the first all atom MD simulation for this system.

Maltoporin is a trimer of three identical 18-stranded antiparallel β-barrel monomers. In each monomer, the L3 loop folds into the β-barrel to form an hourglass-shaped constriction region with a helical twist that mimics the shape of maltodextrin. This allows maltodextrin to slide through the constriction without any energetically expensive conformational changes. Furthermore, a sequence of aromatic residues, referred to as the "greasy slide", aligned by polar track residues form a specific sugar translocation pathway within the constriction region of the channel.

Our equilibrium MD simulations provided valuable information about the conformational stability of maltoporin, while nonequilibrium SMD simulations revealed the microscopic details of glucose permeation in maltoporin.

Jason Gallia

Major: Bioengineering
University: Binghamton University
Faculty Mentor: Dr. John Critser
Mentor Department: Veterinary Pathobiology
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Parameter estimation and data reduction for cellular biophysical analysis

Jason Gallia, James Benson and John Critser

Accurate estimation of cellular permeability parameters are an important part of designing and developing optimized cryopreservation protocols. Electronic Particle Counters measure cell volume by detecting changes in electrical conductivity. However, data that are obtained from these machines are noisy, making immediate application of curve fitting algorithms impossible. We attempted to reduce or eliminate noise due to both the population variance and the instrument. To eliminate the noise we grouped the original data into evenly spaced time bins, compared the point density of each bin to the average density over all the bins, and discarded those bins whose density fell outside a predetermined range that was centered around the average. Next an averaging scheme was created to remove the noise from the top and bottom. This was accomplished by grouping the remaining bins and applying a third order polynomial fit to the high and low ends of their volume histogram. Minima where found for each end in each time bin and their average was used as our high and low cut off. Any remaining noise was eliminated through the use of a Fast Fourier Transform and a high pass filter. After noise reduction a curve was then fit to the remaining data points using a least squares parameter estimation technique and a conjugate gradient method to find optimal parameters of the differential equations which model cell volume flux. These parameter values that were acquired using the best fit technique could then be used in models to more accurately represent the data that was collected.

Angelique Garrido-Gibbs

Major: Biology
University: Medgar Evers College
Faculty Mentor: Dr. Joel Maruniak
Mentor Department: Biological Sciences

Funded by: NSF-REU Program in Biological Sciences & Biochemistry

The effect of caloric restriction on the mitotic rates of mice

Angelique Garrido-Gibbs and Joel Maruniak

Caloric restriction has been shown to cause a number of biological changes in animals including the retardation of the aging process. Calorically- restricted animals show an average increase in life span of 30 - 50 %. In the present study we wanted to test the hypothesis that caloric restriction leads to a generalized slowing of mitotic rates in the body that at least in part, underlies caloric restriction's ability to extend lifespan. The subjects in this study were 22 six month old CD-1 male mice that were obtained from the colony of our animal facility. They were group housed from weaning to 4 months of age and then isolated and singly housed for a month before being used in this study. The 11 experimental mice were calorically restricted until they experienced a 20% loss in body weight.The experimental group was given approximately 25% less food than controls but received water ad lib. When necessary, the food ration was adjusted slightly so that their weight was maintained between 80-82% of their initial weight. The control mice were given water and food ad lib and both control and experimental groups were weighed daily. After the weights of the calorically restricted mice stabilized for 3 days, they were injected with bromodeoxyuridine (BrDu) for another 3 consecutive days. They were then sacrificed and their brains, nose, and ears were collected to be assessed by using immunohistochemistry for BrDu. The results of this study are yet to be determined. We will quantify the number of mitotic cells in each tissue as evidenced by BrDu staining.

Alison Ghormley

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Susan Nagel
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Effects of prenatal exposure to xenobiotic estrogen and the development of endometriosis in adulthood

Alison Ghormley, Katie Hurrelmeyer, Kathy L. Sharpe-Timms and Susan C. Nagel

Endometriosis is an estrogen-dependent disease that affects millions of women worldwide, causing pain and infertility. While it is known that retrograde menstruation places endometrial tissue in the peritoneal cavity, it is unclear why it invades and proliferates in women with endometriosis. Studies have shown that other hormone-dependent diseases have a fetal basis (e.g. breast cancer), suggesting that the presence of different hormones before birth may alter the incidence of endometriosis in adulthood. For example, women whose mothers took the synthetic estrogen diethylstilbestrol (DES) during pregnancy had an eighty percent increased incidence of endometriosis. Thus, our hypothesis is that prenatal exposure to xenobiotic estrogen will increase the severity of endometriosis in adulthood in a mouse model of surgically-induced endometriosis. To test this hypothesis, mice were time mated and dosed with vehicle control, 100 ng/kg DES or 10,000 ng/kg DES from days 11-17 of gestation. Surgical induction of endometriosis was performed in adulthood by autotransplantation of one uterine horm. The horn was removed, opened, divided into three pieces, and sutured to the arterial cascade of the intestinal mesentery. The implants became vascularized and formed endometriotic lesions. The mice were then collected at 2 or 4 weeks post-surgery, and the following endpoints were measured: 1) uterine weight; 2) implant size; and 3) implant weight. Additionally, implants were set aside for further analysis of 1) histology; 2) estrogen receptor indicator reporter gene activity; and 3) endometriosis-related gene expression. At the conclusion of this ongoing study, we expect to show whether there is an estrogen-mediated fetal component to endometriosis.

Cortnae' Gullatt

Major: Psychology
University: Hampton University
Faculty Mentor: Dr. Jessica Summers
Mentor Department: Educational, School & Counseling Psychology
Funded by: Summer Pre-Graduate Research Experience for Students in the Humanities

A study of teen pregnancy: At-risk teens and their motivation to stay in school

Cortnae' Gullatt and Jessica Summers

This study utilized Deci and Ryan's self-determination theory of motivation to examine pregnant and parenting teenage girls who attended an alternative education program in Kansas City, MO and mainstream high schools in Kansas City, KS. Self determination theory provides a theoretical basis that explains the different intrinsic and extrinsic motivational regulations that affects teenage girls who are pregnant or have already mothered a child in determining what motivates them to stay in school. In today's society, teenage pregnancy is becoming more and more prevalent, where it is affecting children as young as fourteen years of age (MMVS, 2002). If they are given available resources, and the proper education on intercourse and the risks involved, then such deterrence would not be affecting our young generation. The purpose of the study was twofold: 1) to examine the use of contraception among girls who were already pregnant or parenting; and 2) to determine what factors motivate at-risk teens in attaining a high school education. After carefully running analyses, results indicated there were many significant differences on the various regulation levels and contraceptive methods. For example, teens who were pregnant more likely to have sex and less likely to use condoms compared to teens who were already mothering a child. Also, the higher their mother's education level, the more likely popular contraceptive methods were used by the girls, such as condoms and the Depo-Provera shot. Another significant finding indicated that girls who were pregnant were more amotivated at Time 1 than girls who already had their baby at Time 2. There were also correlations with regards to basic psychological needs (competence, autonomy, and relatedness), parental support (mother autonomy, mother warmth, and mother involvement), and the various motivational scales. These findings are instrumental to other educational psychologists to help build further research on the different aspects of the motivation system associated with at-risk teenagers.

Timothy Hackmann

Major: Biology and Animal Science
University: University of Missouri-Columbia
Faculty Mentor: Dr. James N. Spain
Mentor Department: Animal Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Modeling the flow of digesta through the ruminant reticulorumen

Timothy J. Hackmann, James N. Spain and Ronald L. Belyea

Ruminants possess a specialized gastrointestinal (GI) tract that enables them to efficiently digest fibrous feeds. The first stomach compartment of the ruminant GI tract, the reticulorumen (RR), is the site of most fiber digestion due to the presence of cellulolytic microorganisms in conjunction with selective retention of feed particles; undigested fibrous feed particles are selectively retained and fermented by cellulolytic microorganisms in the RR until certain digestive processes are completed, enabling the particles to pass. Selective retention and the overall process of digesta flow in the RR affect feed digestibility, feed intake, and microbial efficiency—all important animal performance parameters in ruminant production. It is imperative to model digesta flow in the RR to better predict these animal performance parameters for use in ruminant production systems. Mathematical models have indeed been developed to describe the flow of digesta in the RR, typically with the RR represented as one or more mathematical compartments with flow between compartments defined by kinetic rate variables or constants. Mathematical models developed to the present use either fractional rate constants or rate variables based on the gamma distribution. The Yule distribution has also been suggested for modeling RR digesta flow kinetics, but its development has been cursory. It remains unseen what, if any, benefits may arise from applying the Yule distribution to describe the kinetics of RR digesta. In this study, a model incorporating the Yule distribution is fully developed. Physiological justification for using the Yule distribution is also provided on the basis of selective retention. A comparison between the model developed herein and a previously published model using the gamma distribution reveals that both models give similar mathematical results under certain cases. Still, it is suggested that the physiological relevance of the model treated here may make it superior. Animal feeding trials are currently being conducted to validate the structure of model. Additionally, mathematical models are being developed to describe small and large intestinal flow in ruminant and non-ruminant species, thereby expanding this modeling effort to include most of the GI tract.

Tiffanie Hamilton

Major: Fisheries & Wildlife Science and Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Matthew E. Gompper
Mentor Department: Fisheries and Wildlife
Funded by: Life Sciences Undergraduate Research Opportunity Program

Sex and age specific infestation rates of raccoons (*Procyon lotor*) by American dog ticks (*Dermacentor variabilis*)

Tiffanie Hamilton, Ryan Monello and Matthew Gompper

American dog ticks (*Dermacentor variabilis*) can have profound direct and indirect effects on human and wildlife hosts. However, there is little information on their short- or long-term rates of parasitism in free-ranging wildlife populations. In Missouri, raccoons (*Procyon lotor*) are the principal host of dog ticks, with tick prevalence reaching up to 90%. Our goal was to determine the intensity of non-engorged (short-term) and engorged (long-term) tick infestations among different age, sex, and reproductive classes of raccoons. From May to July 2005 we captured 105 raccoons across eight populations residing in predominantly forested ecosystems of central Missouri. Raccoons were sexed, weighed, and aged by examining tooth wear, genital morphology, and body size. Ticks were sampled by direct, two-minute timed observations to estimate tick abundance. Non-engorged and engorged ticks infested males, lactating females, and non-lactating females in decreasing levels of intensity. There was no correlation between weight and the intensity of tick infestation, but tick burdens generally increased with age.

Daniel Hanneken

Major: Social Work
University: University of Missouri-Columbia
Faculty Mentor: Dr. Anne Dannerbeck
Mentor Department: Social Work
Funded by: MU Undergraduate Research Scholars Program

Metro and nonmetro youth: Evaluating differential pathways to delinquency

Daniel Hanneken and Anne Dannerbeck

Although much research has been conducted on risk factors and behaviors of delinquent youth, little is known about the nonmetro population and how they may differ from their metro counterparts. The purpose of this study is to test the hypothesis that metro and nonmetro youth experience significant differences in risk factors, behaviors, and experiences leading to delinquency. The findings are the result of a multi method approach incorporating both quantitative and qualitative analysis. An assessment of a pre-existing data set of 1706 delinquents identified initial differences between metro and nonmetro delinquents. Major risk factors between the two groups were then identified through a literature review. Next, to identify nonmetro pathways to delinquency a content analysis was performed on interview transcripts of 28 youth recently housed in Missouri Division of Youth Services Treatment Facilities. The above hypothesis was supported as several themes appeared. Significant differences were found in parent attributes between the two groups as well as how the youth experience and respond to parenting. Nonmetro youth were found to be referred for the first time at an earlier age and their referral was predicted by more and different variables than that of metro youth. A difference in resources and services along with diminished social support due to community size affect how nonmetro youth cope with fewer economic opportunities as well as greater poverty rates. Although more study is needed, this research improves our understanding of metro and nonmetro differences in delinquency and can be used to develop prevention and intervention strategies specific to nonmetro youth.

Stefan Harris

Major: Biology
University: Prairie View A&M University
Faculty Mentor: Dr. Jay J. Thelen
Mentor Department: Biochemistry
Funded by: Plant Genomics Internship @ MU

Oil bodies isolated from Brassica napus mature seed

Stefan Harris, Vesna Katavic, Martin Hajduch, Ganesh Agrawal and Jay J. Thelen

Plants store seed triacylglycerols in discrete lipid monolayer storage organelles called oil bodies. Only two proteins have been characterized from oil bodies, namely oleosin and caleosin, which are both integral membrane proteins. To better understand the protein composition this organelle, oil bodies were isolated from Brassica napus (cultivar westar) mature seed. Oil bodies were isolated using two published methods that utilize phase separation in aqueous media. Method 1 employed iterative washes in aqueous media containing sucrose, and 2M NaCl while method 2 made use of only one type of aqueous media (minus NaCl) put through multiple washes. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) showed method 1 to yield isolated oil bodies with higher purity based on the absence of the storage protein napin that was present in the total protein of isolated oil bodies from method 2. The oil bodies isolated with method 1 were subjected to washes in 2M NaCl or 8M urea to determine the nature of protein association to oil bodies. The isolated oil bodies were fractionated through petroleum ether to extract neutral lipids (triacylglycerols) that are contained by the monolayer membrane. Polar lipids were then extracted with chloroform/methanol. The interfacial pad which contained the associated proteins was suspended in water, sonicated, and subjected to acetone precipitation. Analysis of salt and urea washed oil body proteins by SDS-PAGE revealed abundant bands of the proper molecular weight for oleosins as well as at least 10 other additional proteins. Identification of these proteins by mass spectrometry will reveal novel proteins associated with oil bodies.

Kate Hart

Major: Biochemistry and Anthropology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Judy Wall
Mentor Department: Biochemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Construction of a *tatA Desulfovibrio vulgaris Hildenborough*

Kate E. Hart and Judy D. Wall

tatA Desulfovibrio vulgaris Hildenborough is a member of the obligately anaerobic bacteria growing by sulfate respiration and involved in environmental biocorrosion of ferrous metals. It also shows potential for bioremediation of toxic metals. Because these important metabolic activities of *D. vulgaris* are directly linked to electron flow, a better understanding of energy generation is needed. A model for augmenting respiratory energy production through hydrogen cycling has been proposed. This controversial model requires a periplasmic hydrogenase. The genome sequence of *D. vulgaris* reveals genes for four different periplasmic hydrogenases, the roles of which are currently unclear. There are two primary systems of transport of proteins such as hydrogenases to the periplasm or outer cell membrane. Both the Sec and Tat protein export systems translocate proteins across the cytoplasmic membrane. The Sec pathway exports short unfolded proteins, while the Tat system (Twin Arginine Translocation) translocates longer prefolded proteins. The latter generally contain redox cofactors and share a consensus motif (S/T)-R-R-x-F-L-K recognized for export. The Tat system is found in most prokaryotic plasma membranes. The Tat protein export system is encoded by four genes *in E. coli, tatA, tatB, tatC, and tatE*. However, only three of these genes, *tatA, tatB,* and *tatC*, have been putatively identified in *D. vulgaris*. Removal of one or more tat genes from *E. coli* causes deficiency in the transport of proteins by the Tat system. We propose to test the hydrogen cycling model for energy generation by creating a tatA deletion mutant in *D. vulgaris* that should block the production of all periplasmic hydrogenases. An examination of the deletion mutant should reveal the contribution of the hydrogen cycle to the energy economy of *D. vulgaris*.

Colleen Hayes

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Allison Welch
Mentor Department: Biological Sciences
Funded by: REU Supplement to A. Welch and C. Gerhardt

Does genetics play a role in feeding behavior of gray tree frogs?

Colleen Hayes and Allison Welch

Models of sexual selection suggest that, in some animals, females choose mates of genetically superior quality. In the gray tree frog Hyla versicolor, it has been shown that females prefer male advertisement calls of long duration. Studies have also found that offspring of long-calling males have a performance advantage over the offspring of short-calling males. This research focuses on the feeding habits of H. versicolor tadpoles in an attempt to understand the contribution of paternal genetic quality to tadpole behavior. The tadpoles used in this study were offspring from long-calling males and short-calling males, reared individually in the lab. Tadpoles were individually weighed and then observed on three different occasions over the course of a week: one day after food administration, immediately after food administration, and one day after a subsequent food administration. Tadpole behavior was classified as either feeding, resting, or swimming. Results reveal that feeding behavior did not change with age, though feeding behavior was significantly higher immediately after food administration. In addition, larger tadpoles spent more time feeding than smaller tadpoles. Preliminary analyses indicate that the offspring of short-calling males were, on average, larger in size than offspring of long-calling males and, probably as a consequence of their larger size, spent more time feeding. In summary, paternal genetic quality appears to affect feeding behavior of their offspring, although further investigation is needed to determine whether tadpole feeding behavior affects performance later in life.

Zachary Henderson

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Steve Nothwehr
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

A search for regulators of a yeast synaptojanin

Zachary Henderson and Steve Nothwehr

The yeast S. cerevisiae expresses three synaptojanins: Inp51p, Inp52p, and Inp53p. These enzymes are characterized by two specific characteristics. They contain an inositol 5'-phosphatase and a polyphosphoinositide phosphatase. Together, these enzymes play a crucial role in the membrane trafficking of yeast cells. The synaptojanins are important to yeast because the cells ability to survive is dependent on them. It has been shown that a complete knockout of the three genes causes lethality in yeast. The synaptojanin that we are focusing on in this experiment is Inp53p. Inp53p is involved in intra-cellular membrane trafficking within yeast. Loss of Inp53p function results in quicker membrane protein movement towards the prevacuolar compartment from the trans-Golgi network. Although it is known that these enzymes are regulated, the method of regulation is unknown. We wish to identify proteins in yeast that activate Inp53p. At the current time, we are constructing a strain of yeast that codes for a knockout of all three synaptojanins, which would have lethal results, and introducing a gene containing the INP53 gene fused to a weak promoter from *GAL4* resulting in lower than normal expression of Inp53p. At the current time, no results have been recorded. However, in the near future we will transform the created strain with a gene library (YEp351) and look for proteins that, when over expressed, enhance the activity of Inp53p. On a broader scale, due to the large responsibility of synaptojanic activity in membrane trafficking in humans, any further research in the field would be beneficial to human health.

Jessica Hodge

Major: Biology
University: Xavier University of Louisiana
Faculty Mentor: Dr. Satish Nair
Mentor Department: Mechanical & Aerospace Engineering
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

The impairment of the prefrontal cortex due to high levels of dopamine and norepinephrine in relation to ADHD

Jessica Hodge and Satish Nair

Attention- Deficit/ Hyperactivity Disorder (ADHD) affects many people from various backgrounds; however, not much is known about the disorder aside from clinical symptoms. Researchers are just beginning to dissect ADHD and its effects on the brain, specifically in the prefrontal cortex (PFC) region. The PFC controls attention, motivation, planning, and most importantly working memory. Working memory is temporary storage for short-term memory; it is essential for sequencing tasks and assists with internalized language. The working hypothesis implicates increased levels of Dopamine (DA) and Norepinephrine (NE) in the impairment of PFC cells, leading to inhibition of working memory, and the development of disorder. The interaction of pyramidal neurons in the various layers of the PFC is studied in order to discover the impact of the network level plasticity on the disorder. This interdisciplinary research examines the relative impact of DA and NE, and the relevant pathway interactions on affected cells. Relevant neurophysiological experimentation data is used to examine mechanisms of ADHD in rat PFC, and to develop a computational model of the pyramidal neurons located in the six layers of the PFC. An analysis of the cognitive effects of ADHD via computational modeling may predict brain function, uncover emergent properties, and assist in the development of treatment. Reliable computational modeling will help save money and time as well as avoid the frequent use of human trial subjects.

