

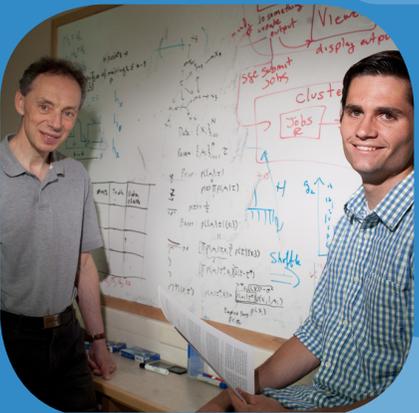
COS-JAM 2014

College of Science Joint Annual Meeting

Friday, May 2

Jordan Hall of Science

The eighth annual College of Science Joint Annual Meeting (COS-JAM) will take place on Friday, May 2 as part of the seventh annual Undergraduate Scholars Conference. The intent of COS-JAM is to highlight the achievements of undergraduate students conducting scientific research.



UNIVERSITY OF
NOTRE DAME

College of Science



COLLEGE OF SCIENCE - JOINT ANNUAL MEETING

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Schedule - Biological Sciences

Oral Presentations I

Jordan Room 105

1:00 - 2:30 p.m.

Moderator: Karim Ahmed

- 1:00 Gary Lamberti, Chair, Dept of Biological Sciences - Opening remarks
- 1:05 John McLaren - Evaluation of soundscape analysis as a tool for monitoring grassland bird diversity and abundance
- 1:20 Mary Schreck - Identifying Novel Olfactory Ligands by Exploiting Evolutionary Dynamics
- 1:35 Dayna Smith - Heavy Metal Contamination in Lake Michigan Wetland Turtles
- 1:50 Katia Fernandez Soto - The Role of APC in Chemotherapeutic Responsiveness of Breast Cancer
- 2:05 Rebecca Marton - Molecular characterization of actin cytoskeletal proteins during retinal regeneration

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

- Philip Allen, Ralph Hauke, Sarah Motter, Betel Ali, and Kelley Chan - Establishing a Functional Link Between StARD9 and NPC1-mediated Cholesterol Transport
- Patricia Amorado - Effects of glucose and phosphorus limitation on growth and uptake kinetics of freshwater bacteria
- Nicholas Anderson - The effects of a parasitic mite (*Ectrombidium locustorum*) on the competitive interactions between two pest grasshopper species *Melanoplus sanguinipes* and *Ageneotettix deorum*.
- M. Olivia Balmert - Investigating ARF6-mediated regulation of melanoma invasion
- Claire Bedalov - COX-2 expression and activity in *APC*-mutant breast cancer
- Alexandra Below - Dissecting the role of CCL2 signaling pathway in acquired resistance to anti-HER2 therapy
- Taylor Boland - Transcriptome shifting in brain metastasis and the role of the microenvironment
- Elena Brindley - Characterizing the Role of Vision in Mosquito Vector Competency
- Anna Carmack - Compartmental Epidemiological Modeling of Influenza in the United States with Wavelet Analysis
- William Chronister - The Prairie Peninsula: Where Was It, and Why?
- Kyle Cowdrick - Window to Discovery: Spatial and Temporal Delineation of Brain Metastatic Colonization
- Bonnie Leigh Crusier - Identification of a Novel Gene Required for Secretion in *Mycobacterium marinum*

Ryan Davila - Effects of ammonia and copper on Brine Shrimp (*Artemia franciscana*) populations in the Great Salt Lake

Nicholas Deason - Malaria Prevalence and Epidemiological Characteristics of Western Province, Solomon Islands

Allison Dianis - Swapping Spit: An assessment of demographics and habituation on simian salivary sampling

Margaret Dickson - The Evolution of Reproductive Isolation in the Seed Beetle *Callosobruchus maculatus* (Coleoptera: Chrysomelidae)

Michael Dinh - Specific Long-range Targeting of Amygdala Neurons onto Cortico-PAG and Corticoamygdalar Neurons in the Medial Prefrontal Cortex

Eric Donahue - A Chemical Genetic Screen of the ICCB Known Bioactives Library for Effects on Zebrafish Pronephros Development

Jonathan Dowd and Joshua Junge - Characterization of Putative Bacteriocins in *Lactobacillus ramosus* ATCC 21052

Lauren Firanek - A Revolutionary Molecular Diagnostic Method for Detection of Lymphatic Filariasis

Annika Fling - Hard to Swallow - Role of Food Material Properties on Chewing Patterns in Mammals

Gary George, Seung Yu, and Erin Clark - Light-regulated blood-feeding and flight behavior and a light phase response curve for the *Anopheles gambiae* malaria mosquito

Jeffrey Hansen - The Effect of Baboon Hybridity on Parasite Resistance Mechanisms

Katherine Hayman - Light Threshold and Preference Behavioral Studies in *Aedes aegypti*

Andrew Hildreth - Effect of Climate Change on the Endangered Karner blue Butterfly

Sara Hockney - Generation and Validation of a pax6b:GFP Transgenic Zebrafish Line

Alyssa Hummel - Ablation of the Id2 gene results in altered circadian feeding behavior, and sex-specific enhancement of insulin sensitivity and elevated glucose uptake in skeletal muscle and brown adipose tissue

Jonathan Jou - Deducing the role of fibroblast growth factor signaling in the regenerating zebrafish kidney

Jeanae Kaneshiro - Characterizing the Phosphorylation of Zwilch by the MPS1 Kinase

Sarah Khan - Multimodal Lymph Node Imaging with Nanoparticles Incorporating Fluorescent and Radioactive Reporters

Michael Kraft - Plants and mosquitoes: What do we need to know and why?

Alexandria Kristensen Cabrera - The Effects of Inhibiting Myosin II and PTEN on Neurite Formation and Axon Extension

John Kwon - Overlapping Roles of P31comet and Dynein in Silencing the Spindle Assembly Checkpoint

Elaine Lee - Feeding Frenzy: Diet and Symphyseal Biomechanics in Strepsirrhine Primates

Eunice Lee, Audrey Kelly, Megan Kilbride, and Anna Poteraj - Effect of RNA inhibition of JNK on the body size of *Aedes aegypti*

Miranda Madrid - Exploring the effect of climate on the voltinism and phenology of a butterfly hybrid zone using an individual-based simulation model

Michael McGraw, Josiah Nieto, Daniel Chrzanowski, Alexander Graves, and Christian Urbina - Influence of TNF α and Notch on Müller glia dedifferentiation and the role of Stat3 and Ascl1a in the cellular regeneration response

Amelia McReynolds, Brennan Sullivan, Alexander Rizk, Maribeth Golm, and Kaitlyn Dawson - Resistance to miltefosine in *Leishmania major*

Frank Mezzacappa - Ecdysone-induced protein 78C function in plasmatocyte survival and crystal cell fate commitment

Rachel Miceli - Genetic analysis of podocyte development

Melanie Mironovich - Interaction between the gut microbiome and intestinal parasites in wild baboons

Michelle Mueller - How Much Does Error Matter? Statistical Analysis of Data Entry Discrepancies in the PaleON Project

Rebecca Noble - TAG-320 Functions as a Brake on the Unfolded Protein Response in *Caenorhabditis elegans*

Michael O'Brien - Regulation of epithelial morphogenesis by Adenomatous Polyposis Coli

Elizabeth Owers - Imaging and 3D Printing of Trabecular Bone

Riley Parrott - Evaluating the Cost “Diapause Strategies” in the Overwintering Pupae of *P. glaucus*, *P. canadensis*, and Their Hybrids in a the Context of Climate Change

Andjela Pehar - Gene expression changes downstream of APC loss predict tumor phenotype

Steven Penny, Galvin Loughran, David Schmitz, and Miranda Burnette - Targeting the Polyamines in *Drosophila* Models for Tumorigenesis and Development

Samantha Piekos - Characterization of rod precursor proliferation and differentiation in the adult zebrafish retina

Stephanie Prince - Development of Imaging Protocols for X-ray Computed Tomography of Rats

Erika Rivera - Using Th40:Treg Ratio as a Predictor of Multiple Sclerosis and Other Autoimmune Diseases

Sarah Rohrman and June Tome - Gut Feelings: Diagnosis and Subtyping Analysis of *Blastocystis* Parasites in *Macaca fascicularis*

Elyssa Schwendy - A comparison of the components contained in hydrofracking fluid of three companies in three geographic regions

Joseph Scollan and Erin Franks - Diet-Induced Integration and Evolution of the Skull in a Rabbit Model

Alexandra Searle - The effect of light availability on zooplankton predator avoidance behavior and growth

Kaitlyn Simmons - Wnt/ β -catenin Signaling in Pancreatic Cancer

Erica Smith - Bioinformatic Approaches to Identify Novel Polyamine-Relevant Genes in *Drosophila Melanogaster*

Lucy Smith - Pancreatic Stem Cell Function Through Matrix Metalloproteinase-3

Kristin Springer - Roles of the notch and retinoic acid signaling pathways during zebrafish kidney regeneration after acute injury by gentamicin injection

Anna Szentirmai and Vincent Riccelli - Are You Really What You Eat? Cross-Sectional Bone Distribution in the Mandibles of Strepsirrhine Primates

Denise Tarnowski - Incorporation of Monoclonal Antibody Genes in Transgenic Silkworms

Christopher Tricarico - Regulation of Epithelial Glandular Architectures
Tyler Wagner - Are allozymes found in two species of butterflies leading to differential enzymatic performance and affecting species' ranges?
John Werner - A dissociation between diurnal cycles in locomotor activity, feeding behavior and hepatic PERIOD2 expression in chronic alcohol-fed mice
Andrew Wilson - Patterns of Contaminant Transport by Pacific Salmon in Great Lakes Tributaries
Clare Yarka - Sox2 is necessary and sufficient for Müller glial proliferation in the zebrafish retina
Abraham Yu - The Role of the Streptolysin-Associated Gene (*sag*) cluster in *Staphylococcus aureus*
Jessica Zic - Understanding the binding mechanism of VU0404251, a positive allosteric modulator of metabotropic glutamate receptor 5 a novel target for treatment of schizophrenia and cognitive disorders

Oral Presentations II
3:30 - 5:00 p.m.

Jordan Room 105

Moderator: Jon Savakus

- 3:30 Young Moon - Maturation and Retention of Rhodopsin in *Anopheles gambiae* Photoreceptors
3:45 Manuel Rocha - Patterned Expression of Two Rhodopsins in *Aedes aegypti* Larval Visual System
4:00 Nicholas Pagani - Ras mediated regulation of apoptosis in extracellular matrix attachment and detachment
4:15 Roger Smith - Validating Small Molecule Responses in *Plasmodium falciparum*

Schedule - Chemistry and Biochemistry

Oral Presentations I

Jordan Room 101

1:00 - 2:30 p.m.

Moderator: Steven Wietstock

- 1:10 John Rieth - Synthetic Pathway to Zampanolide
- 1:30 Michael Ahlers - Synthesis of GEX1A Analogues: A Potential Lead for Niemann-PickType C Disease
- 1:50 Ansel Nalin - Total Synthesis and Biosynthetic Investigation of Ambruticin J
- 2:10 Jennifer Martynowicz - Exploration of Nitroso-Ene Reactions

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

- Kathleen Anthony - RNA localization in *Xenopus* oocytes
- Gabrielle Going, Anna Heffron, and Mariana PradoAnaya - How do γ -Trimethylsilyl Groups Stabilize Carbocations?
- Kevin Hendzel - Squaramides and Thiosquaramides: Synthesis, Structure, and Chloride Binding
- Carolyn Keefe - Development of Novel Catalysts for the Copolymerization of CO[~2~] and Epoxides
- Megan Kennelly - Synthesis of (Z)-Methyl 4-(3-((5-(4-bromophenyl)furan-2-yl) meth-ylene)-2-oxo-5phenyl-2,3-dihydro-1H-pyrrol-1yl)benzoic Acid, A Possible Niemann-Pick Type C Therapy
- Maggie Kerper - Molecular profiling of aggressive breast cancer in a unique patient population from Kenya
- Kyle Lewellen - Monitoring Vascular Endothelial Growth Factor and CD31 Expression to Assess a Possible Link Between Obesity and Ovarian Cancer
- Megan McGarel - Influence of Matrix Metalloproteinase-3 on Metastatic Burden and Progenitor Cell-Driven Chemoresistance in Aggressive Breast Cancers
- Evan Merryman - The Effects of FLASH Knockdown on the Polyadenylation of Histone Transcripts
- Matthew Messina and Megan Fabry - Regulation of the Oncogene ZNF217 by Localization in Breast Cancer
- Matthew Metzinger - Correlation of X-ray Computed Tomography with Quantitative Nuclear Magnetic Resonance Methods for Pre-Clinical Measurement of Adipose Tissues in Living Mice
- Ellen Norby - Computational Studies of the Effect of Nucleation on Microtubule Steady-State Dynamics
- Matthew O'Neill - Synthetic Progress Towards Concanamycin F, A Potent Inhibitor of Vacuolar ATPase

Brian Shannon - ADAM10/Kuzbanian is Upregulated During Neuroendocrine Prostate Carcinogenesis
Laura Shute - Inhibiting EYA3 Tyrosine Phosphatase Activity Sensitizes Ewing's Sarcoma Cells to Etoposide Treatment
Rebecca Shute - Isolation of LpA-I and LpA-I/A-II Particles from HDL for Proteomic Characterization
Anna Sliwinski and Vincent Riccelli - Synthesis of Low Band Gap Conducting Polymers for High Performance Solar Cells
Joy Tao - The Maximum Loading Capacity of Copper on Cerium Oxide Catalysts
Toby Turney - The Use of Per-Acetylated Oligosaccharides to Study the Conformations of Glycans
Meredith Vieira and Andrew Gasparini - Heterologous Production of Linear Polyketide Analogs from Advanced Synthetic Substrates

Oral Presentations II

Jordan Room 101

3:30 - 5:00 p.m.

Moderator: Steve Wiestock

- 3:30 Sean McGee and Nicholas Myers - The incorporation of green design into iodine deficiency test: The Iron Nanoparticle "Kill Switch"
- 3:50 Joseph Ong - Using Yeast as Biosensor for Mutagenicity
- 4:10 Alexander Dang - Therapeutic Potential of Conantokins for Stroke
- 4:30 Maria Moreno Caffaro - The Role of Coagulation and Platelet Activation Markers in Platelet Dysfunction for a Rat Model of Traumatic Brain Injury

Schedule – Mathematics

Oral Presentations I

Jordan 310

1:00 - 2:30 p.m.

Moderator: Sonja Mapes

- 1:00 Jacob Haley - Graph Theory and Graceful Labelings
- 1:15 Monica Gorman - Zero-knowledge Proofs
- 1:30 Dillon Bak - A Study of Partial Differential Equations
- 1:45 Maria Corsaro - Modeling the Human Tear Film during a Blink while Wearing a Contact Lens
- 2:00 Austin Rodgers - On Matrix Invariants of Knots

Poster Presentation

Jordan Galleria

2:30 - 3:30 p.m.

Thomas Cziperle - Literature Review on Options Pricing Models and Delta Hedging
Caroline Jansen and Jack Burkart - Implementing methods in algebraic graph theory in Macaulay2

Oral Presentations II

Jordan 310

3:30 - 5:00 p.m.

Moderator: Sonja Mapes

- 3:30 Mitchell Faulk - Geometric vertex operator algebras: An approach to conformal field theory
- 3:45 Daniel Irvine - Knot Theory and Knot Invariants 2: Multi-Crossings
- 4:00 Jonathan Sheperd - Characteristic classes of complex vector bundles
- 4:15 Matthew Cole - Complex Tori and Elliptic Curves

Schedule - Physics

Oral Presentations I

Jordan 322

1:00 - 2:30 p.m.

Moderator: Jacek Furdyna

- 1:00 Sean Brudney and Benjamin Guerin - Bringing the Sun Down to Earth
- 1:15 Sean Howard - Radiocarbon Dating using Accelerator Mass Spectrometry at Notre Dame
- 1:30 Steven Jepeal, Sean Howard, James Miller, Sean Brudney, Kirby Hermansen, Benjamin Guerin - Radiocarbon Dating at Notre Dame
- 1:45 James Miller - Carbon-14 Graphitization Chemistry
- 2:00 Joon Seok Suh - The Risks and Benefits of an Alternative Source of Technetium-99
- 2:15 Sarah Russel and Elaine MacDonald - Experimental investigation of bone drilling performance

Performance / Film Presentation

Jordan Digital Visualization Theater

- 2:30 Matthew Cole - Visualizing Objects on the Galactic Scale

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

- Ian Broderick - Phase 2 CMS Upgrade Scintillating Materials
- David Howe and Joseph Hagmann - Magneto-transport study of topological insulator materials
Bi₂Se₃ and Bi₂Te₃
- Edward Kielb, Robert Stoddard and Taylor Corpuz - iLocator: An NIR Doppler Spectrometer
- Kyle McCall - A Scattering Theory Model of Molecular Graphene

Oral Presentations II

Jordan 322

3:30 - 5:00 p.m.

Moderator: Jacek Furdyna

- 3:30 William Cantrell - Computational Examination of Electron-Induced Dissociation of Hypoxanthine and Adenine
- 3:45 Andrew Jensen - Damage to DNA with Various Flow Rates by Atmospheric Pressure Plasma Jet
- 4:00 Emily Kunce - Effects of Atmospheric-Pressure Helium Plasma on Cysteine Solutions
- 4:15 Joanna Kabuye - Dissociative Electron Attachment to DNA in a DNA-Glycine mixture
- 4:30 Grace Meikle - Solar Cells: Understanding and Amending the Technology Transfer Disconnect
- 4:45 Christopher Sander - Optical Properties of Human Cancer and Normal Cells

Schedule – Advanced Diagnostics & Therapeutics

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

Elizabeth Huschke - Improvement of a Low-Cost, Field-Portable Thermocycler through Thermal Modeling and Imaging

Ireere Kwihangana - Investigation of DNA Amplification via Polymer Chain Reaction Using Open Source Technology

Robin Lawler - Integrated platform for nucleic acid sensing

Ivan Leung - Measuring urinary iodine at parts per billion level using a paper device

Sean McGee - The incorporation of green design into iodine deficiency test: The Iron Nanoparticle “Kill Switch”

Joseph Ong - Using Yeast as Biosensor for Mutagenicity

Schedule – Research in Compassionate Care

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

Jill Briody, Matthew Gervais, Matthew Harbrecht, Ivan Leung, John Mueller, Thomas O’Callaghan, Michael Russell, John Vernon, and R.J. Weir - Qualitative Study of Patient Perceptions of Physicians Who Have Broken Bad Medical News in the Best Manner Possible

Schedule – Spirit of Science Award Winners

Poster Presentations

Jordan Galleria

2:30 - 3:30 p.m.

Samuel Alber - How do bacteria move on different surfaces?

Patrik Bauer – Solar Tracker

Anthony Kavanagh - The Effects of Road Salt on *Daphnia magna*

Eric Liu - Encryption: The Perfect Hash

Sarina McCabe – Suffocated: A study of cellular damage due to smoking

ABSTRACTS

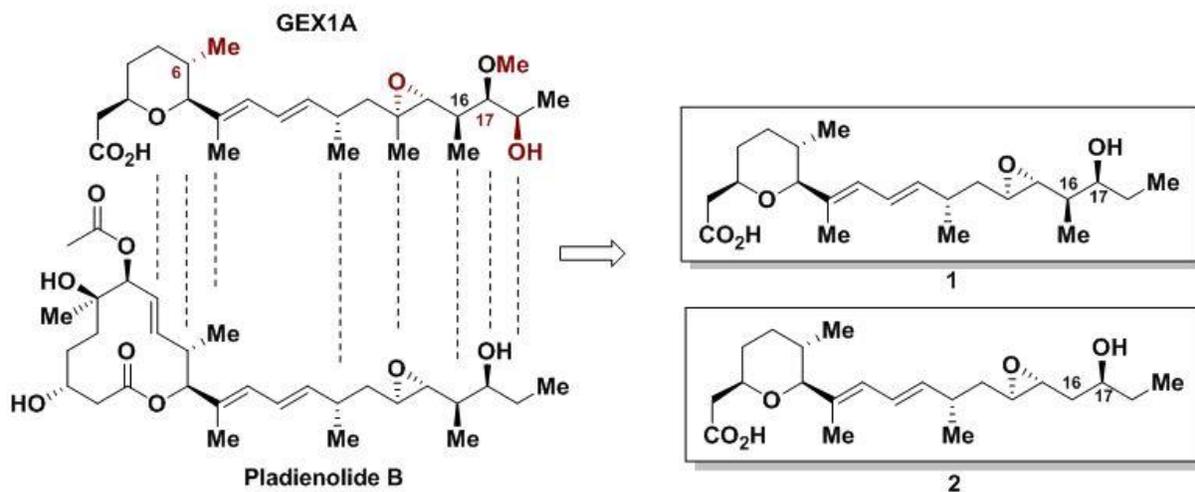
Oral Presentation

Synthesis of GEX1A Analogues: A Potential Lead for Niemann-Pick Type C Disease

Michael Ahlers
College of Science
Chemistry

Jarred Pickering and Eve Granatosky, Dept. of Chemistry and Biochemistry
Advisor: Richard Taylor, Dept. of Chemistry and Biochemistry

Niemann-Pick disease Type C (NPC) is a rare and fatal lysosomal storage disease that typically presents before the age of 10. Specifically, NPC is characterized by mutations to either the NPC1 or NPC2 proteins that result in defective cholesterol trafficking. Although hydroxypropyl β -cyclodextrin (HP β CD) and histone deacetylase inhibitors (HDACi) such as Trichostatin A are current therapeutic candidates for NPC, there remains no current FDA approved treatment. Our laboratory has recently demonstrated the ability of GEX1A, a type I polyketide natural product isolated from *Streptomyces chromofuscus*, to restore cholesterol trafficking in NPC1 mutant cell lines. The observed biological activity was of comparable levels to Trichostatin A, yet GEX1A is not an HDACi. In addition, we have observed the ability of GEX1A to restore cholesterol trafficking in HUVECs induced with the NPC phenotype. Thus, the synthesis of GEX1A analogues to be tested in NPC1 and NPC2 mutant cell lines is necessary in order to determine the minimal functionality required for activity against NPC as well as the mechanism of action of GEX1A. Intriguingly, novel anti-cancer natural product pladienolide B shares both structural and biosynthetic similarities with GEX1A. Accordingly, we are currently engaged in the synthesis of an analogue that incorporates the linear side chain of pladienolide B while retaining the western hemisphere of GEX1A (Figure 1). The synthesis is highlighted by novel crotylation chemistry¹ in order to set the requisite stereochemistry at C16 and C17 of analogue 1. As the synthesis of analogue 1 is nearing completion, efforts have been focused towards the synthesis of analogue 2 by modifying the Leighton crotylation to an allylation.



Poster Presentation

How do bacteria move on different surfaces?

Samuel Alber
Schmucker Middle School

Texture of shark's skin was noticed to control bacteria spreading which inspired development of new materials. How skin pattern regulates bacterial movement is not well understood. In order to study how the surfaces might affect the growth and movement of bacteria, we will use standard microbiology tests that grow bacteria on agar petri dishes. We will modify the surface in several ways to determine if the growth of the bacteria is influenced. The bacteria that will be used is a common non-pathogenic bacteria called *Myxococcus xanthus* (*M. xanthus*). This bacteria exhibits complex social behavior and is used to study the movement patterns of bacteria on surfaces.

To test how surfaces affect bacteria growth, we will change the surface of an agar plate by adjusting the percentage of agar used. This will result in harder or softer agar. We will also change the surface by squeezing the agar which will change the surface that the bacteria are growing on. Additionally, we will scratch the surface to create imperfections on the surface similar to shark skin.

To observe how well the bacteria are able to grow under the different conditions, the size of the bacteria colony will be measured over the course of 7-10 days. If the different surfaces affect the ability of the bacteria to grow and move, we hypothesize that this will determine how quickly the bacteria colonies' grow. We will also try to make microscope movies of the bacteria. The supervising adult Dr. Cameron Harvey will perform the microscopy and make movies, while the student will examine obtained movies to characterize movement of the bacteria on different surfaces.

Poster Presentation

Establishing a Functional Link Between StARD9 and NPC1-mediated Cholesterol Transport

Philip Allen, Ralph Hauke, Sarah Motter, Betel Ali, and Kelley Chan

College of Science

Biological Sciences

Ali Raja and Kevin Vaughan, Dept. of Biological Sciences

Advisor: Kevin Vaughan, Dept. of Biological Sciences

Neimann-Pick Type C (NPC) disease is a pediatric neurodegenerative disease characterized by pathological accumulation of cholesterol and other lipids in lysosomes. 95% of NPC cases result from a mutation in NPC1, a transmembrane protein with cholesterol binding activity. Although the exact nature of the disease remains unclear, lipid accumulations are thought to disrupt autophagy in neurons and other cell types. In the process of elucidating how mutant NPC1 leads to defects in cholesterol transport, the transmembrane protein StARD9 was identified as a new component of the cholesterol trafficking pathway. StARD9 contains a C-terminal cholesterol-binding StART domain, an N-terminal kinesin motor domain and is proposed to play a role in transporting cholesterol from the lysosomes to the Endoplasmic Reticulum. By analyzing the results of shRNA knockdown of StARD9 and comparing the phenotype to defective NPC1, we will characterize StARD9 and its role in cholesterol transport pathway. We will analyze the locations of cholesterol and other lipids using imaging assays as well as tests for defective autophagy and defective lysosomal tubulation. Similarities between mutant NPC1 and StARD9 knockdown would suggest the importance of StARD9 in the cholesterol transportation. Additionally, we will test if StARD9 induces HMG CoA reductase expression, a result which reflects an inability to sense endocytosed cholesterol. Our research is designed to provide a more complete understanding of StARD9's role in cholesterol transport.

Poster Presentation

Effects of glucose and phosphorus limitation on growth and uptake kinetics of freshwater bacteria

Patricia Amorado
College of Science
Biological Sciences

Advisors: Hildamarie Caceres-Velazquez and Stuart Jones, Dept. of Biological Sciences

While freshwater microorganisms play crucial roles in aquatic environments such as nutrient cycling, little is known about tradeoffs amongst microbial traits and how these traits affect overall ecosystem dynamics. Freshwater bacteria survival is dependent upon the availability of carbon resources like glucose and mineral nutrients including phosphorus. Previous research suggests tradeoffs between maximum growth rate and substrate affinity (half-saturation constant) and between capacity to capture carbon and phosphorus. In this study, we examined the uptake kinetics of glucose and phosphate for six species of freshwater bacteria. For each bacterial species, the maximum growth rate and the half-saturation constant was calculated for glucose-limited and phosphorus-limited experiments. Glucose-limited experimentation shows a general inverse relationship between the growth rate and half-saturation constant; but for phosphorus-limited experimentation, this inverse relationship is not as pronounced. We then compared our kinetics data to the genome sequences of the bacterial strains to look for possible correlations between growth kinetics and genes present in the genome. The observed tradeoffs in our study suggest potential resource-mediated coexistence amongst aquatic bacterial species. Finally, relationships between genome content and resource acquisition traits can improve our ability to predict bacterial functions and contributions to freshwater ecosystems based upon the genetic diversity present in a given aquatic environment.

Poster Presentation

The effects of a parasitic mite (Ectrombidium locustorum) on the competitive interactions between two pest grasshopper species, Melanoplus sanguinipes and Ageneotettix deorum

Nicholas Anderson
College of Science
Biological Sciences

Advisors: Gary Belovsky and Angela Laws, Dept. of Biological Sciences

To date, many studies have examined the effects of a natural enemy, such as a predator or a parasite, or competitor on an organism. Far fewer studies have examined how a natural enemy effects the interaction between competitors. Presently there is an increasing interest in integrating these traditionally separate fields with the goal of better understanding the true interactions between organisms. One of the possible applications for increased understanding of natural interactions is in the development of effective Integrated Pest Management (IPM). In keeping with these themes, this study explored the effects of an ectoparasitic mite, *Eutrombidium locustorum* (Walsh), on the interspecific competition between two pest grasshopper species, *Ageneotettix deorum* (Scudder) and *Melanoplus sanguinipes* (Fabricius). We hypothesized that parasitism by *E. locustorum* would increase *M. sanguinipes*' feeding activity and thereby increase its competitive impact on *A. deorum*. Field experiments were conducted to determine the effects of these combined interactions on the grasshopper species, while laboratory-feeding trials were done to examine changes in feeding behavior caused by parasitism. The results of these experiments suggest that *E. locustorum* increases the competitive ability of host *M. sanguinipes* by increasing its feeding activity and competitive ability both in late instar and adult grasshoppers. While many studies have shown the potential of *E. locustorum* as a biocontrol agent, the results of this study suggest that use of this mite should be more carefully considered, as the use of this mite to control one pest species may be countered by an increase in the destructive capabilities of another species. This suggests that further research is needed to better document *E. locustorum*'s potential as a biocontrol agent.

Poster Presentation

RNA localization in Xenopus oocytes

Kathleen Anthony
College of Science
Biochemistry

Advisor: Paul Huber, Dept. of Chemistry and Biochemistry

An essential aspect of development is the distribution of maternal information to specific regions of the egg prior to fertilization. In *Xenopus* oocytes, localization of specific mRNAs to either the animal or vegetal hemispheres reflects this cellular polarity. Vg1 mRNA is localized to the vegetal hemisphere, and a 340-nucleotide segment in the 3'-untranslated region, called the Vg1 localization element (VLE), is sufficient for proper localization. Six proteins bind directly to the VLE to form a ribonucleoprotein (RNP) complex that directs localization; however, these six proteins also bind to mRNAs that move to the opposite hemisphere of the oocyte. This observation indicates that there must be other, unidentified, factors that comprise the RNP complex and determine mRNA destination. To test this hypothesis, I am using RNAs that contain the VLE fused to affinity tags, known as aptamers. These tagged RNAs can be injected directly into oocytes to allow formation of the RNP localization complex *in vivo*; the aptamer allows for subsequent affinity purification. The protein composition of the retrieved ribonucleoprotein complexes will be determined using mass spectrometry. Three constructs, containing a Sephadex, streptavidin, or tobramycin aptamer, are being characterized for protein binding activity and recovery from cell extract. The RNA containing the tobramycin aptamer seems to be the most promising construct for microinjection. It specifically binds the six core proteins, indicating that the aptamer sequence does not inhibit formation of the ribonucleoprotein complex. The tobramycin matrix also recovered its cognate RNA more specifically and much more efficiently (>50% of input) than the other two. Current experiments are testing the activity of these aptamer constructs in whole cell extract before initiating microinjection of the RNA into live oocytes.

Oral Presentation

A Study of Partial Differential Equations

Dillon Bak
College of Science
Mathematics

Advisor: Jeffrey Diller, Dept. of Mathematics

Physical systems often can only be described by models that include more than one independent variable. As such, one cannot depend on ordinary differential equations, which only involve one independent variable, to describe such systems. Instead a proper description can only be obtained through partial differential equations, which depend on multivariable functions and their partial derivatives. One of the most popular examples of partial differential equations is the heat equation, which describes the flow of heat through a medium. The heat equation can then be used as an example by which the technique of separation of variables can be introduced. Other examples of partial differential equations important to the study of physics, namely the wave equation and Laplace's equation, will then be explored. Lastly, more generalized topics, such as Sturm-Liouville problems and generalized Fourier series, will be covered.