Clifton Holland

Major: Biology
University: Xavier University of Louisiana
Faculty Mentor: Dr. Dennis Lubahn
Mentor Department: Biochemistry
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Estrogen receptors in TRAMP C2 cells

Clifton Holland, Jinghua Liu and Dennis B. Lubahn

According to a 2005 study done by the American Cancer Society, prostate cancer is the second most common type of cancer among American men. It has been shown that estrogen receptors alpha and beta play significant roles in the development and inhibition of prostate cancer. To further understand the roles ERs play in prostate cancer, a Transgenic Adenocarcinogenic of the Mouse Prostate (TRAMP) model was utilized. Simply put, these DNA engineered mice are highly likely to develop a prostate cancer similar to the type experienced by humans. Similar to humans, in TRAMP mice there are different stages of prostate cancer; well differentiated carcinoma (WDC) and poorly differentiated carcinoma (PDC) are the stages being we study extensively. It has been shown that double transgenic ER alpha knockout/ TRAMP mice have decreased incidence of PDC, while ER beta knockout/ TRAMP mice have increased incidence of PDC, which implies different roles for ER α and ER β in prostate cancer. The TRAMP C2 cell line is derived from TRAMP mice and potentially serve as a good model for in vitro studies of prostate cancer. This cell line would be useful for studying estrogen effects on prostate cancer, if it contained ER α and β. Our hypothesis is that TRAMP C2 cells are ER α and ER β positive. The goal of this research is to test for the presence of these proteins in the TRAMP C2 cell line. To test for the presence of ER alpha and ER beta, the Western blot method was used. Western Blot is a widely accepted and efficient method for detecting a specific protein among a mixture of many different ones. In conclusion, both estrogen receptor α and β are present in TRAMP C2 cells. With this confirmation, the cure to prostate cancer is one step closer because this TRAMP C2 cell line will be well suited for determining the benefits of ER alpha and ER beta manipulation.

Antonio Howard

Major: Mathematics
University: Lincoln University
Faculty Mentors: Phil Buckley and Darren Rodke
Mentor Department: Midwest Research Insitute Kansas City
Funded by: NSF Program Alliance for Collaborative Research in Alternative Fuel Technology and MU Access in Engineering

Fuel system design for an absorbed natural gas vehicle

Antonio Howard, Stephen Eastman, Darren Radke and Phil Buckley

With energy and environmental concerns mounting as the global energy demand increases, alternative fuels are drawing more and more attention. Natural gas is one such alternative fuel. However, the major shortcoming of natural gas is that it must be highly compressed in order to store at a comparable energy density to liquid fuels. For this reason, The Alliance for Collaborative Research in Alternative Fuel Technology (ALL-CRAFT) aims to develop low-pressure, high-capacity storage technologies for natural gas (methane).

Midwest Research Institute (MRI), an ALL-CRAFT partner, is assigned the task of developing a fuel tank and fuel delivery system for a natural gas-powered vehicle modified to store the natural gas using adsorbed natural gas (ANG) technology. The design work done thus far has dealt with the logistics of modifying the vehicle's fuel delivery system to accommodate the use of the ANG tank in addition to the pre-existing compressed natural gas (CNG) tank.

The fuel system of a 2005 Honda Civic GX will be modified by installing an ANG fuel tank to serve as an auxiliary tank to the existing higher pressure CNG tank. Additional capabilities will be added while maintaining all of its original functions. One such capability is running either from its CNG or the ANG tank, with emphasis on maximizing mileage from ANG tank use. Moreover, the CNG tank will be equipped to simultaneously fuel the engine and refill the ANG tank upon the latter's depletion. An on-board CPU will be installed to control this modified fuel delivery system and record data such as mileage accrued from each tank.

The MRI involvement in the project is only at the end of the first of two stages towards completion but this initial research should provide a solid foundation to complete the design.

Alice Hui

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Kathleen Newton
Mentor Department: Biological Science
Funded by: MU Monsanto Undergraduate Research Fellowship

Analysis of mitochondrial DNA insertions into a nuclear chromosome of the maize B73 line

Alice Hui, Leah Westgate, Jonathan Lamb, James Birchler and Kathleen Newton

Mitochondrial DNA (mtDNA) is known to have integrated into the nuclear DNA of plants and animals. The purpose of this project is to investigate the on-going migration of mtDNA into the nuclear DNA of maize plants. Specific objectives are to discover the amount of DNA incorporated, whether it is the whole mitochondrial genome or sections, and to see if it has replicated after migration. The maize inbred line B73 has a particularly large mt DNA insert on chromosome 9. Using the fluorescent in situ hybridization (FISH) method, the arrangement of inserted mitochondrial DNA was examined. The FISH method uses fluorescently labeled mtDNA as probes for hybridization to chromosomes. Regions of the chromosomes that contain mtDNA can then be detected using a compound microscope with fluorescent attachments. Locations that contain more mtDNA are brighter. Three combinations of probes that cover different parts of the mitochondrial genome were employed. In order to analyze the arrangement of the DNA, the chromosomes were prepared from a stage of meiosis called pachynema in which the chromosomes are elongated and have not yet begun to condense. The results have confirmed the presence of all three probes within the large insertion of mtDNA on chromosome 9 of B73. The data suggest that either different parts of the mitochondrial genome are incorporated preferentially or that there is selective replication of portions of the mitochondrial genome after incorporation.

Charles Hunter

Major: Biology
University: Prairie View A&M University
Faculty Mentor: Dr. Michael R. Lewis
Mentor Department: Veterinary Medicine and Surgery
Funded by: Louis Stokes Missouri Alliance for Minority Participation

In vitro evaluation of In-111-DOTA-anti-bcl-2-PNA-Tyr-3-octreotate in Chronic Lymphocytic Leukemia cells

Charles Hunter, Fang Jia and Michael R. Lewis

The B-cell lymphoma/leukemia-2 (bcl-2) gene is overexpressed in many cancers. This gene increases cell survival by blocking apoptosis, or programmed cell death. The objective of this study was to evaluate radiolabeled peptide nucleic acid (PNA)-peptide conjugates targeting bcl-2 gene expression. DOTA-anti-bcl-2-PNA-Tyr-3-octreotate conjugate was labeled with In-111. Uptake, internalization, and efflux studies were performed in the human chronic lymphocytic leukemia (CLL) cell line Mec-1, which expresses both somatostatin receptors and bcl-2 mRNA. In the conjugate, octreotate is the somatostatin receptor ligand. Receptor and mRNA binding were also evaluated. Internalization of In-111-DOTA-anti-bcl-2-PNA-octreotate increased from 58.29% at 1min to 67.9% at 15min and reached 81% at 4h, whereas the internalized In-111-DOTA-Tyr-3-octreotate in Mec-1 cells started from 31.1% at 1min and gradually increased to 49.28% and 66.1% at 15min and 4h, respectively. Efflux analysis of Mec-1-In-111-DOTA-anti-bcl-2-PNA-Tyr-3-octreotate showed that 84.9% of radioactivity remained in the cells after 1min incubation and 60.0% of cell associated radioactivity was retained 4h later. Analysis of In-111-DOTA-Tyr-3-octreotate showed the cell associated radioactivity dropped from 85.1% at 1min to 69.1% at 4h.The western blot assay study showed a 51.0% bcl-2 protein synthesis inhibition by treatment with DOTA-anti-bcl-2-PNA-Tyr-3-octreotate. As a result, a peptide conjugate, which contains two molecular functions, was developed. These functions are receptor mediated tumor cell delivery and oncogene mRNA targeting. This agent has the potential to be used for detection of tumor bcl-2 expression by non-invasive molecular imaging.

Louis Jamtgaard

Major: Nuclear Medicine
University: University of Missouri-Columbia
Faculty Mentor: Dr. Vladislav Glinskii
Mentor Department: Biochemistry
Funded by: Molecular Imaging Program

Analysis of PDGF-AB and -BB in serum of intact and ovariectomized (OVX) pigs

Louis D. Jamtgaard, Tsghe W. Abraha, Olga V. Glinskii and Vladislav V. Glinsky

Previous studies in our group demonstrated that terminal microvascular networks in dura mater of ovariectomized (OVX) pigs undergo significant remodeling characterized by a decrease in microvessel density, capillary rarefaction, and increase in blood vessel permeability. It was postulated that post OVX vascular remodeling is estrogen-dependent and could involve changes in expression levels of relevant growth factors and receptors on both systemic and local levels. Comparison of 41 relevant growth factors and receptors in serum of intact female and OVX animals using antibody array revealed most robust changes in the expression levels of platelet-derived growth factors (PDGF) -AB and -BB, both of which are potent regulators of growth and survival in a vascular tissue. To corroborate the data from the antibody array, we conducted SDS-Page and Western blot analysis using monoclonal antibody directed against B chain of PDGF, which recognizes both PDGF-AB and PDGF-BB. The Western blot analysis revealed several species of PDGF-AB and BB possibly existing in porcine serum, notably p24, p36 and p54, which are consistent with differing stages of posttranslational processing and maturation of PDGF. Densitometry analysis confirmed antibody array results showing significant decrease in PDGF-AB and PDGF-BB expression levels in post OVX animals compared to intact female swine. Our ongoing experiments aim at isolating and verifying specific bands, and analysis of the expression levels and autophosphorylation of PDGF receptors alpha and beta in different vascular compartments.

Paula Jemes

Major: Biology
University: Tennessee State University
Faculty Mentor: Dr. John Walker
Mentor Department: Biological Sciences
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Peptidomics of *Arabidopsis thaliana*

Paula Jemes, Kevin Lease and John Walker

Peptidomics is study of all the peptides in an organism, some of which are signaling molecules. Peptides are polymers of amino acids. For the purpose of this work, peptides are defined as proteins being less than 15 kDa in size. Peptides can arise either from genes with small open reading frames or by proteolytic processing of a larger polypeptide precursor. Known peptides have many different physiological functions. We hypothesize that plants have many peptides that have not yet been discovered. To test this hypothesis, we are attempting to identify the peptidome of the plant *Arabidopsis thaliana*. Arabidopsis proteins were extracted, fractionated by size, separated by reverse phase chromatography, and analyzed by mass spectrometry. To date, we have identified several proteins using this methodology.

Jessica Jenkins

Major: Cell and Molecular Biology
University: Southwest Missouri State University
Faculty Mentor: Dr. Troy Zars
Mentor Department: Biological Sciences
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

A century later another surprise: A non-visual behavioral function of the *white* gene

Jessica Jenkins, Soeren Diegelmann and Troy Zars

Discovery of the *white* mutation in *Drosophila melanogaster* has broadly influenced our understanding of the mechanisms of inheritance. We recently discovered a role of the *white* gene in memory formation. Thus, the *white* gene continues to provide insight into basic biological functions. We use two conditioning methods to routinely measure learning and memory in *D. melanogaster*, the heat-box, and classical olfactory conditioning. In the heat box experiments, *white* mutant flies' learning performance was notably impaired. However, in olfactory conditioning studies the mutant flies performed the same or better than wild-type flies. This differentiates the molecular mechanisms that support these conditioned behaviors. To better understand the regulatory elements that control *white* expression, we have initiated a molecular characterization of the *white* genomic locus. We identified the necessary regulatory elements by defining the deletion in the w1118 null allele. Using PCR methods we found that the deletion is about 7 kb long, and includes 5' regions, exon 1, and part of the first intron. Experiments to determine the sufficient set of regulatory elements for conditioned behavior were initiated. Two results argue that existing genomic transgenes do not contain all regulatory elements. First, mutations that affect eye color have molecular lesions outside a 14 kb genomic transgene. Second, attempted behavioral rescue experiments with this transgene fail. We interpret the failure of the 14 kb transgene to rescue as a consequence of incorrect *white* expression. Thus, we are creating a genomic construct that is 18 kb long that includes genomic DNA up to the next known gene. These approaches should define the regulatory regions necessary and sufficient for behaviorally important *white* expression.

Robert Jinkerson

Major: Biological Engineering
University: University of Misssouri-Columbia
Faculty Mentor: Dr. Gabor Forgacs
Mentor Department: Physics and Astronomy
Funded by: Life Sciences Undergraduate Research Opportunity Program

The evolving technology of bio-printing

Robert Jinkerson, Karoly Jakab, Colin Weston and Gabor Forgacs

Bio-printing is a novel method of tissue engineering that uses living cell spheroids as the 'bio-ink' and biocompatible gels as the 'bio-paper' with a three dimensional printer that deposits these aggregates into the gel with great precision. The deposited aggregates fuse into three dimensional tissue structures of the desired conformation due to the liquid like nature of cells and tissues, serving as the driving force of biological self assembly. Successful results from previous experiments and theoretical modeling of the fusion process prompted the development of a standardized and automated method that increases the speed, accuracy and reproducibility of printing. To fulfill these requirements, a cell packer, an aggregate cutter and bio-printer was developed, calibrated and tested. The tools produced more uniform and spherical aggregates as compared to the manual protocols, allowing the standard size and shape necessary for rapid and precise printing. The printed structures (ring and grid-like arrangements of aggregates) fused into toroids and compact sheets, fundamental building blocks of a living organism. The precision of the printing, combined with the cell packer and aggregate cutter makes bio-printing a feasible technology. The automated process using organ specific cells could allow histologically analogous tissues to be produced and used for tissue repair and regeneration.

Omega Johnson

Major: Biology
University: Florida Agricultural and Mechanical University
Faculty Mentor: Dr. Grace Y. Sun
Mentor Department: Biochemistry
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Aβ toxicity to SHSY-5Y human neuroblastoma cells

Omega D. Johnson, Phullara B. Shelat, Agnes Simonyi and Grace Y. Sun

Alzheimer's disease (AD) is a progressive neurodegenerative disorder that results in the loss of memory, language deterioration, confusion, restlessness, and eventually destroyed cognition. It is characterized by an accumulation of beta amyloid (Aβ) plaques and tangels in the brain. Increased oxidative stress has been regarded as an early event underlying the progression of AD and there is evidence that Aβ can cause oxidative stress. In our lab, we are using SHSY-5Y human neuroblastoma cells (SH cells) as a model to look at NADPH-oxidase, an enzyme that may be involved Aβ induced toxicity to the cells. NADPH-oxidase is a multi-subunit enzyme that catalyzes molecular oxygen to form reactive oxygen species (ROS). In order for this enzyme to be activated, its cytosolic components must translocate to the membrane. One of its cytosolic components is p47-phox. We stimulate cells with oxidative agents such as menadione and H2O2 to monitor the translocation of p47-phox to the membrane. Because the production of ROS may be one of the factors leading to neuronal death, we chose to look at the activation of NADPH-oxidase. SH cells were treated with menadione (stimulator), H2O2 (stimulator) and DPI (inhibitor) for different time intervals. After treatments, the cells were harvested and treated with a lysis buffer to lyse the cells. After the cells were lysed, we put them through ultra-centrifugation and collected the membrane and cytosolic fractions. Western Blots were performed on both the membrane and the cytosolic fractions to look for the presence of p47-phox. From the Western Blot we saw that there was an increase in the p47-phox levels in the membrane fraction after exposing the cells to menadione and H2O2. Our results show that treating the cells with oxidative agents caused an increase in the p47-phox level in the membrane fraction thus leading to the activation of NADPH-oxidase.

Manu Johny

Major: Biomedical Engineering
University: Saint Louis University
Faculty Mentor: Dr. Mark A. Haidekker
Mentor Department: Biological Engineering
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Characterizing polymerization dynamics using fluorescent molecular rotors and magnetoelastic sensors

Manu Ben Johny and Mark A. Haidekker

The dynamics of polymerization are critical in many medical applications; for instance, polymers used to fill aneurysms must be timed accurately. Two distinct methods were examined for their ability to probe the polymerization kinetics of different polymers and to predict the onset of polymerization. Molecular rotors are a class of fluorophores with two de-excitation pathways: fluorescence emission and intramolecular rotation. Highly viscous solvents provide a constrained environment in which intramolecular rotation is inhibited, and radiation is the preferred pathway. It is hypothesized that during polymerization steric hindrance of the intramolecular rotation leads to increased fluorescence emission intensity. Magnetoelastic (ME) sensors have been used to measure fluid viscosity. In a time varying magnetic field, a magnetoelastic strip oscillates at its viscosity-dependent resonant frequency creating a magnetic flux that is detected. Subsequently, viscosity can be analyzed by measuring quantities such as resonance frequency, signal voltage, and Q-factor. In this study, fluorescent molecular rotors and magnetoelastic sensors were evaluated for their efficacy in monitoring the polymerization dynamics of acrylamide gels, collagen, and sol-gels. The ME sensor was effective in characterizing the polymerization dynamics of acrylamide and sol-gel, where a reduced Q-factor indicated mechanical dampening of the oscillation in the polymerized state. For unknown reasons, the ME sensor was unable to characterize the polymerization of collagen. However, the molecular rotors sensed the polymerization of collagen and sol-gel though a marked increase of emission intensity. Molecular rotors deteriorate from ammonium persulfate (APS), a strong oxidant and catalyst for cross-linking in the acrylamide system. While ME sensors are effective in characterizing several polymerization reactions, molecular rotors are more effective in monitoring the polymerization of proteins such as collagen. The results also demonstrate the possibility of using molecular rotors as novel probes capable of characterizing the polymerization dynamics of various biopolymers significant to medicine.

Jill Jouret

Major: Biological Engineering
University: University of Missouri-Columbia
Faculty Mentor: Dr. Andrew McClellan
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Imaging reticulospinal neurons in the lamprey brainstem using calcium indicator

Jill Jouret and Andrew McClellan

Imaging reticulospinal neurons in the lamprey brainstem using calcium indicator In the lamprey, a lower vertebrate, reticulospinal (RS) neurons in the brain are the output elements of the command system that activate spinal pattern generators and initiate swimming. In order to better understand the locomotor command system in the lamprey, it is necessary to determine the locations of neurons in the network, as well as their connectivity and patterns of activity. Calcium indicator dyes are an important technique for labeling and monitoring neuron activity. During impulse, calcium enters neurons and binds to the dye, increasing the fluorescence of the dye and creating an optical image that can be recorded and analyzed. In the present study, Calcium Green dextran amine was applied to the transected spinal cord at 20% body length (BL). After retrograde transport of the dye and labeling of RS neurons, the brain and spinal cord were removed and placed on a slide for viewing under a microscope equipped for fluorescence. Electrical stimulation of the spinal cord activated labeled RS neurons in the brain, resulting in a fluorescence increase that was recorded by an S-VHS video camera. The next step will be to image RS neuron activity during actual swimming movements. For this purpose, RS neurons will be labeled in a semi-intact preparation in which the brain and upper spinal cord are exposed and the lower half of the body is free to produce swimming movements. As a control experiment, the spinal cord was transected and Calcium Green applied at 60% BL. Semi-intact preparations were observed to produce swimming movements. Imaging of the isolated brain and rostral spinal cord showed RS neuron labeling and fluorescent changes similar to when tracer was applied at 20% BL. These results lay the groundwork for imaging brain neuron activity during actual swimming behavior.

Marcus Judy

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. John Faaborg
Mentor Department: Biological Sciences
Funded by: Missouri Ozark Forest Ecosystem Project

The effect of timber stand improvement practices on the abundance of Pileated Woodpeckers

Marcus Judy, Paul Porneluzi and John Faaborg

The Pileated Woodpecker (Drycopulus pileatus) is a large woodpecker that requires large dead trees within a mature forest. I investigated how forest management practices affect the Pileated Woodpecker. Timber stand improvement (TSI) is the practice of girdling live trees to allow adjacent trees more space and light in which to grow. Areas treated with TSI have more dead snags which may be used by pileated woodpeckers. I surveyed total snag abundance and woodpecker density in these TSI areas compared to unmanaged (control) areas to determine the effect of TSI on Pileated Woodpeckers.

Motunrayo Kemiki

Major: Chemical Engineering
University: Pennsylvania State University
Faculty Mentor: Dr. Rusty Sutterlin
Mentor Department: Chemical Engineering
Funded by: NSF Program Alliance for Collaborative Research in Alternative Fuel Technology and Louis Stokes Missouri Alliance for Minority Participation

Conversion of waste corn cobs to activated carbons for natural gas (methane) adsorption

Motunrayo Kemiki, Peter Pfeifer, Rusty Sutterlin, Galen Suppes and Parag Shah

Adsorbed Natural Gas (ANG) is an alternative energy source technology that uses micropores in adsorbent materials to store natural gas. Activated carbons, which are useful adsorbents with a highly porous form of carbon are promising adsorbent materials that can be used to store methane. In this study, dried crushed corn cobs were used to produce activated carbons, using a chemical activation method. A set of experiments was performed under various conditions to determine the optimum conditions for preparing the activated carbons. The activation process varies depending on the concentration of the activating agent (phosphoric acid), the impregnation temperature, the carbonization temperature, and the heating rate. The resultant activated carbon is further immobilized into monolithic form, to increase the density. The micro porosity of the activated carbons produced from corn cobs can have a methane uptake capacity of 150v/v or greater, and a BET surface area of 800m2/g–1600m2/g.

Matt Keuss

Major: Chemical Engineering
University: University of Missouri-Columbia
Faculty Mentor: Dr. Kent S. Gates
Mentor Department: Chemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Developing proteomics approaches for identifying new, redox-regulated proteins

Matthew Keuss and Kent S. Gates

For many years it was thought that hydrogen peroxide was only a toxic substance to cells. However, recent work has revealed that hydrogen peroxide can be utilized by organisms as a cellular signaling molecule. Hydrogen peroxide has the ability to react with proteins involved in signal transduction causing the activity of these proteins to be turned on or off. One such example is protein tyrosine phosphatase 1B (PTP1B) whose enzymatic activity is turned off by reacting with hydrogen peroxide. A cysteine residue in the active site of PTP1B is oxidized by hydrogen peroxide to form a sulfenic acid which then reacts with a neighboring amide nitrogen in the protein backbone to form a cyclic sulfenamide. The formation of this heterocycle causes PTP1B to lose its activity. In order to discover new proteins that are oxidatively regulated by hydrogen peroxide, chemical tools for selective detection of cyclic sulfenamide residues in cellular probing need to be developed. We describe results obtained using simple chemical models to identify reagents that have the ability to selectively tag protein derived sulfenamide residues.

Eric Ladd

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Dennis Lubahn
Mentor Department: Biochemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Studying DNA methylation changes of CpG islands in different stages of prostate cancer by pyrosequencing

Eric R. Ladd, Yi Zhuang, Amos Burks, Anna Slusarz and Dennis B. Lubahn

Prostate cancer is one of the most common forms of cancer in men. Our lab is currently investigating changes in DNA methylation that occur during cancer progression, and in response to the soy phytoestrogen genistein treatment. We analyze genome-wide methylation differences by using the mouse DMH (mouse-Differential Methylation Hybridization) assay, a form of microarray. We are specifically looking at broad sets of CpG islands, areas rich in cytosine-guanine dinucleotides, that are subject to epigenetic modifications. The hypermethylation of CpG islands is correlated with the silencing of a gene while hypomethylation is correlated with a gene being actively transcribed. We were looking for potential new oncogenes or tumor suppressors. To study these genes we have a mouse model called TRAMP (TRansgenic Adenocarcinoma of the Mouse Prostate), which is a good model to study the progression of prostate cancer and metastasis because it is similar to human prostate cancer. We are using double transgenic mice that are WT or KO for the transcription factor estrogen receptor alpha, on a TRAMP background. The removal of ERα has been correlated with DNA methylation changes. These methylation changes showed up in our microarray screen that led us to find a set of genes that were differentially methylated across cancer progression. We selected one gene: Kinesin superfamily protein 9 (K3_E17) which has been shown on our microarrays to be methylated in well differentiated carcinoma and unmethylated in hyperplasia and poorly differentiated carcinoma. To confirm the methylation status we performed pyrosequencing, a new method to specifically study short sequences of DNA for methylation at specific CG sites. Our hypothesis is that in well differentiated carcinoma Kinesin 9 is hypermethylated, which will correlate with this gene being turned off. This would mean that Kinesin 9 might be acting as a tumor suppressor.

Regina Lehman

Major: Animal Science
University: Pennsylvania State University
Faculty Mentor: Dr. David Ledoux
Mentor Department: Animal Sciences
Funded by: F.B. Miller Undergraduate Research Program in Animal Sciences

Efficacy of high levels of microbial phytase in improving phytate Phosphorus utilization by turkeys

Regina Lehman and David Ledoux

A 14-day study was conducted with 750 female turkey poults to determine the efficacy of high levels of phytase in improving turkey performance and percent and milligram toe ash. Six dietary treatments were assigned to five replicate pens of 25 poults each. A National Research Council (NRC) corn-soybean meal diet, adequate in all nutrients, was fed to all birds for the first week. Dietary treatments fed from 8 to 21 days of age included: 1) a positive control NRC diet (0.6% non-phytate phosphorus [npP] and 1.2% Ca); 2) a low P negative control basal diet (B) (0.36% npP and 1.01% Ca); 3) B + 250 U/kg phytase; 4) B + 500 U/kg phytase; 5) B + 10,000 U/kg phytase; and 6) B + 20,000 U/kg phytase. Feed intake and body weight gain were significantly higher ($P < .05$) in birds fed high phytase diets (diets 5 and 6) compared with those fed the NRC, basal, or low phytase diets (diets 1, 2, 3 and 4). Feed conversion was also found to be lowest (most efficient; $P < .05$) for the birds fed high phytase diets compared to the birds fed the other diets. Percent toe ash for the three highest phytase diets (4, 5 and 6) was similar ($P > .05$) to the NRC positive control diet but significantly higher ($P < .05$) than the negative control birds (diet 2). Milligrams of toe ash was also significantly higher ($P < .05$) for the birds fed the highest two levels of phytase compared to the birds fed the other diets. Feeding high levels of phytase (≥10,000 U/kg) to turkeys was effective in increasing phytate phosphorus utilization and in improving growth performance above the birds fed the NRC control diet.

Lauren Lewis

Major: Biology
University: Furman University
Faculty Mentor: Dr. Mark Milanick
Mentor Department: Medical Pharmacology and Physiology
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Development of an assay to measure cortisol using a standard glucose meter

Lauren Lewis and Mark A. Milanick

When an animal is stressed many changes occur, such as altered behavior and reduced resistance to disease, and these effect population performance (Millspaugh 2004). Cortisol is a stress hormone produced by the adrenal glands to regulate cardiovascular function, and energy utilization. Clinicians and wildlife biologists monitor cortisol levels in animals to determine their stress levels . Current tests must be done in a research lab; I want to develop a test that can be used at home or in the field. Four methods were compared: a glucose meter, FOX (ferric-xylenol orange complex) assay, o-dianisidine assay, and a lanthanide-based luminescent sensing probe, all of which detect H2O2, which is produced by glucose oxidase. The glucose oxidase will be used as a label for cortisol in an immunoassay. I assessed the sensitivity of the four methods. O-dianisidine assay detected 2.5 µM H2O2, lanthanide detected 5 µM H2O2, FOX detected 25µM H2O2, the glucose meter detected 500µM H2O2. I have found that the OneTouch Sure Step® glucose meter detects H2O2 in the absence of glucose. The optimal method for field/home testing has to have great sensitivity and also be easy to quantitate. Even though the meter had the lowest sensitivity, it is the most convenient and inepensive approach for quantitation. We are using modeling and other approaches to develop the best method(s) for cortisol measurement that will not only aid conservation biology, but it can also be used to monitor patient hormonal levels for treatment of endocrine disorders including Cushing's syndrome.

Giovanni Lleonart

Major: Mechanical & Aerospace Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. Sudarshan Loyalka
Mentor Department: Nuclear Science & Engineering Institute
Funded by: Louis Stokes Missouri Alliance for Minority Participation

University of Missouri-Columbia Research Reactor (MURR) flux trap design using Fluent Computational Fluid Dynamics (CFD)

Giovanni Lleonart and Sudarshan Loyalka

The University of Missouri-Columbia Research Reactor Center (MURR) is the center of a world class, totally unique environment for the research, development, and production in major advances in nuclear medicine. The reactor operates at a ten megawatt power level. Samples are placed in three strategically positioned canisters situated in the flux trap zone of the nuclear reactor core. Heat is removed from the core by water flowing through it, as well as through the flux trap. The trap consists of three vertical cylinders 4 meters long which are encased inside one bigger cylinder, inside every cylinder there is one canister, where the samples are placed. Pool water at a high mass flow rate is pumped inside and around the cylinders to partially cool the reactor core (the main portion of the flow is directly through the core). The purpose of the research is to model the MURR using Fluent Computational Fluid Dynamics (CFD) software, to visually project the pool water flow and heat transfer in the flux trap to enable possible improved positioning of the irradiation samples. In other words, our focus is on being able to create a model of MURR, and understand the effects of geometry in the flux trap for the pool water flow to the fullest extent possible. In conclusion, the geometry of the MURR flux trap has been successfully modeled using GAMBIT, in addition water velocity, temperature, pressure and turbulence have also been successfully computed using FLUENT. The results show regions of high turbulence, strain and velocity in the flux trap. For Future work it will be useful to obtain functional data so these computer results can be verified, also the model that we have constructed should be improved to include all details of the reactor, and finally, the model should be further used to optimize the flow geometry and canister placement of the reactor.

Jonathan Lowe

Major: Mass Communications
University: Alcorn State University
Faculty Mentor: Dr. Cynthia Frisby
Mentor Department: Advertising
Funded by: Summer Pre-Graduate Research Experience for Students in the Humanities

Death by the pounds: The effects of television on the obesity of African-American children and adolescents

Jonathan Lowe and Cynthia Frisby

This study examined the direct effects that television programming has on the obesity of African-American children and adolescents based upon the top three stations viewed by African-American children and adolescents during prime time viewing hours. A self-concept theory was implemented to determine whether or not the content of television programs helped develop a child or teenagers concept of obesity. While it has not been possible to provide definite answers to our research questions, we project that the results will be that majority of children and adolescents who view a significantly amount of television a day will indeed have a distorted view of the realities of obesity and its causes. Future studies will explore the same self-concept theory of the African-American children and teenagers on obesity using advertisements as the medium. Also I will explore the usage and depiction of African-American endorsers in health food ads in popular African-American periodicals.

Abraham Lueth

Major: Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Shuqun Zhang
Mentor Department: Biochemistry
Funded by: MU Monsanto Undergraduate Research Fellowship

Functional analysis of conserved amino acid residues in the C-terminus of ACC synthase

Abraham Lueth, Njabulo Ngwenyama, Yidong Liu and Shuqun Zhang

Ethylene is an important plant hormone that regulates growth, development, and stress response. Synthesis of Ethylene from its immediate precursor, 1-aminocyclopropane-1-carboxylic acid (ACC), is catalyzed by ACC oxidase. ACC is produced from S-Adenosy1-L-Methionine (SAM) in a reaction catalyzed by ACC synthase (ACS). ACS is the rate limiting enzyme of ethylene biosynthesis. Selected isoforms of ACS are substrates of MPK6 and MPK3, the two Arabidopsis stress-responsive mitogen-activated protein kinases (MAPKs). Phosphorylation of ACS6 by MPK6 stabilizes the ACS protein, thus, elevating the levels of cellular ACS activity and ethylene production. Expression of ACS6DDD, a gain-of-function ACS6 mutant that mimics the phosphorylated form of ACS6, shows constitutive ethylene production and ethylene-induced phenotypes. Analysis of Arabidopsis ACS6 and its orthologs from other species in the database revealed conserved charged amino acids (AAs) in addition to the MAPK phosphorylation sites in their C-termini. We hypothesized that these conserved residues may be involved in the regulation of ACS stability. We used site-directed mutagenesis to mutate the conserved residues to Ala, Ile, or Leu in the ACS6WT or ACS6DDD background using the polymerase chain reaction (PCR). Mutation was confirmed by DNA sequencing. ACS6 mutant gene was transformed into Arabidopsis plants. The stability of ACS6 protein was tested in vivo to determine if the mutation enhances or diminishes its stability. Ethylene production was used as an output reading and the levels of ACS6 protein were determined by immunoblot analysis. Mutation of positively charged AAs makes the ACS6 protein more stable, whereas the mutation of the negatively charged AAs which are close to the phosphorylation sites destabilizes it. Interestingly, deletion of the C-terminus stabilizes the ACS6 protein, suggesting that C-terminus is required for ACS6 degradation. We observed ethylene-regulated morphologies like short hairy main roots and epinastic leaves in ethylene-overproducing seedlings.

Rachel Mahan

Major: English and Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Raymond D. Semlitsch
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Effects of forest management practices on treefrog oviposition site choice

Rachel D. Mahan, Betsie B. Rothermel, Daniel J. Hocking, J. Whitfield Gibbons and Raymond D. Semlitsch

Globally, amphibian populations are declining faster than those of birds or mammals. Habitat destruction is considered the primary cause of these declines; however, what remains partly unexplored is the idea that some species may be more greatly affected than others by deforestation. Treefrogs (Family: Hylidae), because of their mobility, may be expected to circumvent disturbed habitats; however, because of their dependency on arboreal habitat, they may be adversely affected by different forms of forest management. As part of the LEAP (Land-Use Effects on Amphibian Populations) study, four forest management practices—clearcut with coarse woody debris (CWD) removed, clearcut with CWD retained, thinning of 25% basal area, and uncut forest—were implemented at four wetlands at the Savannah River Site. In May 2005, we placed wading pools 25 m into each treatment and allowed them to fill with rainwater. To monitor time to first oviposition event and to determine the number of events per treatment, pools were checked daily, eggs were counted, and tadpoles were raised to confirm that all eggs were indeed those of hylids. We measured water depth, canopy cover, and surrounding vegetation. These data will be analyzed to determine if suitable calling/breeding habitat (microhabitat) is a more reliable predictor of oviposition than treatment (macrohabitat). At three of the four wetlands, first oviposition events occurred in the thinning treatments, and second events occurred in the clearcuts with CWD retained. We found that more oviposition events also occurred in the thinning treatments (43%) and the clearcuts with CWD retained (33%) than in the clearcuts with CWD removed (13%) or the uncut forest controls (10%). One explanation for these findings is that hylids have evolved to locate openings in the forest canopy which could indicate a wetland or a fallen tree whose uprooting has caused an ephemeral pool to form.

Elizabeth Maricle

Major: Animal Science
University: University of Nebraska-Lincoln
Faculty Mentor: Dr. William Lamberson
Mentor Department: Animal Sciences
Funded by: F.B. Miller Undergraduate Research Program in Animal Sciences

Effect of feed restriction and hypothermia on fetal mice

Elizabeth Maricle and William Lamberson

Low birth weights result in high mortality in highly prolific pigs. Anecdotal evidence in sheep and cattle suggests restricting feed early in gestation and/or cooling late in gestation increase birth weights. Therefore, the objective of this study was to determine the effect of early gestation feed restriction in combination with late gestational chilling on term decidual and fetal weights, and prenatal survival in mice. The study used 37 ICR male mice each mated with 4 females except for one male with 5 females. Once a female had a vaginal plug, she was removed from the male and placed into her own cage. Pregnant females were allocated to four groups: full feed-normal temperature, full feed-chilled temperature, restricted feed-normal temperature, and restricted feed-chilled temperature (n = 18, 19, 23 and 16, respectively). The restricted feed females were fed 80% of their previous five day's average intake from day 5 to 10 of gestation while full feed females were fed ad libitum. All females were fed ad libitum from day 10 to 18. On day 14 the chilled temperature females were moved to an 18 °C environmental chamber while the normal temperature females were housed at 22 °C. On day 18 the females were sacrificed and the fetal weight, respective fetus's decidual weight, and number of corpora lutea and implantations were recorded. During restriction, intake of restricted mice was 68% of full feed mice. Immediately after restriction, there was a compensatory increase in intake by restricted mice, but overall, restricted mice consumed 93.8% that of full feed mice. There were no significant differences in survival rates among the four groups. There was also no significant difference between chilled temperature and normal temperature for decidual or fetal weights. However, full feed mice had greater ($P<0.05$) birth weights than restricted feed mice (1.36 vs. 1.31 g). In conclusion, restricting feed and chilling during gestation did not increase birth weights in mice.

Amber McCadney

Major: Psychology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Debora Bell
Mentor Department: Psychological Sciences
Funded by: Louis Stokes Missouri Alliance for Minority Participation

The relation of childhood depressive symptoms to behavior during a speech task

Amber McCadney and Debora Bell

This study examined the relation of child depressive symptoms to their observed behaviors during a speech performance task. Previous work (Mavers & Bell, 2005) has demonstrated that children's anxiety was related to several observed difficulties during a speech task, including rate of speech that was too fast or too slow to be easily understood, short utterance lengths, substantial pauses in responding, soft voice volume, unclear speech content, and low eye contact. Because children's anxiety and depression share many behavioral features, the present study extended this work by examining whether similar relations would be evident for child depressive symptoms. A sample of 79 third to sixth grade children completed self-report measures of anxiety and depression, and then completed a 5-minute speech task, which was videotaped and coded for several verbal and motor behaviors. Parents and teachers also reported on children's anxiety and depressive symptoms. Results indicated that child and parent reports of child depression were related to difficulties in two verbal behavior categories: children with more depressive symptoms demonstrated more awkward rates of speech and less clear speech content than children with fewer depressive symptoms. In contrast, for teacher reports, observed behaviors tended to be related to the absence of externalizing symptoms rather than the presence of internalizing (e.g., depression) symptoms. Implications of our findings and future directions are discussed.

Jon McRoberts

Major: Fisheries & Wildlife
University: University of Missouri-Columbia
Faculty Mentor: Dr. Josh Millspaugh
Mentor Department: Fisheries & Wildlife
Funded by: Life Sciences Undergraduate Research Opportunity Program

Resource selection of black-footed ferrets based on black-tailed prairie dog distributions

Jon McRoberts and Josh Millspaugh

This study investigates how black-footed ferrets (*Mustela nigripes*) select their habitat in relation to the distribution of black-tailed prairie dogs (*Cynomys ludovicianus*). Ferrets are one of the rarest and most endangered mammals in North America. An intensive captive breeding program has allowed for reintroduction of ferrets on the Charles M. Russell National Wildlife Refuge in Central Montana, the study site of this project. However, despite over two hundred individual ferrets released in the last ten years, a self-sustaining population has not been established. Because 90% of a ferret's diet consists of prairie dogs and prairie dog burrows provide exclusive shelter sites for ferrets, understanding how ferrets select their habitat within a prairie dog colony could have important management implications. I hypothesize that ferrets will select patches of high prairie dog density. The first component of data collection involved GPS (Global Positioning System) mapping of 26,000 prairie dog burrows within the prairie dog colony. Ferrets were located within the prairie dog colony by spotlighting for their reflective eye shine at night. Once located, a PIT (passive integrated transponder) reading identified each individual ferret, and GPS coordinates were recorded. In the 10 week spotlighting period 60 GPS ferret observations were recorded. A Kernel analysis was done to determine the level of habitat utilization by ferrets within the prairie dog colony. This information was overlaid on the prairie dog colony map that identified patches of different burrow densities using GIS (Geographic Information System) software. A Chi-squared test was then performed to analyze the relationship between prairie dog distribution and ferret habitat selection. The results of this study can hopefully help wildlife managers better manage ferrets and possibly adjust or modify their ferret management plan based on prairie dog colony structure.