Poster Presentation

Investigating ARF6-mediated regulation of melanoma invasion

M. Olivia Balmert
College of Science
Biological Sciences

Alanna Sedgwick, Dept. of Biological Sciences

Advisor: Crislyn D'Souza-Schorey, Dept. of Biological Sciences

Metastatic melanoma is an aggressive disease with poor prognosis. While the five-year survival expectancy for those diagnosed with localized disease is over 98%, it declines to approximately 15% for those with distant metastasis. Early in disease, tumor cells leave their *in situ* environment and develop the ability to invade the surrounding tissue. Extensive efforts have been focused on elucidating the mechanisms of this invasive behavior. Our lab and others have identified ARF6 as a key modulator of tumor cell invasion, and recently, downstream of Wnt5a during melanoma invasion. The ARF6 exchange factor, GEP100, that facilitates GTP loading of ARF6 and identified to promote ARF6 activation in this pathway, is antagonized by SLIT2-ROBO1 signaling, which appears to recruit as-yet unidentified ARF6 GTPase activating proteins (GAPs). Ongoing studies are aimed at understanding the role of ARF6 GAPs in melanoma and how they may impact signaling downstream of Wnt5a.

Poster Presentation

Solar Tracker

Patrik Bauer
Mishawaka Catholic School

My hypothesis is that I can make a simple system with solar cells that can follow a light source. The procedure is connecting the solar cells to the motors, putting the cells on a turnable object, then shining light on the cells. My results were that when the cells were adjusted to the smallest degree (60 degrees) they tracked the light source much better. Overall, my hypothesis was indeed correct.

Poster Presentation

COX-2 expression and activity in APC-mutant breast cancer

Claire Bedalov
College of Science
Science Business

Advisors: Jenifer Prosperi, Indiana University School of Medicine – South Bend, Harper Cancer Research Institute, and Dept. of Biological Sciences, and Monica VanKlombenberg, Indiana University School of Medicine – South Bend

Breast cancer is the leading cause of cancer-related death in non-smoking women, and the most commonly diagnosed cancer in women. The Adenomatous Polyposis Coli (APC) tumor suppressor gene is mutated or silenced by hypermethylation in 18-70% of sporadic breast cancers depending on subtype; however, the molecular mechanisms downstream of APC loss in the breast remain largely unexplored. While inactivation of APC most commonly leads to increased signaling through the Wnt/ β -catenin pathway, there are multiple, less-investigated functions of APC, including regulation of GSK3 β -mediated signaling, proliferation, epithelial polarity, cytoskeletal organization, and DNA repair. Given that restoration of tumor suppressors is a hurdle in treating tumors arising from loss of gene function, it is critical to investigate and understand the downstream signaling pathways involved in tumorigenesis. Our laboratory is particularly interested in investigating the effect of APC loss or mutation in breast cancer, and the complex Wnt-independent signaling downstream of APC loss in the breast. We previously demonstrated that Apc mutation accelerates the mouse mammary tumor virus-Polyoma middle T antigen (MMTV-PyMT) transgenic model of breast tumorigenesis independently of Wnt/ β -catenin signaling. Interestingly, focal adhesion kinase (FAK)/Src/JNK signaling was up-regulated and required for the enhanced proliferation and squamous phenotype mediated by Apc mutation. Despite the lack of Wnt/ β -catenin pathway activation, Apc-mutant mammary tumor cell lines demonstrated enhanced expression of Cyclooxygenase-2 (COX-2) and production of prostaglandin E₂ (PGE₂), known to be important in triple-negative and inflammatory breast cancers, two aggressive breast cancer subtypes. While treatment with the Src inhibitor (PP2) decreases COX-2 protein expression, there is no effect on the level of phosphorylated JNK, indicating a non-linear signaling pathway. Consistent with this, treatment with an inhibitor of JNK (SP600125) has no effect on COX-2 expression. These data suggest that while Src activation downstream of Apc mutation enhances COX-2 in a Wnt-independent manner, the pathway does not travel through activation of JNK. Therefore, the mechanisms by which Apc mutation initiates this stream of events to enhance mammary tumorigenesis, and the contribution of COX-2 to the phenotypes acquired in APC-mutant breast cancer remain unclear.

Poster Presentation

Dissecting the role of CCL2 signaling pathway in acquired resistance to anti-HER2 therapy

Alexandra Below
College of Science
Biological Sciences

Advisor: Siyuan Zhang, Harper Cancer Research Institute and Dept. of Biological Sciences

Trastuzumab (Herceptin®) is a successful targeted therapy for HER2 overexpressing breast cancer. Despite initial therapeutic success, more than half of trastuzumab-treated patients exhibit a poor response with continual progression of the disease due to acquired resistance after subsequent rounds of treatment. The dynamic interactions between tumor and tumor microenvironment (TME) contribute to the development of acquired resistance to targeted therapy. Acquired resistance poses challenges both in the clinic and the lab, as management of HER2+ breast cancer and knowledge of mechanisms underlying resistance elude physicians and scientists. To effectively explore acquired resistance, we must better understand the crosstalk between the tumor and its local stroma. Reports have shown that not only do trastuzumab-resistant breast cancer cells overexpress the inflammatory chemokine (C-C motif) ligand-2 (CCL2), it is excessively released by surrounding TME cells, suggesting a role of CCL2 in the development of acquired resistance to trastuzumab. To elucidate the molecular mechanism driving acquired resistance by CCL2 and its receptor C-C chemokine receptor type 2 (CCR2), human cytokine arrays and transcription activator-like effector nuclease (TALEN)-mediated knockdown were initiated. Primary investigation via human cytokine array suggested that common cytokines of interleukin 6 (IL-6) and interleukin 8 (IL-8) are upregulated in human trastuzumab-resistant mammary cells (BT474.R) over parental line (BT474.P) expression. Surprisingly, CCL2 expression decreased in BT474.R in comparison to the parental line. Further studies are needed to confirm these results. In addition, required building halves of CCR2-specific TALENs, the ultra-precise restriction enzymes that cleave DNA through dimerization, were constructed and agarose gel verified. Completion of the TALEN is still needed through future Golden Gate reactions to perform CCR2 knockdown. Comprehensive understanding of the critical role of CCL2 in TME will allow for physicians and pharmaceuticals to make appropriately combined therapeutic approaches which will target both tumor cells and TME in order to improve drug efficacy over resistance.

Poster Presentation

Transcriptome shifting in brain metastasis and the role of the microenvironment

Taylor Boland
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Biological Sciences

Advisor: Siyuan Zhang, Harper Cancer Research Institute and Dept. of Biological Sciences

Metastasis is responsible for 90% of all cancer mortality and has remained an elusive area of cancer research and treatment. A degree of this complexity is due to the seed-and-soil hypothesis, which claims that metastatic cells seed in areas with a particular microenvironment with which the tumor cells can favorably interact. This leads to successful proliferation and survival of the cancer cells. Previous studies have suggested that this cross-talk between metastatic cells and the tumor microenvironment can impact expression within metastatic cells. That is, the ‘soil’ can induce unique changes within the ‘seed.’ Thus, it is possible that this tumor cell evolution leads to the development of the aggressive, fatal characteristics so often seen in metastatic cancers. So, identification of these changes is imperative in order to further understand the mechanisms by which metastatic cancer act. After analysis of publically available proteomic and cDNA tissue microarray data, we first observed a stark contrast between the molecular profiles of *in vitro* cancer cell cultures and *in vivo* metastatic tissue, further suggesting an impact of the microenvironment cells on metastatic tumor cell expression. Further analysis of these datasets revealed two distinct transcriptome shifts within the metastatic tumor cells. First, we witnessed a surprising global decrease of metabolic pathways in metastatic cells, unlike the Warburg effect-like metabolic changes commonly seen in primary tumors. However, metabolic pathways specific to the brain, such as the GABA pathway, were increased within the metastatic tumor cells. Second, we observed within the tumor cells an upregulation of several pathways responsible for classic neuronal characteristics, such as synaptic signaling, neuronal channels, and neuronal transmitters. These results support the role of the microenvironment in the successful evolution of disseminating cancer cells into metastatic tumors. Furthermore, these results suggest potential novel approaches for the treatment of brain metastasis.

Poster Presentation

Characterizing the Role of Vision in Mosquito Vector Competency

Elena Brindley

College of Science and College of Arts & Letters
Biological Sciences and Psychology

Matthew Leming and Michelle Whaley, Dept. of Biological Sciences

Advisor: Joseph O'Tousa, Dept. of Biological Sciences

Dengue and yellow fevers afflict over 400,000 people annually and are transmitted by the mosquito vector, *Aedes aegypti*. Because there are no known cures for these diseases, research has shifted to focus on vector control as a method to prevent disease transmission. Recent studies in our lab have revealed a very complex visual system in *Aedes aegypti*, suggesting that vision may play a crucial role in mosquito behavior. The mosquito retina contains photoreceptor cells that express opsin proteins responsible for initiating the visual transduction cascade. *Aaop1*, the primary opsin in *Ae. aegypti* adults, displays a light-dependent localization pattern within the R1-6 photoreceptor cells. This study focuses on generating visually impaired mosquitoes by developing TALEN transgenic lines that contain a knock out of the *Aaop1* gene, RNAi lines that have significant knockdown of *Aaop1* through nanoparticle feeding, and Vitamin A deprived lines that have decreased levels of all mature opsins. Following molecular verification of opsin knockout or knockdown and electrophysiological verification of visual impairment, these mosquitoes will be placed into behavioral assays. The first behavioral studies will measure the minimum light pulse time interval necessary to evoke a change in activity, the light intensity threshold at which adult mosquitoes stop responding to light, and light preference. These mosquitoes will then be studied in assays to measure vector competence behaviors such as blood-feeding, sugar feeding and oviposition efficiency. These approaches will test the hypothesis that visually impaired mosquitoes will demonstrate increased light response threshold, increased light intensity threshold, decreased light preference, and decreased behavioral efficiency. Comparison of results from wild type and visually impaired mosquitoes will demonstrate the role of vision in mosquito behavior. This could lead to novel interventions in the mosquito life cycle to reduce vector competency.

Poster Presentation

Qualitative Study of Patient Perceptions of Physicians Who Have Broken Bad Medical News in the Best Manner Possible

Jill Briody, Matthew Gervais, Matthew Harbrecht, Ivan Leung, John Mueller, Thomas O'Callaghan,
Michael Russell, John Vernon, and R.J. Weir
College of Science
Science Preprofessional
Elizabeth Moriarty, University of Notre Dame
Advisor: Dominic Vachon, Dept. of Preprofessional Studies

The ability for a physician to break bad news to a patient and his or her family has been shown to be of high importance in patient care and patient satisfaction. The research literature has generally focused on problems physicians have had in conveying bad news to patients or on training methods to help physicians develop this skill. While there have been studies examining patient preferences in how patients would prefer to be told bad news, there appears to be little research investigating what patients have actually experienced with breaking bad news done in the best manner by a physician. The goal of this research project was to interview patients and/or the patient's family or significant others and learn what they perceive when this is done well by physicians. Individual intensive interviews were conducted with ten participants using a qualitative grounded theory method with an appreciative inquiry approach. Research participants were recruited by advertisements in local media inviting people who felt their doctor did a good job of conveying bad news of their medical condition. Interviewers were trained in the nonbiased appreciative inquiry qualitative method and digitally audio recorded the interview sessions. Interviews were transcribed and analyzed using the NVivo10 software program with high levels of interrater agreement. Over 60 physician behaviors were identified as being important components for optimum delivery of bad news by a physician. Furthermore, participants described the optimum method of delivering bad news as involving three phases: the preparation for delivery of bad news, the actual delivery of the bad news, and the follow-up phase of physician support. These results will help physicians in practice and physicians in training gain important insights into what is perceived as helpful from patient perspectives in this very serious circumstance.

Poster Presentation

Phase 2 CMS Upgrade Scintillating Materials

Ian Broderick
College of Science
Physics

Advisor: Mitchell Wayne, Dept. of Physics

Phase 2 upgrades of the Compact Muon Solenoid (CMS) detector at the Large Hadron Collider (LHC) includes longer-term optimization projects that will be installed within the next decade. In particular, our research involves investigating the properties of various scintillators (both solid and liquid) as candidates for these particle-detector upgrade projects. The scintillators we tested include waveshift quenching liquids from Elgen Technologies (named 10 A&B, 11 A&B, 12 A&B, 13 A&B, 14 A&B, 15 A&B), as well as more standard solid scintillators including 201T and 3HF. We tested the scintillation properties of these scintillators by bombarding the scintillator with beta particles from a strontium-90 source and measured counts using a silicon-photomultiplier (SiPM) and oscilloscope setup. In addition, we also tested for the attenuation length of the liquid scintillators by placing them in small capillary tubes, exposing them to a violet LED in a light-tight box, and measuring the light received at the end of the tube using a photodiode. Because of the high levels of radiation inside the detector, we also exposed each scintillator to various levels of radiation at the Notre Dame Radiation Laboratory, re-running these tests to see how well each material stands up to radiation. Preliminary results show that these promising scintillators are fairly rad hard; we plan to continue researching these and other materials in order to optimize upgrades for the CMS detector.

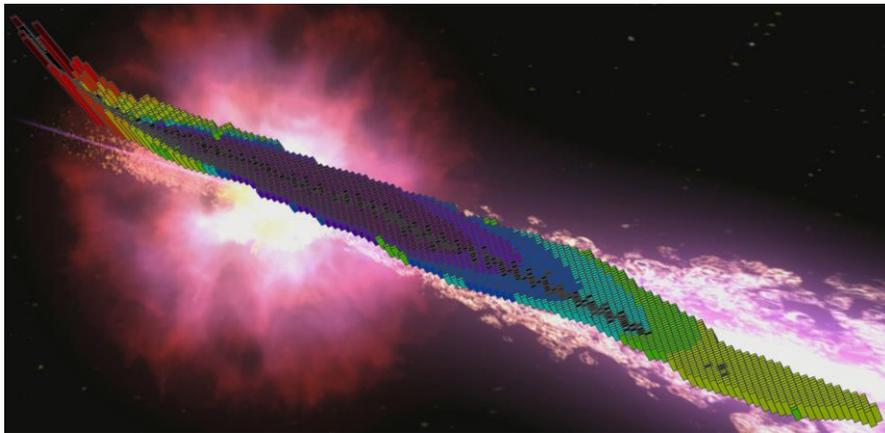
Oral Presentation

Bringing the Sun Down to Earth

Sean Brudney and Benjamin Guerin
College of Science
Physics

Advisor: Philippe Collon, Dept. of Physics

A critical aspect of doing research in science is communicating to others what your results mean. For those who are blessed to have it, some use their own drawing abilities to make diagrams and graphs. Basic computer programs that graph and diagram with precision are essential to accurately displaying scientific findings. Unfortunately, not everyone can read a 2D spectrum or an experimental diagram. If it were not for the amazing 3D videos developed by CERN when explaining how the LHC works, it is unlikely the world would have been as transfixed with particle physics and the search for the Higgs-Boson. This is why visualizing research in a creative yet scientifically accurate way is important for the science community to exchange discoveries internally and especially keeping the rest of the world involved. As animators for the Nuclear Science Lab, it is our job to depict science in a visually appealing and exciting way to engage audiences to learn. We work closely with the Accelerator Mass Spectrometry Group making charts, graphs, and animations that showcase the physical ideas behind their research. One of the most useful products so far is a 3D rendering of the entire nuclear physics lab. Not only does this provide a wonderful schematic markup for logistical purposes, but it also provides a medium through which an experiment that uses an accelerator can be explained, visualized, and even partially simulated such as PIXE, which uses X-rays to identify specific isotopes in a sample. Another project that a great amount of effort has been put into are the various basic nuclear reactions that take place in stars and that not only produce energy but also produce heavier elements that are the basis of life on Earth. These simulations can be especially useful as reference for those who do not have a perfect understanding of this process or simply as a learning tool for those who wish they did. The talk will cover not only the creative process but also the science behind it and show some of the rendered 3D simulations.



Oral Presentation

Computational Examination of Electron-Induced Dissociation of Hypoxanthine and Adenine

William Cantrell
College of Science
Science Business

Advisors: Sylwia Ptasińska, Dept. of Physics and Nicole Brinkmann, St Marys College

High-energy ionizing radiation (such as x-rays, gamma rays, and other quanta) is well-known to induce damage in biomolecules. One possible mechanism in which this can be done is the formation of unstable positive ions, which then dissociate into a radical and a positive ion, through interaction with low energy electrons. Two molecules in which this process is very important are the nucleobases adenine and hypoxanthine. Adenine is one of the four nucleobases that make up DNA, and hypoxanthine is a close relative of adenine that has been found in outer space. Through theoretical calculations, we have examined the fragmentation process in both adenine and hypoxanthine upon low energy electron impact resulting in the production of positive ions and neutral radicals.

In order to study this, the supercomputers at the Notre Dame Radiation Laboratory (NDRL) were used. The five most prevalent fragment masses detected experimentally were selected to be studied computationally¹. With those guidelines, we calculated the absolute energy for every possible conformer at each mass. We then compared the resulting energies and predicted the most likely conformer to be produced by identifying the conformer of the lowest (most stable) energy.

¹ M.M. Dawley, K. Tanzer, W.A. Cantrell, P. Plattner, N.R. Brinkmann, P. Scheier, S. Denifl, S. Ptasińska- Electron Impact Ionization of the Nucleobases Adenine and Hypoxanthine (in preparation)

Poster Presentation

Compartmental Epidemiological Modeling of Influenza in the United States with Wavelet Analysis

Anna Carmack

College of Science

Applied and Computational Mathematics and Statistics and Biological Sciences

Advisor: Benjamin Ridenhour, Dept. of Biological Sciences

Each year, between 5% and 20% of United States residents contract seasonal influenza. Most epidemiological models depend on influenza-like illness (ILI) reports, collected weekly by the CDC from outpatient practices, resulting in noisy and incomplete counts for influenza across the country. To obtain a more accurate picture of seasonal influenza, wavelet analysis was employed to filter the available ILI data for each region of the United States and find the wavelet remainder best correlating with regional positive lab tests (an indicator of a true presence of influenza). That wavelet remainder was then fit to an SEIR compartmental model using a Markov chain Monte Carlo selection method to determine epidemiological parameters such as basic reproduction number (R_0) and generation time (t_{gen}) for each region during the influenza seasons. The average basic reproduction number was found to be 1.379 (1.34, 1.39), and the average generation time was found to be 2.563 days (2.45, 2.68). Using the nine US Census regions over ten years, the SEIR model fit to the wavelet analysis output estimated 26.30% (23.83%, 28.76%) of ILI regional reports to be true cases of influenza. Region and influenza season (year) were found to have little to no significance on influenza epidemic parameters or ILI proportion estimates, suggesting homogeneous influenza dynamics across the United States.

Poster Presentation

The Prairie Peninsula: Where Was It, and Why?

William Chronister
College of Science
Biological Sciences

Advisor: Jason McLachlan, Dept. of Biological Sciences

The Prairie Peninsula is an important but poorly understood historical feature of the American Midwest that can be better understood by collecting vegetation data in settlement era Public Land Survey (PLS) notes. Edgar Transeau's 1935 map of the region depicted a bulge of prairie extending from the Mississippi River east through Illinois and into Indiana, surrounded on the north, east, and south by forest. This hand-drawn map has been widely accepted in the decades since its publication, but the paper lacks any accompanying data to support the mapped regions of prairie and forest. As part of the Paleo-Ecological Observatory Network (PaleON) Project, forest data (density and species composition) were gathered from pre-Euro-American settlement Illinois and Indiana surveys and used to reconstruct the landscape as it existed prior to widespread European settlement. In the process, Transeau's map was tested for accuracy and potential causes of the geographical location and shape of the Peninsula were examined. These findings will not only provide greater clarity for an historical ecological feature but also point out potential drivers of prairie and forest ecosystems. Knowing the environmental factors that contribute to the maintenance of ecosystems, especially irregular regions such as the Prairie Peninsula, has important implications for understanding the processes of modern global change.

Oral Presentation

Complex Tori and Elliptic Curves

Matthew Cole
College of Science
Mathematics

Advisor: Gabor Szekelyhidi, Dept. of Mathematics

I will explain what a torus is and how modding out the complex plane by a lattice produces a torus. Then I will introduce elliptic curves and explain how their points may be made into a group. Finally, I will bring complex tori and elliptic curves over \mathbb{C} together by stating their equivalence and giving a partial explanation of it.

Performance / Film Presentation

Visualizing Objects on the Galactic Scale

Matthew Cole
College of Science
Mathematics

Advisor: Keith Davis, Dept. of Physics

The Milky Way is close to 100,000 light years in diameter, while the farthest man-made object from the Sun is less than a light-day away. Consequently, it is difficult to determine even such simple facts as how far away or how big objects in our galaxy actually are. Astronomers' best guesses at an object's distance often have large margins of error, and it is not uncommon for new data to revise calculations by 50% or more. Moreover, even when good data are available for an object, it is hard to visualize that object's place relative to the other things in the sky. We choose several supernova remnants and globular clusters in or nearby the Milky Way. Globular clusters are clumps of millions of stars that are gravitationally bound together, and supernova remnants are the expanding remains of exploded stars. Using the Digital Visualization Theater, we explain what these objects are, including their historical significance, and show them as they appear from Earth. We then show their actual sizes and positions at the galactic scale, as measured by astronomers' current best guesses. We attempt to explain why it is hard to measure distance accurately, and we show how our reckoning of an object's absolute size varies with our reckoning of its distance and the large margin of error thereof. Finally, we simulate the orbits of stars in a globular cluster, and conclude by showing how small the entire galaxy is, globular clusters, supernova remnants, and all, compared to the universe.

Oral Presentation

Modeling the Human Tear Film during a Blink while Wearing a Contact Lens

Maria Corsaro
College of Science

Mathematics and Psychology

Advisors: Zhiliang Xu, Dept. of Applied and Computational Mathematics and Statistics, Daniel Anderson, George Mason University, Dept. of Mathematical Sciences, and Padmanabhan Seshaiyer, George Mason University, Dept. of Mathematical Sciences

Millions of people worldwide wear contact lenses. The presence of a contact lens on the eye changes the behavior of the human tear film. This paper examines this relationship during the period of the blink when the upper eyelid is opening. A model is created through the use of standard thin film assumptions and is then reduced to a nonlinear partial differential equation for the thickness of the tear film. Two different models for the lipid layer are incorporated into the model. Additionally, expressions that describe the motion of the eyelid, the motion of the contact lens and the tear fluid flux are utilized. These expressions are designed to correlate with experimental data. A numerical solution to the partial differential equation is then calculated, using the method of lines. This solution is used to discover the shape of the tear film for the specific set of conditions being explored. The results obtained by this method are then compared to experimental data for similar conditions. In this way an accurate model that describes the behavior of the human tear film during a blink and while a contact lens is placed on the corneal surface will be created.

Poster Presentation

Window to Discovery: Spatial and Temporal Delineation of Brain Metastatic Colonization

Kyle Cowdrick
College of Engineering
Chemical Engineering

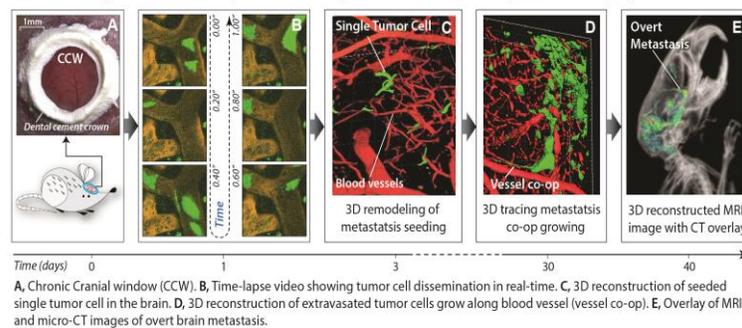
Wendy Alvarez Barrios and Ian Guldner, Dept. of Biological Sciences
Advisor: Siyuan Zhang, Harper Cancer Research Institute and Dept. of Biological Sciences

The molecular mechanisms regulating early metastatic colonization of disseminated tumor cells are among the greatest unsolved mysteries of metastasis. The crosstalk between the disseminated tumor cells and the distant metastatic microenvironment (TME) influences how the single metastatic cell will evolve and form a secondary tumor, and how this micro-metastasis will respond to therapeutic intervention. Despite significant clinical advancements in metastasis research, it remains elusive how disseminated tumor cells colonize and adapt to dynamic surroundings, thrive at distant organ sites vastly different from the microenvironment of the primary site, and ultimately form life-threatening overt metastatic tumors. By nature, metastatic colonization is a dynamic process with unique spatial and temporal characteristics. There are no approaches established that can accurately address the spatial and temporal dynamism of metastasis within an intact tissue.

Taking a novel approach to decipher the molecular mechanisms of metastatic colonization, we integrated cutting-edge rapid prototyping, intravital imaging, tissue clearing techniques and an *in vivo* brain metastasis animal model to portray the metastatic cytotype – here defined as the cellular identity, quantity, and location of various cell types that comprise a tumor and its microenvironment – down to the single cell level. First, we utilized cranial imaging windows coupled with two-photon intravital imaging to track the behavior of single metastatic tumors cells in real-time. We visualized the temporal dynamics of an early stage tumor in its native metastatic niche and observed striking vessel cooperation during brain metastasis development. Second, we successfully adapted novel tissue clearing approaches for unprecedented imaging of intact brain metastatic TME in 3D space up to 2mm depth. More importantly, through immunofluorescence staining and computer-aided reconstruction of multiphoton imaging datasets, we demonstrated specificity and reproducibility of molecular delineation of cytotypes in the 3D brain metastatic microenvironment.

As demonstrated in our preliminary study, these advancements are a faithful characterization of tumor and its metastatic microenvironment during the critical stage of colonization. Furthermore, they provide an unprecedented capability to explore the cytotypes of early stage metastases and the molecular mechanisms that are vital for developing future novel therapies for brain metastasis.

Figure 6 Multimodality real-time tracing of the brain metastasis by intravital imaging



Poster Presentation

Identification of a Novel Gene Required for Secretion in Mycobacterium marinum

Bonnie Leigh Cruser

College of Science and College of Arts & Letters

Biological Sciences and Philosophy

George Kennedy, Rachel Schluttenhofer, and Patricia Champion, Dept. of Biological Sciences

Advisor: Patricia Champion, Dept. of Biological Sciences

Tuberculosis (TB) killed 1.3 million people and infected 8.6 million in 2012. It is well established that the causative agent of TB, *Mycobacterium tuberculosis*, requires a functional ESX-1 protein secretion system to cause disease in humans. However, the basic molecular mechanisms of ESX-1 mediated protein secretion are not fully understood. We aim to gain a better understanding of the ESX-1 secretion system so secretion can be blocked in *M. tuberculosis*. To accomplish this, *M. marinum* is used as a model system for *M. tuberculosis*. A *M. marinum* transposon insertion library was screened to discover novel genes required for ESX-1 secretion. A mutant strain, 246A9, was identified by smooth colony morphology, a phenotype previously linked to ESX-1 deficient strains. Further analysis revealed that the 246A9 *M. marinum* strain was ESX-1 deficient by red blood cell lysis and failed to secrete ESAT-6 or CFP-10, two known protein substrates of the ESX-1 system. DNA sequencing of the 246A9 strain showed that the transposon is located 21 base pairs downstream of MMAR_4414. Since 246A9 is ESX-1 deficient, MMAR_4414 must encode a necessary component of the ESX-1 system. We conclude that MMAR_4414 is involved in mycobacterial secretion. Further study is needed to investigate the function of the MMAR_4414 encoded protein in the ESX-1 secretion system. To more effectively fight *M. tuberculosis*, the mechanism of mycobacterial secretion must be understood. This research lays the groundwork for new vaccinations and treatments of TB.

Poster Presentation

Literature Review on Options Pricing Models and Delta Hedging

Thomas Cziperle

Mendoza College of Business and College of Science

Finance and Applied and Computational Mathematics and Statistics

Advisor: Huy Huynh, Dept. of Applied and Computational Mathematics and Statistics

Financial options have been traded in great volumes by both financial institutions and retail investors in the past few decades. In this paper two popular models for pricing options are discussed: binomial model and the Black-Scholes model. We also review a portfolio strategy titled delta hedging, a type of hedge that is widely used by derivative dealers and financial institutions to reduce or eliminate a portfolio's risk exposure to an underlying. Finally, we perform a simulation study for delta hedging and compare its performance to other trading strategies.

Oral Presentation

Therapeutic Potential of Conantokins for Stroke

Alexander Dang
College of Science
Biochemistry

Advisors: Rashna Balsara and Francis Castellino, W.M. Keck Center for Transgene Research
and Dept. of Chemistry and Biochemistry

Ischemic stroke is a global health problem and is a major cause of death and disability in developed countries. The release of excess glutamate during an ischemic stroke leads to hyperactivation of the N-methyl-D-aspartate receptor (NMDAR) that is expressed throughout the central nervous system. In particular, the GluN2B subunit of the functional heterotetramer is hyperactivated during this neuropathology. Conantokin-G (con-G), a peptide that has antagonistic activity towards the NMDAR and exhibits selectivity for the GluN2B subunit, was utilized in this stroke study. The stroke model employed was the Middle Cerebral Artery Occlusion (MCAO), as >80% of stroke cases in humans are ischemic stroke. Brains from rats that were either stroked, or stroked and intrathecally injected with 2 μ M con-G were sacrificed at 4 hr or 24 hr, stained with TTC, and imaged to assess edema and infarct size. Additional histological analyses performed to evaluate the therapeutic effect of con-G, included hematoxylin and eosin, FluoroJade B, Von Kossa, and Microtubule associated protein-2 staining. Treatment with con-G significantly decreased the number of degenerated neurons and average number of calcium deposits in the penumbra region of the brain. Con-G decreased ischemia-induced brain infarct size and damage to the brain cytoarchitecture. Stroke-mediated surface expression of GluN1 was diminished in the penumbra of the con-G treated rat brains compared to untreated rat brains. Also, con-G treated rats displayed improved neurological deficits compared to untreated rats. These results suggest that con-G has therapeutic properties in ischemic stroke. Further studies that will be performed to include the immunohistological staining for GluN2A and GluN2B subunits. The aim of this research is to utilize this data to develop safe and effective therapeutic agents that can specifically antagonize the NMDARs for treatment of ischemic stroke.