Julie Meyer

Major: Agriculture
University: Truman State University
Faculty Mentor: Dr. James Birchler
Mentor Department: Biological Sciences
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Retension of knobs in chromosome tips in maize

Julie Meyer, Jonathan Lamb and James A. Birchler

Knobs are deeply staining chromosomal sites on maize chromosomes. Molecularly, they are composed of a 180 base pair repeat. Their positions on the chromosomes are variable but usually internal in maize. In relatives, the knobs are usually found on the tips of chromosomes. They have been observed for a long time, yet their function remains a mystery. Knobless maize lines do not appear to have knobs. I used fluorescence in situ hybridization (FISH) to test whether cryptic knob sequences exist at the chromosome tips in maize but have avoided normal detection. Long exposure time detects weak signals near the ends of most chromosomes and some cryptic internal sites. Knobless lines are ideal because they do not have the large knobs which can make such detection difficult, if not impossible. I found the Knobless Tama Flint and Knobless Wilbur Flint lines to have cryptic knobs on most chromosomes. *Zea diploperennis* exhibited knobs on every chromosome, usually at the tips. Thus, although knobs as usually detected in maize are internal, maize has cryptic knob sequences at the ends of most chromosomes in a similar situation as its relatives suggesting a conserved function at chromosome termini.

Amanda Meyer

Major: Chemistry
University: University of Missouri-Rolla
Faculty Mentor: Dr. Susan Z. Lever
Mentor Department: Chemistry
Funded by: Molecular Imaging Program

The synthesis of peptide-PNA conjugates

Amanda E. Meyer, Fabio Gallazzi, Michael R. Lewis and Susan Z. Lever

In two long term studies of non-Hodgkin's Lymphoma (NHL), the only clinical feature associated with a high relapse rate and treatment resistance is the presence of the *B-cell lymphoma/leukemia-2(bcl-2)* proto-oncogene in an over-active state. Regulation of this gene has shown promise as a means for better treatment in patients with relapsed NHL. At MU, in the past, many antisense and nonsense peptide-peptide nucleic acid (PNA) conjugates that target the *bcl-2* proto-oncogene were synthesized and radiolabeled for mRNA binding evaluations.

This summer, we synthesized two new peptide-peptide nucleic acid conjugates. The first of these was a nonsense sequence of PNA monomers attached to the peptide Tyrosine-3-Octreotate (1), and the second was the anti-*bcl-2* sequence attached to Alanine-box Octreotate (2). The PNA sequences attached to the peptides correspond to the first fourteen bases of the *bcl-2* proto-oncogene (ccagcgtgcgccat) in the case of the anti-*bcl-2* compound (2) and correspond to no matching sequence in the human genome in the case of the nonsense sequence (1). They are both for later use as a negative control in mRNA binding evaluations (the previously synthesized positive agent being anti-*bcl-2* attached to Tyrosine-3-Octreotate). The peptides were synthesized using standard Fmoc solid phase peptide synthesis on a resin using a very low substitution level. The peptides were synthesized in an automatic peptide synthesizer, and then elongated with the addition of the PNA monomers manually in a reaction vessel. Each peptide-PNA construct was then coupled to DOTA (1, 4, 7, 10-tetraazacyclododecane-*N, N', N'', N'''*-tetraacetic acid), a ligand to provide a site for subsequent radiometal chelation. The correct molecular weight with a high purity was observed in the LC-MS results for the peptide-PNA compound 1 after two attempts, and compound 2 was successful after the first attempt. The amount of each construct synthesized should be enough for the later mRNA binding study.

Matthew Meyer

Major: Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Georgia Davis
Mentor Department: Plant Sciences
Funded by: MU Monsanto Undergraduate Research Fellowship

Identifying Lepidopteran resistance within *hcf* mutants

M. Meyer, D. Davis, T. Musket and G. Davis

Southwestern corn borer (SWCB) and fall armyworm (FAW) feeding on maize causes extensive crop damage in the United States. Previous proteomic analysis comparing resistant and susceptible lines of maize indicates genes found in the photosystem II pathway are highly expressed in the resistant line. The *high chlorophyll fluorescence (hcf)* mutants have defects in photosystem I or photosystem II genes. A preference test was performed comparing *hcf* mutants to their wild-type siblings. *Oy, pg,* and *g* mutants were also compared to their wild-type siblings to ensure that color was not a factor in feeding differences. SWCB preferred the wild-type over *hcf11-N1205A* and *hcf49-N1480* mutants, indicating these genes may be resistance factors. *Oy1-Andrew* and *hcf13-N1097B* mutants were preferred by SWCB compared to their wild-type siblings, indicating these genes increase susceptibility to feeding damage. *hcf49-N1480, hcf7-N1029D*, and *pg15-N340B* had reduced FAW damage compared to wild-type siblings, indicating they may increase resistance to feeding damage. *hcf44-N1278B* showed increased susceptibility to FAW feeding compared to its wild-type sibling. An antibiosis test was performed using *hcf* mutants. Photographs and larval weights were taken at the end of the four days. Tissue damage areas were analyzed using AlphaEaseFC software. From the data, *hcf7-N1029D* and *hcf50-N1481* had reduced larval weights for both FAW and SWCB indicating these genes have antibiotic properties and can reduce larval feeding damage. The mutants evaluated for effects of pigmentation displayed varying results indicating color differences associated with some *hcf* mutants are unlikely to be responsible for the differences in feeding behavior observed. These genes identified here may be useful in increasing resistance to FAW and SWCB in commercial hybrids.

Kelly Moncheski

Major: History and Political Science
University: University of Missouri-Columbia
Faculty Mentor: Dr. Ted Koditschek
Mentor Department: History
Funded by: MU Undergraduate Research Scholars

How the revolutionary thought of two West Indian intellectuals predicts and explains post-independence African problems

Kelly Moncheski and Ted Koditschek

Though most of Africa gained independence from European colonial rule by 1960, today the continent is still plagued by poverty, ignorance, corruption, internal conflict, and external control. These results are now clear to everyone but there were a few black individuals even at the time of decolonization who foresaw the situation that would result if decolonization were not carried out carefully and properly. My paper focuses on two West Indian intellectuals, C.L.R. James and Frantz Fanon. C.L.R James' book *Black Jacobins*, though written during the 1930s, addresses the colonial problem and calls for revolution in the form of a mass-organized revolt and an awareness of each nation's identity as distinct from that of the colonial aggressor. I will explain the way in which James recognizes the physical and cultural oppression of the peoples of underdeveloped countries, the dual-world of those well-educated by the mother country, and the problems resulting from the probable inability or aversion of black political and intellectual leaders to recognize the necessity of a complete break from the colonial ruler and the oppressive imperialist capitalism it represents. Frantz Fanon, in *Black Skins, White Masks* and *The Wretched of the Earth*, approaches the problem of decolonization as a psychiatrist. He understands the psychological oppression of third-world peoples as a diametrically opposed slave-master relationship found between settlers and natives and within the native himself. Fanon prescribes a violent revolution as the only action that will provoke a response of change in the colonial country and the only way to rid the native of his inferiority complex; only after a violent revolution will the native be free to reclaim his history and culture and begin a new society in which each man is respected for who he is.

Courtney Morriss

Major: Biotechnology
University: Brigham Young University
Faculty Mentor: Dr. Georgia Davis
Mentor Department: Plant Sciences
Funded by: Plant Genomics Internship @ MU

Quantitative trait loci for seminal root angle and number in the maize IBM population

Courtney Morriss, Doug Davis, Michael Gerau and Georgia Davis

In maize, seminal roots develop and the primary root system deteriorates as the plant matures. The seminal roots comprise the majority of the root system of the adult plant and give the plant stability against lodging. Because seminal roots are the primary means of water uptake in the adult plant, their development under drought conditions is vital. Previous research has suggested that seminal root angle and abscisic acid (ABA) level are correlated in maize. Additional research has shown that ABA levels are related to drought tolerance. This study focuses on identifying quantitative trait loci (QTL) that affect seminal root angle and the number of seminal roots entering the soil from each node. The QTL generated for seminal root angle and number per node can then be used to evaluate the relationship with drought tolerance. A set of 94 mapping lines from the intermated B73 x Mo17 (IBM) mapping population was used to measure the angle between the seminal root and the stalk. The number of seminal roots entering the soil from the first two nodes was measured as well. Molecular markers evenly distributed throughout the genome were used to run the QTL analysis using QTL Cartographer Version 1.16. The following QTL analyses were run: seminal root angle, number of roots entering soil from the first node above ground, and number of roots entering soil from the second node. Three QTL were found for seminal root angle, two QTL for the number of roots at the first node above ground, and three QTL for the number of roots at the second node above ground. These QTL positions were then compared to previously known QTL for drought tolerance and root traits.

Njabulo Ngwenyama

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Shuqun Zhang
Mentor Department: Biochemistry
Funded by: MU Monsanto Undergraduate Research Fellowship

Functional analysis of MAP kinases in Arabidopsis thaliana: Fully rescuing the mpk3/mpk6 mutant phenotypes

Njabulo Ngwenyama, Huachun Wang, Yidong Liu, John Walker and Shuqun Zhang

Mitogen Activated Protein Kinase (MAPK) cascades are three-stage modules involved in signal transduction. MAPKs function at the lower tier of these cascades and they phosphorylate transcription factors and other protein kinases upon activation, ultimately leading to cellular responses. Twenty genes coding for MAPKs were identified in the fully sequenced Arabidopsis genome. MPK3 and MPK6 are the most closely related. Analysis of T-DNA insertional lines revealed no phenotype in the mpk3 and mpk6 single mutants; however, female sterility is observed in MPK3+/-/MPK6-/- plants and embryo lethality results from knocking out both genes. This indicates overlapping function of MPK3 and MPK6. To better understand the function of these two kinases, an attempt was made to rescue these phenotypes by introducing a Dexamethasone (DEX) inducible: MPK6 transgene. This construct led to only partial rescue of the lethal double mutants, and no signs of fertility were evident in MPK3+/-/MPK6-/- plants. In an attempt to attain complete rescue of these phenotypes, new MPK3 and MPK6 constructs were engineered with the following features: • Transgenes regulated by endogenous promoters were used in order to maintain normal cell/tissue specific expression of the protein, which may be essential for normal plant function. • The transgene products were tagged with Yellow Florescent Protein and Green Florescent Protein in order to ascertain their expression patterns. • Genomic DNA, as opposed to complementary DNA, was used as the coding regions in order to ensure the presence of introns, which may be significant for gene function. Currently, T1 generation transgenic plants have been isolated and transgenic lines with good expression of the transgene proteins, in vivo, will be identified by Western Blot analysis. Indication of a full rescue will be verified in the T2 generation. Failure to observe completely rescued lines may indicate protein tag interference, and untagged constructs will then be attempted.

Zachary Nichols

Major: Math and Biology
University: University of South Carolina
Faculty Mentor: Dr. Dong Xu
Mentor Department: Computer Science
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Protein secondary structure prediction: Creating a meta-tool

Zachary Nichols, Rajkumar Bondugula and Dong Xu

Protein structure prediction is a growing field of interest for a many varied reasons, owing not only to its obvious utility, but also the success that applying newer mathematical tools has garnered in recent years. Despite the intractability of determining optimal protein structure directly by finding a lowest-energy conformation among a huge amount of candidates, many heuristic methods have emerged that sacrifice some degree of accuracy for reasonable speed of execution. Through the use of numerical techniques such as neural networks(1), neural networks bolstered by position-specific scoring matrices generated by psi-blast(2), and k-nearest neighbor algorithms(3), the success rate of protein structure prediction has been increasing over the past decade and a half. Each of these tools has particular strengths and weaknesses. To address this and to improve prediction accuracy, we are constructing a three-part meta-tool that combines k-nearest neighbor methods, neural network methods, and hidden markov models to predict the secondary structure of proteins based on their position-specific scoring matrices. The results from each of the individual tools will be integrated and filtered to form a final prediction. This tool will be available on the web through a simple interface for those wishing to evaluate or utilize it. References: 1: Rost and Sander. Predictions of protein secondary structure at better than 70% Accuracy; J. Mol. Biol. (1993) 232, 584-599 2: Jones. Protein secondary structure prediction based on position-specific scoring matrices; J. Mol. Boil. (1999) 292, 195-202 3: Bondugula, Duzlevski, Xu. Profiles and fuzzy k-nearest neighbor algorithm for protein secondary structure prediction; (unpublished).

Carolynn O'Dell

Major: Biology
University: The College of Saint Elizabeth
Faculty Mentor: Dr. Brenda Peculis
Mentor Department: Biochemistry
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Binding properties of X29 protein and RNA

Carrie O'Dell and Brenda Peculis

The Peculis Lab previously demonstrated that X29 protein binds U8 snoRNA with high affinity and specificity in Xenopus Laevis [1]. U8 snoRNA is a C/D box RNP required for pre-rRNA maturation of 5.8s and 28s rRNA in the nucleolus. X29 is a Nudix hydrolase that decaps the U8 RNA at the m^7G and $m^{227}G$ caps [2]. Together these two components may interact in vivo to regulate the rate of ribosome biogenesis and thus, the rates of cell growth and cell division. My work has focused on characterizing the interaction between these two molecules and I have been working on two interrelated projects. The first project involves generating mutations to alter one amino acid in the protein sequence. Based on crystal structure data, the amino acid tryptophan, at position F49, lies in the putative RNA binding site on the X29 protein. The mutation will substitute a tryptophan for the 'wild type' phenylalanine residue at this position. After the mutagenesis, the protein is expressed in bacteria in BL21 cells and the mutated protein is purified. We predict the protein would contain a fluorescence property such that when analyzed by flourimitry we will be able to determine RNA binding and possibly address stoichiometry and dimer formation. The second project involves cross-linking wild type X29 protein to U8 RNA and mapping the cross-link on the RNA. Cross-linking reactions followed by reverse transcription using 5' end-labeled oligo DNA primers will identify 'stops' which are UV- and protein-dependent. We will be able to map the precise nucleotide on the RNA and interpret this in the framework of the proposed secondary structure for U8 snoRNA. The results of these experiments will greatly aid the research of the X29 protein and its binding capabilities to RNA.

References

1. Tomasevic, N. And B. Peculis, Identification of a U8 snoRNA-specific binding protein. J Biol Chem, 1999. 274: p. 35914-20. 2. Ghosh, T., et al., Xenopus U8 snoRNA binding protein is a conserved nuclear decapping enzyme. Mol Cell, 2004. 13: p. 817- 828.

Joselyn M. Ocasio Escobales

Major: Chemical Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. William Miller
Mentor Department: Nuclear Science & Engineering Institute

Funded by: NSF-REU/NIH Program in Radiochemistry

Environmental report actualization for the license renewal of the University of Missouri Research Reactor Center

Joselyn M. Ocasio Escobales, Jeancarlo Torres Llenza and William Miller

Licensing requirements for power as well as non-power reactors must address environmental concerns related to radioactive emissions. The purpose and need for the renewal of the operating license for the Missouri University Research Reactor (MURR) is to allow continued studies in nuclear related undergraduate and graduate level degree programs along with continued production of radioactive isotopes for cancer treatment and research for an additional 20 years beyond the current license of 40 years which expires on November 21, 2006. The MURR is a multi-disciplinary research and education facility that provides a wide range of analytical, radiographic, and irradiation services to the research community and the commercial sector. The licensing requirements are established by the U.S. Nuclear Regulatory Commission in 10 CFR § 51.45 Environmental Reports - General Requirements. As part of the license renewal process the environmental report which was created on 2001 needed to be updated and revised to assure of the quality of the information. To study the hypothetical dose received by the public from the radioactive emissions that are released by the MURR during normal operations, the Environmental Protection Agency (EPA) COMPLY program was utilized. This program is intended for use by NRC licensees and non-DOE federal facilities to determine if they meet the radiation dose standards imposed by EPA under the Clean Air Act. COMPLY was utilized using an average of the last 10 years of the stack effluent which was measured in Curies per year. The results obtained from the program indicated that the MURR is in compliance for the emission released to the atmosphere.

Vanessa Palmer

Major: General Studies
University: University of Missouri-Columbia
Faculty Mentors: Dr. Carol Grove and Dr. Benyamin Schwarz
Mentor Department: Art History; Architectural Studies
Funded by: MU Undergraduate Research Scholars Program

Landscape design for Bear Creek Prairie in Columbia, Missouri

Vanessa L. Palmer, Carol Grove and Benyamin Schwarz

Bear Creek Prairie is a proposed conservation development in Columbia, Missouri whose vision statement is “to develop a residential community that is environmentally responsible, pedestrian friendly, encourages community interaction and is a model for sustainable land use development”. The well-accepted definition of sustainability is meeting the needs of the present without compromising the ability of the future generations to meet their own. The fact that there are countless contributions people can make towards sustainability is very exciting to me and finding my place within the movement landed in design. I have been researching how to design the common area in Phase One of the development plan. There are an infinite number of contributions that can be made to design a site that manages storm water well, is beautiful for people so that they enjoy the space, is nourishing for wildlife, and is a place for children to play. The three areas of contribution I chose to focus on are techniques to manage storm water, landscaping with conservation and nurturing in mind, and a play structure for the children of the neighborhood. The discerning quality of the Bear Creek Prairie site was the discovery of a prairie and the diversity it possessed. At the time of European settlement 15,000,000 acres of Missouri was prairie. Today, fewer than 90,000 acres remain. For the Bear Creek Prairie developers, the preservation of the prairie found on the site is the most important consideration towards the development of the property. Further study of prairie plants shows that their deep root systems are also very valuable as a tool for managing storm water. Wet mesic prairie plants are necessary components of raingardens, because of their ability to absorb and cleanse storm water before it percolates to the water table. Including a play structure, into the design of my landscape, was necessary for the children of the neighborhood. I also studied the use of native plants and all vegetation, identified to be used in my design, is native to Missouri and in some cases have already been identified at the site. Overall, I believe my design addresses the variety of concerns one has to deal with when designing for an urban environment. In an urban environment we must not only seek to meet the diversity of needs for human beings, in all stages of life and culture, but also the needs of the environment within which we choose to inhabit.

Kimberly Palmer

Major: Biology
University: Stephens College
Faculty Mentor: Dr. Jim Schoelz
Mentor Department: Plant Sciences
Funded by: Plant Genomics Internship @ MU

Characterization of *N* gene homologs in *Nicotiana* species

K.Plamer, B.E. Wiggins, C.A. Angel, B. Balaji and J.E. Schoelz

We have developed a new variety of *Nicotiana, N. edwardsonii* var. Columbia, that can be used as a bridge plant to move virus resistance genes from *N. glutinosa* to *N. clevelandii*, and have made crosses between *N. edwardsonii*. var. Columbia and *N. clevelandii* to characterize a single dominant gene that specifies resistance to Tomato bushy stunt virus (TBSV). We have also developed a gene silencing assay that specifically targets host resistance genes that fall into the NBS-LRR category and have used this assay to show that TBSV resistance gene has sequence similarity to the *N* resistance gene. As a prelude to cloning the TBSV resistanc gene, it is now important to understand how many *N* gene homologs exist in crosses with *N. glutinosa.* To examine the diversity of *N* gene homolog sequences, we developed PCR primers that amplified a 516 bp DNA segment of Exon 2 of the *N* gene. This PCR reaction yielded multiple products, which were cloned and sequenced. In *N. clevelandii*, two *N* homologs predominated. These sequences differed from the *N* gene by approximately 10%. The analysis of *N* homologs in *N glutinosa* is still being completed, but preliminary results indicate that this *Nicotiana* species contains a broader array of *N* gene homologs than *N. clevelandii.*

Ryan Peterson

Major: Biochemistry
University: The University of Minnesota-Twin Cities
Faculty Mentor: Dr. John R. Lever
Mentor Department: Radiology
Funded by: NSF-REU/NIH Program in Radiochemistry

Synthesis and binding studies of novel sigma receptor ligands

Ryan M. Peterson, Rong Xu, Jennifer L. Gustafson, Rachel L. Allmon, John R. Lever and Susan Z. Lever

Sigma receptors are binding sites that are found in the brain, in the endocrine and immune systems, and also in the lungs, kidneys, intestines, muscles and especially the liver. They are classified into two subtypes, sigma1 and sigma2, both of which have unique characteristics. Sigma receptors in the central nervous system are thought to be involved in disorders such as psychoses, Alzheimer's disease, and schizophrenia. A number of human tumors also show high densities of sigma receptors. In this study, three novel compounds were synthesized with the intent of characterizing how their structural differences affect affinity for the sigma1 and sigma2 receptors. We investigated derivatives of a potent sigma1 selective agonist, 1-(3',4'-dimethoxyphenethyl)-4-(3''-phenyl propyl)piperazine, developed by Santen Pharmaceutical Co. Specifically, the 4'-methoxy moiety was replaced by benzyloxy, phenethyloxy and 3-phenylpropyloxy substituents. These were prepared by reaction of the corresponding 4'-phenol with base and treatment with phenethyl bromide, 3-phenylpropyl bromide or benzyl bromide. For the phenethyl and 3-phenylpropyl derivatives, a mixture of 40% KOH and tetrabutylammonium hydroxide (1M in MeOH) was used as the base. Column chromatography provided these target compounds in 81 - 94% purified yields. The benzyl derivative proved difficult to obtain using this procedure, and different conditions were used to synthesize this compound. The 4'-phenol was reacted with benzyl bromide and potassium carbonate in ethanol to give the benzyl ether in 35% yield after purification by column chromatography. All three compounds were characterized by 1H NMR, and were analyzed by elemental analysis and HPLC. Currently, competition receptor binding studies are being run on the synthesized compounds to measure their affinities for sigma1 and sigma2 receptors.

Sarah Price

Major: Biology
University: Xavier University of Louisiana
Faculty Mentor: Dr. Vincent DeMarco
Mentor Department: Child Health
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Brain natriuretic peptide decreases pulmonary artery pressure in rats with pulmonary hypertension

Sarah Price and Vincent DeMarco

INTRODUCTION: B-type or Brain natriuretic peptide (BNP) was first isolated from the porcine brain, but it is primarily secreted from the cardiac ventricles in humans. As a cardiac hormone it has a physiologic regulatory function in the cardiovascular system. Along with atrial, and C-type natriuretic peptides, BNP aids in the natriuretic, diuretic, and vasorelaxant responses intended to reduce blood pressure and fluid volume homeostasis. Its vasodilator properties are known to be present in the pulmonary circulation; therefore, we hypothesized that BNP can be used as a therapy to lower the pulmonary artery pressure in an animal model of pulmonary hypertension.

METHODS: Male Sprague-Dawley rats were given a one-time subcutaneous injection of 60 mg/kg monocrotaline to induce PH over a five week period. After establishment of PH, rats were anesthetized and ventilated. A catheter was placed in the right jugular vein and passed into the right ventricle to record right ventricular pressure (RVSP), an estimate of pulmonary artery pressure. A second catheter was placed in the right carotid artery to measure mean arterial pressure (MAP). RVSP and MAP were recorded before, during, and after infusions of BNP.

RESULTS: One hour infusions of 5, 25, 50 or 150 ng/kg min BNP caused 24, 31 38, or 36% decreases in RVSP, respectively. There was no evidence of systemic hypotension at these doses of BNP.

CONCLUSION: These preliminary findings suggest that BNP causes dose dependent decreases in pulmonary artery pressure in rats with pulmonary hypertension. Further study is needed to confirm these preliminary results.

Valerie Rahing

Major: Chemical Engineering
University: University of Missouri-Columbia
Faculty Mentor: Dr. Gary Ehrhardt
Mentor Department: MU Research Reactor
Funded by: MU Research Reactor

Development of a portable source for production of Re-188

Valerie Rahing, Gary Ehrhardt and Alan Ketring

Rhenium 188 is a radioisotope that is potentially useful for treatment of certain types of cancer including bone cancer and circulating tumors. Its short half-life of 16.7h however makes it an awkward choice for clinical use as much of the product will decay during shipping. This project focuses on the development of a portable source of producing high specific activity Rhenium188 from a longer lived (t1/2 = 69.4d), low specific activity source; Tungsten 188. Tungsten 188 is obtained by double neutron capture from $Na_2{}^{186}WO_4$. Peroxide complexes of the Sodium Tungstate ($Na_2{}^{186}WO_4$) and Zirconyl Nitrate ($ZrO(NO_3)_2$) are formed and then mixed with heating to yield a $ZrO^{186}WO_4 \cdot XH_2O$ gel precipitate. This is loaded into a column and washed with saline. As the W-188 decays to Re-188, high specific activity Sodium Perrehnate ($Na^{188}ReO_4$) will be eluted from the column. This can then be reduced to form the final drug on location. Future studies may include a similar method of production for a Mo-99/Tc-99m generator, another drug commonly used for imaging. The final poster will also discuss crystalline content of the $ZrO^{186}WO_4 \cdot XH_2O$ gel, which must be minimized to maximize the yield of Re-188.

Joey Ransdell

Major: Neuroscience
University: University of Minnesota-Twin Cities
Faculty Mentor: Dr. Abrahan Eisenstark
Mentor Department: Biological Sciences and the Cancer Research Center
Funded by: Cancer Research Center

Diversity of progeny from a single colony of Salmonella typhimurium after 19 months in sealed agar stabs

Joey Ransdell, Dustin Newman, Alison Fea and Abraham Eisenstark

Recent studies at the Cancer Research Center revealed numerous mutations in *Salmonella typhimurium* that had been sealed in agar stab vials and stored for over forty years. The bacteria that were conserved in over 20,000 vials were all progeny of the same *S. typhimurium* strain. However, they were not progeny from a single colony (thus, a single parental cell), but from cultures used in genetic studies in several laboratories. To continue the evolutionary and mutational study of *S.typhimurium*, a new set of 100 similar agar stabs were inoculated 19 months ago from a single colony (thus, a single parental cell), and sealed. Cells from this set were assayed to see if mutations had occurred. Through motility tests, colony growth on three media, re-streaking of unique colonies, and phage spot testing, genetic variability was observed after 19 months storage. In this amount of time enough mutation did occur to display diverse phenotypes among progeny of the single strain of *S. typhimurium*. To confront any concerns that the mutations may have been present 19 months ago, a -80 °C stock of the parent colony was used as a control. While the phenotypic changes were significantly less then the vials stored for forty years, it is obvious that 19 months was enough time for genetic variability to occur in *S. typhimurium* from a single parent.

Support from Cancer Research Center. Special thanks to Dustin Newman and Alison Fea for technical instruction.

Lelande Rehard

Major: Undeclared
University: University of Missouri-Columbia
Faculty Mentor: Dr. Raymond Semlitsch
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Desiccation rates of *Rana sylvatica*, *Rana clamitans*, and *Bufo americanus* in a fragmented forest

Lelande Rehard, Tracy Rittenhouse, Elizabeth Harper and Raymond Semlitsch

Habitat loss and fragmentation are the primary causes in the declines of amphibian populations. Farming, urban sprawl, and logging have created a mosaic of developed and undeveloped land that may create barriers between aquatic breeding sites and terrestrial refuges. While ponds and wetlands are important in early development and breeding, many species spend their adult lives foraging in the terrestrial environment surrounding a breeding site. An amphibian's ability to move and forage in a terrestrial environment is determined by their capacity to remain hydrated. We compared desiccation rates of wood frogs *(Rana sylvatica*), green frogs (*Rana clamitans*), and American toads (*Bufo americanus*) juveniles in different microhabitats of a forest and a clear-cut to determine how they might affect the terrestrial activity of amphibians. Using the experimental arrays created by LEAP (Land use Effects on Amphibian Populations) at Daniel Boone Conservation Area we set up cylindrical wire mesh enclosures in forest drainages, forest ridges, brush piles in clear cuts, and open areas in clear cuts at two ponds. Animals were placed in the enclosures during the evening and weighed every six hours for twenty-four hours. Soil moisture, and soil temperature were also measured every six hours. Analysis of variance with repeated measures was used to compare percent water loss in the habitat treatments. All frogs lost water; however, water loss was greater in the day compared to night. Brush piles within the clear cut slowed water loss compared to open areas in the clear cuts, and animals on forest ridges lost more water than those in forest drainages. Our results reinforce the need to protect forest drainages as terrestrial refuges and illustrate that clear cutting, even with brush piles as cover, may negatively affect the delicate balance of mortality and survivorship in juveniles, therefore threatening the future of a population.

Derrick Reynolds

Major: BioAgribusiness Management: Biotechnology Emphasis
University: Brigham Young University
Faculty Mentor: Dr. Henry T. Nguyen
Mentor Department: Plant Sciences
Funded by: Plant Genomics Internship @ MU

Genetic mapping of QTL conditioning resistance to soybean cyst nematode in PI464925B

Derrick Reynolds, Geung-Joo Lee, Sean Blake, Kathleen Pyatek and Henry T. Nguyen

Soybean cyst nematode (SCN) (*Heterodera glycines* Ichinohe) is estimated to cause the greatest yield losses to soybean [*Glycine max* (L.) Merr.] of any pest worldwide. It has been determined that host plant resistance is the most cost-effective and environmentally conscious method of controlling SCN. Phenotypic resistance appears to be quantitative and few cultivars exhibit resistance to one or more races of SCN. Identification of genetically resistant lines will be needed to compensate for various environmental SCN populations. Plant introductions (PIs) from the USDA Soybean Germplasm Collection have been screened for resistance to SCN and relatively few sources have been identified as new sources of SCN resistance. A wild soybean PI464925B (*Glycine soja* Siebold & Zucc.) is a soybean plant introduction from China shown to have resistance to SCN race 3. In this study, PI464925B was crossed with the SCN susceptible cultivar 'Hutcheson' to generate F_1 hybrids. One hundred twenty-two F_2 derived F_3 progenies were evaluated for reaction to SCN race 3 in a thermo-regulated waterbath (27±1 °C) in the greenhouse at the University of Missouri for reaction to SCN race 3. DNA from leaf tissue of the parents and progeny was extracted and one hundred seventeen of the progenies were used for construction of linkage maps and location of the QTL(quantitative trait loci) by using SSR(simple sequence repeats) markers. Multiplex PCR was performed using fluorescent labeled primers with subsequent analysis on an ABI 3100 DNA sequencer to increase high-throughput of genetic mapping. Genemapper (v3.5) was used for automatic allele sizing and genotyping. Parental testing showed 201 polymorphic SSR markers (56%), providing an average genomic coverage of 12 cM between two markers. Among them, genotypic data from 113 labeled SSR markers on the F_3 progeny were collected to analyze association with the SCN response. QTL locations and genetic contribution of the favored alleles will be discussed.

Gerard Robertson

Major: Psychology and Philosophy
University: St. John's University in New York
Faculty Mentor: Dr. Kevin Cokley
Mentor Department: Educational, School, and Counseling Psychology
Funded by: Summer Pre-Graduate Research Experience for Students in the Humanities

A study of academic self- concept, academic motivation, and self- esteem: Their relationship to academic achievement in college students

Gerard Robertson and Kevin Cokley

This study examined the reliability of the Academic Motivation Scale in a group of 263 undergraduate students enrolled in undergraduate psychology classes at a large Midwestern public university. Ethnicity, sex, age, and class status (i.e., year in college) differences in academic self- concept were investigated as well as factors that predict academic self- concept. Participants completed the Academic Self- Concept Scale, Academic Motivation Scale, and the Rosenberg Self-Esteem Scale. This study also examines construct comparison to test for any differences in the levels of motivation, and self-esteem as it relates to GPA between African American and European American college students. While it was found that African American students are highly motivated and have a higher academic self- concept when compared to European Americans, this does not seem to be related to how African Americans perform academically. Analyses revealed that among African American students and European American students, the relationship between academic self- concept and GPA showed a slight difference. However, reported self- esteem for both ethnic groups was relatively similar. Self-determination theory has been introduced as an additional motivational framework to understand African American students' motivation relative to European American students.

Chris Robinson

Major: Cell and Molecular Biology
University: Southwest Missouri State University
Faculty Mentor: Dr. Gary Weisman
Mentor Department: Biochemistry
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Point mutation of an RGD sequence in the human P2Y2 receptor to a QGD sequence conserves Go-mediated signal transduction

Chris Robinson, Sriparna Bagchi and Gary Weisman

The $P2Y_2$ nucleotide receptor is a $G_{o/q}$ coupled receptor that is activated equipotently by extracellular nucleotides such as ATP or UTP and is upregulated in a variety of tissues in response to injury or stress. The biological effects of extracellular nucleotides are mediated through activation of P1 and P2 purinergic receptors. P1 receptors are responsive to adenine and P2 receptors are activated by a variety of nucleotides including ATP and UTP. The P2 receptors are subdivided into two distinct categories, the ionotropic ligand-gated channel (P2X) receptors and G-protein coupled P2Y-receptors, with seven transmembrane domains. Previous studies have shown that the human $P2Y_2$ nucleotide receptor contains an arginine-glycine-aspartic acid (RGD), integrin-binding domain. This domain is located in the first extracellular loop of the receptor and binds specifically to the $\alpha_v\beta_3/\beta_5$ group of integrins. The $P2Y_2$ receptor interacts with the α_v integrins by the RGD domain to activate G_o and induce cell migration. The human and murine $P2Y_2R$'s have the RGD integrin-binding domain, whereas the rat homologue has a QGD domain. However, this change in the arginine position in the RGD integrin-binding domain is considered to be a conservative substitution that maintains integrin binding. In order to confirm this assumption we changed the RGD domain of the human $P2Y_2$ receptor into the QGD domain by in vitro mutagenesis. The wild-type and the QGD mutant $P2Y_2$ receptors were transiently transfected into P2 receptor null, 1321 N1 astrocytoma cell line. Preliminary data suggest that the QGD mutant can stimulate PLC dependent intracellular Ca2+ mobilization and also activate cofillin and extracellular signal-regulated kinases (Erk) with equal efficacy and agonist potency as the wild type receptor. Further tests need to be done to verify that integrin bindin and signaling by the Rac and Rho pathways remain unaffected in the QGD mutant to induce integrin dependent cell migration in response to UTP and ATP.

Katherine Roehrick

Major: Advertising and Marketing
University: University of Missouri-Columbia
Faculty Mentor: Dr. Paul Bolls
Mentor Department: Advertising
Funded by: MU Undergraduate Research Scholars Program

The effects of arousing video on attention and memory for attack vs. non-attack political advertisements

Katie Roehrick and Paul Bolls

During the election season, it may appear that television viewers are bombarded with political advertisements. Furthermore, it may also appear that the majority of these advertisements are routinely negative. It has been said that candidates use attack advertisements because they work; that is to say, attack advertisements are more memorable than non-attack advertisements. Much research has been done on political advertisements, with mixed conclusions on the effectiveness of attack versus non-attack advertisements. My research on the effect of arousing advertisements attempts to add clarity to the question of if and why attack advertisements affect memory to a greater degree than non-attacks advertisements. I will directly test the hypothesis that memory is not necessarily affected by the content of the advertisements (i.e. attack or non-attack), but rather by the production values of the advertisements (i.e. how arousing the advertisement is). If this hypothesis is true, the direct implication is that candidates do not have to design a negative attack advertisement to be successful in their campaign, but rather they can create arousing, positive advertisements that focus solely on themselves and their position. Consequently, I believe that advertisers will be able to use the results of my research to help them create more suitable and effective advertisements.

The study will test the dependent variables of attention, emotional valence, memory, and attitude. Attention to the advertisements will be measured by obtaining a participant's heart rate. Deceleration of heart rate is indicative of attention to the message. Emotional valence will be measured through facial EMG (measurement of smile and frown muscle activity). Memory will be tested through a recognition test. Attitudes toward the advertisements will be measured through the use of a questionnaire.

Rebecca Rone

Major: Biological Engineering
University: University of Missouri-Columbia
Faculty Mentor: Dr. Per Stromhaug
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

Making the Cvt pathway/autophagy in vitro

Rebecca Rone and Per Stromhaug

Autophagy, Greek for “self eating”, occurs in all eukaryotic cells to remove damaged or unwanted organelles or to provide a source of nutrients during starvation. In autophagy, a double membrane surrounds a cluster of contents, damaged organelles, bulk cytoplasm, and aminopeptidase I (Ape1), forming an autophagic vesicle to be sent to the vacuole. A unique Cvt pathway occurring in *Saccharomyces cerevisiae*, includes a membrane encapsulation of only Ape1 to be transported directly to the vacuole. Most of the proteins needed for autophagy and the Cvt pathway have been identified, but their roles have yet to be determined. In the Cvt pathway, the Ape1 aggregates to form a dodecamer before forming a Cvt complex by combining with the protein Atg19. The Cvt complex affixes to the autophagic membrane presumably with the aid of Atg11 and Atg8. An array of proteins, Atg9-Atg2 complex, Atg1, and Pi3-kinase complex, help complete the formation of the autophagic vesicle encompassing Ape1. The autophagic vesicle then fuses with the vacuole releasing the Ape1 into the lumen of the vacuole. Until now, only whole cells have been used to examine autophagy. Due to the complexity of the whole cell, the functions of the all proteins needed for autophagy have not been determined. Our main goal is to be able to construct the Cvt pathway in vitro. We have begun inserting the *APE1* gene from *S. cerevisiae* into another strain of yeast, *Pichia pastoris*, where the Cvt pathway does not occur. Once the proteins are expressed in *P. pastoris*, we will study the interaction of Ape1 with other Cvt proteins. From *P. pastori* we will extract Cvt proteins for examining in a test tube. While *in vitro*, it will be possible to determine the molecular function each protein contributes to autophagy. A better understanding of the process of autophagy will be beneficial to understanding and treatment of many diseases such as cancer, liver disease, muscular disorder, neurodegeneration and bacteria infections.