Poster Presentation

*Effects of ammonia and copper on Brine Shrimp (*Artemia franciscana*) populations in the Great Salt Lake*

Ryan Davila

College of Science and College of Arts & Letters

Biological Sciences and Political Science

Advisor: Gary Belovsky, Dept. of Biological Sciences

The Great Salt Lake (GSL) is a unique ecosystem being the fourth largest and the least human-impacted hypersaline lake in the world. Brine shrimp (*Artemia franciscana*) are the dominant grazers in the GSL food web, a relatively species poor ecosystem due to its high salinity. These invertebrates are abundant and are the main source of food for many resident and migrating water birds meaning that they have important ecological and conservation value. Also, in the present day, brine shrimp cysts are harvested and sold because of their use as a food source for larval fish and crustaceans. The annual economic value of this business is an estimated US \$50-100 million. In this project, brine shrimp acute toxicity assays using ammonia and copper are performed in order to create water quality criteria for the GSL. These two pollutants are actively being discharged into the GSL and were identified as priority pollutants by the State of Utah Division of Water Quality and were selected because of their potential threat to invertebrate species. It is hypothesized that as toxicity levels increase, survivorship levels of brine shrimp will decrease and that there will be a level for each toxin where survivorship will be zero. We are in the process of gathering data for this project and we expect that the data will tell us the maximum concentration of toxin possible before brine shrimp populations will be in trouble of rapid decline, putting the fragile GSL ecosystem in danger of collapse and the brine shrimp business in peril of crashing. Future directions for this project include expanding testing to include lead, another identified potential pollutant, and expanding experiments to include chronic assays to determine long-lasting effects of these chemicals on brine shrimp populations, ultimately being more representative of what will actually occur in the GSL.

Poster Presentation

Malaria Prevalence and Epidemiological Characteristics of Western Province, Solomon Islands

Nicholas Deason
College of Science
Biological Sciences

Diego Echeverri Garcia, Neil Lobo, and Frank Collins, Dept. of Biological Sciences
Thomas Burkot and Tanya Russel, Faculty of Medicine, Health and Molecular Sciences
and Australian Institute of Tropical Health Medicine, James Cook University
Advisor: Neil Lobo, Dept. of Biological Sciences

Malaria is a mosquito-borne disease that affects millions of people each year, with over 600,000 deaths globally in 2012. Recently, Solomon Islands set a goal of nationwide malaria elimination. Decades of long-lasting insecticidal nets (LLIN) and indoor residual spraying (IRS) interventions have greatly reduced, but not eliminated malaria in Solomon Islands. Instead, the primary malaria vector, *Anopheles farauti*, has undergone a shift from late-night endophagic bloodfeeding to early-evening exophagic bloodfeeding. Presumably, these behaviors are selected for by LLINs and IRS, which may have reached the limit of their effectiveness. Thus, behavioral resistance could be a contributing factor to the persistence of malaria transmission. Before novel interventions that target changing vector behaviors can be tested, basic knowledge is needed about the malaria prevalence and epidemiology of Solomon Islands. We conducted a baseline survey of malaria prevalence in 19 villages across 5 islands in Western Province, Solomon Islands. The survey of 3,837 volunteer subjects revealed an overall malaria prevalence of 16.59%, with prevalences in individual villages ranging from 5.13% to 44.04%. Of 188 samples chosen for additional analysis to determine parasite species, 95.2% were *Plasmodium vivax* while 4.8% were *Plasmodium falciparum*. Our method of malaria diagnosis was direct PCR amplification of *Plasmodium* 18s rRNA from human blood-spots collected on filter paper. A series of tests performed on cultured parasites of known dilution showed the PCR method to be sensitive to at least 1.6 parasites/ μ l of blood. Other characteristics of the sample population were recorded including sex, age, and tympanic temperature. Overall, malaria prevalence in Western Province was higher than expected, with a large number of asymptomatic cases. The asymptomatic population likely serves as a parasite reservoir for continued malaria transmission. The data collected in this survey will allow us to pair similar villages for a planned case-control study evaluating the effectiveness of a novel intervention: insecticide impregnated barriers.

Poster Presentation

Swapping Spit: An assessment of demographics and habituation on simian salivary sampling

Allison Dianis
College of Science
Biological Sciences

Hope Hollocher, Dept. of Biological Sciences

Agustin Fuentes, Dept. of Anthropology

Amy Klegarth, Dept. of Biological Sciences

Michael Gumert, Crystal Riley Koenig and Jayasri Narayanan,

Dept. of Psychology, Nanyang Technological University

Advisor: Agustin Fuentes, Dept. of Anthropology

Saliva samples can be used to obtain DNA, hormone profiles, and nutrient analyses. Here we describe the use of cotton oral swabs for the collection of DNA from wild long-tailed macaques in Singapore (*Macaca fascicularis*). Urban macaques are particularly well suited for the collection of saliva samples via swabs, as their habituation to humans enables researchers to approach, offer, and recollect swabs with relative ease. Although poised to become an increasingly utilized sampling method, little is known about sampling biases that may arise due to differences in demographic structure and habituation level. To investigate this question, we looked at instances of multiply sampled individuals in terms of troop demographics and independently assessed habituation metrics to determine if and when particular subgroups of individuals are likely to be over-represented. From 675 saliva samples collected from wild *M. fascicularis* on Singapore, 127 individuals were multiply sampled. Within the sample subset, 46 locations were represented, across which trends were investigated using a variety of statistical analyses. Individuals represented by multiple samples from the same collection day were first sorted by sex and age class. Locations were then sorted by a habituation score measured based on distance measures for flight response and attraction to food. Statistical tests including one-way ANOVAs and two-tailed t-tests were performed between the full data set of individuals and within each location by habituation division. I hope to determine if group demographics or habituation has a stronger influence on which sex or age class is multiply sampled more frequently by looking at these test both in relation to and independent of habituation score. Data suggests that multiple sampling occurs significantly more in adults than the other age classes, and that males multiply sample significantly more frequently than females, but statistical analyses must be performed to determine the influence of habituation. This information can be used to predict and account for which age class or sex is most likely to be over-represented in field collected saliva samples.

Poster Presentation

*The Evolution of Reproductive Isolation in the Seed Beetle *Callosobruchus maculatus* (Coleoptera: Chrysomelidae)*

Margaret Dickson
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Biological Sciences

Glen Hood, Jeffrey Feder, Scott Egan, and Meredith Doellman, Dept. of Biological Sciences
Frank Messina, Dept. of Biology, Utah State University
Advisor: Jeffrey Feder, Dept. of Biological Sciences

Ecological speciation is the process by which barriers to gene flow evolve between populations due to ecological divergent selection between different environments. As new species form, barriers to gene flow evolve that reproductively-isolate diverging populations. One type of pre-zygotic isolating barrier, sexual isolation, reduces the rate of copulation between diverging populations during secondary contact. In many taxa, the evolution of sexual isolation is rapid. However, without knowing when diverged lineages initially split, knowing how rapid is difficult. To better understand the rate and pace of the evolution of sexual isolation in a historical proximate context, I conducted mating experiments using the seed beetle, *Callosobruchus maculatus* (Coleoptera: Chrysomelidae). *Callosobruchus maculatus* is a specialized pest of dried, stored legumes. We induced a host shift of *C. maculatus* from the ancestral mung creating three separate and independently derived populations established on lentil in the laboratory and allowed each lentil population to persist for 80 generations. To determine if sexual isolation has evolved between the ancestral mung and the three independently derived lentil lines of *C. maculatus* we performed a total of 546 no choice mating trails. Males and females from conspecific (control) and heterospecific (each mung x lentil combination) populations were placed inside a petri dish and observed for 30 minutes. During these mating trails, we measured the following six variables: (1) presence of copulation, (2) time to first copulation, (3) length of first copulation (4) total number of copulations, (5) length of the longest copulation and (6) total time spent copulating. With the exception of the length of the first copulation, ANOVA revealed no significant differences between in the remaining five variables. Our results could be attributed to insufficient period of time since divergence (only 80 generations) to detect the sexual isolation and/or weak selection pressures between environments. Alternatively, other types pre- and post-zygotic reproductive isolation may have evolved that will form the basis of future studies of host plant adaptation in this system.

Poster Presentation

Specific Long-range Targeting of Amygdala Neurons onto Cortico-PAG and Corticoamygdalar Neurons in the Medial Prefrontal Cortex

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Ashley Ferreira, Indiana University School of Medicine – South Bend
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Advisor: Patrick Sheets, Indiana University School of Medicine – South Bend
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The medial prefrontal cortex (mPFC), periaqueductal gray (PAG), and amygdala are brain regions important for stress and fear responses. Elucidating specific connectivity and circuit physiology for these regions is crucial for understanding the biology of anxiety and related disorders. Reciprocal pathways between the mPFC and amygdala are known. However, specific connections onto defined neurons within these regions are unknown. We hypothesized that amygdala inputs to the mPFC specifically target neurons projecting back to the amygdala and to neurons projecting to the PAG. Using the mouse as a model, we identified cortico-PAG (CP) and corticoamygdalar (CA) neurons in mPFC using retrograde tracers. Concurrently, we injected the amygdala with an adeno-associated virus (AAV) to express channelrhodopsin-2 (ChR2) in neurons projecting to the mPFC. Neurons expressing ChR2 can be specifically activated using 470 nm light. In acute brain slices, synaptic connections were recorded in CP and CA neurons following activation of amygdalar axons in mPFC. This identified specific amygdalar axonal targets in the mPFC. These findings suggest that input from the amygdala to the mPFC is crucial for regulating mPFC output to the PAG and amygdala.

Poster Presentation

A Chemical Genetic Screen of the ICCB Known Bioactives Library for Effects on Zebrafish Pronephros Development

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Advisor: Rebecca Wingert, Dept. of Biological Sciences

Chemical genetic screening is a relatively new technique that allows for the phenotypic assessment of small molecules to determine if they can alter signaling pathways affecting development, organogenesis, and/or other biological processes *in vivo*. Zebrafish have emerged as a valuable model for chemical genetics due to their high degree of genetic conservation with humans. Additionally, zebrafish embryos can be easily drug treated by adding small molecules to the embryo media, making them an ideal model for chemical genetics. The zebrafish embryonic kidney comprises basic functional units called nephrons, which are similar to their human homologues. Here, we performed a chemical genetic screen using the ICCB Known Bioactives Library to gain novel insights into molecules that affect nephron development. We found that 78/480 compounds induced morphological defects in the pronephros. Of these, 2 compounds promoted podocyte development, whereas 7 hindered it; 24 compounds promoted proximal convoluted tubule development, whereas 36 hindered it; and 21 compounds promoted distal early tubule development, whereas 14 hindered it. To further identify any potential hits, a second round of screening will be conducted using the ICCB library at multiple drug concentrations. This screen will be completed by July 2014, which will enable several compounds to be selected for in-depth characterization. Specifically, we seek to delineate these compounds' relationships to the retinoic acid-signaling pathway, which induces proximal segment development during nephrogenesis. Elucidating these pathways will provide useful information to better understanding of kidney development and to provide a basis for drug discovery with inherent translational value.

Poster Presentation

Characterization of Putative Bacteriocins in Lactobacillus rhamnosus ATCC 21052

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Probiotics have found recent popularity in the food industry as a way to promote good health. A subset of probiotics are bacteriocins, small proteinaceous compounds that bacteria produce to kill other competitor bacteria. Lactic acid bacteria, found in the human gastrointestinal and urogenital tracts, are common producers of bacteriocins. One such bacteria strain is *Lactobacillus rhamnosus* ATCC 21052. This strain was previously identified to produce bacteriocins having antibacterial activity against several notable competitor species, including *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes*, and *Staphylococcus aureus*. After identifying bacteriocin activity, the goal was to isolate the specific genes responsible for the production of bacteriocins. Using genomic analysis and homologies to known bacteriocins, three putative bacteriocins were identified in the *Lactobacillus rhamnosus* ATCC 21052 genome. RT-PCR was performed to confirm that these genes were transcribed by the strain. Next, the conditions of bacteriocin production were altered in the hope that they would affect both the level of antibacterial activity and the transcription levels of the putative bacteriocins, establishing a correlation between the transcription of the genes and bacteriocin activity. The pH and media type for *L. rhamnosus* growth were altered. *L. rhamnosus* was also co-cultured with *E. coli* to determine whether direct competition could induce bacteriocin production. The results demonstrated that transcription of the putative bacteriocins, especially GI150 and GI0738, were closely linked to greater antibacterial activity against *E. coli*, indicating that these genes are likely responsible for some sort of bacteriocidal action. The putative bacteriocin genes have since been cloned into a TOPO-TA vector and will subsequently be cloned into a PET-27 plasmid in an effort to artificially generate bacteriocin production. The identified bacteriocins could have wide-reaching applications ranging from food preservatives to antibacterial therapeutics.

Oral Presentation

Geometric vertex operator algebras: An approach to conformal field theory

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Mathematics

Advisor: Katrina Barron, Dept. of Mathematics

In this talk, we present one possible algebraic formulation of a geometric approach to the study of quantum field theory, namely, the notion of a geometric vertex operator algebra, as found in [H]. More specifically, we first introduce a basic geometric substructure consisting of genus-zero world sheets together with a type of composition on this substructure given by sewing these world sheets together. This substructure is studied up to conformal equivalence, that is, up to deformations of these world sheets by angle-preserving maps. Combining the approach of [H] and the results of [BHL], we then introduce a type of algebraic object over this substructure of genus-zero world sheets, which is called a geometric vertex operator algebra. If time permits, we interpret geometric vertex operator algebras as constructions closely related to topological field theories as developed in [ST].

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Oral Presentation

The Role of APC in Chemotherapeutic Responsiveness of Breast Cancer

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Science Preprofessional Studies

Monica VanKlompberg, Indiana University School of Medicine – South Bend
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Advisor: Jenifer Prosperi, Indiana University School of Medicine – South Bend,
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Breast cancer is the leading cause of cancer-related death in non-smoking women. Specific subtypes of breast cancer respond differently to chemotherapeutic and targeted therapies driven by distinct oncogenic events and signaling pathways. The Adenomatous Polyposis Coli (APC) tumor suppressor is mutated or hypermethylated in 18-70% of sporadic breast cancers; however, the effect of APC mutation on tumorigenic properties remains unexplored. APC binds both directly and indirectly to microtubules and regulates multiple components of the DNA repair pathway, suggesting it may play a critical role in therapeutic responsiveness. Through Real-Time PCR, *ApcMin/+* mouse model demonstrated alterations in expression of two ATP-binding cassette transporters, multidrug resistance protein 1 (MDR1) and ATP-binding cassette sub-family G member 2/Breast Cancer Resistance Protein (ABCG2/BCRP), both of which are critical in predicting responsiveness to therapeutic agents. Given that one aspect of therapeutic resistance is an increase in tumor initiating cells (TIC), an ALDEFLUOR assay was performed and surprisingly showed a decrease in TIC population in cells from MMTV-PyMT;*ApcMin/+* mice. In addition, cells from MMTV-PyMT;*ApcMin/+* mice were more sensitive to paclitaxel and 5-fluorouracil via MTS assay. To translate our findings to human breast cancer cell lines, we utilized DU4475 cells, which harbor a mutation in APC in the β -catenin binding region, and MDA-MB-157 cell with shRNA lentiviral APC knockdown. We have generated stable DU4475 cell lines expressing the middle region or C-terminal domain of APC, and demonstrated that these cell lines have increased sensitivity to paclitaxel, 5-fluorouracil, cisplatin, and doxorubicin. Combined, these data suggest that APC does modulate therapeutic resistance in breast cancer cells in a context-dependent manner. Future studies will involve testing the specificity of APC in regulating the therapeutic response in the PyMT-derived cell lines, as well as in both human breast cancer cell lines, DU4475 cohort and APC knockdown MDA-MB-157 cells.

Poster Presentation

A Revolutionary Molecular Diagnostic Method for Detection of Lymphatic Filariasis

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Science Preprofessional Studies

Advisor: Gregory Crawford, Dept. of Physics

Lymphatic Filariasis (LF) is a neglected tropical disease that affects nearly 120 million people worldwide. Though this disease is not generally fatal, it is considered the leading cause of disability worldwide due to clinical symptoms. Recently, the World Health Organization (WHO) classified LF as potentially eradicable, and launched a global program to eliminate the disease as a public-health problem. The majority of individuals infected with filariasis, show no external signs of infection, often living completely asymptomatic despite a presence of adult worms and microfilariae. This makes diagnostic tools that can efficiently and cost-effectively diagnose LF increasingly important for the delivery of appropriate treatment, monitoring of the disease, and tracking of disease prevalence globally. Here, we explore the usage of a novel diagnostic method to identify the presence of the parasite that causes lymphatic filariasis, *Wuchereria bancrofti*, in human blood, comparing its sensitivity, specificity, and cost-effectiveness to other available diagnostic methods. The NESDEP IU is a molecular diagnostic device that permits rapid sample preparation and identification of genetic material, from water, food product, or bodily fluid samples. It takes advantage of microfluidic biochip technology with probe-functionalized carbon nanotubes that hybridize target DNA, while allowing the bulk of the fluid and any non-target DNA to flow through undetected. Current identification of genetic materials for medical, environmental, or food safety applications is often limited to processes involving a laboratory and a turnover time that can be more than 24 hours. The NESDEP IU is able to complete the process from sample to measurement and assay in as little as 45 minutes or a few hours without a laboratory, and is transportable and operates at low voltage for field use. Our findings suggest that the device can accurately amplify and detect the *W. bancrofti* DNA. We hope to continue work in elucidating the best overall protocol to decrease the time and cost of each test.

Poster Presentation

Hard to Swallow – Role of Food Material Properties on Chewing Patterns in Mammals

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Matthew Ravosa, Dept. of Biological Sciences
Advisor: Matthew Ravosa, Dept. of Biological Sciences

In evaluating the functional link between diet and mandibular form, prior experimental and comparative studies typically lump together data on foods of different material properties which is often incomplete for the subjects used to characterize a given species. Greater control on within-subject variation in feeding behavior would increase our understanding of the evolution of the mammalian skull by providing information on how dietary properties influence jaw-loading patterns. Here, we use 19 adult rabbits to analyze intraspecific variation in diet-induced chewing patterns during mastication. Three foods that vary in stiffness and toughness were used for our video-based analyses of feeding behavior. Observations consisted of a feeding bout where a rabbit was offered a given mass of hay. Once the hay was processed and ingested, that subject was then fed an equal mass of pellets, a procedure that was ultimately repeated for carrots. This facilitated an intra-individual assessment of the functional ability to process foods of different properties. Three chewing parameters were quantified from video footage shot at 60 frames/second: chewing frequency (chews/sec), chewing duration (sec) and chewing investment (chews/gram). In pairwise comparisons of hay vs. pellets, pellets vs. carrots, and hay vs. carrots, we found that chewing duration and chewing investment was significantly higher for the more mechanically challenging items. Chewing frequency was independent of food material properties, averaging about 4Hz. In all three sets of comparisons, analysis of stress-limited and displacement-limited fragmentation indices for hay, pellets and carrots allowed us to determine that variation in chewing investment and chewing duration is due largely to an item's stiffness. Therefore, stiff, rather than tough, foods underlie repetitive loading of feeding structures, which contradicts previous scenarios emphasizing toughness as a determinant of daily loading cycles. These findings have implications for understanding the evolution of masticatory behavior and diet-induced variation in the mammalian skull.

Poster Presentation

Light-regulated blood-feeding and flight behavior and a light phase response curve for the Anopheles gambiae malaria mosquito

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Seung Yu

College of Science
Science Business

Erin Clark

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Aaron Sheppard, Samuel Rund, and Giles Duffield, Dept. of Biological Sciences

Advisor: Giles Duffield, Dept. of Biological Sciences

Biting behaviors in *anopheline* mosquitoes are time-of-day specific, with a greater abundance of biting occurring during the dark phase of their photoperiod. We investigated how a single light pulse administered at the beginning of the night effected biting behavior. Additionally, *An. gambiae* locomotion has a distinct circadian rhythm, characterized by nocturnal activity bouts. We investigated how precisely timed light pulses delivered throughout the circadian cycle can shift the activity rhythm, leading to the synthesis of an *An. gambiae* Phase Response Curve (PRC). To investigate biting inhibition, two incipient *An. gambiae* species (S and M molecular forms) were treated with white light (10 min, 150-800 lux) at the onset of complete darkness and the percentage taking a blood meal was recorded every 2 hr up to 8 hr. To produce an anchored PRC, S-form mosquitoes received a single 30 min pulse of light at various times during the immediate 24 hr transitioning from LD to DD. The pulse significantly reduced biting tendency in the S-form mosquito for 2 hr after administration (at 0.20 hr and 2 hr), with variable responses observed at 4 hr, and no differences detected at 6 and 8 hr (one factor ANOVA, $p < 0.05$). Conversely, M form mosquitoes, were unresponsive to the light treatment, *i.e.* their biting tendency did not change (*n.s.*). For the PRC analysis, as seen in most other examined species, *An. gambiae* mosquitoes demonstrated distinct delays and advances in circadian phase when light was presented during the early and late subjective night, respectively. These data reveal a strain-specific effect of acute light treatment on biting behavior that is both immediate and sustained. The *An. gambiae* PRC is qualitatively similar to several model insect and vertebrate organisms. At present, insecticidal treated bed-nets designed to prevent mosquito-human contact and kill mosquitoes, are relied upon to prevent malaria transmission; as mosquitoes and malaria parasites are becoming increasingly resistant to insecticidal and drug treatments, respectively, there is a necessity for the development of innovative control strategies. The inhibitory and phase shifting effects of light may prove to be an effective tool in assisting with these strategies.

Poster Presentation

How do γ -Trimethylsilyl Groups Stabilize Carbocations?

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Science Preprofessional Studies and Studio Art and Design

Anna Heffron

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Biochemistry

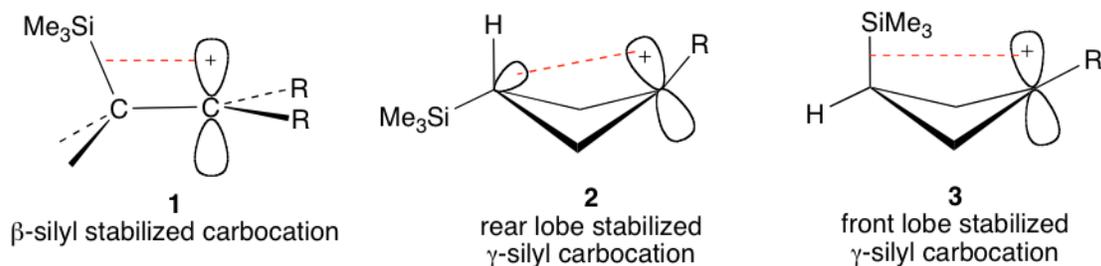
Mariana PradoAnaya

College of Science

Science Preprofessional Studies

Advisor: Xavier Creary, Dept. of Chemistry and Biochemistry

Trimethylsilyl groups are known to have a stabilizing effect on a carbocation when in close proximity. This dramatic effect, as shown below in a β -trimethylsilyl carbocation 1, has been attributed to an interaction of the carbocation vacant orbital with the adjacent C-Si σ -bond. The effect of silicon on a carbocation's stability when in the γ -position, as in cations 2 and 3, has been investigated in less detail. Given the large stabilizing effect of the trimethylsilyl group in the β -position it was anticipated that the trimethylsilyl group in the γ -position would also provide a stabilizing effect. We have evaluated the ability of trimethylsilyl groups to stabilize carbocations of type 2 and 3 using experimental measurements of reaction rates. We have also used computational chemistry to calculate the magnitude of trimethylsilyl stabilization of types 2 and 3. Our results suggest that cations 2 are greatly stabilized by rear lobe stabilization due to the trimethylsilyl group. However, cations 3 show no observable or calculated front lobe stabilization due to the trimethylsilyl group.



Oral Presentation

Monica Gorman 2014 Abstract — Zero-knowledge Proofs

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Chinese and Mathematics
Advisor: Jeffrey Diller, Dept. of Mathematics

Zero-knowledge proofs are a means by which Alice may prove to Bob that she possesses a certain piece of information, without revealing to him or to third parties what that information is. I will discuss zero-knowledge proofs in general as well as their applications in cryptography and information theory, and demonstrate and explain a specific example of zero-knowledge proofs: a proof that Alice has the factorizations of some very large number that does not disclose to Bob how he might factor the number himself.

Oral Presentation

Graph Theory and Graceful Labelings

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Mathematics

Advisor: Sonja Mapes, Dept. of Mathematics

Graph theory is one of the most widely studied areas in the field of combinatorics, and it has numerous applications to fields such as chemistry, computer science, and sociology. One of the disciplines most famous problems is the Ringel conjecture, a 50-year-old problem that concerns the structure of complete graphs. One of the most promising methods of approaching the conjecture concerns what are known as graceful labelings of graphs. In this talk, we will define a graph and introduce some key examples such as paths, cycles, trees, and the complete graph. Then, we will introduce the concept of a graceful labeling, and we will determine when a few important graphs are graceful. Finally, we will define the join of two graphs, and we will introduce some recent results concerning the gracefulness of joins.

Poster Presentation

The Effect of Baboon Hybridity on Parasite Resistance Mechanisms

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Elizabeth Archie, Dept. of Biological Sciences

Susan Alberts and Jenny Tung, Dept. of Biology, Duke University

Advisor: Elizabeth Archie, Dept. of Biological Sciences

The effect of hybridity upon the fitness of individuals varies across species. For instance, the concept of hybrid vigor proposes that hybrid organisms benefit from outbreeding. Alternatively, hybridization may be costly if it disrupts locally-adapted gene complexes or leads to super-optimal MHC diversity that results in T-cell depletion. The baboon population in the Amboseli basin lies in a natural hybrid zone between two sub-species: yellow baboons, *Papio cynocephalus*, and Anubis baboons, *Papio cynocephalus Anubis*. Using genetic hybrid data and measures of gastrointestinal parasitism, this project hopes to explain the effect of hybridity on patterns of parasitism. We predicted that, if parasite diversity is unique to each sub-species and environment, yellow baboons may have better resistance to parasites unique to the Amboseli ecosystem and consequently have a lower parasite load compared to immigrant Anubis baboons and hybrids. In support, preliminary results suggest that in females, both increased hybridity and increased Anubis ancestry correlates with increased burden of the most prevalent and costly parasite, *Trichuris trichiura*. Conversely, in females, greater Anubis ancestry correlates with a decreased burden of *Abbreviata* sp., another relatively common and costly parasite. This study is among the first to explore the effects of hybridity on parasitism in a wild primate setting and results will have implications for understanding the selective forces that may maintain species boundaries.

Poster Presentation

Light Threshold and Preference Behavioral Studies in Aedes aegypti

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Joseph O'Tousa, Dept. of Biological Sciences

Advisors: Michelle Whaley and Joseph O'Tousa, Dept. of Biological Sciences

Yellow fever and dengue fever affect more than 100 million people annually. Increased understanding of the primary vectors of these illnesses, specifically *Aedes aegypti*, may give new insight into avenues for the reduction of disease transmission. Current work has suggested that the visual system in mosquitos is much more complex than might be expected based on other insect models, indicating that vision may play a significant role in vector competence behaviors. This study examined the role of the visual pathway in the light avoidance behaviors of *Ae. aegypti* larvae. The responses of larvae to varying degrees of light stimulus were studied to determine light detection thresholds and light preference. Three types of larvae were compared: wild-type red-eyed larvae, mutant white-eyed (Wh) larvae, and larvae raised on a vitamin A deprived diet. Individual larvae were introduced into a four-quadrant light gradient from a light box below. The amount of light was altered by addition or removal of neutral density filters. Measurements of the amount of time required for larvae to flee the brightest quadrant, the time required before larvae left the dark, and the number of larvae in each quadrant over the course of one minute were analyzed to characterize the light response. We hypothesize that the lack of red pigment molecules in the eyes of the Wh larvae would leave them more sensitive to light, while the vitamin A deprivation would reduce the ability of the larvae to produce functional rhodopsin, rendering them unable to perceive and respond to lower levels of light. Further experiments with TALEN visual mutants will be studied in larval light avoidance behavior. Gaining an understanding of vision-based behaviors in mosquito larvae could lead to developments that decrease their survivability and vector competence.

Poster Presentation

Squaramides and Thiosquaramides: Synthesis, Structure, and Chloride Binding

Kevin Hendzel

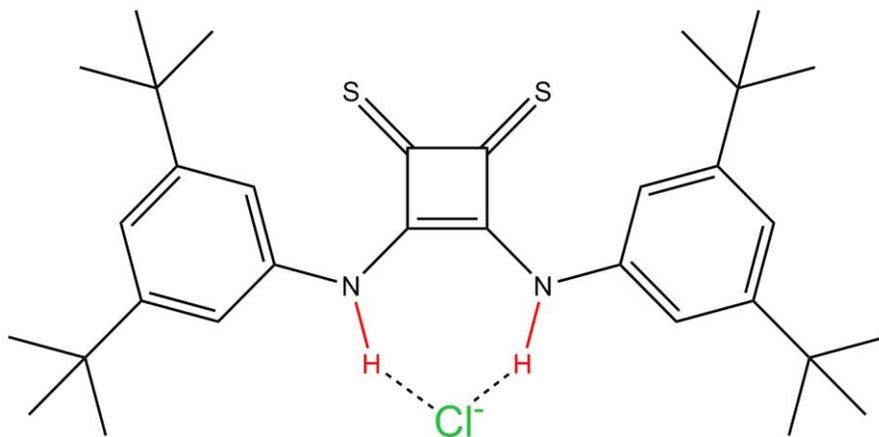
College of Science

Science Preprofessional Studies

Evan Peck, Dept. of Chemistry and Biochemistry

Advisor: Bradley Smith, Dept. of Chemistry and Biochemistry

A goal within the Smith Lab has been to synthesize 'smart molecules' which efficiently target and bind chloride. Within a biological system, the detection of chloride is crucial to recognizing and treating cystic fibrosis. Squaramides are unique in their ability to form up to four hydrogen bonds, offer a large binding pocket, and promote favorable hydrogen bonding directionality, making them ideal candidates to bind chloride. Due to this ability, squaramides have aimed to replace rival ureas and thioureas in the contest for anion and cation recognition. Ureas and thioureas differ only in a substitution of oxygen for sulfur yet have significantly different properties and binding capabilities due to this difference. This led to the synthesis of thiosquaramides, in hopes that the substitution of oxygen for sulfur would promote even greater chloride binding as it has for thioureas when compared to ureas. First, the synthesis of squaramide and thiosquaramide derivatives was optimized, followed by ^1H NMR studies, which revealed dynamic conformational behavior of these species in varying solvents. Finally, squaramide and thiosquaramide derivatives were subject to chloride titrations through ^1H NMR and binding constants were obtained, revealing that thiosquaramides do bind chloride with higher affinity than squaramides.



Poster Presentation

Effect of Climate Change on the Endangered Karner blue Butterfly

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Jason Dzurisin, Dept. of Biological Sciences
Advisor: Jessica Hellmann, Dept. of Biological Sciences

The Karner blue, *Lycaeides melissa samuelis*, is a small-bodied specialist butterfly historically native to the northern parts of the United States and southern parts of Canada that is most often found in oak savannahs and pine barrens. In recent years, a number of Karner blue populations have declined dramatically, some to extinction. Because of this decline, the species was listed as a Federally endangered species and in 2000, declared locally extinct in Canada. The species now inhabits only a few scattered pockets around the Midwest and northeastern United States. In addition to existing global change stressors, shifting climate regimes have the potential to impact the population as well. As ectotherms, the Karner blue is directly affected by changing climate and many of the potential impacts are largely unknown. This study attempts to understand the effects that temperature, and more specifically projected temperature changes, as a result of climate change, may have on the Karner blue and what the overall impacts climate change might have on the already dwindling Karner population. By simulating a number of potential climate regimes in the laboratory, Karner blue butterflies were bred, mated, and allowed to develop in different increased temperatures. Upon eclosing, each adult butterfly was photographed and using image analysis techniques, the morphometrics of the particular butterflies were measured and recorded. Individual measurements of various size and weight characteristics were aggregated and analyzed statistically to determine the effect of each climate treatment. Results suggest that elevated temperature regimes lead to additional voltinism and that these individuals tend to be smaller and lighter than their predecessors. Although the cause of the population decline for the Karner blue remains to be proven, new ideas about potential drivers of the decline have been uncovered.