Heather Rosenblatt

Major: Mathematics
University: University of Missouri-Columbia
Faculty Mentor: Dr. Dorina Mitrea
Mentor Department: Mathematics
Funded by: MU Undergraduate Research Scholars Program

Mean value formulas for differential operators

Heather Rosenblatt and Dorina Mitrea

The main goal of our research is to discuss Mean Value Formulas for solutions of partial differential equations of a certain form (see 1 below) where A is a symmetric, positive definite, real-valued matrix. Such equations arise when modeling various steady state (time independent) phenomena. A mean value formula is a precise way to relate the value of the solution at a point c to the values taken in a neighborhood of that point. A neighborhood being simply a region around the point c. Mean Value Formulas have a rich history stretching back to the early 1800 when the famous mathematician C.F. Gauss initiated their study by considering the case when the matrix A is the identity. This corresponds to the Laplace equation (see 2 below). In this case, the neighborhood around a point c is a sphere. The more general settings we discuss correspond to: integer powers of the Laplacian, the anisotropic (direction dependent) model and the Lame system of isotropic elasticity. We were able to establish mean value formulas in each of these cases. There are many aspects of the project that lend themselves to future study. This includes considering other types of partial differential equations, such as the heat equation and Helmholtz equation, and proving converses to the Mean Value Theorems already established, obtaining the most general version of the Mean Value Formula, valid for all solutions to the Lame system.

Natalie Rosenwasser

Major: Bioengineering
University: Binghamton University
Faculty Mentor: Dr. Mark Milanick
Mentor Department: Medical Pharmacology and Physiology
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Pharmacokinetic modeling of cortisol binding to dietary fiber in the gastrointestinal tract

Natalie Rosenwasser, Mark Milanick and Krista Arnett

Cortisol is a glucocorticoid hormone produced in the adrenal cortex during stressful situations. The purpose of this project was to determine whether cortisol binds to dietary fiber and to design a pharmacokinetic model to predict whether or not fiber has a significant binding capacity in the human gastrointestinal tract. Studies have shown that estrogen binds to dietary fiber. Coumesterol, a cholesterol derived steroid structurally similar to estrogen, is also thought to bind to dietary fiber. The fluorescence of coumestrol bound to oat, wheat and psyllium fiber was analyzed in order to determine the binding capacities of each. This indicates that steroids have different binding capacities important in the pharmacokinetic model. This model would provide useful information capable of predicting physiological changes due to changes in dietary habits as well as medicines such as antibiotics that may alter steroid secretion. If steroids do have a recycling route and dietary fiber has a significant binding capacity in the human body then an increase in dietary fiber may result in a decrease in cortisol.

Courtney-Jamaal Rouse

Major: Nursing
University: Austin Peay State University
Faculty Mentor: Dr. Joanne Banks-Wallace
Mentor Department: Nursing
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Stroke risk factors and awareness study

Courtney-Jamaal Rouse and Joanne Banks-Wallace

Cerebrovascular Accidents, also known as strokes, are the third leading cause of death in the United States. It is estimated that more than 275,000 people die from strokes every year (American Heart Association 2003). In 2002, it was calculated that over 5,400,000 people suffered from a stroke. 2,400,000 of those were males, and 3,000,000 of those who suffered from a stroke were females (American Heart Association 2003). The highest prevalence of strokes occurs within the African American Population. In 2002, around 8% of the total African American population suffered from a stroke, which averages out to be a total of about 111,000 people (American Heart Association 2003). Hispanics are close behind with around 6.4% of their population suffering from strokes in 2002. Strokes occur when the blood supply to the brain is limited or completely cut off. It causes the brain not to be able to function properly and can even cause paralysis on one or both sides of the body. Strokes involve a long recovery process if there is any recovery at all. It seems as though most people do not know and understand how great the risk factors are for strokes. Although the risks for strokes are high, they could be minimized if people take the time and become educated on what are actually those risk factors. People are also unaware of how much it costs our country to provide the health care and aide for stroke victims/survivors. It is estimated that over $393 billion dollars were spent in 2003. People do not seem to think strokes affect as many people as they actually do. The purpose of this research is to see how much peers in the LSMOAMP program actually know about signs and symptoms as wells as risk factors for strokes. A twenty question survey was developed. Questions were derived from a review of the literature. The participants completed the survey. The survey served a dual purpose. It provided information regarding current awareness about strokes among participants in LSMOAMP. It was also a tool to enhance awareness about strokes. If the participants began to think about the questions that they did not know, then that would allow them to delve deeper into the knowledge that they should acquire about stroke risk factors.

Matthew Sailor

Major: Fisheries and Wildlife
University: University of Missouri-Columbia
Faculty Mentor: Dr. John Faaborg
Mentor Department: Biological Science
Funded by: Missouri Ozark Forest Ecosystem Project

The effects of even-aged cutting on density and pairing success of Worm-eating Warblers

Matthew Sailor, Amber Wiewel, Richard Clawson, John Faaborg, and Paul Porneluzi

It is important for researchers to be aware of how timber management practices affect songbird populations. Certain forest management techniques can cause declines in breeding habitat of Neotropical migrant songbirds that require mature forest. The worm-eating warbler (Helmitheros vermivorus) is a common mature forest-dwelling species that may experience a decline in density due to habitat alterations such as clear cutting and selection cutting. As regeneration of the clear cuts occurs, mature forest-dwelling species may be able to utilize these areas as suitable habitat. This summer was the first year that worm-eating warblers settled on the 8 year old clear cuts on the sites of the Missouri Ozark Forest Ecosystem Project. We compared the relative abundance of worm-eating warblers that inhabited even-aged sites with those that inhabited control sites by using point counts of each site. In order to determine pairing success, we followed a singing male until the bird was seen interacting with a female or for 90 minutes if no interaction was seen. We hypothesized that the worm-eating warblers will have lower pairing success on even-aged sites (clear cuts) than control sites. We also hypothesized that the densities of worm-eating warblers would be the highest on the control sites and the lowest on the uneven-aged (selection cuts) sites, with the density of the even-aged sites falling slightly below that of the control sites.

Melanie SanMiguel

Major: Communication Science and Disorders
University: University of Missouri-Columbia
Faculty Mentor: Dr. Judith Goodman
Mentor Department: Communication Science and Disorders
Funded by: MU Undergraduate Research Scholars Program

Development of conversation in toddlers: The role of maternal input

Melanie SanMiguel and Judith Goodman

One of the most important human skills is the ability to engage in conversation. This includes our ability to initiate topics, take turns appropriately, and respond contingently to a partner's utterances. While we know that children learn these skills, a clear understanding of the steps they take in developing them and of the factors that may influence the course and rate of development is currently lacking. The present longitudinal study uses language samples collected from 45 mother-child dyads to analyze how children between the ages of 20 and 30 months develop conversation. In addition, it examines the impact of maternal education on this development. Results indicate that the nature of mothers' and children's contributions to discourse change with age. Children become more adept at contingent responding, and the percent of consecutive utterances and topic initiations made by mothers decreases as the children age. Maternal education does not significantly affect the way mothers and children converse in this study. These results suggest that turn-taking between mother and child increases as mothers respond to their children's growing conversational competence. At least within this population, maternal education does not affect the way that the mothers respond. Future studies might examine a wider range of maternal education and investigate whether children's conversational development depends substantially on their language skills.

Erick Scheerer

Major: Mechanical Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. William H. Miller
Mentor Department: Nuclear Science and Engineering Institute
Funded by: U.S. Department of Energy MNSEC Summer Undergraduate Research Program

TRIAX Upgrade at MURR

Douglas D. Charlton, Olawale B. Oladiran and William H. Miller

Neutron scattering is an extremely powerful tool in the study of elemental excitations in condensed matter. One instrument used for these studies is the triple axis neutron spectrometer (TRIAX). Within the past decade the triple-axis spectrometer located at the 10 MW University of Missouri Research Reactor (MURR) was upgraded with triple-axis spectrometer previously located at the Oak Ridge Research Reactor (ORR) and owned by Ames Laboratory. The TRIAX located at the MURR serves two purposes. The first is to carry out condensed matter research, and the second as a training tool for educating a new generation of neutron scatters. An upgrade of this instrument is needed to ensure that the TRIAX can continue to fulfill this dual role and remain in good working order. In order to upgrade the TRIAX, several components need to be replaced and a new control system is being added which will be compatible with a similar instrument at Oak Ridge National Laboratory. SPICE “spectro and instrument control analysis” is software from Ames Laboratory, which is being installed to communicate the TRIAX with the user. During this upgrade it was noted that a drive mechanism on the TRIAX had backlash between the worm gear and the gear that it drives. To resolve this problem experiments were performed to measure the applied load necessary to move the part that the worm gear is moving. It was found that a different force was necessary to move the part in different directions. For movement in the clockwise direction it took 1 pound of force while in the counter-clockwise direction it took approximate 8 pounds of force. The reason for the backlash between the gears is that the drive didn’t have sufficient torque to drive the 8 pounds of force. To verify this assumption, calculations were prepared using Actual Mechanism torque analysis that demonstrated insufficient torque from the combination of the motor and the reduction gears. To resolve this problem, a new motor of the same frame size and larger torque was identified and, based on the same calculations used before; a new gear ratio has developed to provide approximate 9.5 pounds of force. The engineering design for this new drive was implement with AutoCAD and Solid Works software and will be implemented on the TRIAX as part of the system’s upgrade. This material is based upon work supported by the US Department of Energy Innovations in Nuclear Infrastructure and Education program under Award No. DE-FG07-03ID14531.

Michael Schulte

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Karen Cone
Mentor Department: Biological Sciences
Funded by: Arts & Sciences Undergraduate Research Mentorship Program

The effect of reduced chromatin gene expression on an epigenetically regulated maize gene

Michael Schulte and Karen Cone

In virtually all eukaryotic organisms, not just plants, genes are regulated at the level of chromatin. In a genomics approach to understand how expression of a gene can be regulated by its chromatin configuration, a series of maize mutants in which chromatin gene expression has been knocked down by RNA interference are being analyzed.

Mutants of three different types of chromatin genes, which all are thought to have normal roles in gene silencing, were examined. The maize gene *chr101* is orthologous to the Arabidopsis gene *DDM1*, which codes for an ATPase-dependent chromatin remodeling protein responsible for maintaining DNA methylation and gene silencing patterns. The maize genes *dmt101*, *dmt102*, and *dmt106* show sequence homology to the Arabodopsis genes *MET1*, *CMT1*, and *DRM3*, respectively, all of which code for DNA methyltransferases. The maize *mbd* genes show sequence homology to the Arabodopsis AtMBD genes, which code for methyl-CpG-binding domain proteins responsible for binding specifically to methylated DNA and recruiting histone deacetylases, which aid in tightening chromatin structure.

To look at the effect of reduced chromatin gene expression, plants carrying transgenes targeting *chr, dmt,* or *mbd* genes were crossed to a line carrying a gene that acts as a reporter for chromatin-level regulation. The reporter, *P1-Blotched*, activates synthesis of purple anthocyanin pigments to produce a variegated phenotype that is correlated with closed chromatin and a distinct pattern of DNA methylation. Mutations in genes that are necessary for maintaining a closed chromatin configuration--like *chr*, *dmt*, and *mbd* genes--may lead to increased *P1-Blotched* expression, which should be evident phenotypically as higher anthocyanin levels. To test this idea, I measured pigment levels in plants carrying chromatin-gene mutations. Increased pigmentation in the transgenic plants will provide evidence that the targeted genes play a role in regulating *P1-Blotched*.

Laura Shannon

Major: Biology and Anthropology
University: Grinnell College
Faculty Mentor: Dr. Tim Holtsford
Mentor Department: Biological Sciences
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Development of CAPS markers for Nicotiana

Laura Shannon, Dulce Figueroa-Castro and Tim Holtsford

The area in which the ranges of *Nicotiana longiflora* and *Nicotiana plumbaginifolia* overlap presents an ideal system for studying the interaction and hybridization of a selfing and an outcrossing species. *N. longiflora* is characterized by long corollas and self compatibility but sets little fruit on its own due to anther stigma separation. *N. plumbaginifolia* exhibits shorter corollas and self pollinates almost all of it's flowers. A third morph with medium length corollas is found in populations comprised of both species. It seems likely that this morph is a hybrid. In order to better understand how hybridization occurred and the genetic consequences of species interaction, we plan to perform pollen races in which we will allow self, out crossed, and inter-specific pollen to compete on the same style. Pollen competes and is selected through a variety of mechanisms including stigma and/or style clogging, pollen tube germination success and speed of growth, and differential seed abortion.

The winners of the races will be determined through paternity tests of the resulting off spring. Using this method allows us to examine the genetic consequences of all the stages of pollen competition. We will test for paternity using molecular markers in the form of single nucleotide polymorphisms in restriction enzyme recognition sites (CAPS markers). We used DNA sequences of randomly chosen genetic loci to develop CAPS markers. We found a high degree of variability within our population, however only loci at which an individual is heterozygous are useful, so most of the polymorphisms we found cannot serve as markers. At this point the most promising marker seems to be SNPs in the recognition site for Taq I on the gene for Cu-Zn superoxide dismutase.

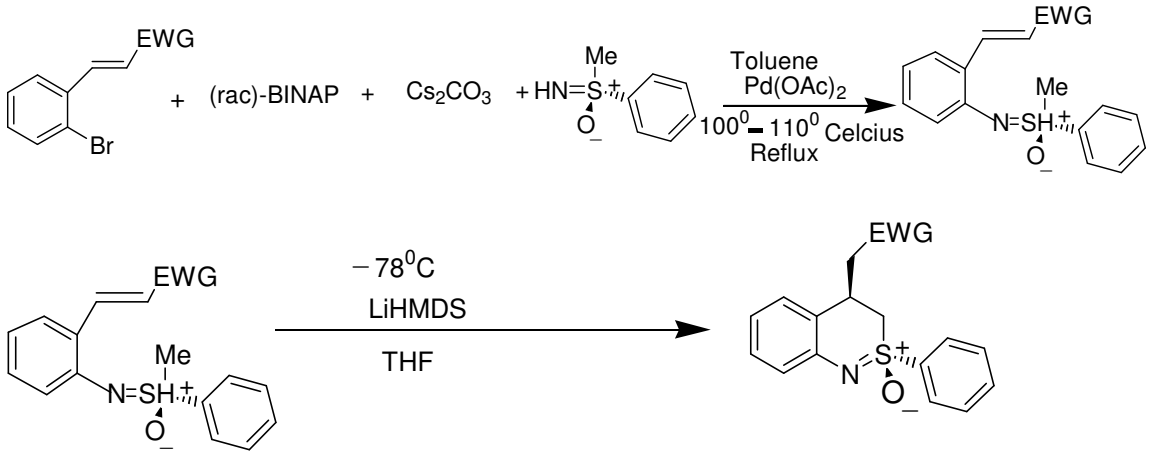
Vikas Sikervar

Major: Chemistry
University: Indian Institue of Technology, Kanpur, India
Faculty Mentor: Dr. Michael Harmata
Faculty Department: Chemistry
Funded By: Stevens' Chemistry Program

The intramolecular, stereoselective addition of sulfoximine carbanions to electron deficient alkenes

Vikas Sikervar and Michael Harmata

Chiral Benzothiazine play important roles in synthetic organic chemistry since they can be used in the preparation of enantiomerically pure compounds. We have studied the synthesis of these species using the intramolecular, stereo selective addition of sulfoximine carbanions to general electron deficient alkenes. Details on the synthesis of starting material and cyclization reaction will be presented.



Christian Simpson

Major: Biochemistry

University: North Carolina State University
Faculty Mentor: Dr. Jan A. Miernyk
Mentor Department: Biochemistry
Funded by: Plant Genomics Internship @ MU

Subcellular localization of the *Arabidopsis thaliana* atDjC37 molecular chaperone protein

Christian H. Simpson, Mark L. Johnston and Jan A. Miernyk

There are 94 genes encoding J-domain molecular chaperone proteins in the *Arabidopsis thaliana* genome. These genes have been grouped into 51 families (Miernyk 2001 Cell Stress Chaperones 6: 209-218). Family 4 consists of two proteins, atDjC6 and atDjC37. It has been previously determined that atDjC6 is nuclear localized (Suo & Miernyk 2004 Protoplasma 224: 79-89). We now wish to determine the subcellular localization of atDjC37. In silico analysis of the atDjC37 deduced amino acid sequence (http://maple.bioc.columbia.edu/predictNLS/) yielded the prediction that residues $-R_{253}$RSSKKS- comprise a nuclear localization signal (NLS) sequence. Our experimental strategy has been to construct plasmids that encode full-length atDjC37 protein and a C-terminal truncated version that lacks the NLS sequence, fused to the red fluorescent protein. These proteins will be transiently expressed in biolistically-transformed tobacco BY2 cells, and localized using laser-scanning confocal microscopy. The transformed cells will be simultaneously incubated with a fluorescent nuclear stain to test for signal coincidence. Four nuclear stains are being evaluated for their utility; propidium iodide (PI), DAPI, SYTO Green, and Hoechst 33342. The SYTO and Hoechst 33342 stains are considered cell-permeant, while DAPI is "semi-permeant" and PI is impermeant. The PI and DAPI stains are UV blue-fluorescent, while PI is red and SYTO Green is, naturally, green.

Ashwin Singh

Major: Biology
University: University of Maryland-Baltimore County
Faculty Mentor: Dr. Patrick Shiu
Mentor Department: Biological Sciences
Funded by: Life Sciences Fellowships/Meyerhoff Scholars Program

Detection of *Sad* genes in various species of *Neurospora*

Ashwin Singh, Ryan Morris and Patrick Shiu

Neurospora crassa is a haploid fungus that reproduces asexually during vegetative growth. However, in a nitrogen deficient environment, the two mating-type cells, *A* and *a*, can fuse together and enter the sexual cycle. During this transient diploid stage, a post-transcriptional gene silencing (PTGS) mechanism silences the expression of any unpaired gene. This mechanism is called meiotic silencing by unpaired DNA (MSUD) (Shiu, *et al*., 2001; Cell 107: 905-916). MSUD occurs when a gene is not paired with a homologue during meiosis. The unpaired DNA segment generates a sequence-specific signal, causing any paired or unpaired copies of that gene to be silenced. Two required genes for meiotic silencing have been identified; *sad-1* encodes an RNA-directed RNA polymerase while *sad-2* encodes a novel protein. Interspecific crosses between *N. crassa* and other related species are known to be infertile. This infertility may be due rearrangements caused by inversion and/or translocation. These could disrupt the pairings of genes needed for meiosis and ascus development, causing these genes to be silenced, resulting in sterility. This hypothesis is validated by observing that interspecific crosses within the genus *Neurospora* become much more fertile when the *N. crassa* parent contains a *Sad-1* mutation. If MSUD is in other *Neurospora* species, it may represent another mechanism for speciation. This research project focuses to determine whether *sad-1* and *sad-2* are conserved in related species of *Neurospora*. Homologues of the sad genes were amplified in several fungal isolates by PCR (Polymerase Chain Reaction), using primers designed for those sequences. We have discovered that *sad-1* and *sad-2* can be found in several different *Neurospora* species; *sad-1* is present in *N. sitophila, N. tetrasperma, N. dodgei, N. galapagosensis*, and *N. africana*, while *sad-2* is found *in N. sitophila, N. tetrasperma*, and *N. intermedia*. The presence of *sad* genes in these species suggests MSUD may contribute to their reproductive isolation.