Poster Presentation

Generation and Validation of a pax6b:GFP Transgenic Zebrafish Line

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Kristin Ackerman, Dept. of Biological Sciences
Advisor: David Hyde, Dept. of Biological Sciences

Over one million people in the U.S. suffer from blindness resulting from retinal diseases characterized by progressive and irreversible retinal cell death (National Eye Institute). Zebrafish (*Danio rerio*) are a valuable degenerative/regenerative model system because unlike humans, zebrafish can regenerate lost retinal neurons in response to damage and ultimately restore vision. Upon damage to the zebrafish retina, Müller glia reenter the cell cycle, produce progenitors that continue to proliferate, migrate to the site of damage, and differentiate into the lost retinal cells (Vihtelic et al 2006). The mechanisms that induce Müller glia dedifferentiation to generate neuronal progenitors and the subsequent regeneration process are not fully characterized. Previously, our lab demonstrated that the undamaged retina expresses Pax6 in amacrine and retinal ganglion cells, but upon retinal damage, Pax6 is upregulated in columns of proliferative progenitor cells (Thummel 2008). Quantitative PCR demonstrated that two Pax6 paralogs, *pax6a* and *pax6b*, are differentially regulated and morpholino-mediated gene knockdown indicates they possess different functions: Pax6b knockdown stops neuronal progenitor cells from undergoing the first progenitor cell division, while Pax6a knockdown prevents subsequent cell divisions (Thummel et al 2008). As a first step to determine the role of Pax6a and Pax6b in neuronal progenitor cell proliferation during zebrafish photoreceptor regeneration, I generated a transgenic line using transposon-mediated BAC transgenesis that expresses GFP from the *pax6b* promoter. Pax6b expression is localized to the brain, spinal cord, and retina of the developing zebrafish embryo. Retinal cross sections demonstrate GFP-positive cells in the INL and RCG and immunohistochemistry confirmed that GFP expression is confined to neuronal progenitors, amacrine cells, and retinal ganglion cells in the transgenic line. A *pax6b* specific DIG-labeled anti-sense RNA probe was generated to validate the endogenous expression of *pax6b* in the transgenic line using *in situ* hybridization.

Oral Presentation

Radiocarbon Dating using Accelerator Mass Spectrometry at Notre Dame

Sean Howard
College of Science
Physics

Advisor: Philippe Collon, Dept. of Physics

Current development of a local radiocarbon dating methods using Accelerator Mass Spectrometry (AMS) seeks to provide sensitive, reproducible, and accurate measurements for future interdisciplinary projects with the Biology and Anthropology departments. While AMS has been used as the premier radiocarbon dating method for a few decades, repurposing Notre Dame's FN Tandem accelerator for radiocarbon dating provides many unique challenges. The talk will focus on previous and upcoming radiocarbon experiments done on said accelerator. Previous experiments have shown that radiocarbon dating is possible and reproducible using the FN Tandem accelerator, found optimal settings for said accelerator, and established sensitivity limits comparable to dedicated radiocarbon dating facilities. In addition, there is ongoing work to create a local chemistry lab to convert organic artifacts into graphite to be used with the accelerator. Once the chemistry side has been completed, several artifacts from the IAEA's radiocarbon intercomparison have been procured and analyzed. Dating these artifacts (with actual dates known from intercomparison) will provide an additional measure on the accuracy and repeatability of both the accelerator and chemistry treatment. Provided that these IAEA artifacts are dated successfully, exciting projects will ensue, such as the authentication of artwork and dating of anthropological samples.

Poster Presentation

Magneto-transport study of topological insulator materials Bi₂Se₃ and Bi₂Te₃

David Howe and Joseph Hagmann
College of Science
Physics
Xinyu Liu, Dept. of Physics
Advisor: Jacek Furdyna, Dept. of Physics

The topological insulator is a novel quantum state of matter that behaves as an insulator along the bulk of the material, but along the surface exhibits a topologically non-trivial band gap, which in turn interacts with band structures of the insulator bulk and of the vacuum on either side of the surface to form topologically-protected electron states. These states have two novel properties – the electrons locked in these states display linear dispersion, closely akin to normal photon dispersion relations; and the spin of the electron is “locked” perpendicular to its momentum, which in turn drastically reduces back-scattering, making the state interesting to study. They are extremely robust, which has immediate implications for technology, where such robustness of electronic states can be put to use by designing and forming new devices which are “fault-tolerant”, i.e., which can withstand perturbations which typically occur due to charge carrier scattering and other forms of instabilities. Manganese doped Be₂Se₃ and Be₂Te₃, materials grown using MBE in Professor Jacek Furdyna’s lab, were taken through various magneto-transport measurements to characterize their electronic properties, including SQUID and cryogenic (below 2K) measurements. Through these measurements, topologically characteristic weak anti-localization curves were found in the mobilities and magnetization. A major issue in the study of TI’s is to be able to distinguish electrical transport in the bulk from that occurring on the surface that represents the novel topological effects. To this end, I co-designed and fabricated micron-scale Hall-bar circuits on our samples in order to isolate the surface conduction from the bulk contributions. The six-step process produced limited results due to the small sample sizes and previously unforeseen interactions between the novel materials and typical IC processes. The results of both the measurements before and after the hall-bar construction are shown.

Poster Presentation

Ablation of the Id2 gene results in altered circadian feeding behavior, and sex-specific enhancement of insulin sensitivity and elevated glucose uptake in skeletal muscle and brown adipose tissue

Alyssa Hummel
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Biological Sciences

Peng Zhou, Deepa Mathew, Cameron M. Pywell, Daan R. van der Veen, Jinping Shao, Yang Xi, Nicolle A. Bonar, Dept. of Biological Sciences

Sarah Chapman and W. Matthew Leevy, Notre Dame Integrated Imaging Facility
and Dept. of Biological Sciences

Giles Duffield, Dept. of Biological Sciences

Advisor: Giles Duffield, Dept. of Biological Sciences

Inhibitor of DNA binding 2 (ID2) is a helix-loop-helix transcriptional repressor rhythmically expressed in many adult tissues. Our earlier studies have demonstrated a role for ID2 in the input pathway, core clock function and output pathways of the mouse circadian system (Duffield et al., 2009, *Cur Biol* 19:297-304; Ward et al., 2010, *JBC* 285: 38987-39000; Hou et al., 2009, *JBC* 284:31735-45). We have also reported that Id2 null (Id2^{-/-}) mice are lean with low gonadal white adipose tissue deposits and lower lipid content in the liver. These results coincided with altered or disrupted circadian expression profiles of liver genes including those involved in lipid metabolism. In the present phenotypic study we intended to decipher, on a sex-specific basis, the role of ID2 in glucose metabolism and in the circadian regulation of activity, important components of energy balance. We find that Id2^{-/-} mice exhibited altered daily and circadian rhythms of feeding and locomotor activity; activity profiles extended further into the late night/dark phase of the 24-hr cycle, despite mice showing reduced total locomotor activity. Also, male Id2^{-/-} mice consumed a greater amount of food relative to body mass, and displayed less weight gain. Id2^{-/-} females had smaller adipocytes, suggesting sexual-dimorphic programming of adipogenesis. We observed increased glucose tolerance and insulin sensitivity in male Id2^{-/-} mice, which was exacerbated in older animals. FDG-PET analysis revealed increased glucose uptake by skeletal muscle and brown adipose tissue of male Id2^{-/-} mice, suggesting increased glucose metabolism and thermogenesis in these tissues. Reductions in intramuscular triacylglycerol and diacylglycerol were detected in male Id2^{-/-} mice, highlighting its possible mechanistic role in enhanced insulin sensitivity in these mice. Our findings indicate a role for ID2 as a regulator of glucose and lipid metabolism, and in the circadian control of feeding/locomotor behavior; and contribute to the understanding of the development of obesity and diabetes, particularly in shift work personnel among whom incidence of such metabolic disorders is elevated. Supported by the NIGMS (R01-GM087508) and the American Heart Association (10SDG4030011).

Poster Presentation

Improvement of a Low-Cost, Field-Portable Thermocycler through Thermal Modeling and Imaging

Elizabeth Huschke
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Electrical Engineering

Advisor: Scott Howard, Dept. of Electrical Engineering

Thermocyclers are a standard tool in procedures requiring analyzable quantities of DNA. Thermocyclers can amplify small DNA samples by several orders of magnitude by heating it to temperatures at which the two strands separate and subsequently cooling it to temperatures at which new base pairs assemble on each of the separated strands. Thus, DNA quantities double with each cycle and sample sizes can be significantly increased in a relatively short period of time. The NDPCR project aims to make DNA analysis practical on a low-cost, field-portable scale, extending the applications of DNA analysis to work in remote, low-resource settings. Compared with conventional thermocyclers, the NDPCR can be manufactured for a fraction of the cost and operate on very low power. My project aims to improve performance of the NDPCR by investigating and optimizing heat distribution in the DNA sample heating block. Both theoretical work with COMSOL modeling and thermal imaging of the actual block as it is heated and cooled are employed to better understand and ultimately improve the heat transfer characteristics of the device.

Oral Presentation

Knot Theory and Knot Invariants 2: Multi-Crossings

Daniel Irvine
College of Science
Mathematics

Advisor: Colin Adams, Dept. of Mathematics and Statistics, Williams College

Traditionally, knot theorists studied knot projections in which two strands of the knot interact at each crossing. The recently defined *n-crossing projection* breaks this norm. An *n-crossing* is a singular point in a knot projection where n strands are allowed to cross in such a way that each strand completely bisects the crossing. The *n-crossing number* of a knot K is the least number of crossings possible in any *n-crossing projection* of K . In this talk I will present joint work from my time at the Williams College REU 2013. My research group was able to generalize a classical result of Kauffman, Murasugi, and Thistlethwaite which relates the crossing number of a knot to the span of its bracket polynomial, an easily-computable knot invariant. We reformulate the result to give a lower bound on the n -crossing number of a knot in terms of the bracket polynomial for any n :

$$\text{Span}\langle K \rangle \leq \left(\left\lfloor \frac{n^n}{2} \right\rfloor + 4n - 8 \right) c_n(K).$$

In this talk I will explore how n -crossing projections relate to the bracket polynomial, and I will outline a proof of the above result. This talk will be a continuation on the theme from my talk last year: *An Introduction to Knot Theory and Knot Invariants*. All the relevant background knowledge from that presentation will be reviewed in this talk.

Poster Presentation

Implementing methods in algebraic graph theory in Macaulay2

Caroline Jansen and Jack Burkart
College of Science
Mathematics

Advisors: Sonja Mapes and David Cook, Dept. of Mathematics

There are significant interactions between commutative algebra and combinatorics, particularly graph theory. It is of growing importance for mathematicians to be able to do computations on graphs, among other objects. We wrote a package for Macaulay2, a program used to do algebraic computations, which implements methods for graphs and digraphs. We will discuss some of these connections and how we implemented them.

Oral Presentation

Damage to DNA with Various Flow Rates by Atmospheric Pressure Plasma Jet

Andrew Jensen
College of Science
Science Preprofessional Studies
Advisor: Sylwia Ptasinska, Dept. of Physics

Currently there are many techniques to treat cancer. One of these techniques is radiation therapy. A potentially alternative form of treatment, and one that is currently being tested, is the irradiation of tumors with an atmospheric pressure plasma jet (APPJ). The purpose of my experimental research is to further explore the effect AAPJ on the DNA molecule. An APPJ has been shown to induce both double strand (DSB) and single strand (SSB) breaks¹. The resulting damage to the DNA from the APPJ is the result of the plasma, which contains highly reactive species which include radicals, free electrons and ultraviolet light. The plasma jet can be projected with various flow rates (L/min). It has been shown that at different flow rates, the effect that the plasma has on the DNA breakage varies. In light of this, I am characterizing the jet with respect to flow rate in order to optimize its functionality. These experiments will be conducted using DNA mixtures which will be prepared using 10 μL of diluted 100 ng DNA and 5 μL of deionized water. These 15 μL aqueous DNA samples will be irradiated with the APPJ. The flow rate of the AAPJ will vary with each trial run. Following the irradiation of each sample, the DNA will be analyzed for SSBs and DSBs. This will be done using an agarose gel electrophoresis technique. I expect an increase in the amount of double strand breaks as the flow rate increases since more reactive species can be delivered to the sample.

References: ¹. S. Ptasinska , B. Bahnev, A. Stypczyńska, M. Bowden, N.J. Mason, St.J. Braithwaite, 2010. DNA strand scission induced by a non-thermal atmospheric pressure plasma jet. *Physical Chemistry Chemical Physics*, 12, 7779-7781.

Oral Presentation

Radiocarbon Dating at Notre Dame

Steven Jepeal and Sean Howard
College of Science
Physics
James Miller
College of Science
Mathematics and Physics in Medicine
Sean Brudney
College of Science
Physics
Kirby Hermansen
College of Science
Economics and Physics
Benjamin Guerin and Louis Hiza
College of Science
Physics

William Bauder, Wenting Lu, Karen Chamberlin, Michael Skulski, Tyler Anderson, Dept. of Physics
Advisor: Philippe Collon, Dept. of Physics

Initial experiments conducted by our group have proven that the technique of ^{14}C measurement for radiocarbon dating through accelerator mass spectrometry (AMS) is viable in the Nuclear Science Laboratory using the FN Tandem Accelerator. The next step in the development of an established radiocarbon dating procedure at Notre Dame is a demonstration of the validity of our measurements. The Third Radiocarbon Intercomparison (TIRI) is a wide-scale and evolving program of intercomparisons of very specific sample materials that allows laboratories and users to fine-tune their AMS techniques. In the following month we plan to take ^{14}C measurements of the sample material previously used in TIRI in order to examine our measurement capabilities. By utilizing the data that TIRI has provided on these samples, the accuracy of our measurements can be analyzed and our technique reevaluated. This project consists of obtaining measurements for the ^{14}C abundance in several samples that have been previously dated through TIRI. The project begins with the preparation of the sample material, transforming samples of organic carbon to cathodes containing graphitized carbon. The cathode preparation consists of two steps, the graphitization of the sample material through a process that is currently being developed by James Miller, and the construction and filling of the metal cathodes. Once the cathodes have been prepared, the ratio of ^{14}C to ^{12}C will be measured using the FN accelerator. These measurements will be analyzed, after which they will be compared to the results for the same materials from TIRI. The talk will present both the details of the upcoming measurements as well as how reliable dates can be determined from the ^{14}C measurements.

The long-term goal of the ^{14}C AMS project is to develop a procedure for the radiocarbon dating of organic material through AMS. This procedure would allow carbon-dating projects to be performed in collaboration with other academic colleges of Notre Dame such as anthropology and biology. These projects would be performed completely by Notre Dame Undergraduates, who would be responsible for performing every step from the collection of sample material to the analysis and interpretation of the results.

Poster Presentation

Deducing the role of fibroblast growth factor signaling in the regenerating zebrafish kidney

Jonathan Jou
College of Science
Biological Sciences

Advisor: Rebecca Wingert, Dept. of Biological Sciences

Kidney damage begins at the nephrons, the individual tubules that constitute the functional units of the kidney. The nephrons filter the blood, acting as an important component of removing waste and nutrients from the blood to maintain homeostasis. Kidney dysfunction results when nephron cells are injured and destroyed, which can lead to acute or chronic renal disease. Research toward the development of regeneration-based treatments utilizes zebrafish as a model organism because of its robust regenerative capacities and high degree of conservation between the fish and mammalian nephron structures. The regeneration phenomenon of the zebrafish kidney is termed neonephrogenesis, the molecular basis of which is still unknown today. This project assesses the role of fibroblast growth factor (Fgf) signaling as a trigger for neonephrogenesis processes. The Fgf family is closely associated with its ability to protect cells from damage, trigger cell proliferation, and enhance cell mobility, and is conserved between all vertebrate model animals. Thus, we hypothesized that Fgf signaling may be a potential trigger for the regeneration process. Our preliminary data allowed us to narrow down a receptor and ligand mRNA of the Fgf pathway that show punctate expression in the regenerating kidney, namely *fgf8a* and fibroblast growth factor receptor (*fgfr*) 1a using *in situ* hybridization techniques. Quantitative real time polymerase chain reaction assays showed an increased expression of both *fgf8a* and *fgfr1a* mRNA at the established time points of regeneration. Further, mRNA transcripts were co-localized between *fgfr1a* and transcription factors associated with nephron differentiation, namely *wt1b* and *lhx1a*. This suggests that Fgfr1a and Fgf8a may play roles in the regeneration response. Future experiments will use transgenic models missing Fgfr1a expression to further analyze the effect of the loss of the Fgf pathway on regeneration of the nephrons in the kidney after injury.

Oral Presentation

Dissociative Electron Attachment to DNA in a DNA-Glycine mixture

Joanna Kabuye
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Science Preprofessional Studies
Advisor: Sylwia Ptasinska, Dept. of Physics

Damage to DNA induced by radiation can result in single and double strand breaks, which can frequently lead to apoptosis or cell death. In the cell, DNA is surrounded by proteins consist of amino acids. This summer our aim was to use amino acids as a model to better understand the effect of proteins on the DNA damage. Our aim was to investigate the impact of the amino acid, glycine, on DNA damage induced by low energy electron irradiation. Irradiation of DNA using low energy electrons, which are highly abundant products of ionizing radiation, induces strand breaks by a process known as dissociative electron attachment via the formation of transient anions. Low energy electrons (<10 eV) induce single strand breaks in the sugar phosphate backbone of DNA whilst higher electron energies induce both double and single strand breaks. To study this damage, we tried to find a procedure for the preparation of DNA samples, which could be introduced to a vacuum chamber for irradiation. As the simplest amino acid, glycine was used for the first trial, where glycine was mixed with DNA. Although originally we found that Gold on Silicon substrate induced the least amount of damage, placing the lyophilized Gold on Silicon substrate into the high vacuum chamber overnight (which achieved pressures as low as 10-8mbar), uncovered severe problems including minimal recovery and extremely fragmented DNA upon recovery. This semester I have shifted my focus to the dissociative electron attachment (DEA) of gas phase dimethylformamide (DMF). Dimethylformamide is a derivative of formamide and thus contains a peptide bond, which allows it to serve as a model peptide. Understanding the interaction of low energy electrons with biomolecules is a progressive step towards the analysis of larger peptides and proteins.

Poster Presentation

Characterizing the Phosphorylation of Zwilch by the MPS1 Kinase

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Biological Sciences

Ali Raja, James Kasuboski, and Patricia Vaughan, Dept. of Biological Sciences
Advisor: Kevin Vaughan, Dept. of Biological Sciences

The Spindle Assembly Checkpoint (SAC) ensures the proper segregation of chromosomes during mitosis by delaying anaphase until all kinetochores are properly attached to spindle microtubules and aligned at the metaphase plate. Important proteins of the SAC are recruited to the kinetochores and form part of the fibrous corona, where they regulate anaphase onset. Loss of function studies revealed that the Monopolar Spindle 1 (MPS1) kinase plays a key role in maintaining the SAC. However, the direct link between the kinase and the SAC remains unclear. The Rod-Zw10-Zwilch (RZZ) complex is thought to play an important role in maintaining the function of the SAC, as individual knockdown of each component of the complex leads to defects in prometaphase. The Vaughan Lab discovered Zwilch as a novel substrate for MPS1, where inhibition of MPS1 with a small molecule inhibitor, Reversine, leads to loss of the RZZ complex and proteins upstream of RZZ in the fibrous corona. LC/MS/MS analysis of *in vitro* phosphorylated Zwilch identified three novel phosphorylation sites. Constitutively dephosphorylated (3A) mutants and constitutively phosphorylated (3E) mutants were tagged with mcherry for transfection studies to define the role of phosphorylation. Both 3A and 3E Zwilch mutants were characterized transfection studies. Transfection with 3A Zwilch resulted in loss of kinetochore proteins distal to Zwint, similar to MPS1 inhibition by Reversine. However, transfection with 3E Zwilch did not result in the loss of kinetochore proteins, and 3E Zwilch rescued kinetochore assembly during Reversine treatment. Assessing the mechanism, 3E Zwilch pulled down Zw10 from mitotic cell lysates whereas wild type Zwilch was unable to pull down Zw10. This suggests that MPS1 phosphorylation of Zwilch plays a role in the assembly of the RZZ complex, linking MPS1 to the SAC.

Poster Presentation

The Effects of Road Salt on Daphnia magna

Anthony Kavanagh
Trinity School at Greenlawn

I was interested in how road salt affected the population of aquatic life. Using *Daphnia magna*, I could test the effect of road salts on their population. I wondered what would happen if I compared snow, a road sample, and a plain salt solution to their natural spring water environment (control). I believed that out of the four solutions the road sample would decrease population the most followed by the salt concentration, than the snow, and finally the spring water. I put 36 *Daphnia magna* into four different containers each containing a different liquid inside it. The *Daphnia* would stay in the containers for 24 hours being checked on the 8th, 10th, 12th, 16th, and 24th hour. I would check the *Daphnia magna* by counting the population and observing the vitality of the organisms. After looking over my data, I saw that each non-control liquid had a smaller population when compared to the control. On the 16th hour, the results (by decreasing population) were spring water (control), snow, the road sample, and lastly the salt solution. My experiment partially supported my hypothesis. Though the salt solution had a lower population the majority of the time, it eventually mirrored the road salt sample. The spring water had the highest population followed by the snow as my hypothesis predicted.

Poster Presentation

Development of Novel Catalysts for the Copolymerization of CO₂ and Epoxides

Carolyn Keefe

College of Science and College of Arts & Letters

Chemistry and Spanish

Advisor: Kenneth Henderson, Dept. of Chemistry and Biochemistry

Use of CO₂ in an economically profitable fashion will help offset costs of carbon capture and storage while providing a renewable alternative to petroleum as a carbon source. One application is the copolymerization of CO₂ with an epoxide yielding polycarbonates. Current technology utilizes transition metal catalysts that often require high pressures (100 bar), can discolor the product, and are toxic. The use of environmentally friendly zinc, magnesium, and calcium metal centers is proposed as a less expensive, “greener” alternative, without sacrificing reactivity or selectivity. Two classes of ligand system are investigated: salen-type and macrocyclic. The salen-type ligand system has been shown in the literature to increase reactivity, control selectivity, and provide a scaffold that facilitates reagent binding in similar polymerization reactions. Several salen-type catalysts, typically including imine-ethylene arms capped with polar functional groups, are synthesized in simple and inexpensive reactions with high yields. The second class of ligand system investigated is a macrocyclic system, which has been shown in the literature to operate with relatively good TON and TOF at ambient pressure. Magnesium and zinc-coordinated macrocyclic complexes with the basic salen skeletal structure are synthesized for this study in simple reactions with good yield. These synthesized salen-type and macrocyclic catalysts are tested in copolymerization reactions at atmospheric pressure and a relatively mild temperature, 80°C. Almost all of the catalysts tested show activity, forming a white, water-insoluble solid. Interestingly, this product is not the desired polycarbonate but rather polyether, a less versatile class of polymer. NMR analysis of the residue after all solvent had been removed shows trace amounts of the desired polycarbonate.

Poster Presentation

Synthesis of (Z)-Methyl 4-(3-((5-(4-bromophenyl)furan-2-yl) meth-ylene)-2-oxo-5phenyl-2,3-dihydro-1H-pyrrol-1yl)benzoic Acid, A Possible Niemann-Pick Type C Therapy

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Biochemistry

Gang Liu, Dept. of Chemistry and Biochemistry
Advisor: Paul Helquist, Dept. of Chemistry and Biochemistry

Niemann-Pick Type C is a rare autosomal disorder that is characterized by accumulation of cholesterol in lysosomal storage organelles. In 2006, the Maxfield laboratory used an automated filipin-base high-throughput screening procedure to screen a library of 14,956 compounds for potential Niemann Pick Type C therapies. Of the compounds tested, 14 compounds showed significant reduction of cholesterol accumulation in CT60 and CT43 NPC1 mutant Chinese hamster ovary cells. Several pyrrolinones exhibited significant cholesterol reduction above the other compounds tested. This combined with their mild toxicity has made pyrrolinones an ideal target for further investigation for a possible NPC therapy. The goal of this project is to synthesize one of the original 14 compounds, (Z)-4-(3-((5-(4-bromophenyl)furan-2-yl)methylene)-2-oxo-5-phenyl-2,3-dihydro-1H-pyrrol-1-yl)benzoic acid, with the addition of an ester linkage. It is our hopes that with the addition of the ester linkage, the pyrrolinone will have improved solubility within the cell. We report the synthesis of (Z)-Methyl4-(3-((5-(4-bromophenyl)furan-2-yl)methylene)-2-oxo-5phenyl-2,3-dihydro-1H-pyrrol-1yl) benzoic Acid for use in further biological studies of its cholesterol reduction properties..

Poster Presentation

Molecular profiling of aggressive breast cancer in a unique patient population from Kenya

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Emilia Ivanova and Zonggao Shi, Dept. of Chemistry and Biochemistry

Jenifer Prospero, Harper Cancer Research Institute and Dept. of Biological Sciences

Sharon Stack, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

Sunil Badve, Indiana University School of Medicine – South Bend

Rispah Torrorey and Simeon Mining, Moi University

Advisor: Laurie Littlepage, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

Breast cancer rates of incidence and mortality vary significantly between different nations and racial groups. African nations have the highest breast cancer mortality rates in the world, even though the incidence rates are below those of many other nations. In Kenya, breast cancer tumors are often highly aggressive at presentation and occur at a significantly earlier age (as early as the teens and 20s), relative to North American women. In the United States, non-Hispanic white women have the highest incidence of breast cancer, but African-American women have the highest mortality. These striking racial disparities are due not only to inequities in screening and treatment but also to variations in the rates of aggressive breast cancer. Differences in disease progression suggest that aggressive breast cancer tumors may harbor components of a unique molecular signature that result in racial disparities. We aim to identify drivers of poor prognosis breast cancer growth by identifying molecular signatures with high prognostic value from tumor samples of patients with aggressive disease. We hypothesize that changes in the DNA, RNA, and post-translational protein regulation contribute to aggressive disease. To characterize the tumors from this patient population, we used samples from >100 Kenyan breast tumor tissue samples. We stained tissue microarray sections for clinical breast cancer markers including lymphocyte markers. Using DNA and RNA that we isolated from these patient-derived breast tumors, we are characterizing these tumors by analyzing them for gene expression, genome sequencing, proteomics, and pathology analysis coupled with bioinformatics to develop signatures of aggressive breast cancer growth and metastasis. Our data will be foundational in understanding how aggressive, lethal breast tumors of Kenyan breast cancer patients differ from less aggressive tumors and will enhance our ability to diagnose and eliminate outcome disparities in breast cancer patients.

Poster Presentation

Multimodal Lymph Node Imaging with Nanoparticles Incorporating Fluorescent and Radioactive Reporters

Sarah Khan

College of Science

Science Preprofessional Studies

Advisors: W Matthew Leevy, Dept. of Biological Sciences and Raghu Kannan, Dept. of Bioengineering, University of Missouri – Columbia

Reliable, high-resolution imaging is essential for accurate diagnosis of cancer, especially when searching for small metastatic lesions, including those within lymph nodes. Modern imaging methods depend on both the modality being used along with a corresponding contrast agent to highlight and visualize the targeted area. For diseases such as cancer, nanoparticles that have been specifically developed to reach tumor sites may be developed to provide enhanced contrast. For this purpose, we are pursuing a collaborative project using PMMA polymeric nanoparticles encapsulated with Indocyanine green dye (ICG), which is detected via near infrared fluorescence imaging. In addition, the PMMA NP are functionalized for labeling with radioisotopes that may be detected via Single Photon Emission Computed Tomography (SPECT). The first goal of our project is to validate that it is indeed possible to make the nanoparticles fluorescent and radioactive, and can then be detected through tissue during *in vivo* imaging of mice. In order to achieve these objectives, images of the injected mouse were taken immediately after injection of PMMA NP, and then at 30 min, 1, 2, and 4 hrs after injection, using a Bruker In-Vivo Xtreme which allows for fluorescence, radioactive, X-ray and reflection images to be taken. Then, 24 hours after injection, *ex-vivo* imaging of blood, liver, spleen, kidney, heart, lung and lymph nodes was completed. Our results indicate that these particles may be detected during multimodal *in vivo* imaging experiments, and are ideal candidates for future studies that target cancer cells residing within the lymph nodes.

Poster Presentation

iLocator: An NIR Doppler Spectrometer

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Applied and Computational Mathematics and Statistics and Physics
Robert Stoddard
College of Science
Environmental Sciences
Taylor Corpuz
College of Science
Physics
Advisor: Justin Crepp, Dept. of Physics

The iLocator project involves designing, coding, and constructing a near-infrared (NIR) Doppler spectrometer built to interface with the Large Binocular Telescope (LBT) in Arizona. This instrument will, among other things, detect planets around other stars using the Doppler method. iLocator's location at the LBT gives the instrument several distinct advantages. The LBT has the largest collecting area of any telescope, giving it the highest spatial resolution, and its two mirrors allow for the monitoring of internal radial velocity drifts. Its "extreme" adaptive optics (AO) correction at near-infrared wavelengths gives iLocator the opportunity to be the world's first diffraction-limited spectrometer. Attaining such a high spectral resolution provides for a smaller size when compared to other instruments, leading to greater optical and thermal stability, less expensive optics, and a design that can use a single-mode fiber that will eliminate modal noise. A major part of this project is creating the radial velocity extraction method whereby the instrument will extract a radial velocity/time graph from the light absorption lines present on the detector, as well as simulating reliable stellar spectra to test the method on. Additionally, iLocator's user interface will allow users to both control and track in real time nearly every aspect of the instrument, like temperature and pressure. Users will be able to monitor local observing conditions, tweak detection parameters as needed, directly control the detector and adaptive optics system, and choose stars to observe from any local database. Finally, iLocator will provide data on planet formation around multiple star systems via determining the characteristics and frequency of such planets, allowing for the exploration of new parameters regarding planet formation in a variety of stellar configurations as well as confirming or refuting current trends seen in existing samples of extrasolar planets.

Poster Presentation

Plants and mosquitoes: What do we need to know and why?