Nebiat Sisay

Major: Chemistry
University: Southern University at New Orleans
Faculty Mentor: Dr. Silvia S. Jurisson
Mentor Department: Chemistry
Funded by: Stevens' Chemistry Program

Reduction of rhenium (V) oxo Schiff Base Complexes with triphenyl phosphine ligands

Nebiat Sisay, Stephen A. Williams, Stephanie R. Lane and Silvia S. Jurisson

One approach to the treatment of cancer is to direct beta-emitting radionuclide to the cancer site where the radiation destroys the cancer cells. This can be achieved by coordinating the radioisotope in a very stable environment and linking it to a specific biological targeting molecule, which interacts specifically with particular cancer cells. It is necessary to have extremely stable *in vivo* radionuclide complexes so that limited amounts of radiation are released to other parts of the body before the radionuclide can reach the cancer cells. Isotopes of radioactive Rhenium are characteristic of such a nuclide. Our emphasis was to obtain a Rhenium (III) metal ligand complex since the lower oxidation state is more kinetically inert relative to Rhenium (V).

The method employed was to first produce the Re^{V}-ligand complex, $[Re^{V}OCl(Sal_2phen)]$, by reacting a 1:2 molar ratio of $TBA[Re^{VII}OCl_4]$ to Sal_2phen. Next, $[Re^{V}OCl(Sal_2phen)]$ was reacted with three equivalents of triphenylphosphine to determine whether a mono-substituted Re^{V} complex or a di-substituted Re^{III} complex was formed. After purifying the product by solvent extraction, the coordinated complex was reacted with ammonium hexaflurophoshate, NH_4PF_6, to induce crystallization of the target compound, $[Re^{III}(PPh_3)_2(Sal_2phen)][PF_6]$. Preliminary ^{1}H NMR, and FT-IT spectra suggest formation of trans-$[Re^{III}(PPh_3)_2(sal_2phen)]PF_6$. The Re=O stretch at 951.36 cm^{-1} observed for $[ReOCl(sal_2phen)]$ in the IR spectrum is missing from our product, implying the Re (III) product has been formed.

Emily Stanley

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Gary Weisman
Mentor Department: Biochemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Up-regulation of the P2Y2 receptor by cytokines in neuronal cells

Emily M. Stanley, Jean M. Camden, Laurie Erb, Cheikh I. Seye and Gary A. Weisman

Alzheimer's Disease (AD) is characterized by inflammation and neurodegeneration in the brain due to the presence of extracellular amyloid beta (A β) plaques and neurofibrillary tangles. Microglial and astrocyte cells associated with these plaques and tangles have been shown to release cytokines in AD patients, which have a proinflammatory effect on the brain. The P2Y2 receptor (P2Y2R) is a receptor protein that is up-regulated in response to damage or stress in a variety of tissues, including blood vessels and salivary gland epithelium. Recently our laboratory has shown that activation of the P2Y2R enhances α -secretase-dependent amyloid precursor protein (APP) processing. APP is proteolytically processed by β - and γ -secretases to release neurodegenerative A β. Alternatively, APP can be cleaved within the A β domain by α -secretase releasing the non-amyloidogenic product, sAPP α, which has been shown to have *neuroprotective* properties. Primary neurons have low P2Y2R expression, however, it has been demonstrated that cytokines up-regulate P2Y2R in smooth muscle cells. Therefore, this study will explore if cytokines up-regulate P2Y2R expression in primary rat neurons and in SH-SY5Y human neuroblastoma cells. Primary rat neurons and SH-SY5Y human neuroblastoma cells were plated on glass cover slips 24 or 48 hours with individual treatment, or a combination of, human interleukin-1 β (IL1- β), tumor necrosis factor α (TNF α), and interferon γ (IF γ). P2Y2R activity was measured by increases in intracellular calcium concentration ([Ca2+]i) in response to the P2Y2R agonist UTP. Results support the hypothesis that P2Y2R is up-regulated by cytokines in neuronal cells. Furthermore, real-time PCR results indicate a two-fold increase in P2Y2R mRNA after cytokine treatment. Therefore, activation of the up-regulated P2Y2R in stressed neurons generates a neuroprotective (sAPP α) rather than neurodegenerative (A β) peptide. These results could have a substantial impact on the understanding and treatment of neurological disorders such as AD.

Phillip Strawbridge

Major: Biology and Chemistry
University: University of Missouri-Columbia
Faculty Mentor: Dr. Lené Holland
Mentor Department: Medical Pharmacology and Physiology
Funded by: Life Sciences Undergraduate Research Opportunity Program

Interaction of a heterodimerization partner with glucocorticoid receptor (GR), androgen receptor (AR) and GR/AR hybrids

Phillip A. Strawbridge, Lené J. Holland and LaNita A. Nichols

Steroid hormones are a class of compounds that play a role in regulating many functions. Glucocorticoid hormone is a compound in this class, which helps maintain homeostasis, including regulation of production of γ-fibrinogen, a protein that plays a major role in blood clotting. Glucocorticoid hormone acts by binding to an intracellular receptor protein called the glucocorticoid receptor (GR). GR bound to glucocorticoid then moves to the nucleus, where it interacts with another protein, *Xenopus* Glucocorticoid Receptor Accessory Factor (XGRAF), to form a heterodimer. This heterodimer binds to an upstream regulatory region of the DNA coding for the γ-fibrinogen gene that is composed of a binding site for XGRAF adjacent to a half GR recognition site (a classical GR response element consists of two elements). Binding of this heterodimer to the recognition sites regulates transcription of the γ-fibrinogen gene. The dimerization interaction relies on specific amino acid sequences on both proteins. These experiments will examine the amino acids on GR that are involved in heterodimerization with XGRAF. Androgen receptor (AR), is very similar to GR, so examining the differences in binding in the presence of XGRAF due to the substitutions could help determine what regions of GR are essential to XGRAF binding. To study the heterodimerization, several constructs that incorporate AR at different parts of GR in place of the normal sequence were expressed in a bacterial system and then isolated for analysis. The proteins were used in gel mobility shift assays which allow detection of the interaction between the nuclear receptors and XGRAF. After studying the binding of these constructs we have determined that the parts of AR that were substituted for GR still allow heterodimerization with XGRAF. Since both GR and AR have the ability to interact with XGRAF, we can speculate that similar types of heterodimerization mechanisms for nuclear receptors could be more common than previously thought.

Jessica Struckhoff

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Mark D. Kirk
Mentor Department: Biological Sciences
Funded by: Life Sciences Undergraduate Research Opportunity Program

The effect of Camgaroo-2 incorporation on the differentiation potential of embryonic stem cells

Jessica Struckhoff, Katie Spears, Chris Pierret and Mark D. Kirk

Embryonic stem (ES) cells are capable of differentiating into any cell type in the body and are a promising therapeutic agent. Our research focuses on the differentiation of ES cells into functional neurons and/or glial that can nurture host cells of the nervous system that are damaged due to disease. Cells must express the appropriate phenotype and perform the proper function after transplantation. Camgaroo-2 is a fluorescence protein that provides a basal fluorescence and responds to a rise in intracellular calcium by producing an increase in fluorescence emission. Our lab transfected a mouse ES cell line (GSI-1) with the Camgaroo-2 gene and is testing this fluorescence indicator to determine the physiological function of cells grown in vitro. There is concern that the incorporation of the Camgaroo-2 gene could alter the cell phenotype, potentially decreasing their differentiation potential. GSI-1 cells were plated on culture slides following a neural induction protocol that uses retinoic acid and allowed to proliferate. Immunohistochemisty of slides was performed to label for neural precursors, immature and mature neurons, astrocytes, and oligodendrocytes (anti-O4). GSI-1 labeling was compared to corresponding immunohistochemistry performed on another ES cell line that had also been 'neuralized' to determine if the differentiation potential of the GSI-1 cells was similar to that of the other ES cell line. Similar labeling was seen for all markers except O4 which did not label for the GSI-1 cells, indicating the GSI-1 cells have the potential to differentiate into all cells of neural lineage except possibly oligodendrocytes. GSI-1 cells retained the ability to differentiate post-transfection with the Camgaroo-2 gene. Because of their unique ability to respond to an influx of intracellular calcium, GSI-1 cells expressing Camgaroo-2 can be transplanted into rodent models for human disease, and can be tested post transplantation for their ability to function as neural cells.

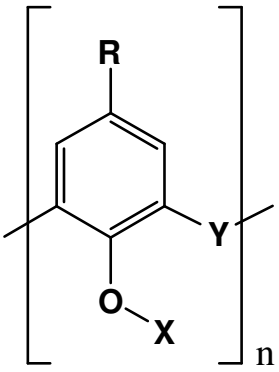
Harry Tabi

Major: Chemistry
University: Southern University at New Orleans
Faculty Mentor: Dr. Jerry Atwood
Mentor Department: Chemistry
Funded by: Stevens' Chemistry Program

Calix[n]arene derivatives for gas storage

Harry Tabi, Praveen Thallapally and Jerry Atwood

The calix[*n*]arenes are versatile inclusion compounds (Scheme 1) comprise of cyclic, polyphenolic compounds that can be tailored synthetically by altering X, Y, R and *n*. In solid state, we found simple calixarenes are quite interesting for example separation of hydrogen from mixture of gases so our attention turned into the closely related calixarenes for sorption studies.



n = 4, 5, 6, 8

Scheme 1

With this little back ground on calixarenes and their uses in solid state, we designed and synthesized *tert*-butylsulfonylcalix[4]arene and Tetra-*p*-*tert*-butyl-tetramethoxysulfonylcalix[4]arene from *tert*-butylthiacalix[4]arene by oxidizing in the presence H_2O_2 or $NaBO_3$ in exceptional yield.

Furthermore, asymmetric bridging of two calix[4]arene molecules to form a calixarene tubes with a larger and easily accessible cavity was also attempted to synthesize. Finally, H^1NMR spectral and X- ray crystallographic modeling studies was done to reveal the conformational characteristics of the synthesized compounds.

Demetrius Taylor

Major: Physics
University: University of Missouri-Columbia
Faculty Mentor: Dr. Peter Pfeifer
Mentor Department: Physics and Astronomy
Funded by: NSF Program Alliance for Collaborative Research in Alternative Fuel Technology and MU Access in Engineering

Synthesis and analysis of activated carbon briquettes as an adsorbent for natural gas

Demetrius Taylor and Peter Pfeifer

Activated carbon has been used for many years for its adsorptive properties. These adsorptive properties are a result of its high surface area to density ratio. It achieves this through its activation process. During activation a network of pores forms throughout the carbon matrix. These pores give the carbon a very large surface area for outside molecules to adsorb to. By maximizing the distribution of different pore widths one can tailor the carbon to adsorb molecules of differing sizes and during various conditions. Our goal is to develop a natural gas (95% methane) fuel tank that uses corncob produced activated carbon as an adsorptive medium. To do this we need to maximize the distribution of pore diameters that are between 1~2 nanometers (10~20 Angstroms). We are currently studying different activation methods and their effect on the carbon's adsorptive properties. We have obtained volumetric nitrogen and methane isotherms, gravimetric methane analysis data, both scanning and tunneling electron micrographs, and small-angle x-ray analysis data obtained from Argonne National Labs. From this data we have begun producing activated carbon briquettes that will form the "core" of our tank. We hope to expand the use of these briquettes to not only automotive fuel tanks but to natural gas trapping and storage as well.

Michael Tempesta

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Charlotte Phillips
Mentor Department: Biochemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Promotion of functional heterotrimeric type I collagen via transfection in osteogenesis imperfecta fibroblasts

Michael Tempesta and Charlotte Phillips

Osteogenesis imperfecta (OI) is a heritable disorder due to mutations in type I collagen. Normal type I collagen forms a heterotrimeric protein comprised of two proα1(I) chains and one proα2(I) chain [α1(I)$_2\alpha$2(I)]. The osteogenesis imperfecta murine (*oim*) model mouse contains a single nucleotide deletion in the proα2(I) gene (COL1A2) resulting in non-functional proα2(I) chains and production of homotrimeric type I collagen containing three proα1(I) collagen chains, [α1(I)$_3$], resulting in small body size, increased bone fragility and altered bone mineralization.

The overall goal of this study is to correct the *oim* defect by introducing normal COL1A2 genes into *oim* cells. *Oim* dermal fibroblasts were transfected with a series of COL1A2 gene constructs containing the full-length murine proα2(I) collagen cDNA driven by various lengths of the murine COL1A2 promoter (1.5kb, 3.0kb, and 6.0kb) along with a COL1A2 enhancer. These DNA constructs were cotransfected with pcDNA3 containing a neomycin resistance gene, which allows for selection of stably transfected cell lines. Various assays have been developed to monitor proa2(I) collagen expression at the DNA, RNA and protein levels. A PCR assay was used to confirm genomic incorporation of transgenic COL1A2 gene constructs and an RT-PCR assay used to confirm expression of normal proα2(I) collagen mRNA. Denaturing urea-SDS polyacrylamide gel electrophoresis along with Western blotting analyses using anti-murine α1(I) and α2(I) collagen antibodies were used to confirm normal proα2(I) collagen expression at the protein level as well as its incorporation into normal heterotrimeric type I collagen.

All the necessary tools have been established for evaluating the efficacy of transfection. Currently, the first series of stably transfected *oim* cell lines are being expanded for analyses as described above. Although this study is aimed at 'fixing' the *oim* mutation via gene therapy, valuable data will also be collected regarding the effectiveness of the variable length promoter regions in enhancing the expression of the normal COL1A2 gene.

Michelle Thoma

Major: Biology
University: University of Missouri-Columbia
Faculty Mentor: Dr. Susan Deutscher
Mentor Department: Biochemistry
Funded by: Molecular Imaging Program

Anti-galectin-3 peptides increase apoptosis in galectin-3 expressing human breast cancer cells

Michelle Thoma, Linda Landon and Susan Deutscher

A critical factor in the proliferation and the metastatic nature of carcinoma cells appears to be their resistance to natural programmed cell death (apoptosis). However, the molecular mechanisms that enable carcinoma cells to become resistant to cell death are unclear. Galectin-3 (Gal-3) is a protein that is found at elevated levels in a variety of primary and metastatic tumor cells that may play a key role in chemo-resistance and proliferation of carcinoma cells. Gal-3 has also been found to play a key role in the regulation of common apoptosis commitment pathways. Therefore, we hypothesize that peptides, which bind to and inhibit Gal-3 functions, could be used to reduce the anti-apoptotic activity of Gal-3 thus increasing the occurrence of cell death in carcinoma cells. Two cell lines were cultured, the human breast cancer cell line BT549 and a Gal-3-transfected derivative of BT549 (BT549/V). After undergoing apoptosis induction with 0.5 M staurosporine, apoptosis markers were detected fluorescently using flow cytometry. Our preliminary data suggests that, in the absence of anti-galectin-3 peptides, the parent BT549 cell line exhibits mitochondrial damage (decrease in mitochondrial membrane potential as detected by using MitoTracker Red fluorescence) by 6 hours of staurosporine treatment, whereas the BT549/V cell line shows little change in MitoTracker Red fluorescence even after 8 hours of apoptosis induction. A similar pattern is observed when changes in MitoTracker Red fluorescence are correlated with changes in phosphatidylserine translocation from the inner to outer surface of the plasma membrane. The current data suggest that cells transfected with Gal-3 have an increased rate of survival after apoptosis induction. In the next phase of this ongoing project, flow cytometric studies of changes in membrane permeability and DNA damage in parent and galectin-3 transfected BT549 cells will be conducted to further define the time-dependent apoptotic response of the BT549 parent versus BT549/V cells. Finally, we will observe and compare the effect of anti-Gal-3 peptides on induction of apoptosis in these two cell lines in order to determine if Gal-3 plays a key role in the anti-apoptotic nature of carcinoma cells and to test if anti-Gal-3 peptides are efficacious in inhibiting the anti-apoptotic functions of Gal-3.

Stefanie Timpe

Major: Chemistry
University: Bradley University
Faculty Mentor: Dr. J. David Robertson
Mentor Department: Chemistry
Funded by: NSF-REU/NIH Program in Radiochemistry

Effects of washings and treatments on the usefulness of hair as a biomarker

Stefanie Timpe, John Brockman, Vickie Spate and J. David Robertson

Hair is a useful matrix for the analysis of many trace elements found in the human body. Studies show that hair can incorporate trace metals into its structure during the growth process. Hair is an attractive monitor because unlike blood serum and urine, it is a metabolic end product and therefore inert. It is collected non-invasively, easily stored and disposed. Many studies in the literature attempt to correlate trace elements measured in hair to health, pollution exposure or to disease. Trace elements in hair can be accurately measured by Instrumental Neutron Activation Analysis (INAA). Hair samples must be cleaned before analysis to remove external contamination, there are many methods of sample cleaning, however there is not a standardized washing procedure. This study investigates pre and post collection cleaning techniques that may alter observed trace element concentrations in the hair. Two separate, post collection washing methods were studied: the International Atomic Energy Agency, IAEA, method, and the University of Missouri Research Reactor, MURR, method. The samples were then analyzed for Se, Ti, Mg, Mn, V, I and Zn using INAA at MURR. Selenium concentrations were unchanged. However, all other elements showed a significant reduction in concentration from the MURR to the IAEA method. It was also hypothesized that pre-collection cleaning with shampoos containing EDTA, a chelating agent, may be responsible for leaching some trace metals from hair. In order to determine the effects of shampoos on the sample, hair from a single subject was treated with three different types of shampoo. Two solutions of each shampoo were prepared in a 1:4, shampoo:water ratio. The hair was then washed in these solutions for either 1 or 24 hours for each type of shampoo. Hair washed with shampoo containing selenium sulfide resulted in a large selenium contamination despite cleaning with both the IAEA and MURR methods. The large variability between the post-collection cleaning techniques shows that a standard preparation method must be established before hair can be accurately used as a biomarker. Further studies must be done to determine if pre-collection shampoo treatment affects the validity of hair as a biomarker for trace elements.

Jeancarlo Torres

Major: Environmental Engineering
University: Polytechnic University of Puerto Rico
Faculty Mentor: Dr. William Miller
Mentor Department: Nuclear Science & Engineering Institute
Funded by: U.S. Department of Energy MNSEC Summer Undergraduate Research Program

Environmental report actualization for the license renewal of the University of Missouri Research Reactor Center

Jeancarlo Torres, Jocelyn M. Ocasio, Ronald J. Dobey and William Miller

Licensing requirements for power as well as non-power reactors must address environmental concerns related to radioactive emissions. The purpose and need for the renewal of the operating license for the Missouri University Research Reactor (MURR) is to allow continued studies in nuclear related undergraduate and graduate level degree programs along with continued production of radioactive isotopes for cancer treatment and research for an additional 20 years beyond the current license of 40 years which expires on November 21, 2006. The MURR is a multi-disciplinary research and education facility that provides a wide range of analytical, radiographic, and irradiation services to the research community and the commercial sector. The licensing requirements are established by the U.S. Nuclear Regulatory Commission in 10 CFR § 51.45 Environmental Reports - General Requirements. As part of the license renewal process the environmental report which was created on 2001 needed to be updated and revised to assure of the quality of the information. To study the hypothetical dose received by the public from the radioactive emissions that are released by the MURR during normal operations, the Environmental Protection Agency (EPA) COMPLY program was utilized. This program is intended for use by NRC licensees and non-DOE federal facilities to determine if they meet the radiation dose standards imposed by EPA under the Clean Air Act. COMPLY was utilized using an average of the last 10 years of the stack effluent which was measured in Curies per year. The results obtained from the program indicated that the MURR is in compliance for the emission released to the atmosphere.