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Science Preprofessional Studies
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Advisor: Zainulabeuddin Syed, Dept. of Biological Sciences

Mosquitoes act as vectors for several life threatening diseases such as malaria, dengue, and West Nile virus. Females transmit these diseases while blood-feeding from a host. Though vast literature exists on blood-feeding behavior in mosquitoes, little is known about their sugar feeding habits. Plant sugars are the sole energy source for both male and female mosquitoes. I conducted experiments to gain further insight on plants that are preferred as food source in adult mosquitoes. Earlier behavioral investigations in *Culex* mosquitoes in the North Eastern United States have shown certain plants such as *Solidago hybrida* 'Dansolitem,' *Achillea millefolium*, and *Leucanthemum x superbum* to be attractive to females (Mauer and Rowley, 1999). To gain a global understanding of what plants mosquitoes consume, I employed molecular identification of plant material from mosquitoes. Plant chloroplast DNA has highly conserved genomic regions across plant species, but is interrupted with non-coding sequences that are highly variable and are usually unique to plant genera. DNA was extracted from individual mosquitoes that were fed restrictively on known host plants. By using several primers that were designed across exon-intron-exon boundaries, amplified fragments were reliably identified based on their unique size via gel electrophoresis and DNA sequencing. This process is currently being evaluated on field captured *Anopheles farauti* from the Solomon Islands. By identifying plants preferred by mosquitoes in the field, we aim to identify odors from these plants and use them as baits to capture significant mosquito population, thereby inhibiting the spread of disease.

Poster Presentation

The Effects of Inhibiting Myosin II and PTEN on Neurite Formation and Axon Extension

Alexandria Kristensen Cabrera
College of Science
Science Business

Advisors: Paul Letourneau and Jose San Miguel-Ruiz,
Dept. of Neuroscience, University of Minnesota Medical School

Normal behavior depends on the correct formation of neural circuits during development of the nervous system. Developing neurons sprout axons that reach out to other neurons, specifically to dendritic extensions, to complete electrical connections. We investigated how to promote initiation and growth of immature axons and dendrites (neurites) by neurons from chick embryo forebrains. To answer this question we conducted three groups of experiments. First, the pharmaceutical drug Blebbistatin was used to inhibit Myosin II; which produces a contractile force on axon growth. Second, the pharmaceutical drug bpV was used to inhibit PTEN; a protein that regulates cell growth through different pathways including the synthesis of proteins needed for axon extension. The third experiment determined if the two pharmaceutical drugs combined had an additive effect. For each group of experiments, various concentrations of the drug were tested in a tissue culture system containing dissociated chick embryonic forebrain neurons cultured in a defined growth medium. Both Blebbistatin and bpV increased the proportion of cells with neurites. Cells treated with Blebbistatin had longer axons, while cells treated with bpV had more neurites per neuron. When we combined Blebbistatin and bpV we saw the effects of individual treatments, more neurites and longer axons, and perhaps an additive effect on axon length. This project showed that the formation and growth of axons by chick embryonic neurons can be promoted using pharmaceutical drugs that target a contractile protein Myosin II, and PTEN, which is a negative regulator of cell growth.

Oral Presentation

Effects of Atmospheric-Pressure Helium Plasma on Cysteine Solutions

Emily Kunce
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Physics in Medicine

Advisor: Sylwia Ptasinska, Dept. of Physics

As the number of lethal cancer cases is expected to rise nearly 45% in the upcoming two decades, there is a profound need for the development of targeted cancer therapies¹. Current research has shown that plasma can selectively induce apoptosis in cancer cells, which avoids the inflammation associated with cell necrosis². However, the reactive pathways of plasma are not fully understood and the consequences of treatment on healthy cells must be investigated. This research aims to characterize the interaction of plasma with healthy cell components by studying the effects of helium plasma radiation on solutions of cysteine.

Initially, the control sample of non-irradiated cysteine solution was analyzed using Fourier Transform Infrared (FTIR) spectroscopy and the resultant peaks were assigned to the functional groups found within the compound. This data was later compared to the spectra recorded following irradiation to identify the groups damaged in the treatment process. Then, for each time point tested, three samples were irradiated under the plasma jet. Each sample was then analyzed using FTIR and the data for each time point was averaged to reduce any random variations in absorbance due to sampling.

Preliminary data suggests that there is quantifiable damage to selected groups within the cysteine compound after it is subjected to irradiation times greater than one minute in length. These results will be confirmed using Raman spectroscopy. Additionally, future experiments are planned to characterize the reactive species produced in this interaction using a series of colored scavengers. The data gathered from their absorption spectra after irradiation will provide insight into the reactive oxygen and nitrogen species produced.

¹ World Health Organization, Ask the Expert 2008

² Woedtke T, Reuter S, Masur K, Weltmann K. "Plasmas for Medicine." Physics Reports 530. (2013): 291-320. Print.

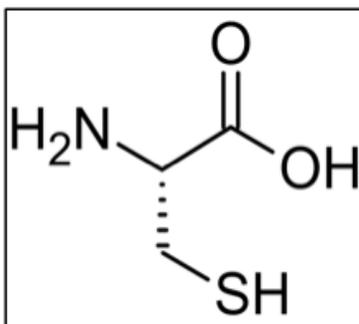


Figure 1. Chemical structure of the amino acid cysteine, which shows the -CH₂SH (thiol) side chain.

Poster Presentation

Investigation of DNA Amplification via Polymer Chain Reaction Using Open Source Technology

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College of Science

Engineering, Science, Technology and Entrepreneurship Excellence Program

Advisor: Scott Howard, Dept. Electrical Engineering

DNA/RNA detection is one of the most commonly and effectively employed methods to confirm the presence of pathogens in samples. However, deployment in low resource settings (i.e., deployment in the field or developing economic regions) is impeded by the lack of low-cost and low-power DNA/RNA amplification. Thus, a low cost, low energy and reliable portable nucleic acid identification platform would allow distributed measurements and rapid identification at the point of identification in places where current PCR and detection systems cannot go. To solve this problem, we investigated what open source technologies are available and whether they are effective. This poster investigates the feasibility of DNA/RNA polymer chain reaction using the openPCR and the IORodeo mini illuminator box, both of which are open source technologies.

Poster Presentation

Overlapping Roles of P31comet and Dynein in Silencing the Spindle Assembly Checkpoint

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Kevin Vaughan, Dept. of Biological Sciences
Advisor: Kevin Vaughan, Dept. of Biological Sciences

The Spindle Assembly Checkpoint (SAC) is a robust surveillance system that monitors chromosome alignment during mitosis. The SAC prevents anaphase onset during prometaphase while chromosomes attempt to align at the metaphase plate. However, the SAC is silenced in response to chromosome alignment, thereby allowing anaphase onset. Cytoplasmic dynein has been implicated in SAC silencing through disassembly of the checkpoint signaling complex. Recently, p31comet has been identified as a Mad2 binding protein that also contributes to checkpoint silencing. Because p31comet and dynein both play a role in SAC silencing, we investigated if these two components are part of the same silencing pathway. Previous work reveals that dynein is recruited to kinetochores during prometaphase. To assess if p31comet mimics dynein recruitment, we generated fluorescently-tagged p31comet for imaging in cultured cells. We treated cells with nocodazole to emphasize kinetochore recruitment during prometaphase. P31comet colocalized with known kinetochore markers, suggesting that p31comet and dynein are both recruited to kinetochores during prometaphase. Studies have shown that Rod/Zwilch/Zw10 (RZZ) and associated anaphase inhibitors are recruited onto kinetochores during prometaphase, but undergo poleward streaming with dynein at metaphase. We interrogated recruitment of RZZ and dynein to kinetochores after inhibition of Aurora B (AurB) or Polo like kinase-1 (Plk-1) to determine whether p31comet recruitment to kinetochores is dependent on RZZ. AurB inhibition abrogated the recruitment of p31comet to kinetochores, however Plk-1 inhibition did not impact kinetochore recruitment of p31comet. Expression of triple-alanine zwint (3A zwint) disrupts both p31comet and RZZ recruitment to kinetochores. These results suggest that p31comet recruitment is dependent on the RZZ complex. To determine if p31comet mimics dynein during metaphase, we transfected in mcherry-tagged p31comet and tested for localization to spindle poles. Nordihydroguaiaretic acid (NDGA) was utilized as a tool to enrich streaming proteins at spindle poles during metaphase. Treatment with NDGA induced p31comet accumulation at spindle poles, suggesting that p31comet mimics streaming proteins, including dynein. Taken together, our studies suggest that p31comet and dynein share some degree of functional overlap in silencing the SAC at metaphase.

Poster Presentation

Integrated platform for nucleic acid sensing

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Advisor: Hsueh-Chia Chang, Dept. of Chemical and Biomolecular Engineering

Pathogen detection technology has had a revolutionary impact on human healthcare and environmental surveillance. However, current methods such as DNA microarray and real-time PCR are impractical, bulky, and costly, especially for developing areas. An inexpensive, portable device would revolutionize global diagnostics. The purpose of our research is to integrate various novel nucleic acid separation, concentration, and probing technologies into an affordable, handheld pathogen detection chip. The biological fluid pretreatment and nucleic acid preconcentration mechanisms were optimized separately, and successfully assembled into a platform that prepares nucleic acids for sensing. The separation technology uses a current to pass negatively charged nucleic acids from lysed biological samples through agar gel, thereby removing debris that may interfere with the sensing process. Gel electrophoresis and fluorescent labeling imagery confirmed the mechanism's effectiveness in adequately moving the nucleic acids through the agar into the testing channel. After loading the nucleic acids into the channel, the preconcentration mechanism focuses them in preparation for sensing. An ion exchange membrane (IEM) and an applied potential create an ion-depleted region that acts as a non-mechanical barrier for large anions. Nucleic acids are pumped toward the region and accumulate adjacent to it, as confirmed through imaging of colored dyes and fluoresceinated nucleic acids. The sensor consists of an anion exchange membrane pre-functionalized with short oligonucleic acid probes specific to the target DNA/RNA sequence. The presence of the target molecules is detected through a change in current voltage characteristic of the membrane. Finally, these technologies are integrated into a single automated chip. This device will revolutionize the world of nucleic acid sensing, transforming an expensive and impractical procedure into a routine process and aiding healthcare in third-world countries.

Poster Presentation

Feeding Frenzy: Diet and Symphyseal Biomechanics in Strepsirrhine Primates

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Advisor: Matthew Ravosa, Dept. of Biological Sciences

Among the strepsirrhini, a suborder of primates including lemuriforms and loriforms, there is a wide range of mandibular morphologies potentially related to the diversity of dietary material properties and feeding behaviors. Species-specific masticatory stresses related to such variation also appear to underlie variation in the degree of ossification of the mandibular symphysis, which is the midline joint between left and right lower jaws. While prior work has attempted to link diet and mandibular form in strepsirrhines and other mammals, it has largely relied on external dimensions to evaluate such functional associations, which vary in the extent to which they accurately reflect the biomechanical characteristics of a skeletal element. Using novel microCT data on the cross-sectional geometry of the mandibular symphysis in 72 adult specimens from 25 strepsirrhine species that differ in the degree of symphyseal fusion, this study tests the hypothesis that phenotypic variation in the internal anatomy of lower jaw reflects a dietary signal. Biomechanical parameters for the symphyseal, first incisor, and canine regions were analyzed by generating a 3D visualization based on microCT scans of each lower jaw via Amira software. Log-linear bivariate regression was used to perform standard allometric analyses of mandibular cross-sectional geometry ($p < 0.05$). Results indicate that cortical bone area in all three anterior mandibular regions scales with positive allometry in strepsirrhines. This indicates that larger taxa exhibit relatively more robust mandibles designed to counter the increased masticatory stresses associated with the exploitation of more mechanically challenging foods differentially exploited at larger body sizes. Such an interpretation is consistent with the finding that larger strepsirrhines also tend to develop greater fusion or ossification of the mandibular symphysis. Characterization of this phenotypic pattern is likely to prove helpful in generating hypotheses regarding other mammal groups and for the paleobiological reconstruction of diet in fossil species.

Poster Presentation

Effect of RNA inhibition of JNK on the body size of Aedes aegypti

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Advisors: Molly Scheel, Indiana University School of Medicine – South Bend and Dept. of Biological Sciences, and Michelle Whaley, David Severson, and Anthony Clemons, Dept. of Biological Sciences

Mosquito-borne illnesses have had catastrophic impacts, particularly in developing countries, where recent resurgences make them especially threatening. Genome sequencing projects for several well-known vectors, including the yellow and dengue fever vector *Aedes aegypti*, have yielded new putative targets for genetic manipulation as a method of pest control. In this study, we hope to find evidence that an association exists between the stress signaling JNK pathway and vector competence in *Aedes aegypti*. Based on preliminary studies that successfully use RNA interference within this insect vector, we believe that inhibition of jnk in the Moyo-R subline of *Aedes aegypti*, which is refractory to infection and characterized by a small body size, will allow us to partially or totally reverse the dengue refractory phenotype of this subline. This will generate insects that more closely resemble the larger, disease-susceptible Moyo-S subline in body size and susceptibility. JNK protein expression, which will be quantified with a western blot at each stage of mosquito development, will be targeted by feeding Moyo-R larvae dsRNA. Body size will be determined by wing length and is expected to be larger as a result of a loss of JNK signaling. It is anticipated that loss of JNK signaling will also result in increased susceptibility to disease, characterized by greater dissemination of DENV-2 virus. Conversely, it is predicted that upregulation of JNK signaling will decrease susceptibility to dengue infection. These studies may promote the elucidation of novel strategies for vector control.

Poster Presentation

Measuring urinary iodine at parts per billion level using a paper device

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Marya Lieberman and Nicholas Myers, Dept. of Chemistry and Biochemistry
Advisor: Marya Lieberman, Dept. of Chemistry and Biochemistry

The World Health Organization reports that more than 1/3 of the world's population is iodine deficient. Iodine is an essential nutrient and deficiency leads to hypothyroidism and mental impairment in children. Thus, urinary iodine (UI) monitoring is important in assessing a population's iodine intake. Conventionally, a UV method based on the Sandell-Kolthoff reaction is used to quantify iodine in urine. Redox indicators have been used to ease the detection of color change where spectrophotometers are not available. However, these methods require that the urine samples be boiled in strong oxidizers and acids, which restricts the procedure to a laboratory setting. To allow UI detection in areas that do not have access to a laboratory, a field-friendly paper analytical device (PAD) has been devised. After a simple urine preparation, the user places drops of urine onto the reaction areas and measures the time needed for the indicator to turn from blue to red. In less than ten minutes, the PAD can measure physiologically relevant iodine concentrations between 25 and 300 parts per billion (ppb). Reading the PAD by eye will allow semi-quantification, but a cell phone image analysis app will be developed to achieve more refined quantification. This poster focuses on two innovations in the implementation of the Sandell-Kolthoff reaction on paper millifluidic devices: 1) development of a redox indicator with a reasonable shelf life that gives strong colorimetric results suitable for interpretation by eye or by image analysis programs and 2) standard addition method which minimizes the matrix effect and potentially eliminates the urine digestion process. This research project and poster are affiliated with the AD&T program.

Poster Presentation

Monitoring Vascular Endothelial Growth Factor and CD31 Expression to Assess a Possible Link Between Obesity and Ovarian Cancer

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Yueying Liu and Sharon Stack, Harper Cancer Research Institute
and Dept. of Chemistry and Biochemistry

Advisor: Sharon Stack, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

While it is considered more treatable than it was in previous eras, ovarian cancer is still the fifth leading cause of cancer death among American women. Becoming increasingly prevalent in the United States, obesity is generally associated with poorer prognoses in the treatment of many diseases. The purpose of this experiment was to investigate the possible relationship between obesity and ovarian cancer progression and metastasis. The experiment was performed in a murine model. At 14 weeks of age, genetically modified obese mice and control mice were injected with eight million ID8 ovarian cancer cells and were then sacrificed at 21.5 weeks of age. Both Vascular Endothelial Growth Factor (VEGF) and CD31 (an endothelial cell marker) play important roles in angiogenesis and endothelial migration, both important factors in tumor metastasis. Therefore, to determine whether vasculature is altered in tumors growing in control vs. obese mice, the respective expressions of VEGF and CD31 were monitored. Tissues were cut into 4-5 micron sections, mounted on microscope slides and immunostained using anti-VEGF or anti-CD31 and anti-mouse Ig conjugated secondary antibodies. Quantification of results is in progress. VEGF receptor inhibitors are currently used in the treatment of ovarian cancer. If obese murine tissue show upregulated VEGF expression, this would suggest that obese patients may be better candidates for ovarian cancer therapies involving VEGF receptor inhibition.

Poster Presentation

Encryption: The Perfect Hash

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In a world of information sent across great distances every day, it is necessary to protect this information with encryption. This is commonly done by using a password. To most securely protect information a good password must be used. A password's strength depends on the length and types of characters. This was tested by use of multiple programs to randomly generate and crack a given password based on specific guidelines. This process was timed and recorded. The data collected ranged from over two minutes to a few milliseconds. The longest it took to crack a password was 133.33 seconds, for passwords of 4 characters consisting of letters and numbers. This was followed by 4 character passwords consisting of all types of characters and 4 character passwords consisting of only numbers, respectively. This pattern of types of characters was present in passwords of 3 characters and two characters, which followed the passwords of 4 characters. This is due to the way the brute force attack used to crack the passwords worked, starting with simple punctuation, such as commas and periods, then numbers, letters, and special punctuation such as pipes and backslashes. This did not support the hypothesis, in which, characters consisting with all types of characters would precede characters consisting with letters and numbers.

Poster Presentation

Exploring the effect of climate on the voltinism and phenology of a butterfly hybrid zone using an individual-based simulation model

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Advisor: Jessica Hellmann, Dept. of Biological Sciences

Phenology—the timing of life cycle events—and voltinism—the number of generations a population has in a given year—are predicted to be affected by climate change in insect populations. However, little is known about what impacts climate change will have on the dynamics and genetics of populations as a result of a change in phenology and voltinism. Here we investigated how climate-induced changes in phenology and voltinism would affect patterns of hybridization between two hybridizing species of butterfly, *Papilio glaucus* and *Papilio canadensis*, in Wisconsin. To explore the effect of climate on their phenology and voltinism, we used an individual-based simulation model. We created a previously adapted model and parameterized the model using one set of growth chamber experimental data that was used to determine specific developmental rate based on developmental stages. Another set of growth chamber experimental data allowed us to test the model for predictions. Next, we ran the model for various genotypes to look at the patterns across hybrid zones and predicted voltinism transition zones. Finally, we used real climate data to compare our model's predictions with those of citizen science field observations to determine how well our model could predict phenological and voltinism patterns within Wisconsin. Preliminary results from this work strongly suggest that changes in climate is influencing the genetic composition of this hybrid zone, by differentially affecting traits associated with voltinism and phenology, in turn affecting the amount of introgression between the two species. We found that not only did climate influence voltinism patterns, but hybridization may vary between warm and cool years because of the timing of emergence dates of the various genotypes.

Oral Presentation

Molecular characterization of actin cytoskeletal proteins during retinal regeneration

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Manuela Lahne, Dept. of Biological Sciences
Advisor: David Hyde, Dept. of Biological Sciences

In response to light-induced photoreceptor cell death, Müller glia residing in the inner nuclear layer of the retina divide and give rise to neuronal progenitor cells that continue to proliferate and ultimately differentiate into new photoreceptors. During retinal development, neuronal progenitor cells undergo interkinetic nuclear migration (IKNM), in which their nuclei migrate from the basal region of the retinal neuroepithelium, where DNA is replicated, to the apical surface, where cells divide. A comparable process of Müller glial nuclear migration in the regenerating adult retina has recently been described. Studies in retinal development implicated actin/myosin interactions as a driving force of IKNM. To test whether the actin cytoskeleton also mediates IKNM during retinal regeneration, dark-adapted Tg[*gfap:EGFP*] zebrafish, that express EGFP in Müller glia, were light-damaged and retinal sections were labeled with phalloidin, which binds filamentous (f-) actin. At 35 hours of light, the onset of IKNM, f-actin accumulates in processes of migrating Müller glia. Moreover, upregulation of α -actinins, actin cross-linking proteins known to play a role in cell migration was detected in Müller glia at 35 hours by immunocytochemistry. Using quantitative real-time PCR, we determined that α -actinin 1 and 3a mRNA expression levels were upregulated prior to the onset of IKNM, suggesting that these isoforms may be increased in Müller glia. In contrast, the mRNA levels of α -actinin 2 and 3b were decreased. Whole embryo in situ hybridizations revealed the ubiquitous expression of all α -actinin isoforms at 24 hrs post fertilization (hpf) when neuronal progenitor cell proliferation is high, while unique expression patterns of each isoform was observed by 96 hpf. In situ hybridization experiments demonstrated an upregulation α -actinin1 mRNA in Müller glia undergoing IKNM. These results suggest α -actinin1 as a potential target to inhibit Müller glial nuclear migration during retinal regeneration.

Oral Presentation

Exploration of Nitroso-Ene Reactions

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Advisor: Marvin Miller, Dept. of Chemistry and Biochemistry

The focus of this project evolved over time. The first goal was to synthesize a library of compounds based on the structure of a novel class of antibiotics called nikkomycin and then use this library to explore the structure activity relationship of nikkomycin. Activity of select intermediates led to a second goal, which included exploring the nitroso-ene reaction as a means of modifying different systems. As chitin synthase inhibitors, nikkomycin have the potential for anti-fungal drug therapy with high selectivity. Work on the nikkomycin library began with synthesizing a side chain containing a hydroxamic acid, which has not been explored as functional group for this scaffold. After step five, problems with protection and decompositions stalled progress. All intermediates were screened for possible biological activity and several showed activity against *S. aureusi*, *M. Leuteus* and *M. vaccae*. These results led to further exploration of the reaction used to create the active intermediates. In exploring the nitroso-ene reaction, a simplified protected system of a Boc protected hydroxyl amine was used and combined with several substrates of varying complexity and functionality. A particular focus was on natural product modification. There were problems with the stability of the nitroso intermediate but capture using a Diels-Alder reaction and then subsequent controlled release using a retro Diels-Alder significantly improved results. A small library was assembled and screened.

Poster Presentation

Suffocated: A study of cellular damage due to smoking

Sarina McCabe
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For the 2014 Science Fair, I wanted to execute an investigative project that would contribute to the knowledge of myself and my peers in a way that could positively impact our futures. To fulfill this aspiration, my driving question focused on a controversial issue present in today's society; smoking. My project revolved around the problem of how smoking impacts lungs on a cellular level. My procedure consisted of infusing cigarettes into the growth medium of *Tetrahymena thermophila* cells, which share characteristics with lung cells, such as cilia. Cilia are what allow the *Tetrahymena* to move, and the lungs to filter out unwanted substances. My hypothesis stated that if *Tetrahymena* cells' growth medium is infused with cigarette smoke, then the chemicals will inhibit and reduce their growth and movement. During the study, I observed the growth and behavior patterns of the cultures over the course of about a week. My investigation revealed that the chemicals in cigarettes inflict a very gradual death of the cultures. During their time of decline, the cells' characteristics changed entirely. The *Tetrahymena* became unable to undergo Mitosis, which led to a low reproduction rate, and also struggled to swim.

After the completion of my primary procedure, I persisted to explore the topic of damage due to smoking. I replicated the respiratory system and 'smoked' a cigarette, using a syringe to pull the smoke through the trachea of the model and to simulate inhalation. To conclude, my project's purpose was to highlight the harm caused by smoking.

Poster Presentation

A Scattering Theory Model of Molecular Graphene

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The goal of this research was to accurately model scanning tunneling microscopy (STM) data acquired by Professor Gomes during his time at Stanford University. The work of Prof. Gomes at Stanford made use of Scanning Tunneling Microscopy (STM) to engineer a 2-dimensional system with unparalleled precision. Molecular graphene was constructed by the creation of a triangular lattice of adsorbed CO molecules, which caused the surface electrons to scatter into the familiar honeycomb hexagonal lattice exhibited by graphene. The focus of the work is to accurately reproduce the interaction between the wavefunctions of the electrons and the scattering potential that the adsorbed atoms represent. This would allow for the prototyping of such systems computationally, without expending the time and energy required to assemble such precise structures. Toward this end, we use a scattering theory based in free-electron Green's functions as done by Heller in 1994, and demonstrate that a similar model can be used to fit the STM data with a few appropriate improvements. Using this theory, a model with free parameters was implemented in MATLAB. These parameters were examined in the context of our system and best fit values were determined. Finally, we compare our results with a group (H. Hammar et. al.) in Sweden which last year modeled the same system in a similar manner, and show that our model reflects a marked improvement, and merits further study in the context of other systems.

Poster Presentation

Influence of Matrix Metalloproteinase-3 on Metastatic Burden and Progenitor Cell-Driven Chemoresistance in Aggressive Breast Cancers

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Ann Zeleniak, Integrated Biomedical Sciences Graduate Program

Advisor: Laurie Littlepage, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

This year more than 40,000 women will die of breast cancer. Most of these deaths arise not from the primary cancer itself, but rather from the evolution of metastatic and chemoresistant tumors at secondary tumor sites. Even though overall breast cancer death rates have been declining, the death rates of aggressive breast cancers are not changing. A different strategy is required to combat these highly aggressive breast tumors that still kill patients. An area at the forefront of this search for the cure is the ever-changing tumor microenvironment. One of the members of the tumor microenvironment is the stromal protease matrix metalloproteinase-3 (MMP3) that promotes an increase in tumor progression in the mammary gland. While MMP3 itself normally is expressed by the surrounding stromal cells and not by normal epithelial cells, during cancer MMP3 also is upregulated in human breast cancer epithelial cells. Here we investigate the overexpression of MMP3 and its contribution to metastasis and chemoresistance. We find that MMP3 overexpression in mouse tumorigenic epithelium causes an increase in invasive pathology and an increase in metastatic tumor burden *in vivo*, indicating that MMP3 promotes an aggressive and potentially motile breast cancer in these mouse models as compared to vector controls. We also determined the contribution of MMP3 to chemoresistance. MMP3 overexpressing mice develop tumors that are resistant to chemotherapeutics compared to vector control mice. This research identifies MMP3 as a novel biomarker in the microenvironment that promotes both metastasis and chemoresistance. Our future research will focus on determining the mechanisms by which MMP3 contributes to metastasis and chemoresistance. We also will determine if MMP3 is a prognostic biomarker of patient outcome and will utilize our cancer models to identify therapies for the most lethal breast cancers.

Oral and Poster Presentation

The incorporation of green design into iodine deficiency test: The Iron Nanoparticle “Kill Switch”

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Advisors: Kathleen Eggleston, College of Engineering
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Iodine deficiency is one of the leading causes for preventable cognitive impairment across the globe. To help track the iodine nutrition status of populations at risk for iodine deficiency, the Sandell-Kolthoff (SK) reaction has been adapted to run on a paper analytical device, or PAD. The identification and characterization of potential harms at any stage of the product life cycle is part of green design, and evaluation of the PAD in this way suggests there may be a potential risk in addition to the benefits it would bring. The formulation of the PAD requires 0.075 mg of arsenic, which exceeds the safe levels for disposal as determined by the toxic characteristic leaching procedure (TCLP) of the US Environmental Protection Agency. Since the cards will be used in developing areas where the likely mode of disposal is landfilling, the arsenic must be put into a non-leachable state before disposal in order to minimize the impact on the local environment and human health. Testing from the summer of 2013 has demonstrated that the introduction of a 10:1 excess of iron oxide nanoparticles to leachates from the test immobilizes >99.7% of the arsenic by adsorption to the surface of the particles. Characterization of the nanoparticles by XRD and BET shows they are made of magnetite (Fe_3O_4), a common and relatively innocuous mineral, further minimizing any impact on the environment. Over the course of the school year the PAD has been redesigned to incorporate the iron nanoparticle “kill switch” into the test design, and testing by ICP-OES has shown that the tests are no longer qualified as toxic according to EPA standards. Future development seeks to mature the PAD into a marketable product.

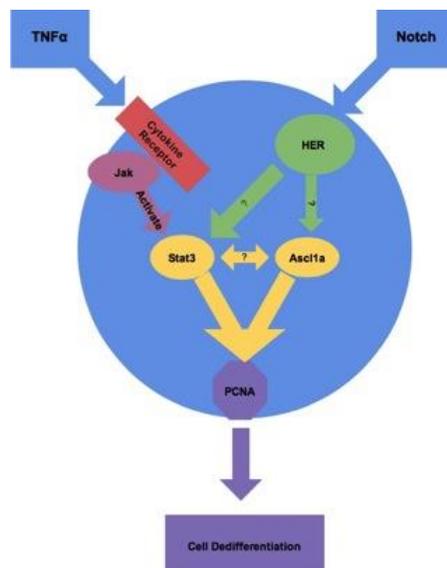
Poster Presentation

Influence of TNF α and Notch on Müller glia dedifferentiation and the role of Stat3 and Ascl1a in the cellular regeneration response

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Retinal damage in zebrafish induces robust Müller glia-mediated regeneration of lost neurons. Dying photoreceptors stimulate the Müller glia to dedifferentiate and reenter the cell cycle to produce neuronal progenitor cells that proliferate and migrate to the outer nuclear layer to differentiate into rod and cone photoreceptors. It has been shown that tumor necrosis factor alpha (TNF α) is produced by dying neurons and is necessary to stimulate Müller glia dedifferentiation and proliferation. Additionally, intravitreal injection of the soluble recombinant TNF α is able to induce Müller glia dedifferentiation and proliferation in the absence of retinal damage. Morpholinos and pharmacological inhibitors have demonstrated that TNF α signaling is activated through a Jak1/Stat3 signaling pathway. Notch signaling maintains Müller glia in a quiescent state in the undamaged retina. Repressing Notch signaling, through injection of the γ -secretase inhibitor RO492, stimulates Müller glia to reenter the cell cycle without retinal damage. This RO492-induced Müller glia proliferation is mediated by repressing Notch signaling and requires both Ascl1a expression and Jak1-mediated Stat3 phosphorylation/activation, analogous to the light-damaged retina. Expression of TNF α in Müller glia increases levels of Ascl1a and Stat3, resulting in further Müller glia recruitment. Knockdown of either Stat3 or Ascl1a has been shown to decrease the activation of the other. It is unknown how Stat3 and Ascl1a regulation change when Notch is inhibited in the presence of RO492. In order to find the underlying regulatory mechanisms between Ascl1a and Stat3 on the process of Müller glial proliferation, we subjected zebrafish to a variety of treatments by directly manipulating the TNF α and Notch pathways *in vivo* to observe changes in expression of Stat3 and Ascl1a using immunofluorescent staining and rt-PCR.



Oral Presentation

Evaluation of soundscape analysis as a tool for monitoring grassland bird diversity and abundance

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Multiple human effects, particularly livestock grazing, have completely changed the landscape and bird community in the Great Plains and Northwest grasslands. Current methods to monitor bird populations and grassland health can be time-consuming, disturb bird breeding, damage habitat, and require trained personnel. An emerging technique, the capture and analysis of the soundscape—the assemblage of sounds in an area—solves some of the problems with traditional monitoring techniques. The soundscape is captured by remote recording stations; this technique can be conducted with minimal expense and disturbance to the environment. However, few studies have tested the value of this new tool for monitoring bird diversity and abundance. For three grazing regimes, small ungulate grazed, livestock-grazed, and bison-grazed, we compared measures of Shannon’s Diversity Index and Species Richness found through point counts, a traditional method for monitoring bird communities, with seven soundscape analysis metrics: Technophony, Biophony, Normalized Difference Soundscape Index (NDSI), Total Energy, Recorded Richness, Acoustic Diversity, and Acoustic Evenness. AIC model selection found Species Richness best related to Recorded Richness, the number of bird species on the audio recordings; and Biophony, the power of biological sound in a recording ($R^2= 0.8892$, $F= 57.15$, $p<0.0001$). Species Diversity was also found to best relate with Recorded Richness, Biophony, and also with NDSI, the normalized ratio of biological-based sound to anthropogenic-based sound ($R^2= 0.8348$, $F= 24.59$, $p<0.0001$). In addition, livestock grazing adversely affects grassland birds and the grassland soundscape. Species Diversity ($df=2$, $F=11.23$, $p=0.002$) and Richness ($df=2$, $F=6.527$, $p=0.01$) were higher in small ungulate and bison grazed habitats, and the soundscape metrics Biophony ($df=2$, $F=4.14$, $p=0.04$) and NDSI ($df=2$, $F=6.119$, $p=0.01$) followed the same pattern. Our results indicate that soundscape analysis, particularly the metrics Biophony and NDSI, has potential as a cost-effective and non-invasive monitoring tool.

Poster Presentation

Resistance to miltefosine in Leishmania major

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Cutaneous leishmaniasis is caused by sandfly-transmitted *Leishmania major* (*L. major*) parasites and characterized by lesions on the skin. This disease is widespread in South America, Africa, and the Middle East and causes approximately 60,000 deaths per year. Current treatments for leishmaniasis include antimonials, paromomycin, amphotericin B, miltefosine, and pentamidine. Though miltefosine is currently the only approved oral drug and is widely available, resistance has already been observed in clinical trials in India and Nepal. Previously cyclophilin 40, a potential resistance marker, has been shown to be downregulated in miltefosine-resistant *L. major*. Cross-resistance markers allow detection of miltefosine-resistant *L. major* and treatment with appropriate antileishmanials. The objective of this study is i) to determine cross-resistance of miltefosine-resistant parasites to four common antileishmanial drugs, ii) validate cyclophilin 40 as a broad resistance marker via Western blot and iii) use comparative proteomics to investigate new potential resistance markers in miltefosine-resistant *L. major*.

Oral Presentation

Solar Cells: Understanding and Amending the Technology Transfer Disconnect

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Solar cells and transistors were invented at roughly the same time, by the same individuals, at the same institutions, but their development over time has been radically different. While technologically similar, solar cells and transistors play very different roles in commercial industry. Historically, the figure of merit for transistors has always been scale which follows the trend of Moore's Law. Scaling transistors has the unique property of simultaneously reducing cost and advancing the technology. By contrast, the solar industry has always been subject to the cost of electricity as its figure of merit, which follows the trend of Swanson's Law. Unlike scaling, reducing the cost of solar power historically has not led to improvements in commercial solar cell technology. This difference partly explains why the microcomputer revolution of the late 20th century succeeded and the cleantech revolution of the early 21st century is still searching for a future. By virtue of sharing the same figure of merit, academic researchers and corporations involved with transistor technology are interested in studying the same problems to achieve the same goals. As a result, I observe that transistors experience a very fluid technology transfer process from research to industry. By contrast, academic researchers and corporations involved with solar technology do not share the same figure of merit, leading to what I perceive as a disconnect in the solar cell technology transfer process. In this paper, I will attempt to demonstrate this disconnect, firstly by comparing the histories of transistor and solar cell technologies and secondly by providing some examples based upon my experience. Finally, I will suggest that one way to amend this disconnect is to find a figure of merit for solar power systems that simultaneously reduces cost for solar companies and improves overall system technology.

Poster Presentation

The Effects of FLASH Knockdown on the Polyadenylation of Histone Transcripts

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Advisor: Amanda Hummon, Dept. of Chemistry and Biochemistry

FLICE-associated huge protein (FLASH) has been identified as a protein that is required for the viability of colon cancer cells. Its knockdown causes altered expression of a number of genes involved in cellular growth and proliferation including histone proteins involved in replication. Knockdown of several proteins associated with FLASH, including a protein called Ars2, has been shown to cause the polyadenylation of histone transcripts, which are not normally polyadenylated. Based on these two facts, we are investigating the effects of FLASH knockdown on the polyadenylation of histone transcripts. To do this, SW480 colon cancer cells were transfected with two different siRNAs that target FLASH. RNA was harvested from these cells and used to make cDNA. A poly-dT primer was used so that cDNA would only be synthesized from transcripts that had a poly-A tail. PCR was used to amplify the transcripts of the histones in question. The PCR products were run on an agarose gel to identify which transcripts were successfully amplified by PCR and which were not. The transcripts that were amplified contained a poly-A tail. The histone transcripts were compared to a housekeeping gene, HPRT1, which would be polyadenylated regardless of FLASH knockdown. The agarose gel indicated that some histone transcripts were polyadenylated, but others were not. This polyadenylation was dependent on the family of the histone protein. The H2A, H2B, and H4 families showed polyadenylation, but the H1 and H3 families did not. Future investigations are aimed at teasing out a mechanistic explanation for these differences.

Poster Presentation

Regulation of the Oncogene ZNF217 by Localization in Breast Cancer

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Poor prognosis in breast cancer patients occurs when malignant tumors adapt to environmental insults, become resistant to chemotherapy, evade immune surveillance, and metastasize to other tissues. Tumors are thought to arise from individual cells with multiple mutations, including amplification of genomic regions that provide a growth advantage. A region on human chromosome 20 called 20q13 is increased in ~25% of early stage human breast cancers and correlates with poor prognosis in patients. We have studied a novel oncogene ZNF217 within this region. ZNF217 is key in promoting breast cancer: it is not only a prognostic indicator of breast cancer progression in patients who have the worst prognosis, but also is itself a drug target and/or marker of patient response to therapy. We find that ZNF217 protein is expressed most strongly in a small subset of cells within normal mammary epithelium and localizes predominantly in the nucleus of mammary epithelial cells. In contrast, the localization of ZNF217 is heterogeneous in breast tumors, with localization in both the nucleus and cytoplasm. Moreover, a truncated form of the protein localizes exclusively in the cytoplasm. We hypothesize that ZNF217 truncation and cytoplasmic localization affect ZNF217 function during cancer progression and can be used to predict poor prognosis in breast cancer patients. Thus, we aim to determine which regions of ZNF217 are required for oncogenesis by overexpressing ZNF217 truncation mutants in mammary epithelial cells and using these cells in a variety of assays that model steps in cancer progression—assays that have previously shown that ZNF217 promotes cancer progression. If our data shows that the localization of ZNF217 is implicated in oncogenesis, then future studies will aim to identify the mechanisms of the regulation of ZNF217 localization. This research will aid in the development of innovative cancer diagnostics and therapeutics for breast cancer. Because ZNF217 is overexpressed not only in breast cancer but also in other cancers, this research may be applicable to other cancers.

Poster Presentation

Correlation of X-ray Computed Tomography with Quantitative Nuclear Magnetic Resonance Methods for Pre-Clinical Measurement of Adipose Tissues in Living Mice

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Science Preprofessional Studies and Spanish

W Matthew Leevy, Notre Dame Imaging Facility and Dept. of Biological Sciences

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Advisor: Sharon Stack, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

Obesity is a profound health problem not only in the United States of America, with more than one-third of the adult populations clinically diagnosed as obese, but also in low- and middle-income countries throughout the world [NIH and WHO]. With incidence rates for several clinical conditions, such as type-2 diabetes, heart disease, stroke and some types of cancer, such as ovarian cancer, increasing due to obesity, research efforts into obesity have significantly increased in recent years. Countless obesity studies have used both murine obesity models and non-invasive anatomical imaging methods, such as X-ray computed tomography (CT) and quantitative nuclear magnetic resonance (QMR), to quantify the adipose tissue in these mice. While each of these methods has been validated using other methods of adipose tissue quantification, an analogous head-to-head study of the microCT and QMR methods with small animals had not been conducted. Using *in vivo* experiments, the microCT imaging technique for adipose tissue segmentation, quantification and 3D visualization was validated relative to the QMR method. *In vivo* scans of 28 nude mice (Nu/Nu, Foxn1 knockout) were conducted at three time points over the course of 18 weeks. From these 28 mice, the 16 mice that presented the highest relative increase in mass were chosen for extensive microCT and QMR analysis so as to span the largest possible range in adipose mass. The microCT-obtained adipose mass values were then compared to the QMR-derived adipose mass values to calibrate the microCT image resolution, adipose segmentation range and median filter parameters in order to align the microCT data with that of the QMR method. Across all three parameters, strong linearity was seen between the adipose mass values obtained with both the microCT and QMR methods. However, underestimation in the microCT-derived adipose mass values proves the value of the microCT method, with its 3D region-specific adiposity visualization, as a semi-quantitative method for measuring changes in adipose tissue in mice in longitudinal studies.

Poster Presentation

Ecdysone-induced protein 78C function in plasmatocyte survival and crystal cell fate commitment

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Drosophila melanogaster has emerged as an ideal model system for hematopoietic studies. Similarities between *D. melanogaster* and mammalian hematopoiesis include conserved signaling molecules and transcription factors, a myeloid cell lineage, and biphasic cell differentiation. Additionally, *D. melanogaster* serves as a model organism for studies concerning nuclear receptors. The genome encodes 18 nuclear receptors, with homologues of all 6 major vertebrate nuclear receptor subfamilies. This study focuses on the role of the nuclear receptor Eip78C in plasmatocyte and crystal cell differentiation in the *D. melanogaster* larval hemolymph. Previous studies identified an increase in the crystal cell population, while the total hemocyte population was reduced. These studies suggested that Eip78C supports normal plasmatocyte differentiation while it suppresses excessive crystal cell differentiation. The studies presented here seek to establish the precise point at which Eip78C functions in the *D. melanogaster* hemocyte differentiation cascades. The Lozenge (Lz) protein is required for normal crystal cell development, with loss-of-function mutants lacking this cell type completely. Increased crystal cell differentiation is observed in Lz-Eip78C double mutant fly lines, which suggest that Eip78C interferes with normal Lz function since this protein is necessary for normal crystal cell differentiation. Ongoing studies continue to work towards an understanding of the widespread effects the Eip78C protein seems to have on hematopoiesis in the fruit fly.

Poster Presentation

Genetic analysis of podocyte development

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Advisor: Rebecca Wingert, Dept. of Biological Sciences

The kidneys are key specialized organs consisting of segmented functional units called nephrons. The zebrafish embryo kidney is composed of two nephrons that share a common glomerulus. The glomerulus functions as a blood filter, and the epithelial cells of this apparatus are called podocytes. Mature podocytes are characterized by cellular extensions, called foot processes, from their basal surface. These foot processes interdigitate with the extensions of neighboring podocytes and form cell-to-cell junctions called the slit diaphragm. Previously, our lab has identified and isolated two mutants: zeppelin (*zep*) and lightbulb (*lib*). The *lib* encodes a mutation in aldehyde dehydrogenase 1a2, which is required for retinoic acid (RA) biosynthesis, and disrupts podocyte formation during nephrogenesis. The *zep* mutants exhibit edema at 4 days post fertilization, and have dramatically reduced numbers of podocytes. To gain further insight into *zep* podocyte development, expression of the podocyte genes *wt1a*, *wt1b*, *nephrin*, and *podocin* was assessed at various time points of development using whole mount *in situ* hybridization (WISH). *zep* mutants displayed reduced *wt1b*-expressing podocytes at the 15 somite stage, suggesting that podocyte specification is abrogated. Recently, a morpholino knockdown of *brca2* in wild type zebrafish was found to phenocopy the *zep* mutants, indicating that it is a good candidate gene. To determine if RA acts upstream or downstream of *zep*, I investigated the epistatic relationship between *zep* and RA. RA treated embryos did not show any rescue of the mutant phenotype, suggesting that *zep* acts downstream of RA. Future directions include determining the expression pattern of *brca2* in *zep* and wild type zebrafish using WISH, determining whether *brca2* can rescue the *zep* phenotype, performing a cell death assay using the TUNEL assay or acridine orange test, and investigating the affect of overexpression of *wt1b* and *wt1a* on *zep*.

Oral Presentation

Carbon-14 Graphitization Chemistry

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Advisor: Philippe Collon, Dept. of Physics

Accelerator Mass Spectrometry (AMS) is a process that allows for the analysis of mass of certain materials. It is a powerful process because it results in the ability to separate rare isotopes with very low abundances from a large background, which was previously not possible. It is in essence the perfect toll to look for the “needle in a haystack.” Another advantage of AMS is that it only requires very small amounts of material for measurements. An important application of this process is radiocarbon dating because the rare ^{14}C isotopes, which has a half-life of $t_{1/2} = 5730$ years, can be separated from the stable ^{14}N background that is 10 to 13 orders of magnitude larger, and only small amounts of the old and fragile organic samples are necessary for such a measurement. Our group focuses on this radiocarbon dating through AMS. When performing AMS, the sample needs to be loaded into a cathode at the back of an ion source in order to produce a beam from the material to be analyzed. For carbon samples, the material must first be converted into graphite in order to be loaded into the cathode. My role in the group is to convert the organic substances into graphite. In order to graphitize the samples, a sample is first combusted to form carbon dioxide gas and then purified and reduced into the graphite form. After a couple weeks of research and with the help of various Physics professors, I have developed a plan for the necessary setup to convert the samples. In the near future, we will purchase the needed parts of the setup and begin to construct the apparatus. Once the apparatus is put together, the carbon samples will be graphitized and then loaded into the AMS machine for analysis.

Poster Presentation

Interaction between the gut microbiome and intestinal parasites in wild baboons

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An animal's gut microbiome, the bacteria community that inhabits its digestive tract, is an integral part to its health and survival. These bacteria interact directly with the host organism and the contents of its gut—consuming, redistributing, and storing energy. Similarly, parasites have been shown to have impacts on an animal's health, often leading to higher risks of mortality. Because parasites can reside and flourish based on the nutrients of a host's gut, and because the microbiome plays a role in digestion, it is likely that there is a relationship between the two. My study will be one of the first to quantify this relationship. I will use parasite and microbiome data from a population of well-studied wild baboons to test the hypothesis that there is a relationship between gut microbiome community composition and intestinal parasite load diversity. If such a correlation exists, the relative abundance of different bacteria will vary based on the parasite load and what parasite species are present. Specifically, based on previous research, I predict that fecal samples with a lower parasite load will have greater relative abundance of Gammaproteobacteria and Betaproteobacteria. The data from this experiment will provide a foundation for understanding the relationship between the microbiome and parasites in wild animals.

Oral Presentation

Maturation and Retention of Rhodopsin in Anopheles gambiae Photoreceptors

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Advisors: Joseph O'Tousa and Michelle Whaley, Dept. of Biological Sciences

The tropical disease vector *Anopheles gambiae* possesses 10 rhodopsins, the light receptors that initiate the phototransduction cascade. Each rhodopsin is tuned for specific wavelengths of light. To understand the role of these rhodopsins in mosquito visual behaviors, we are characterizing the properties of these rhodopsins. Here we report the analysis of long wavelength opsins of the Agop1 family (Agop1, Agop3, Agop4). These proteins are >99 % identical and are not distinguished by the antibody used in our analysis. We show that one or more Agop1 family members, hereafter referred to as Agop1, are expressed in the major class of adult photoreceptors. Two different forms of Agop1, immature and mature, are recognized due to their differing mobility in a SDS-denaturing gel. Further, following endoglycosidase treatment, Agop1 migrated in a similar fashion as the mature Agop1, showing that the immature (nascent) form is glycosylated within the N-terminal domain. These results suggest that Agop1 matures by a modification to the N-terminal region of the protein. We monitored mature and immature Agop1 levels during the standard 12-hour light/dark cycle and other conditions. The results show that the level of immature Agop1 stayed constant regardless of the light condition, while the level of the mature Agop1 increased only during dark conditions. Immunohistology shows that Agop1 is retained within the rhabdomere only during dark conditions. Similar results were previously reported for *Aedes aegypti*. Together, our results indicate that Agop1 is maintained in the rhabdomere as a consequence of dark treatment. Conversely, Agop1 is endocytosed within the cytoplasmic compartment as a consequence of light treatment, where it is subjected to degradation. Our results show that photoreceptors of *Anopheles* possess mechanisms for manipulating both rhodopsin cellular location and rhodopsin levels to enhance photoreceptor sensitivity in low light and nocturnal environments.

Oral Presentation

The Role of Coagulation and Platelet Activation Markers in Platelet Dysfunction for a Rat Model of Traumatic Brain Injury

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Advisor: Victoria Ploplis, W.M. Keck Center for Transgene Research
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Coagulopathy is a condition in which the blood's clotting process is dysfunctional and can lead to delayed healing and prolonged bleeding after injury. Coagulopathy is a complication of traumatic brain injury (TBI) that has been studied extensively and recent studies implicate platelet dysfunction in response to agonists adenosine diphosphate agonist and arachonic acid. The mechanism by which platelet dysfunction arises is poorly understood, but the recent development of a rodent model of traumatic brain injury that mimics the coagulopathy observed clinically can aid in its elucidation. In this study immunohistochemistry was used to show the expression and localization of coagulation and platelet activation markers in post-traumatic brain. These results paralleled changes in systemic platelet responsiveness to adenosine diphosphate and arachonic acid potentially the result of brain tissue factor release in blood and thrombin generation leading to early activation of platelets and then platelet exhaustion. The results indicate that changes in expression of local procoagulant proteins in an injured brain are correlated with systemic platelet dysfunction.

Poster Presentation

How Much Does Error Matter? Statistical Analysis of Data Entry Discrepancies in the PaleON Project

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Advisor: Jason McLachlan, Dept. of Biological Sciences

The PaleON project aims to record data regarding tree composition from the 1800's until today in order to recognize trends that can show ecological change over time. This in turn can be used to analyze human impact on the environment and predict forest trends in the future, improving our understanding of how global change affects forests in the Midwest. Historic tree composition data (species, diameter and location from corner post) from the 1800's was gathered for Illinois and Indiana townships from the United States Public Land Survey System (PLS). We aim to characterize the accuracy rate of data entry within the project and use it to adjust our models and account for variability between readers of data. This type of error is known as observational error and is a common, yet under-appreciated problem in scientific analysis. To assess the observation error of our entered data, we created code in R to systematically examine differences between individual townships entered by two different data readers. Differences were categorized as archival and quantitative estimates; archival differences include items such as PLS page number, surveyor name, tree name notation, etc., and quantitative differences are those related to data used to analyze forest composition, and include tree species, diameter and location. The most common discrepancy between readers occurred in archival entries such as surveyor name, notation in the tree name, and quantitative differences included confusing numbers such as 1 and 7 due to indistinguishable handwriting. Understanding the observational error will be used to 1) improve data entry by the readers and 2) render the PaleON models more applicable and transparent for those that will utilize this data in the future. The goal of the PaleON project is to synthesize ecological data from the past and use it to build long-term forecasting models to predict trends in the future, and this type of statistical analysis is vital in maintaining credibility and reliability in our findings.

Oral Presentation

Total Synthesis and Biosynthetic Investigation of Ambruticin J

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Chemistry

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Advisor: Richard Taylor, Dept. of Chemistry and Biochemistry

The natural product (+)-ambruticin S belongs to a class of polyketides first isolated from *Sorangium cellulosum* in 1977 by scientists at Warner-Lambert. In 2006, a research effort led by Christopher Reeves published data regarding the polyketide synthase gene cluster responsible for ambruticin production. Many of the ambruticins have shown antifungal activity and may have further applications in medicinal chemistry. As a result, recent research has worked toward the total synthesis of ambruticin. In the biosynthetic pathway of ambruticin S, it has been previously proposed that ambruticin J exists as an important intermediate in this pathway. Our research aims to synthesize ambruticin J for further analysis of its role in ambruticin biosynthesis. Our synthetic pathway includes a late-stage coupling of three fragments. Our proposed route applies our previously developed methodology for forming substituted cyclopropanes, an important structural feature of ambruticin. Upon completing the synthesis of ambruticin J, we will investigate the downstream biosynthetic transformations with the goal of accessing the complete structure of the natural product ambruticin S. We will identify conditions for the stereoselective epoxidation and subsequent cyclization to form the pyran ring in ambruticin S. These successful transformations will support the proposed role of ambruticin J in the biosynthesis of the natural product.

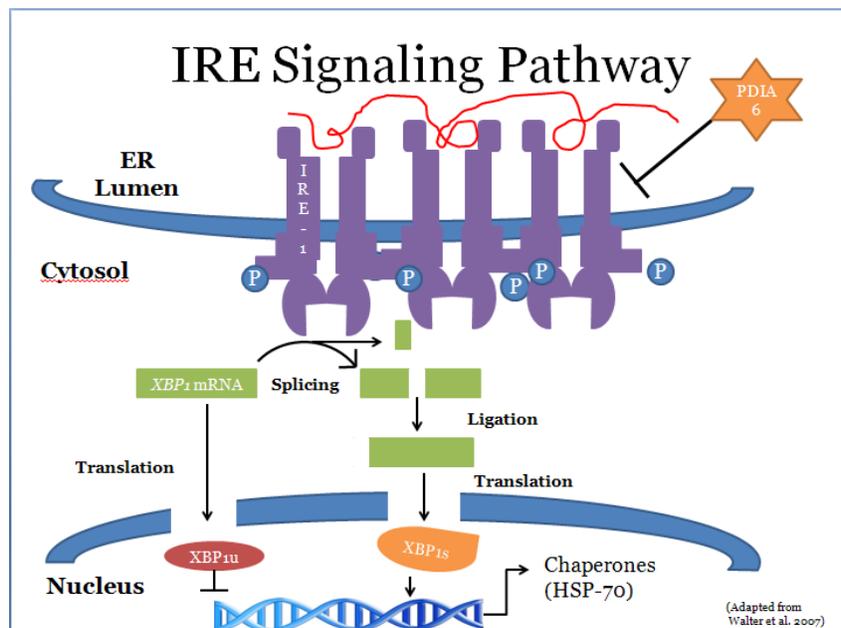
Poster Presentation

TAG-320 Functions as a Brake on the Unfolded Protein Response in Caenorhabditis elegans

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Advisors: Marni Falk, Dept. of Pediatrics, The Children's Hospital of Philadelphia, and Yair Argon, Dept. of Pathology and Lab Medicine, Perlman School of Medicine, University of Pennsylvania, Division of Cell Pathology, The Children's Hospital of Philadelphia

When the level of unfolded or misfolded proteins in a cell exceeds the folding capacity of the endoplasmic reticulum, a process called the unfolded protein response (UPR) is triggered. Part of this process involves the splicing of the *xbp-1* mRNA transcript and its translation into a protein that serves as a transcription factor for UPR target genes, including those encoding many chaperones. Though UPR is necessary for proper cell function, prolonged UPR can cause cell death. PDIA6, a protein disulfide isomerase found in humans, regulates the response by attenuating UPR. This study investigates TAG-320, a protein found in *Caenorhabditis elegans* hypothesized to serve the same function as PDIA6. An assay was developed to quantify the level of *xbp-1* mRNA splicing in order to measure the effect of TAG-320 down regulation. Results showed that *xbp-1* mRNA splicing increases from the basal level when *tag-320* expression is suppressed, suggesting that TAG-320 is an ortholog of PDIA6. If confirmed, these results will allow the use of *C. elegans* as a model organism for studying the modulation of UPR signaling. This could have great implications for diseases, such as diabetes and cancer, as well as numerous neurodegenerative diseases, for which excessive UPR has been identified in the pathology.



Poster Presentation

Computational Studies of the Effect of Nucleation on Microtubule Steady-State Dynamics

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Advisor: Holly Goodson, Dept. of Chemistry and Biochemistry

The cytoskeleton is essential to life because it provides cells with shape, strength, and transportation. Protein-based polymers called microtubules (MTs) are important components of the cytoskeleton, but their behavior is poorly understood because they exist in populations of dynamic polymers that interact in complex ways. Computational modeling provides a way to study these complexities by allowing simple probability-based rules based on the biochemistry of individual subunits to play out over many iterations. These simulations can reveal emergent properties of the system by computing the steady state concentrations of free and polymerized subunits reached under various conditions. My project is part of a larger project studying how the classical theories of polymer assembly (which assume equilibrium polymers that do not require energy input) should be adjusted for steady-state (energy requiring) polymer systems. Specifically, my goal is to understand how changes in the process of nucleation (generation of new filaments) affect the amounts of polymerized and free subunit at steady state. Because MTs must be nucleated by a cooperative initiation event between subunits in order to begin growing, nucleation is an important part of the cell's regulation of the cytoskeleton. This project used a modified version of the published probability-based simulations to compute steady-state concentrations achieved under different nucleation kinetics. Results are still being obtained. While we have already established that the simulated steady-state polymer systems deviate significantly from many of the classical predictions, we predict that the effect of changes to the process of nucleation will in fact be consistent with the equilibrium polymer predictions. Analysis of our simulated steady-state system under different nucleation conditions will reveal whether the effect of nucleation is the same as in the classical models.

Poster Presentation

Regulation of epithelial morphogenesis by Adenomatous Polyposis Coli

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Adenomatous Polyposis Coli (APC) is a multi-functional protein that is lost or mutated in many epithelial cancers. Although APC is well known as a negative regulator of the Wnt/B-catenin signaling pathway, it also binds to microtubules and polarity proteins, suggesting functions in regulation of epithelial polarity and cell migration. The mammary glands of *Apc*^{Min/+} mice demonstrate mis-regulation of epithelial polarity, exhibit early neoplastic changes, and develop more aggressive mammary tumors when crossed to the MMTV-PyMT model of breast cancer. Previous studies from our laboratory demonstrated that APC knockdown in the Madin-Darby Canine Kidney (MDCK) model altered epithelial morphogenesis and resulted in inverted polarity in 3D culture. While restoration of the B-catenin binding domain was unable to rescue the phenotype, introduction of either full-length or a c-terminal fragment of APC partially restored these phenotypes. The current studies investigate the Wnt-independent mechanisms by which APC regulates these processes using the MDCK model. We hypothesize that the interaction between the c-terminal fragment and epithelial membrane protein 2 (EMP2) plays a key role in regulating 3D morphogenesis and polarity. Interestingly, EMP2 and APC have been shown to regulate FAK signaling. Treatment of APC knockdown MDCK cells with PP2, a Src kinase inhibitor, or AIIB2, an integrin inhibitor, eliminated the drastic cyst size changes produced by APC knockdown. In addition, preliminary studies suggest a role for APC in cell motility as shAPC-MDCK cells exhibited increased cell migration. Future studies will aim to dissect the role of the c-terminal fragment of APC in regulating gene expression, cell migration, and polarity and 3D morphogenesis in MDCK cells. Investigating the interactions of APC with several targets such as those in the FAK/Src signaling pathway will help identify key players in the role of APC in Wnt-independent tumor development.

Poster Presentation

Synthetic Progress Towards Concanamycin F, A Potent Inhibitor of Vacuolar ATPase

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Advisor: Paul Helquist, Dept. of Chemistry and Biochemistry

Recent studies have shown vacuolar ATPase inhibitors have therapeutic potential in certain types of cancer, osteoporosis, and Niemann-Pick Type C. Inhibition of vacuolar ATPase leads to disruption of cellular acidification in endosomes and lysosomes, which has important consequences in cells affected by these diseases. The macrolide concanamycin F, a potent inhibitor of vacuolar ATPase, has been shown to possess these properties. Such biological applications have led to our interest in developing a new approach to concanamycin F and its structural analogues, in order to further investigate the structure-activity relationship and optimize therapeutic efficacy. Synthetic development of the molecule will rely on α -alkenylation methodology recently developed in our lab to accomplish key steps, as well employ other organometallic reactions to afford the final product. The initial steps towards the molecule will be presented.

Oral and Poster Presentation

Using Yeast as Biosensor for Mutagenicity

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Julia Philip, Dept. of Chemistry and Biochemistry

Advisor: Holly Goodson, Dept. of Chemistry and Biochemistry

The rise in the production of novel chemicals has resulted in a need to reliably determine the carcinogenic potential of compounds. The Ames test, a common test for mutagenicity, exposes bacteria to a suspected mutagen and uses a histidine-based plate assay to detect mutations in the bacteria. Bacteria that require an external source of histidine to grow are exposed to a suspected compound and grown in an environment without histidine. Consequently, those bacteria that can grow and survive in the histidine-deficient environment are mutants (from his- to his+). The more mutagenic the compound is, the more colonies are obtained. While the Ames test is inexpensive and easy to perform, it uses a high concentration of mutagen and a low exposure time, parameters that generally do not correspond with expected human exposure. We hypothesize that yeast grown in a series of parallel continuous cultures can serve as the basis for an improved test for mutagenicity. Since yeast can be grown for long periods of time in continuous culture systems, we hope to see the effects of exposure to mutagen over a long exposure period and gain increased test sensitivity by seeing results at lower concentrations of mutagen. To test this hypothesis, yeast were grown in continuous cultures at varying levels of known mutagen and the mutagenic potential of the different concentrations of the compound was assessed by two approaches: a plate-based assay similar to the Ames test and whole-genome sequencing. For the plate-based assay, samples of yeast cultures at different times were plated on a plate containing canavanine, an amino acid toxic to WT-yeast. The mutagenic potential of the compound can be inferred by counting the number of surviving (mutant) colonies on a plate containing canavanine. The data obtained thus far suggest that yeast grown in continuous culture systems can detect mutagens at concentrations at least one order of magnitude smaller than the Ames test. The data obtained from the plate-assay is supplemented by sequencing data. Whole-genome sequencing will provide a thorough analysis on the mutagenic potential of a compound in that the changes to the genome can be directly evaluated.

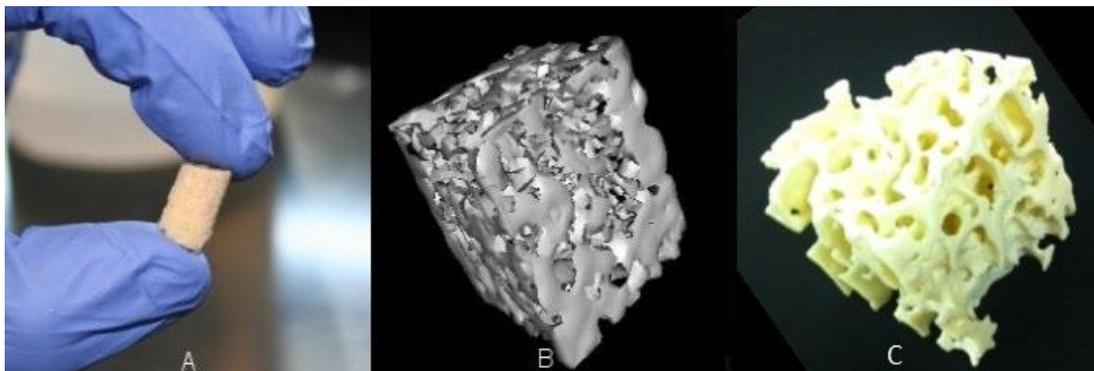
Poster Presentation

Imaging and 3D Printing of Trabecular Bone

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Science Preprofessional Studies
Evan Doney
College of Engineering
Chemical Engineering

Advisors: Glen Niebur, Dept. of Aerospace and Mechanical Engineering and
W. Matthew Leevy, Notre Dame Integrated Imaging Facility and Dept. of Biological Sciences

My research has been conducted jointly between the Tissue Mechanics Lab and the Notre Dame Integrated Imaging Facility (NDIIF) and focuses on developing protocols for imaging and three-dimensional printing of trabecular bone. Previous work in the NDIIF has used 3D printing to produce scale models of rat and rabbit skeletal and soft tissue features from X-ray computed tomographic (CT) data. These techniques of data collection and processing have been applied to imaging trabecular bone, the porous tissue found at the ends of long bones and in vertebrae. This tissue is the site of a dynamic process of formation and resorption, collectively known as remodeling; visualization of this process is useful for the study of bone diseases and cellular response to different treatments. Here, I present a method for converting these CT scans to prints, along with a validation of its accuracy. The resulting analysis of the printed bone cores will be useful for researchers, students, and educators as tangible models will lead to a better understanding of structure and function in healthy and diseased bone, as well as improved interdisciplinary communication.