Jacob Traas

Major: Biomedical Engineering
University: University of Michigan
Faculty Mentor: Dr. Dong Xu
Mentor Department: Computer Science
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Post-Translational modifications and the effects on protein identification through mass spectrometry

Jacob Traas, Zhao Song and Dong Xu

Mass Spectrometry is an effective tool for protein identification. A typical process for protein identification is to break down a protein into smaller peptides and to determine the mass of each of these peptides. These peptide masses are then compared against a database of proteins, to identify the protein which composes these peptides. Most proteins undergo co- and /or post-translational modifications such as glycosylation, phosphorylation etc after they are synthesized. Post translational modifications (PTMs), cause the masses of the peptides to be different than they are in the database, causing the computer programs to predict them incorrectly. While developing a program to accurately predict proteins using Mass Spectrometry, consideration must be given to such PTMs that may occur. The aim of the project was to modify a program currently in development, to allow the users to select some PTMs for consideration. The major challenge was to account for the PTMs without introducing large amounts of error into the system. In order to avoid the possibility of the program matching the mass of selected PTMs to false positive hits, the users will be instructed to only select a small number (less than 5) of PTMs. The actual program will be able to include an infinite number of PTMs, but the prototype only includes 47. There still needs to be some testing done as to which method of scoring gives the best confidence of the predictions. However, taking PTMs into account will definitely allow for a more successful identification of a larger number of proteins.

Kim Khanh Vu

Major: Environmental Science
University: Hartnell College and University of California-Berkeley
Faculty Mentor: Dr. Satish Nair
Mentor Department: Electrical and Computer Engineering
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

How do we know that we have Obsessive-Compulsive Disorder?

Kim Khanh Vu and Satish Nair

The brain is a network of neurons that control our pleasure, emotion, motivation and is important for all types of learning. The objective of the overall research in the OCD's group is to examine the changes in brain circuit, or neuroplasticity that cause Obsessive-Compulsive Disorder (OCD). Such interdisciplinary study requires information of many types: neuroanatomy (relevant regions), neurophysiology (cellular firing) and neurochemistry (neurotransmitters). The specific objectives were to assist with hypothesis development for OCD, to systematically collect information listed above and to work with modelers to develop a computational model for OCD in primates. The basis of this research is the hypothesis that the normal interactions of prefrontal cortical neurons with basal ganglia, thalamus, and amygdala are altered due to OCD, although the primary alterations and interactions remain unknown. Examination of the neuroplastic processes in these pathways will help uncover mechanisms of OCD. This analysis is facilitated by a two-tiered mathematical model for the representation of the brain circuits. At the cellular level (first tier), models can serve to highlight the mechanisms of neuroplasticity affecting firing of the neurons in the circuit. At the network level (second tier) the interactive effects between the brain regions can be studied. Data from primate and rat literature will be used to develop the model. A reliable computation model will help analyze the underlying causes systematically to comprehend the cellular/molecular mechanisms of OCD. After validation, the model can be used for predictive purposes including drug design and to further our understanding of the brain.

Matthew Waterman

Major: Biochemistry
University: University of Missouri-Columbia
Faculty Mentor: Lesa Beamer
Mentor Department: Biochemistry
Funded by: Life Sciences Undergraduate Research Opportunity Program

Structural basis for substrate specificity of the alpha-D-phosphohexomutase superfamily

Matthew Waterman, S.C. Griffith and Lesa Beamer

Phosphoacetylglucosamine mutase (PAGM) is a human enzyme that is the key to the formation of the essential metabolite UDP-N-acetylglucosamine. Bacterial phosphoglucomutase (PGM) from *Acetobacter xylinum* catalyzes the interconversion of glucose 1-phosphate and glucose 6-phosphate. PAGM and PGM are members of the alpha-D-phosphohexomutase superfamily which all catalyze intramolecular phosphoryl transfer on sugar substrates. These two analogs are similar in their mechanism, but dissimilar in their substrate specificity, not only to each other, but also to other well characterized (structurally and mechanistically) members of their superfamily. Protein expression and purification techniques were used to attempt to produce crystals to determine the three dimensional structures of human PAGM and bacterial PGM by X-ray diffraction in order to clarify the structural explanation for substrate specificity within the alpha-D-phosphohexomutase superfamily.

Jeremy West

Major: Chemistry
University: Truman State University
Faculty Mentor: Dr. Jack Tanner
Mentor Department: Chemistry
Funded by: Stevens' Chemistry Program

Expression, purification and initial characterization of *Halobacterium* proline dehydrogenase

Jeremy West and Jack Tanner

Nature recycles proline by converting it to glutamate. This 4-electron oxidation process is catalyzed by two catabolic enzymes, proline dehydrogenase (PRODH) and Δ^1-pyrroline-5-carboxylate dehydrogenase (P5CDH). Inborn defects in PRODH and P5CDH result in the disorders hyperprolinemia I & II, respectively. These conditions are often associated with mental retardation, convulsions, and brain disorders. PRODH has also been implicated in schizophrenia susceptibility, cancer and P53-mediated apoptosis. Despite their importance in human health and disease, these enzymes have not been extensively studied. Thus, the goal of this research is to characterize the structure and function of PRODH. The work presented here focuses on a newly discovered homologue of PRODH found in archaea, which we identified by bioinformatics analysis of genome sequence data. Archaea are also genetically more closely related to eukaryotes than bacteria, so study of their proteins may provide insights into homologous eukaryotic enzymes. Archaea are some of the Earth's oldest life forms and are known for living in extreme environments. The PRODH researched here is from the *Halobacterium* (salt-loving), which can be found in places such as the Dead Sea and the Great Salt Lake. Preliminary results so far include testing the expression of *Halobacterium* PRODH, known as YusM, in two different *E. coli* expression systems, BL21(DE3)pLysS and Rosetta2. The latter strain was used to account for rare codon usage by *Halobacterium*. Parameters varied in these expression tests included time and temperature of induction as well as IPTG concentration. After expression, the cells were broken in a French pressure cell and the cell debris was pelleted with centrifugation. YusM was found to be largely associated with the cell pellet; therefore protein purification under denaturing conditions was investigated. The use of urea as a denaturing reagent has been successful for purifying YusM. Once the protein was renatured it showed improved kinetic activity. We believe the improved activity is due to disruption of improperly folded protein by the denaturant, followed by re-folding into the native, or near-native, state. Further studies will need to be done to determine the cause of misfolding in the *E. coli* cell.

Amber Wiewel

Major: Fisheries and Wildlife
University: University of Missouri-Columbia
Faculty Mentor: Dr. John Faaborg
Mentor Department: Biological Science
Funded by: Missouri Ozark Forest Ecosystem Project

The effects of even-aged cutting on density and pairing success of Worm-eating Warblers

Amber Wiewel, Matthew Sailor, Richard Clawson, John Faaborg, and Paul Porneluzi

It is important for researchers to be aware of how timber management practices affect songbird populations. Certain forest management techniques can cause declines in breeding habitat of Neotropical migrant songbirds that require mature forest. The worm-eating warbler (Helmitheros vermivorus) is a common mature forest-dwelling species that may experience a decline in density due to habitat alterations such as clear cutting and selection cutting. As regeneration of the clear cuts occurs, mature forest-dwelling species may be able to utilize these areas as suitable habitat. This summer was the first year that worm-eating warblers settled on the 8 year old clear cuts on the sites of the Missouri Ozark Forest Ecosystem Project. We compared the relative abundance of worm-eating warblers that inhabited even-aged sites with those that inhabited control sites by using point counts of each site. In order to determine pairing success, we followed a singing male until the bird was seen interacting with a female or for 90 minutes if no interaction was seen. We hypothesized that the worm-eating warblers will have lower pairing success on even-aged sites (clear cuts) than control sites. We also hypothesized that the densities of worm-eating warblers would be the highest on the control sites and the lowest on the uneven-aged (selection cuts) sites, with the density of the even-aged sites falling slightly below that of the control sites.

LaDerrick Williams

Major: Biology
University: University of Arkansas-Pine Bluff
Faculty Mentor: Dr. Miriam Golomb
Mentor Department: Biological Sciences
Funded by: NSF-REU Program in Biological Sciences & Biochemistry

Localized adherence of *Haemophilus influenzae* to human lung cells in tissue culture

LaDerrick Williams, Matthew Bratkowski, Thomas Phillips and Miriam Golomb

The gram-negative coccobacillus *H. influenzae* is part of the respiratory mucosal flora of most healthy humans. Before the era of Hib vaccination, encapsulated *H. influenzae* of serotype b were the leading cause of childhood bacterial meningitis; at present, unencapsulated (nontypeable) strains of *H. influenzae* (NTHi) remain an important cause of respiratory infections such as otitis media, bronchitis, bacteremia, sinusitis, and pneumonia. Occasionally, NTHi strains (which are resistant to Hib vaccination) are isolated from Hib-vaccinated patients with meningitis or septicemia. During the past few years, much has been learned about how other pathogenic bacteria (particularly *E. coli*) colonize host tissue. Less is known about early steps in *H. influenzae* colonization, although a variety of non-pilus adhesins have been identified. We are studying the adherence of clinical NTHi strains to H292 (human lung carcinoma) cells in tissue culture, including the role of the autotransporter Lav, an outer membrane primary protein of unknown function which may play a role in adhesion or persistence. The NTHi being investigated have high molecular weight adhesins (either HMW or Hia). Quantitative adherence assays in which binding time was varied suggested that adherence is a multistep process. Bacteria exposed to H292 cells for 30-60 minutes bound less efficiently than those exposed for longer times (2-4h). The Lav protein did not contribute to short term binding but appeared to improve binding and internalization at 4h. NTHi labeled with a plasmid which expresses GFP (green fluorescent protein) were diluted and bound to H292 on cover slips. While adherence at 30 minutes was diffuse, adherence at 4h was highly localized, with microcolonies of 40-50 bacteria forming at discrete sites on cells. We are constructing a red fluorescent plasmid *for H. influenzae* to determine (by mixing red and green bacteria) whether microcolonies are the progeny of a single bacterial cell or arise by recruitment of multiple bacteria at the same prepared site. We are also staining H292 with fluorescently labeled phalloidin to determine whether microcolonies are associated with actin polymerization and cytoskeletal assemblies.

Stephen A. Williams

Major: Chemistry
University: Southern University of New Orleans
Faculty Mentor: Dr. Silvia Jurisson
Mentor Department: Chemistry
Funded by: NSF-REU/NIH Program in Radiochemistry

Reduction of rhenium^{V} oxo Schiff base complexes with triethylphosphine

Stephen A. Williams, Stephanie R. Lane, Nebiat Sisay and Silvia S. Jurisson

Pioneering techniques for therapeutic treatment of cancers involve targeting cancer sites with strong beta-emitting radionuclides, thereby destroying the cancer cells. This is achieved by coordinating the radioisotope to a very chemically stable environment and linking it to a specific biologically active targeting molecule, which interacts with particular cancer cells. Radioactive isotopes of rhenium possess characteristics of such a nuclide. The focus of our research is to investigate two possible pathways for the reaction of [ReOX(Schiff base)] with phosphine ligands, one a mono-substituted Re^{V} complex and one a di-substituted Re^{III} complex. The preferred Re^{III} complex is lower in oxidation state and more kinetically inert or stable relative to Re^{V}. For practical applications it is necessary to have an extremely stable *in vivo* radionuclide complex which can be conjugated to a suitable biological targeting agent.

The rigid sal_2phen ligand, where Sal_2phen is a tetradentate Schiff base ligand, was investigated to determine if the Re^{III} could be synthesized from the Re^{V} starting complex $[Re^{V}OCl(Sal_2phen)]$. $[Re^{V}OCl(Sal_2phen)]$ was reacted with triethylphosphine (PEt_3) in attempts to yield the Re^{III} complex *trans*-$[Re^{III}(PEt_3)_2(Sal_2phen)][X]$. Previous work indicated that the strongly reducing and strongly nucleophilic PEt_3 might yield the Re^{V} product from $[Re^{V}OCl(Sal_2phen)]$. The synthesized coordinated complex was reacted with an quaternary ammonium salt, ammonium hexaflurophosphate (NH_4PF_6), to induce crystallization of target compound $[Re^{III}(PEt_3)_2(Sal_2phen)][PF_6]$.

Preliminary ^{1}H-NMR, ^{31}P-NMR, and infrared spectroscopy spectra indicate the formation of *cis*-$[Re^{V}O(PPh_3)(Sal_2phen)][X]$. FTIR shows the presence of the Rhenium oxo group; ^{31}P-NMR and ^{1}H-NMR indicate the presence of Re^{V} and a 1:1 PEt_3 : Sal_2phen complex. Single crystal x-ray diffraction, mass spectroscopy, and elemental analysis are additional methods of characterization.

Jennifer Wilmot

Major: English Literature and Communications
University: Chestnut Hill College
Faculty Mentor: Dr. Sw. Anand Prahlad
Mentor Department: English
Funded by: Summer Pre-Graduate Research Experience for Students in the Humanities

"Either he was too weak, or the world was too strong": Motifs of male wounds and healing in African American literature

Jennifer M. Wilmot and Sw. Anand Prahlad

African American men throughout history have tried to establish and define their identities, collectively and individually, beyond those formed, forced, and fashioned by western civilization. Consequently, they have inflicted pain and despair, consciously and subconsciously, on the entire race, Black women, and regrettably themselves. African American literature, fictional and non-fictional, has served as a measure capable of providing a study of the African American experience as a whole. In examining its works, readers meet the achievements and failures, hindrance and progression of its people. HTML In this research I will briefly examine through literary analysis the intense emotional wounds and perspectives of two archetypal males in African American non-fiction and poetry; the severely indignant and the emotionally detached character. I will investigate relationships between the male character, their female counterparts and children if existent through the novels, *Jonah's Gourd Vine, Native Son*, and *In My Father's House*, as well as the poetry of Etheridge Knight. Specifically, I will determine the origin, infliction, and potential healing of their wounds by analyzing certain influences in their lives such as; being slaves or direct descendants of slaves, the household conditions they grew up in physically and psychologically, the presence and/or absence of parents, and the impression of Christianity. Furthermore, I will explore the suggestions made by the authors on how these characters, if possible, can regain their manhood.

Joseph Wilson

Major: Electrical Engineering
University: University of Florida
Faculty Mentor: Dr. Mark A. Haidekker
Mentor Department: Biological Engineering
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

Molecular free volume and viscosity changes in non-Newtonian fluids probed with molecular rotors

Joseph P. Wilson and Mark A. Haidekker

An empirical relationship between molecular free volume and viscosity has been established (Doolittle AK, *J Appl. Phys*. 1952; 23: 236-9). Non-Newtonian fluids hold much importance to scientific study because of their ubiquity in nature - from gelatins to starches to blood. The purpose of this study was to examine the relationship between molecular free volume and viscosity in non-Newtonian fluids under shear-thinning conditions. Molecular rotors are fluorescent probes for free volume. After photoexcitation, these molecules can decay from their singlet state either through radiation (fluorescence) or torsional relaxation (intramolecular rotation). In environments with low free volume, intramolecular rotation is hindered, and the radiative deexcitation pathway becomes dominant. This behavior is accompanied by a measurable increase in fluorescence intensity. Molecular rotors have been used successfully as viscosity probes in various fluids and polymers. Two molecular rotors, CCVJ (9-(2-carboxy-2-cyano)-vinyl-julolidine) and CCVJ-TEG (CCVJ-triethyleneglycol ester), were dissolved at 10µM in an aqueous solution of KelcoGelF (gellan gum) and subjected to shear forces both in a tube shear apparatus for fluorescence measurements and in a Haake VT-550 rheometer to determine the shear-thinning behavior. The gellan solution exhibited power-law behavior with an exponent n=0.48. In spite of this strong shear-thinning behavior, no change in rotor emission intensity was observed. Additionally, a novel behavior of some molecular rotors, a sensitivity towards fluid flow (Haidekker MA et al, *Sensor Lett*. 2005; 3: 42-8), was exploited to observe shear-thinning behavior by probing flow velocity in a tube. Under application of sufficiently high shear rates to cause shear thinning, molecular rotors revealed no change in free volume as observed with fluorescence intensity. This preliminary study suggests that molecular free volume and shear thinning are independent properties. Further studies will be needed to corroborate that the free volume of a fluid is not related to its viscosity in shear-thinning environments.

Lee Wright

Major: Biological Engineering
University: Mississippi State University
Faculty Mentor: Gabor Forgacs
Mentor Department: Physics and Astronomy
Funded by: NSF-REU Program in Biosystems Modeling and Analysis

The role of Periostin in regulating the biomechanical properties of cushion tissue

Lee Wright, Brook Damon, Russell Norris, Corey Mjaatvedt, Vladimir Mironov, Roger Markwald and Gabor Forgacs

During embryonic heart development the atrio-ventricular (AV) cushions swell and fuse to form the valves and septa of the adult heart. Initially, the cushions appear as swellings on the interior wall of the AV canal and eventually fuse to form the septum and valvular leaflets. The morphogenetic event that the cushions undergo during the fusion process is, in part, driven by the cohesive energy of the tissue, which can be described by the tissue's surface tension. It has been shown earlier that many properties of embryonic tissues can be interpreted by using the analogy that they behave as liquids and it is this analogy that gives rise to apparent tissue surface tension. Periostin is hypothesized to affect cushion tissue surface tension, through its possible binding of the extracellular matrix of the tissue. In this study virus containing the sense strand of Periostin DNA is introduced into hanging drops containing living explants of AV cushion tissue. Overnight the tissue explants rounded up to form spheroids allowing their surface tension to be measured and compared to the surface tension of AV cushion tissue explants exposed to a LacZ promoter control virus. The surface tension was determined using a specifically designed apparatus that measures the viscoelastic response of spherical explants due to a compressive force. It was expected that the increased production of Periostin in the cushion explants due to exposure to the virus will result in an increased surface tension compared to that of explants exposed to the control virus. The preliminary results of the experiment have displayed no significant difference of surface tension between the control virus and the Periostin virus. Since earlier research has shown a significant difference in the rate of fusion of cushions exposed to Periostin DNA virus and those exposed to the control virus, and because fusion time is characterized by the ratio of the surface tension and the viscosity of the tissue, we believe that Periostin may be affecting the viscosity of the tissue explants instead of the surface tension.

Mustafa Yousif

Major: Environmental Science
University: Alabama A&M University
Faculty Member: Dr. David Larson
Mentor Department: Forestry
Funded by: Louis Stokes Missouri Alliance for Minority Participation

Issues with scale using very high resolution digital aerial photographs

Mustafa Yousif, David Larsen and Robert Chastain

This study involves the use of remote sensing equipment to observe plant communities. A remote sensor is any instrument that gathers information about an object or area from a distance. Advanced cameras, the most common sensors used in aerial study, take photographs capable of revealing objects (vegetation, trees, etc...) only a few millimeters or inches in width from altitudes of 10 to 150 meters.

The objective of the projective is to determine the resolution to acquire the photographs. In this study, existing and current images are used to classify the vegetation into the classes as needed. The main goal is to classify the images based on the known targets. Images are taken primarily from helium balloons that have a digital attached to capture the image of the intended area of study. The tools used in this project are ERDAS Imagine 8.6 and ArcGIS for image processing and classifying the images into classes using colors and characteristics of the area and surroundings.