Oral Presentation

Ras mediated regulation of apoptosis in extracellular matrix attachment and detachment

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Biological Sciences and Psychology

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Advisor: Zachary Schafer, Dept. of Biological Sciences

Oncogenic Ras protects breast cancer cells from anoikis, an apoptotic process induced by the loss of extracellular matrix (ECM) attachment. Ras is the most common oncogene in human cancer and is found mutated in 20-25% of all human tumors. Mutated ras is only found in 5% of breast cancers. However, multiple growth factor receptors including EGFR and ErbB2 (neu/HER-2) are overexpressed in up to 50% of breast cancers and activate potent downstream signaling through Ras. This suggests that Ras activation and Ras-mediated signaling pathways are critical to breast cancer development. Breast cancer cells overexpressing Ras are able to suppress caspase activation in ECM detachment. Previous literature has demonstrated that Ras suppresses apoptosis by preventing the release of cytochrome c from the mitochondria. Cytochrome c is crucial for the activation of caspases through the formation of the apoptosome. However, we have found that the addition of exogenous cytochrome c to cells overexpressing Ras grown in detachment fails to result in caspase activation. These data suggest that cells overexpressing Ras are able to suppress caspase activation in the presence of cytochrome c and that Ras may be playing a role in anoikis suppression by modulating activity downstream of cytochrome c release, perhaps by disrupting apoptosome formation. Surprisingly, Ras overexpression results in enhanced expression levels of the apoptotic proteins procaspase-3, procaspase-9, and Apaf-1 in attachment and detachment. In contrast to cells grown in detachment, cells overexpressing Ras grown in attachment exhibit increased levels of caspase activation following the addition of exogenous cytochrome c. This indicates that in attachment, cells overexpressing Ras display increased sensitivity to induced cell death due to the enhanced expression levels of apoptotic proteins. Research characterizing the role of Ras in apoptosis in breast cancer is extremely relevant from a therapeutic perspective and could provide insight into the design of novel therapeutics for novel targets.

Poster Presentation

*Evaluating the Cost of “Diapause Strategies” in the Overwintering Pupae of *P. glaucus*, *P. canadensis*, and Their Hybrids in the Context of Climate Change*

Riley Parrott

College of Arts & Letters

Environmental Sciences and Program of Liberal Studies

Sean Ryan, Dept. of Biological Sciences

Advisors: Jessica Hellmann and Sean Ryan, Dept. of Biological Sciences

Climate change has been predicted to change the range of temperatures that species experience in their current geographic ranges and thus could have either positive or negative effects on species, depending on how they respond to these changes. For example, populations occupying the cooler portions of a species' range may benefit from warming temperatures, while those that occupy areas in the warmest portions of their range may be negatively affected by warmer summer temperatures. In Lepidoptera, there are two pathways for development during the pupal stage—direct develop or diapause. One is obligate diapause that only allows the butterfly to undergo one generation in the summer. Facultative diapause allows a butterfly to choose between diapausing directly or emerging and taking another generation in the same summer. *Papilio glaucus* can “choose” which diapause strategy it undergoes, either resulting in a second generation in the summer, or diapausing directly after pupation. *Papilio canadensis*, on the other hand, always diapauses upon pupation. These two species are able to interbreed, forming a hybrid zone that overlaps in the southern most part of *P. canadensis*' range and the northern most part of *P. glaucus*' range, allowing for the direct competition between these two strategies. To test how the fitness of both species and their hybrids are affected by their “diapause strategy” and whether this is dependent on summer temperature, pupae of both *P. glaucus* and *P. canadensis* and their hybrids were subjected to four different summer temperature treatments that represented a range of summer temperatures in the hybrid zone. Pupae were measured throughout the experiment to measure how pupae weight changes as a function of summer temperature and the genotype of the individual. My hypothesis is that *P. canadensis* will lose more weight over the summer than *P. glaucus*. The climate change could cause problems *P. glaucus* continues to outcompete *P. canadensis*.

Poster Presentation

Gene expression changes downstream of APC loss predict tumor phenotype

Andjela Pehar
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Science Preprofessional Studies

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The Adenomatous Polyposis Coli (APC) tumor suppressor is mutated or hypermethylated in up to 70% of human breast cancer cases. Our previous studies demonstrated that Apc mutation advances the MMTV-Polyoma Middle T Antigen (PyMT) model of breast cancer, with an increase in signaling downstream of focal adhesion kinase (FAK)/Src/JNK activation in MMTV-PyMT;ApcMin/+ tumors. In addition, the majority of tumors that arose in the MMTV-PyMT;ApcMin/+ animals were classified as adenosquamous carcinoma as compared to tumors from MMTV-PyMT;Apc+/+ animals, which were solid carcinomas. Given the heterogeneous nature of these tumors, RNA was isolated from tumors with wild-type Apc, mutant Apc yielding solid carcinomas, and mutant Apc resulting in adenosquamous carcinomas. Quantitative real-time RT-PCR was performed to identify gene expression changes responsible for the altered tumor phenotype between tumors from mutant Apc resulting in the different tumor phenotypes. In parallel studies, triplicate samples of the MMTV-PyMT;Apc+/+ and MMTV-PyMT;ApcMin/+ cell lines were analyzed by real-time PCR for gene expression changes. Multiple changes consistent with the phenotypic and proliferative changes downstream of APC loss were identified, including changes in expression of cyclooxygenase-2 (COX-2). Furthermore, 3D cultures of the samples of the MMTV-PyMT;Apc+/+ and MMTV-PyMT;ApcMin/+ cell lines were plated in standard Matrigel and Growth Factor Reduced Matrigel to investigate the role of the microenvironment in gene expression. In parallel with the previous studies, RNA was isolated from the 3D cultures and analyzed for gene expression changes. The findings presented here indicate that APC-mediated gene expression changes can be used to predict tumor phenotype and potentially downstream therapeutic targets.

Poster Presentation

Targeting the Polyamines in Drosophila Models for Tumorigenesis and Development

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Advisor: Jeremiah Zartman, Dept. of Chemical and Biomolecular Engineering

Polyamines are polycationic molecules with pleiotropic roles in cellular processes. In particular, they have been implicated for roles in tumorigenesis and the development of certain tissues. Tumors exhibit increased polyamine biosynthesis, and there is accumulating evidence for roles for polyamines downstream of oncogenes. Thus many attempts have been made to pharmacologically target polyamine biosynthesis as an anticancer therapy. Unfortunately, efficacy of such treatments has been limited by the efficiency of the polyamine regulatory system, for example increased polyamine uptake in response to cellular polyamine depletion. Due to these findings, there is a great need to target polyamine transporter genes in parallel with polyamine depleting therapies. However, little is known about the identity of mammalian polyamine transporters, and less still about the involvement of polyamines in development. Here we use an *in vivo* tumor model system with RNA interference (RNAi)-mediated knockdown of candidate polyamine pathway genes to identify novel effectors of polyamine activity in cancer using the fruit fly (*Drosophila*). Using a secondary, wild type model we can analyze the effects of candidate genes on normal development. We have further begun coupling this genetic approach for cancer modulators with a pharmacological approach using known inhibitors of polyamine biosynthesis to identify potential synergies for future combinatorial therapies. Due to the high level of conservation in the polyamine pathway between *Drosophila* and humans, genes confirmed as having roles in tumor formation and progression in *Drosophila* can provide promising new leads for the next generation of cancer therapeutics.

Poster Presentation

Characterization of rod precursor proliferation and differentiation in the adult zebrafish retina

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David Hyde and Manuela Lahne, Dept. of Biological Sciences
Advisor: David Hyde, Dept. of Biological Sciences

Two hundred eighty-five million people worldwide are visually impaired, and many exhibit a progressive and irreversible loss of vision. If it were possible to regenerate the neurons that were damaged/lost in their retinas, their vision could be restored. In contrast, zebrafish possess the ability to regenerate all their retinal cell types, making it an ideal model organism for studying neuronal regeneration and elucidating the mechanisms that could restore sight to the visually impaired. Zebrafish rod precursor cells were previously shown to be required for the persistent production of rod photoreceptors throughout the life of the fish. It was previously described that the rod precursor cells increase their rate of proliferation in response to light-induced death of rod photoreceptors. We demonstrate that there is no significant difference in the number of rod precursor cells in both undamaged and light-damaged retinas that were previously dark-adapted. However, dark-adapted undamaged fish possess significantly greater numbers of proliferating rod precursor cells relative to fish that are maintained in standard light conditions. These data suggest that prolonged dark adaptation directly or indirectly induces rod precursor proliferation in the central dorsal retina and that light-induced rod photoreceptor cell death does not affect rod precursor proliferation. We further characterized proliferating rod precursors in the *Tg[olig2:EGFP]* and the *Tg[atoh7:GFP]* transgenic zebrafish lines, which upregulate GFP in neuronal progenitor cells that commit to the neuronal lineage during light-damage. While a subset of rod precursors was positive for GFP in the *Tg[olig2:EGFP]* line, no GFP-positive rod precursors were observed in *Tg[atoh7:GFP]* zebrafish. This further supports the hypothesis that the rod precursor cells are not following the normal lineage commitment pathway that is observed in neuronal progenitor cells during rod photoreceptor regeneration.

Poster Presentation

Development of Imaging Protocols for X-ray Computed Tomography of Rats

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Sarah Chapman, Notre Dame Imaging Facility and Dept. of Biological Sciences

Advisor: W Matthew Leevy, Notre Dame Imaging Facility and Dept. of Biological Sciences

X-ray Computed Tomography (CT) is a useful preclinical research tool that non-invasively produces visual and analytical information about anatomical structures and organ functions within living animals. The applications of X-ray CT imaging have been enhanced by a wide variety of contrast agents that selectively visualize specific tissues in animal anatomies. While mouse imaging techniques are well established with a variety of these contrast probes and reagents, there is very little information available on the best practices for imaging of rats, which are up to 10-fold larger by weight. Thus, a wide range of animal disease models in rats are not readily used in conjunction with imaging, since viable strategies have not yet been developed. In order to advance the imaging protocols for X-ray CT in rats, this study aimed to develop the best techniques for the use of three different commercial contrast agents. Here, we present the preliminary methods used to visualize the kidney, liver, and vasculature tissues of rats enhanced by varying amounts of contrast agents, specifically Visipaque, Exitron nano 12000, and Aurovist. By injecting the rats via tail vein and utilizing an Albira X-ray CT system in conjunction with PMOD, ImageJ, and Volview software, the images were analyzed for ideal dosage rates and clearance times in order to develop a more detailed method for image acquisition and examination. Future research will incorporate multi-modal imaging of the same animal through combinations of multiple contrast agents and scanning techniques as well as more refined dosage values. These results will aid researchers in evaluating a wider field of diseases models in rats and open up new opportunities in rat experimentation by providing an established CT imaging protocol.

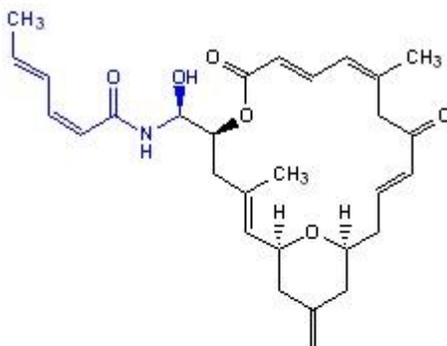
Oral Presentation

Synthetic Pathway to Zampanolide

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Chemistry

Matt Wilson, Dept. of Chemistry and Biochemistry
Advisor: Richard Taylor, Dept. of Chemistry and Biochemistry

Microtubule binding agents have demonstrated effective chemotherapeutic potential for the treatment of multiple cancers. One such compound that has greatly interested our lab is the polyketide, (-)-zampanolide. First isolated in 1996 from the sea sponge *Fasciospongia rimosa*, (-)-zampanolide has potent anti-cancer activity, which makes this compound an interesting small molecule for biological study. Recent studies indicate that (-)-zampanolide behaves as a microtubule stabilizing agent via a unique covalent binding interaction with tubulin in the paclitaxel binding site. This binding process hinders cellular reproduction by disrupting the dynamic nature of microtubules, and specifically affects cancer cells due to their rapid rate of reproduction. Similar to (-)-zampanolide, the compound dactyloide is also produced by *F. rimosa*. Unlike (-)-zampanolide, dactyloide has decreased activity due to the absence of a side-chain that is critical in microtubule binding. It has been hypothesized that the removal of this side-chain in dactyloide is a result of an over oxidation of this side-chain in *F. rimosa*. Currently, a model system of the side-chain of zampanolide is being designed and evaluated. Specifically, the oxidation of the carbon alpha to the amine will be tested for evidence of an oxidation mechanism. Starting with (L)-phenylalanine, a model of the structure will be synthesized. The finished compound will be oxidized with a metallic complex catalyst and evaluated for oxidation potential.



Poster Presentation

Using Th40:Treg Ratio as a Predictor of Multiple Sclerosis and Other Autoimmune Diseases

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Biological Sciences and Psychology

Dan Waid, Jessica Carter, and Gisela Vaitaitis

Webb-Waring Center, University of Colorado Denver

Advisors: John Repine, Dept. of Medicine and Pediatrics, School of Medicine, University of Colorado Denver, and David Wagner, Webb-Waring Center, University of Colorado Denver

Multiple sclerosis (MS) is an autoimmune disease that results in the demyelination of nerves and impedes the efficient transmission of messages. It results in debilitating conditions, including paraparesis, which is the partial paralysis of the limbs, and can lead to disabilities. Currently, the McDonald Criteria is used to diagnose MS. The main criterion to be diagnosed is to have 2 attacks or 2 white matter lesions disseminated in time and space. The presence of lesions is determined through MRI. Even with the McDonald Criteria, it is very difficult, costly and time-consuming to diagnose a patient with MS. Here we describe a cost-effective method that could be used as a predictive tool to help diagnose MS and other autoimmune disorders, such as Type 1 diabetes (T1D). Blood samples were obtained from patients with MS and healthy individuals. Lymphocytes were purified from these samples and were quantified using flow cytometry. We stained for two important immune cell groups: Th40 and Treg cells. Th40 cells are a subset of T helper cells; when the immune system goes awry, as in the case of autoimmune diseases, these cells are involved in attacking the body. Treg cells are regulatory T cells that suppress Th40 proliferation. Treg cells usually occur at the same level as Th40 cells in individuals without autoimmune disease. However, in autoimmunity they are at a lower level and don't regulate to a normal, equivalent activity. Comparing Th40 to Treg levels, we found that Th40 levels were higher than Treg; thus, the Th40:Treg ratio was significantly higher in patients with autoimmune diseases. This ratio can be used to better predict autoimmunity in some disease models. The development of a test using these ratios to predict the likelihood of a patient developing MS, or other autoimmune diseases, could help create a better diagnostic tool.

Oral Presentation

Patterned Expression of Two Rhodopsins in Aedes aegypti Larval Visual System

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Biological Sciences

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Advisor: Joseph O'Tousa, Dept. of Biological Sciences

Vision plays a significant role key mosquito vector behaviors. The larval visual system of *Aedes aegypti* consists of five ocelli that are present at eclosion and persist throughout the larval stage and into the pupal and adult stages. During the L3 stage, photoreceptor cells that form the adult compound eye begins to differentiate. Here, we show a profile for the development of the visual system in *Ae. aegypti* throughout the various larval stages, pupal stage, and adulthood. We also show that Aaop3, the major ocellar rhodopsin, is present in the ocellar cell bodies in light conditions and in the ocellar rhabdomeres in dark conditions, indicating that cell movement of Aaop3 occurs by a light-mediated process. Aaop7 is detected in the central cell of several rows of ommatidia on the anterior edge of the developing compound eye, suggesting that Aaop7 is expressed in newly differentiated ommatidia. Moreover, Aaop7 is detected in the axons originating from these newly differentiated photoreceptor cells. As larval development progresses into the L4 stage, expression of Aaop7 in the ommatidia is down regulated and expression of Aaop1, the major adult rhodopsin, begins. We propose that the patterned expression of rhodopsin may have critical behavioral implications during the larval stage and play a significant role in the development of the adult visual system.

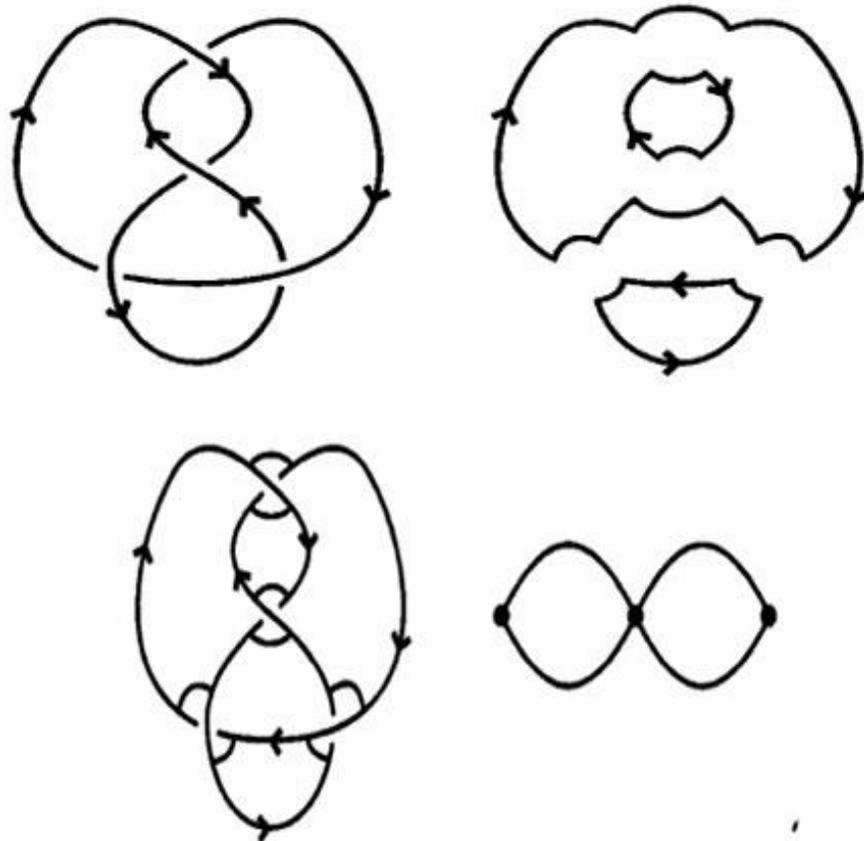
Oral Presentation

On Matrix Invariants of Knots

Austin Rodgers
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Mathematics

Advisor: Jeffrey Diller, Dept. of Mathematics

The study and derivation of matrix invariants of knots is an interesting and beautiful concept in higher mathematics. It brings together several seemingly disparate areas of mathematics into one confluence of theory; incidentally these areas are algebraic topology, graph theory, knot theory, and abstract algebra. Using techniques developed by Seifert and expanded upon by Murasugi and Cromwell, the ideas addressed in my paper are as follows: 1) Construction of Seifert surfaces of knots 2) Construction of Seifert graphs 3) Computation of Seifert matrices 4) Determination of matrix invariants from properties of Seifert matrices.



Poster Presentation

Gut Feelings: Diagnosis and Subtyping Analysis of Blastocystis Parasites in Macaca fascicularis

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June Tome

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Biological Sciences

Justin Wilcox, Dept. of Biological Sciences

Advisor: Hope Hollocher, Dept. of Biological Sciences

Blastocystis is a globally distributed stramenophile parasite with the potential for zoonotic transmission, especially in developing countries with close human-animal contact. Nowhere is this potential for zoonosis greatest than in Southeast Asia where long-tailed macaques (*Macaca fascicularis*) live in very close proximity to human populations. The parasite has been known to produce variable clinical outcomes, including irritable bowel syndrome and ulcerative colitis in human patients; therefore, accurate diagnosis is crucial to public health. Current identification techniques underreport *Blastocystis* prevalence where intrasubtype genetic variability is a major obstacle to precise detection. Presently, *Blastocystis* is most commonly identified by microscopic staining with its subtypes detected by molecular analysis. This research project compares the efficacy of several staining and molecular diagnostic methods to determine if genetic variability associated with the *Blastocystis* subtypes influences detection. The presence of *Blastocystis* was assayed in fecal samples from nine populations across Singapore. Trichrome, Giemsa, and Acid-Fast fecal smear stains were tested for their sensitivity and specificity, ultimately designating trichrome as the preferred staining method for *Blastocystis* identification. Sequencing of the nuclear 18 SSU-rRNA using Bh1 primers and nad2 and nad11 mitochondrial DNA using ST3 primers allowed for intra-subtype diversity investigation. ST3 mitochondrial primers, compared to Bh1 nuclear primers, were most effective in detecting multiple subtype infections. Finally, any subtype-specific staining biases will be determined by comparing the microscopic and molecular data collected. Combining these two techniques provides a more holistic representation of *Blastocystis* pathogenicity and will be vital to accurate diagnosis as new subtypes are identified.

Oral Presentation

Experimental investigation of bone drilling performance

Sarah Russel

College of Science

Physics in Medicine

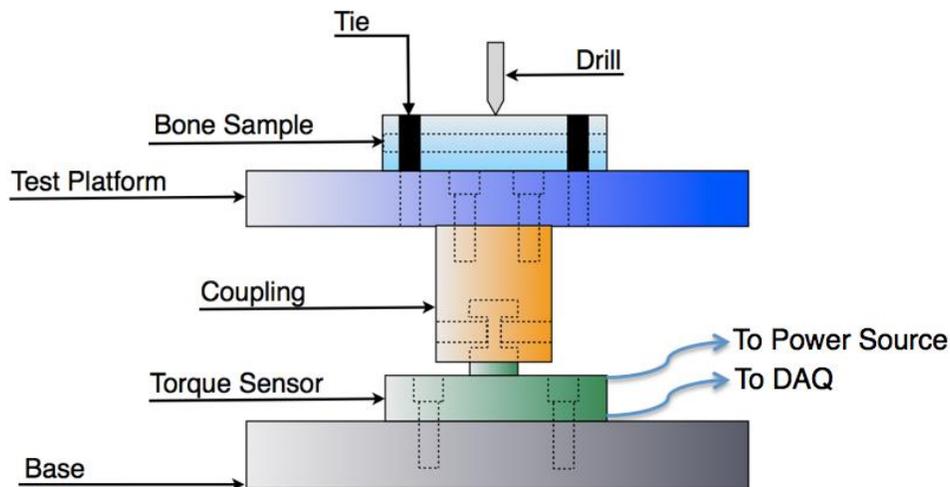
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Mechanical Engineering

Advisors: Steven Schmid, Dept. of Aerospace and Mechanical Engineering
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The drilling of bone is one of the most common orthopedic surgical procedures performed in operating rooms today. Since the performance of surgical drill bits when drilling into bone largely impacts the success of the healing process, special interest lies in developing the most effective tools to accomplish this procedure. The torque can measure such performance, for reducing the torque decreases the rates of drill bit wear and fracture. By developing a mathematical model of the drilling process, one can examine how various aspects of drill bit geometries affect the cutting of bone. To determine the accuracy of this model, drilling experiments were compared to the output of numerical simulations. Additionally, the drill bit in the model was compared to two other drill bits with varying geometries to examine the effectiveness of the bits themselves. This allows for insight into how unique drill bit shapes alter the bone drilling process while providing information on the accuracy of the generalized mathematical model. The torque and feed rate were measured for each drill bit at various thrust forces. Normalization for material removal rate allowed for comparison of the torques without the bias of drill bit diameter, for wider bits generally produce larger torques. Both Zimmer drills (Zimmer two-flute and Zimmer split-point) produced lower torques per unit material removed, but the raw torque data for the Surgibit drill bit was comparable to the slimmer Zimmer split-point drill bit. When compared to the mathematical model, the data was far greater than the idealized value. This indicates a need for a larger model that accounts for the behavior of a larger portion of the cutting lip. By avoiding current simplifications, the model could show not only trends but also more accurate torque values.



Oral Presentation

Optical Properties of Human Cancer and Normal Cells

Christopher Sander

Mendoza College of Business and College of Science
Finance and Physics

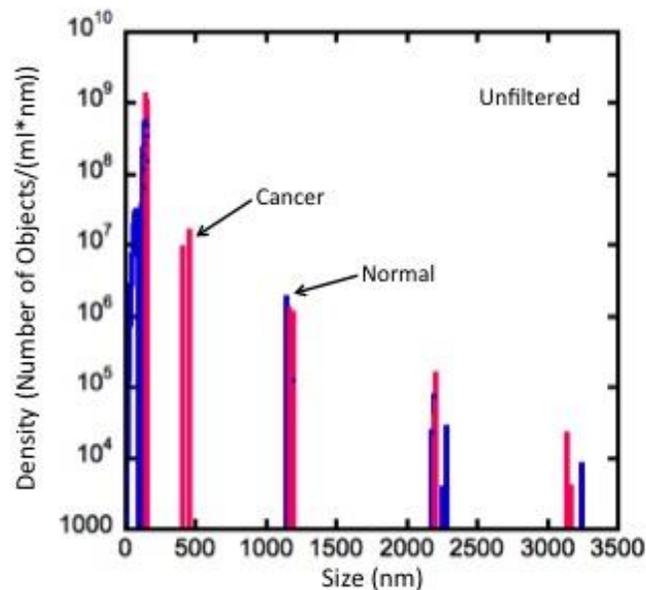
Carol Tanner and Steven Ruggiero, Dept. of Physics
Nan Sun, Dept. of Electrical Engineering

Sharon Stack, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry
Jeffery Johnson, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

Advisor: Steven Ruggiero, Dept. of Physics

We have investigated the optical properties of human oral and ovarian cancer and normal cells. Specifically, we have measured the absolute optical extinction for both whole cells and intra-cellular material in aqueous suspension. Measurements were conducted over a wavelength range of 250 to 1000nm with 1 nm resolution using Light Transmission Spectroscopy (LTS). This provides both the absolute extinction of materials under study and, with Mie inversion, the absolute number of particles of a given diameter as a function of diameter in the range of 1 to 3000 nm. Our preliminary studies show significant differences in both the extinction and particle size distributions associated with cancer versus normal cells, which appear to be correlated with differences in the particle size distribution in the range of ~ 50 to 250 nm.

Filtration's Effect on Inversion



Sander, Sun, Tanner, Ruggiero
University of Notre Dame

Oral Presentation

Identifying Novel Olfactory Ligands by Exploiting Evolutionary Dynamics

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Advisor: Zainulabeuddin Syed, Dept. of Biological Sciences

While not all mosquitoes feed on blood, all of them obtain sugars from plants that are fundamental nutrients for nearly every species. Mosquitoes rely heavily on olfaction for resource tracking, which is modulated by a large family of proteins, the olfactory receptors (ORs). Among the three major mosquito species sequenced to date, a great diversity in OR family is found, yet there is a small group of ORs that are conserved among *Anopheles gambiae*, *Aedes aegypti*, and *Culex quinquefasciatus*. We hypothesized that these conserved ORs are involved in detection of volatile chemicals that guide them to plants. An interesting caveat to this sugar-seeking aspect is the fact that different mosquito species show distinct circadian host/plant seeking patterns and may not respond to similar odorants from the same plants at different diel periods. We performed a detailed analysis of the circadian activity in *Culex* mosquitoes that revealed a pronounced activity peak in males around sunset and somewhat diffused one at sunrise, whereas only one peak of activity was recorded for female mosquitoes around sunset. We identified a few attractive plants from the literature that are known to be preferred by mosquitoes for sugar feeding and identified their headspace odor chemical signatures collected during the day or night by employing Solid Phase Micro Extraction (SPME), or, adsorbent collections. Both quantitative and qualitative changes in volatile emission patterns between the day and night were found. Subsequently, extracts were tested on OR members of the conserved clade that were heterologously expressed in an “empty-neuron” of *Drosophila melanogaster* under UAS-GAL4 system by gas chromatography coupled to single sensillum recording (GC-SSR) revealing natural ligands from plants.

Poster Presentation

A comparison of the components contained in hydrofracking fluid of three companies in three geographic regions

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Depletion of readily accessible natural gas has made hydraulic fracturing (hydrofracking) economically viable. Hydrofracking involves drilling deep vertical wells, directing the drill horizontally into porous shale, and then injecting fluid, consisting of water, sand, and chemicals, to fracture the rock and allow extraction of natural gas. Some hydrofracking fluid flows back to the surface, carrying the original chemicals but also metals, organics, and dissolved solids. Despite efforts of drilling companies to contain and treat hydrofracking wastewater, spills and leakages do occur. To understand potential contaminant issues, knowing the exact chemical composition of hydrofracking fluids is crucial. In this study, the proportions of components used in hydrofracking fluids used in three geographic US regions (west, south, east) by three different companies (Chevron, Whiting, Encana) were compared to determine whether there were differences in the proportions of various chemicals used (e.g., acids, biocides). We predicted that because of differences in underlying geology, there would be differences in chemical proportions between the west (Montana, Colorado), east (Pennsylvania, Ohio, Michigan), and south (Texas, Arkansas, Louisiana). Furthermore, we predicted that there would be no differences in chemical proportions used by different companies because they work under similar conditions, and therefore need similar chemical mixtures. Data were analyzed using a permutational multivariate analysis of variance (PERMANOVA) and differences visualized using non-metric multidimensional scaling. Results showed that there were no significant differences in the proportions of chemicals used by different companies (PERMANOVA, $p=0.157$) or in different regions (PERMANOVA, $p=0.051$). This suggests the impact of hydrofracking contamination likely does not depend on the region or the company responsible for drilling, though there is more variation among regions than among companies. The heterogeneity due to underlying geology should be considered when evaluating the potential impact of hydrofracking fluids on ecosystem and human health.

Poster Presentation

Diet-Induced Integration and Evolution of the Skull in a Rabbit Model

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Erin Franks
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Jeremiah Scott, Dept. of Anthropology, University of Southern Illinois
Matthew Ravosa, Dept. of Biological Sciences
Advisor: Matthew Ravosa, Dept. of Biological Sciences

The evolution of the human skull is one of the more unique aspects of the development of the species, as it has enabled the growth of an enlarged brain cavity. The diet of human ancestors has been shown to significantly affect the size of the skull, as mechanically challenging foods required stronger and thicker masticatory hard tissues to resist the forces associated with the oral breakdown of such items. What remains unclear is the extent to which calvarial and basicranial regions of the skull are influenced by elevated masticatory stresses. Such information is important for understanding functional determinants of cranial covariation and integration, information critical for understanding both the evolution and pathobiology of the mammalian skull. Using New Zealand white rabbits raised 48 weeks from weaning to adulthood on diets of varying mechanical properties, we examined diet-induced plasticity in the growing cranial vault and cranial base. Beginning at weaning (5-weeks old), control-, seasonal- and annual-diet rabbits were scanned biweekly via microCT to document longitudinal growth patterns. Each dietary treatment group contained 10 experimental subjects. Using PMOD software, representative skull dimensions were recorded and analyzed statistically ($p < 0.05$). We found that the postweaning development of linear and angular measures of the cranial vault and cranial base was not significantly affected by the material properties of ingested food items. While trends in certain measures are evident, none approach statistical significance. In comparison to previous work that focused differentially on the jaws, the calvarium and basicranium display less of a dietary signal than areas more directly involved in feeding behaviors. Although the presence and magnitude of diet-induced plasticity has been well documented for a variety of cranial sites, the present study demonstrates that not all hard tissues are sensitive to masticatory stresses and are thus less functionally integrated with variation in the oral cavity.

Poster Presentation

The effect of light availability on zooplankton predator avoidance behavior and growth

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Biological Sciences and French

Advisor: Stuart Jones, Dept. of Biological Sciences

Freshwater concentrations of dissolved organic carbon (DOC) have been steadily increasing over the past two decades, suggesting profound implications for aquatic ecosystems. High DOC concentrations not only influence the global carbon cycle, but they also give water a brownish tint, significantly decreasing light penetration and affecting internal aquatic productivity. Zooplankton play a central role in the aquatic food web, acting as important intermediates between primary production and higher trophic levels. Many taxa exhibit diel vertical migration (DVM), however this cyclical migration pattern remains only weakly understood in terms of causes and effects. It has been previously hypothesized that zooplankton in waters with high concentrations of DOC may migrate to a lesser amplitude, eliciting potential differences in resource use, energetic costs, and ultimately growth. This study utilized a survey of zooplankton migration behavior and production in ten lakes along a naturally occurring DOC gradient to evaluate the indirect effects of DOC concentration on zooplankton productivity through modification of their DVM behavior. The spatial and temporal tendencies of zooplankton were measured, as were biomass production and reproduction. Results will be statistically analyzed in the context of a DOC gradient to achieve a better understanding of both bottom-up and top-down consequences to increasing terrestrial carbon inputs. Preliminary analysis indicates that zooplankton migration generally demonstrated an inverse relationship with concentration of DOC. In cases where it did not, factors such as food quality and predation pressure can often explain the aberrant behavior. My findings confirm proposed models of migration behavior, and suggest that continued increases in concentrations of DOC may have negative consequences for zooplankton populations and thus aquatic food webs. A deeper understanding of the effects of increasing DOC concentrations on zooplankton behavior will help to better inform national and local policy makers, land overseers, and fisheries managers about the indirect implications of their actions on complex aquatic community dynamics.

Poster Presentation

ADAM10/Kuzbanian is Upregulated During Neuroendocrine Prostate Carcinogenesis

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Biochemistry

Advisor: Laurie Littlepage, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry

Prostate cancer (CaP) is the second leading cause of cancer death in men. Advanced prostate tumors often contain neuroendocrine differentiation, which correlates with androgen-independent progression and poor prognosis. Currently, androgen deprivation is the first line of therapy for metastatic CaP. However, CaP often progresses to an androgen-independent bone-metastatic stage, at which point chemotherapy and radiotherapy become the primary therapeutic options. Despite recent advances in therapeutic strategies, many cancers still develop resistance to radiation and therapies, making the identification of new therapies essential to improve the lives and survival rates of patients. We have studied neuroendocrine cancer progression in the cryptdin-2 SV40-TAg (CR2-TAg) mouse model of CaP. Since these cancers do not express androgen receptor, they are refractory to androgen therapy. Therefore, we sought new potential targets. We previously found that matrix metalloproteinases (MMPs), which are capable of degrading many extracellular matrix proteins and cell surface receptors, are upregulated during CR2-Tag tumor progression. In the present study, we examined expression of a family of a disintegrin and metalloproteinases (ADAMs) that is actively involved in these signaling pathways due to their role in releasing the extracellular domain of transmembrane proteins. ADAMs contain features of both adhesive proteins and proteinases. ADAM10 activates the epidermal growth factor receptor (EGFR) and NOTCH signaling systems controlling cell growth, invasion, and metastasis. We found that ADAM10 expression increased during tumor progression and was highly penetrant. We are quantifying the expression levels and localization patterns of ADAM10 in these samples over time. Since MMPs, like ADAMs, are capable of degrading many extracellular matrix proteins and cell surface receptors, we determined if MMPs (MMP 2, 7, and 9) contribute to ADAM10 expression or localization in aggressive hormone refractory CaP. We have stained for ADAM10 in tissue sections from the CR2-TAg mice that are each missing expression of MMPs to determine if that particular MMP contributes to ADAM10 expression or localization. Our research using ADAM10 localization as a potential biomarker and therapeutic target has potential clinical value to identify aggressive CaP earlier in patients. Our study of MMPs and their role in ADAM10 expression will offer insight into the mechanisms of advanced prostate tumor progression.

Oral Presentation

Characteristic classes of complex vector bundles

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Mathematics

Advisor: Francis Connolly, Dept. of Mathematics

Algebraic topology aims to distill the abundant data specifying a topological space into more manageable algebraic invariants. The theory of characteristic classes provides powerful tools for this effort. In my thesis, I derive properties of some of the earliest and most important characteristic classes, the Chern classes associated to complex vector bundles. These are particular elements of the cohomology of the base space that measure how “flat” or “twisted” a bundle is. In this talk, I will describe vector bundles and introduce the universal bundle that motivates the study of characteristic classes. I hope to exhibit some instances where characteristic classes translate hard topological problems into easy combinatorial ones.

Poster Presentation

Inhibiting EYA3 Tyrosine Phosphatase Activity Sensitizes Ewing's Sarcoma Cells to Etoposide Treatment

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Biochemistry

Celvie Yuan, Cincinnati Children's Hospital

Advisor: Rashmi Hegde, Dept. of Pediatrics, University of Cincinnati College of Medicine

Eyes Absent (EYA3) is a tyrosine phosphatase protein which repairs DNA damage, including double-stranded breaks induced by chemotherapeutic agents such as etoposide. It was hypothesized that inhibiting EYA3 could cause cancers in which EYA3 is over-expressed (such as Ewing's sarcoma) to be more sensitive to DNA-damaging agents and therefore serve as useful neo-adjuvant therapies in the treatment of Ewing's sarcoma. The aim of this project was to determine whether the EYA3 inhibitors Benzarone (BZ) and 6-OH-Benzbromarone (6OH-BBR) would decrease cell survival and migration of A673 Ewing's tumor cells in the presence of etoposide. It was found that Benzarone and 6OH-BBR inhibit cell migration of A673 cells, as was previously shown for breast cancer cells and endothelial cells. Benzarone, but not 6OH-BBR, makes A673 cells more sensitive to DNA damaging treatment with etoposide. Reducing EYA3 levels in A673 cells also makes these cells more sensitive to etoposide treatment. Together these results suggest that Benzarone might be a useful lead compound for the development of EYA3 inhibitors to be used in combination therapies as neo-adjuvant therapy for Ewing's sarcoma (BZ) and potentially as anti-metastatic agents (BZ and 6OH-BBR). In future work we would like to delineate the molecular mechanism by which the EYA inhibitors might function in making cancer cells more susceptible to DNA damage and test their efficacy in *in vivo* models. Ongoing experiments using tumor xenografts have shown promising results.

Poster Presentation

Isolation of LpA-I and LpA-I/A-II Particles from HDL for Proteomic Characterization

Rebecca Shute
College of Science

John Melchior, University of Cincinnati

Advisor: W. Sean Davidson, Dept. of Pathology and Laboratory Medicine, University of Cincinnati

Levels of high density lipoprotein (HDL) cholesterol in plasma have been shown to be inversely correlated to the incidence of cardiovascular disease, the leading cause of death in the Western world. HDL particles can be divided into two categories: LpA-I, particles with the most common HDL protein, apolipoprotein (apo)A-I, but none of the second common protein, apoA-II, and LpA-I/A-II, which contain both. However, the HDL proteome is thought to contain over 80 additional minor proteins as well. To determine whether LpA-I and LpA-I/A-II particles have different sets of accessory proteins, LpA-I and LpA-I/A-II particles were isolated by immunoaffinity chromatography, with the intention to analyze these particles for proteomic differences using mass spectrometry. SDS-PAGE gel electrophoresis indicated that the anti-apoA-I immunoaffinity column successfully separated apoA-I protein (LpA-I and LpA-I/A-II particles) from HDL cholesterol. The anti-apoA-II column did not appear to effectively separate exclusively apoA-I (LpA-I particles) from LpA-I/A-II particles. However, anti-apoA-II column elutions appeared to contain other non-identified apoproteins not present in the flow through which contained the LpA-I particles.

Poster Presentation

Wnt/ β -catenin Signaling in Pancreatic Cancer

Kaitlyn Simmons

College of Science

Science Preprofessional Studies

Advisor: Jenifer Prospero, Indiana University School of Medicine – South Bend, Harper Cancer Research Institute, and Dept. of Biological Sciences

Pancreatic ductal adenocarcinoma (PDAC) has an overall median survival of less than one year and is the fourth leading cause of cancer-related deaths in the United States. A severe desmoplastic reaction occurs in PDAC and is believed to create a hypoxic tumor environment and also provide a physical barrier to drug delivery. Research has shown that hypoxia provides an environment for the growth of highly drug-resistant cells that may share characteristics of cancer stem cells (CSCs). CSCs are important targets for PDAC therapeutic interventions because they are self-renewable and can repopulate tumors after treatment. The Wnt signaling pathway is important in progenitor cell expansion and is up-regulated in a mouse model of PDAC. The goal of this research is to characterize the Wnt signaling pathway in human pancreatic cancer cell lines. Seven cell lines (L3.6, Mia Paca, Panc1, BXPC3, HPAF2, Aspc1, Hs766T) were used to investigate activation of the WNT/ β -catenin signaling pathway. Immunofluorescence of β -catenin demonstrated that only the Mia Paca cells exhibit cytosolic β -catenin, the Hs766T cells have membrane and nuclear β -catenin, and the L3.6 and Aspc1 cells have nuclear and cytosolic localization of β -catenin. We have used Dual Luciferase Reporter Assays to assess β -catenin/TCF interaction, and have only found an increase in TCF reporter activity in the Hs766T cell line. None of the cell lines showed a significant increase in expression of Wnt target genes via real-time PCR. Future studies will investigate TCF reporter activity, β -catenin localization, and RT-PCR in hypoxic cells. The long-term goal of this research is to determine the interaction of hypoxia and Wnt signaling in pancreatic cancer. In making this connection, it will allow us to test whether targeting Wnt signaling will impact the features of pancreatic cancer related to hypoxia.

Poster Presentation

Synthesis of Low Band Gap Conducting Polymers for High Performance Solar Cells

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Advisors: Haifeng Gao and Doyun Lee, Dept. of Chemistry and Biochemistry

Solar energy, an invaluable resource in the environmentally conscious world, could be harnessed by various solar cells and converted into electricity. Science has developed many different types of cells, one of the most common being composed of silicon. Recently, there has been research involving polymer solar cells that are made from organic materials and in turn are low cost and lightweight. The efficiency of polymer solar cells relies not only on opto-electrical properties of polymers, such as band gap and charge mobilities, but also on processibility, which is mainly affected by the solubility and crystallinity of the polymers. It is important to note that both the opto-electrical properties and the processibility of the polymers are determined by the polymer structures, while their fundamental relationships are still unclear. In this research, we prepared a series of low-band-gap polymers (PBDTTT) using 4,8-dialkoxybenzo[1,2-b;3,4-b]dithiophene (BDT) and thieno[3,4-b]thiophene (TT) as the repeating units in the polymer backbone. The molecular weights and solubilizing side groups were systematically changed in order to study their influence on the charge mobility and the crystallinity of polymers in thin film. Two types of alkyl groups, dodecyl and 2-ethylhexyl, were attached to the BDT and TT repeating units, which produce polymers with similar solubility in chlorobenzene, but different crystallinity. Studying the variant effects of the alkyl groups can bring about a better perspective on the trade-off between long and short, bulky and linear, alkyl chains, as well as lead to more efficient polymer solar cells in the future.

Oral Presentation

Heavy Metal Contamination in Lake Michigan Wetland Turtles

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Biological Sciences

Jessica Kosiara and Matthew Cooper, Dept. of Biological Sciences
Advisor: Gary Lamberti, Dept. of Biological Sciences

Heavy metal contaminants have been studied in some Great Lakes coastal wetlands and their aquatic organisms. However, turtles have been largely ignored in contaminant analyses, although they are common in many contaminated systems. We sampled turtles from known areas of contamination in Lake Michigan to determine if turtles could be used as indicators of environmental heavy metal contamination. We also compared non-lethal versus lethal sampling techniques for heavy metal analyses. We measured cadmium, chromium, copper, iron, lead, magnesium, manganese and zinc in common snapping (*Chelydra serpentina*) and painted (*Chrysemys picta*) turtles collected from four Lake Michigan wetlands with differing levels of contamination. Non-lethal (claws and shell) and lethal (muscle and liver) samples were collected from all turtles to examine the efficacy of non-lethal techniques. Our results suggest that claw and shell samples accumulate certain metals, whereas lethal samples were best for measuring others. For example, shell accumulated cadmium, chromium, magnesium, and manganese, while copper and iron were concentrated in the liver. We did not find strong correlations between sediment contamination and individual turtle contamination, suggesting that other factors may influence heavy metal accumulation in wetland turtles. In general, however, more contaminated wetlands contained the most contaminated turtles. Because non-lethal samples were effective for measuring certain heavy metals, researchers or managers could choose to sample these tissues rather than using lethal methods. Monitoring of turtles, especially snapping turtles, is important because snapping turtles are often caught and consumed by humans, which may pose a health risk in contaminated areas.

Poster Presentation

Pancreatic Stem Cell Function Through Matrix Metalloproteinase-3

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Advisors: Laurie Littlepage, Harper Cancer Research Institute and Dept. of Chemistry and Biochemistry and Reginald Hill, Harper Cancer Research Institute and Dept. of Biological Sciences

Pancreatic ductal adenocarcinoma (PDAC) is one of the most aggressive cancers and is known for having a poor survival rate. Pancreatic cancer only accounts for 3% of cancers in the US, but accounts for 7% of total deaths caused by cancer. While the five year survival rate has increased three-fold since the 1970s, the five year survival is still only a mere 5%. One of the hallmarks of PDAC is the expansion of the stromal cells in the microenvironment that surround the epithelium to form a dense stromal layer that accounts for ~90% of the tumor bulk. One function of the microenvironment during normal development is to release essential cues that control the behavior of epithelial cells, including stem and progenitor cells. We previously found that matrix metalloproteinase-3 (MMP3) is a regulator of Wnt signaling in mammary stem cells and is required for the mammary stem cell population. MMP3 inactivates Wnt5b, a noncanonical Wnt ligand that inhibits canonical Wnt signaling, in a nonproteolytic manner via its hemopexin (HPX) domain. Because of the important implications of this finding and the lack of good microenvironment markers of PDAC progression, we wanted to see if MMP3 also has an impact on stemness in the pancreas and in PDAC progression. We collected the pancreas from transgenic MMP3 knockout or heterozygous mice and analyzed the stem cell markers CD133+/CD44+ by flow cytometry. We are investigating if mice lacking MMP3 have a reduced pancreatic stem cell population when compared to mice heterozygous for MMP3. For future experiments, we have optimized the pancreasphere protocol and currently are investigating if MMP3 is required for pancreasphere formation and if MMP3 overexpression elevates pancreatic stem cell function, as is seen in mammary epithelial stem cells.

Poster Presentation

Bioinformatic Approaches to Identify Novel Polyamine-Relevant Genes in Drosophila melanogaster

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Polyamines are organic molecules that play important roles in cellular processes such as gene regulation, signal transduction, cell growth, and cell proliferation. There is also evidence for polyamines having roles downstream of certain oncogenes as well as tumors exhibiting increased polyamine biosynthesis levels. Therefore, these molecules have been intensely studied as potential targets for cancer therapies. Unfortunately, therapies targeting polyamine metabolism have had limited efficacy against cancer, due in large part to compensatory mechanisms such as increased intracellular polyamine transport. Thus, a desirable approach is to target polyamine transporters in combination with metabolism targeting therapies; however, the genetic identity of mammalian polyamine transporters is unknown. The purpose of this project is to identify novel candidate polyamine transporter genes by performing a bioinformatics analysis on previously published gene expression data for *Drosophila melanogaster*. Whole genome expression data is available for 25 *Drosophila* cell lines, as well as across 6 stages of larval development and 12 stages of embryonic development. Using techniques such as template matching and clustering analysis with known polyamine metabolism genes, lists of candidate polyamine modulating genes have been generated. The roles of these candidate genes can then be analyzed using the sophisticated genetic tools for *Drosophila*. Due to the high level of conservation between *Drosophila* and humans, identified novel polyamine regulators can serve as targets for the next generation of cancer therapeutics.

Oral Presentation

Validating Small Molecule Responses in Plasmodium falciparum

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Advisor: Michael Ferdig, Dept. of Biological Sciences

Despite much research, malaria remains a formidable global challenge responsible for more than 250 million infections and nearly 1 million deaths annually. Efforts to combat malaria are further complicated by the rapid emergence of drug resistance. New genomics technologies present exciting opportunities to learn about the malaria parasite, and high throughput screens have identified promising candidates for novel antimalarial compounds. However, many of the small molecules currently available and in development have poorly characterized mechanisms of action (MoA) in *P. falciparum*. To prioritize compounds for development, the Ferdig Lab has developed methods for leveraging whole-genome transcription data of chemically perturbed parasites to interpret mechanism of action. The present study seeks to demonstrate the reproducibility and robustness of these chemically perturbed gene expression signatures and their utility in understanding drug mechanism of action. In particular, we perturbed three biological replicates of two lab strains of *P. falciparum* with atovaquone, an experimental compound P4Q-391 and a combination of those two chemicals at their IC50 doses, and whole genome expression profiles were measured. It is believed that these two compounds share molecular targets in the respiratory chain. We show that when biological replicates of each strain are averaged to define a strain-specific signature, biological variation is minimized to the extent that samples receiving atovaquone cluster distinctly from those receiving P4Q-391. GO enrichment analysis revealed that a signal of perturbed biological processes is consistent across strains and with past experiments. High variation between responses of replicate samples obscures signal of MoA and demonstrates the need for averaging signal across replicates to minimize biological variation in the signal of MoA. These results highlight the complexity of interpreting subtle transcriptional responses, specifically when considering drugs with a shared mechanism of action.

Poster Presentation

Roles of the notch and retinoic acid signaling pathways during zebrafish kidney regeneration after acute injury by gentamicin injection

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Kristen McCampbell, Dept. of Biological Sciences

Advisor: Rebecca Wingert, Dept. of Biological Sciences

Kidney disease affects millions of people each year and while procedures such as hemodialysis and transplant are available, no known cure exists. Zebrafish have the ability to regenerate their kidneys upon acute injury; however, the mechanism by which regeneration occurs is not well understood. This ability, coupled with findings demonstrating similar patterns of development between zebrafish and human kidneys, makes studies of kidney regeneration in zebrafish especially promising. Much current research focuses on investigating whether signaling pathways involved in development are again active during regeneration. The Notch pathway and retinoic acid signaling pathway are two such developmentally significant pathways and while they have been implicated in the regeneration of tissues such as the heart and fin, they have not yet been studied in the regenerating kidney. Notch, a family of transmembrane protein receptors, acts during development via a lateral inhibition mechanism to direct the establishment of various renal cell fates. The retinoic acid-signaling pathway, highly important for cell-to-cell signaling, is involved in neurogenesis and organogenesis. The aims of this study were to investigate the potential roles of the Notch and retinoic acid signaling pathways in kidney regeneration upon acute injury by gentamicin injection. Both pathways are essential during kidney organogenesis and thus we hypothesize that they might be likewise essential during regeneration. Through whole-mount *in situ* hybridization (WISH), a method used to assess spatial localization of mRNA in tissues, it was found that Notch ligand jagged2 showed fewer transcripts in injured kidneys suggesting downregulation. Conversely, a second Notch ligand, deltaC, showed transcript expression in cellular casts of injured kidneys. Data from qRT-PCR suggest that components of both pathways are expressed during regeneration. Taken together, these data implicate Notch and retinoic acid signaling in regeneration. Expression studies of Notch and retinoic acid pathway components in kidneys before and after injury are ongoing. Future studies aim to identify the roles for these pathways in renal repair. Additional studies investigating the effects of blocking and over-expressing Notch or retinoic acid may shed further light on the mechanism by which regeneration occurs.

Oral Presentation

The Risks and Benefits of an Alternative Source of Technetium-99

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The first isomer of technetium-99 (^{99m}Tc) is used in about 15 million medical diagnostic imaging procedures annually in the United States. Currently, the most efficient and commonly used method for producing this isomer is through the fission of Highly Enriched Uranium (HEU). However, the Non-Proliferation Treaty (NPT) will compel manufacturers worldwide to phase out this method of production. Therefore, alternative methods of production are actively being examined. One promising non-HEU based method for ^{99m}Tc production is proton-induced nuclear reaction on molybdenum-100 ($^{100}\text{Mo}(p,2n)^{99m}\text{Tc}$). A complication to accelerator-based methods, however, is the large number of other nuclear reaction channels that are open from both ^{100}Mo and trace molybdenum contaminants in the target. These reaction pathways result in the production of not only ^{99m}Tc but also other radioactive technetium isotopes, which are not possible to separate out chemically before injection to the patient. Currently, the amount of radioactive technetium produced has not been conclusively determined. The goal of this work is to theoretically and experimentally evaluate the production yield of all the unstable technetium isotopes produced from proton-induced reactions on molybdenum targets of varying composition. I will present a global context for this project, the theoretical efficacy of accelerators as an alternative ^{99m}Tc production method, and the experimental setup for our measurement at the Nuclear Science Laboratory of Notre Dame.

Poster Presentation

Are You Really What You Eat? Cross-Sectional Bone Distribution in the Mandibles of Strepsirrhine Primates

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Biological Sciences

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Advisor: Matthew Ravosa, Dept. of Biological Sciences

Experimental and morphological analyses of the masticatory system in mammals suggest that mandibular robusticity results from routine processing of mechanically demanding diets. In primates, increased mandibular proportions are posited to resist bending, shear, and twisting of the jaw during repetitive chewing or crushing of hard or tough objects. Most of the comparative evidence for such conclusions is based on external mandibular proportions, which vary in the degree to which they accurately reflect the biomechanical characteristics of a given lower jaw. Using novel data on the internal anatomy of the mandibular corpus, this study assesses the influence of diet on cortical bone geometry in strepsirrhines, which are one of two extant primate suborders. Our sample consisted of 69 adult mandibles from 26 species with diverse diets, which were imaged via microCT to obtain cross-sectional dimensions at three premolar (P2, P3, P4) and three molar (M1, M2, M3) sections. Log-linear bivariate regression was used to perform standard allometric analyses of mandibular cross-sectional geometry at all six corpus sections ($p < 0.05$). Cortical area (CA) and resistance to lateral transverse bending (Ix) scaled isometrically vs. mandibular length at all six sections. Slopes for resistance to parasagittal bending (Iy) were consistently greater than those for CA and Ix in all jaw sections, but not statistically different from isometry. Slopes for CA and Iy were similar between premolar and molar sections, while slopes for Ix increased from the anterior to posterior sections. These data suggest that cortical distribution in the strepsirrhine mandibular corpus does not appear to be linked to size-related increases in food properties. Nonetheless, the premolar to molar increase in Ix slopes suggests that lateral transverse bending of the corpus during mastication may increase anteroposteriorly. Further analysis will be required to determine if this pattern reflects other aspects of functional variation in the strepsirrhine mandible.

Poster Presentation

The Maximum Loading Capacity of Platinum on Cerium Oxide Catalysts

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The water-gas shift (WGS) reaction is essential in the production of hydrogen for fuel cell power generation and carbon monoxide conversion. Carbon monoxide in particular needs to be completely converted because it poisons platinum electrodes, obstructing fuel cell performance, and it is a noxious pollutant. Cerium oxide, when loaded with noble metals such as platinum, is a very effective WGS catalyst at lower temperatures. Transition metals enhance the reducibility of ceria, and single dispersed metals on ceria support are more reactive than clusters of metals because of the enhanced oxygen migration on the CeO₂ surface. In the case of CeO₂ impregnated with platinum, CO molecules absorbed on the platinum is oxidized to CO₂ by the migration of an oxygen to the metal-ceria interface, and water is reduced and dissociates on the oxygen vacancy sites of ceria to H₂. Large clusters of Pt particles will have insignificant interactions with ceria, but the total number of highly dispersed platinum particles will increase with loading. In this experiment, the maximum loading amount of platinum on CeO₂ while still being singly dispersed after reaction was explored. CeO₂ nanorods were prepared via hydrothermal methods at 100°C by mixing cerium nitrate with sodium hydroxide. Platinum supported catalysts at 0.05%, 0.1%, and 0.5% were prepared using deposition-precipitation method. Gas chromatography is used to analyze the efficiency of the Pt/CeO₂ at different loading percentages for catalyzing the WGS reaction. The results of this experiment can be applied to many different nanocatalysts and reactions related to energy systems.

Poster Presentation

Incorporation of Monoclonal Antibody Genes in Transgenic Silkworms

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Advisor: Malcolm Fraser, Dept. of Biological Sciences

Biomedical research and therapeutics have created a high demand for recombinant proteins. Many human proteins that have biomedical significance are glycoproteins, including antibodies, and current systems used for recombinant protein synthesis cannot produce higher eukaryote glycoproteins with the correct carbohydrate side chains at greater than 30 to 40% of the total product composition. This difference in glycosylation could cause an immunogenic response making the proteins unfit for clinical use. Thus, it is important to find a system that cannot only create recombinant proteins in a timely and cost effective manner, but can also correctly glycosylate those proteins. The silkworm, *Bombyx mori*, has been proposed and tested as a potential system because it can synthesize and secrete large amounts of protein in its silk glands making it ideal for the mass production of recombinant proteins. We hypothesize that human N-glycosylated proteins can be proteins that can be synthesized with greater homogeneity for the preferred product and easily recovered from silkworm cocoons. While the entirety of this project will not be completed for a few more months, we have evidence that the silkworms have successfully incorporated into their genome the glycosylated protein genes of interest. Three plasmids utilizing the piggyBac transposon were constructed and injected into the silkworms. The plasmid contained one of three antibody constructs – anti-EGFR (Cetuximab), anti-HER (Herceptin), or anti-CD20 (Rituximab) – under the control of the silk light chain promoter. The plasmids were each injected into two different strains of silkworms. The GG1 strain is a transgenic line that has been genetically engineered with a humanized N-glycosylation pathway. These same plasmids were also injected into the control parental line, w1pnd, to provide a comparison with the GG1 glycosylation strain. After rearing the F1 generation, splinkerette PCR determined insert location and number of the plasmid DNA proving that the antibody genes have successfully incorporated into the silkworm genome.

Poster Presentation

Regulation of Epithelial Glandular Architectures

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Science Preprofessional

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Glandular epithelial organs are composed of a combination of cylindrical tubules and hollow spheroids that are formed from sheets of tightly adherent cells enclosing a central lumen. Here, using three dimensional basement membrane organotypic cultures, we describe a signaling axis that leads to the development of epithelial cysts that are evocative of tumorigenic pathologies and requires signaling from intracellular endosomes. The most conspicuous abnormality is the presence of multiple lumens that resembles the histological phenotype of certain forms of low grade *in situ* breast carcinomas. Formation of signaling endosomes, which serve as long-lived, robust, platforms for ERK signaling, leads to a defect in mitotic spindle orientation and thereby, the formation of cysts with multiple lumens. We are investigating the importance of signaling endosome formation in the disruption of glandular morphogenesis. Our findings till date highlight a previously unknown link between growth factor receptor internalization, mitotic spindle orientation and acquisition of pre-invasive tumorigenic glandular architectures.

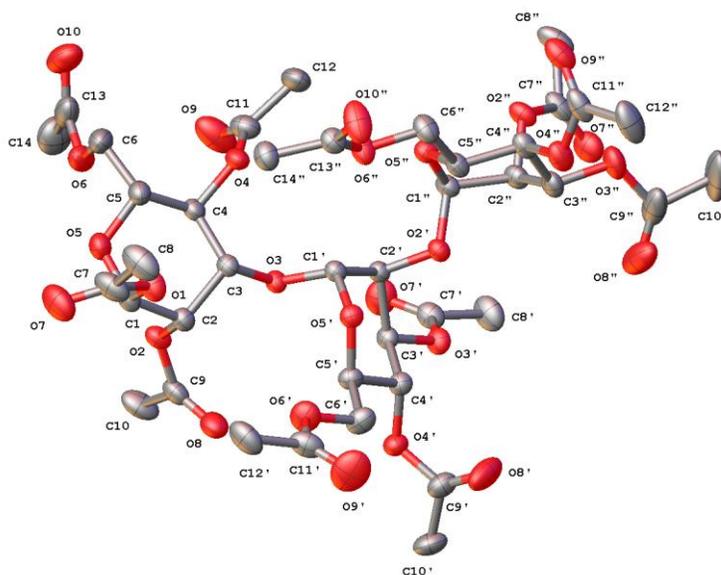
Poster Presentation

The Use of Per-Acetylated Oligosaccharides to Study the Conformations of Glycans

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Advisor: Anthony Serianni, Dept. of Chemistry and Biochemistry

Glycans are involved in numerous functions in the human body, such as cell-cell recognition, modulating protein-protein interactions and shielding proteins from degradation. The reactivity of glycans is dependent upon interactions between exocyclic lone pairs within the molecule. The positions of these lone pairs can be determined through analysis of J-couplings dependent upon the position of the lone pairs, and by examining the crystal structure of the glycan. Unfortunately, crystallographic studies of these molecules have been hampered by the large size of the oligomers and their propensity for hydrogen-bonding. Per-acetylated analogues of these glycans can be synthesized and are smaller, less prone to hydrogen bonding and easier to crystallize. The crystal structures of α -D-mannose pentaacetate and peracetylated α -D-mannopyranosyl(1 \rightarrow 2) α -D-mannopyranosyl(1 \rightarrow 3) α -D-mannopyranose were determined. The effects of adding an acetyl group to the sugars was examined by comparing these structures to the J-couplings in ^{13}C labeled 3-acetyl-6-deoxy- β -D-glucopyranoside. By studying the conformations of per-acetylated oligosaccharides, information about the conformation of unprotected glycans can be derived, which may lead to a greater understanding of the reactivity of these molecules.



Poster Presentation

Heterologous Production of Linear Polyketide Analogs from Advanced Synthetic Substrates

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Our lab is interested in the pharmacophoric link between the myriaporones, tedanolides, and gephyronic acid. These structurally similar, geographically distinct natural products are potent eukaryotic-specific protein synthesis inhibitors. Significant effort in our lab has been applied to the syntheses, structural assignments, and biological investigations of both the myriaporones and gephyronic acid. Investigation of the biological impact of the distinct chemical diversity exhibited by these molecules has been limited due to poor access, both biologically and synthetically. To address these needs, a new heterologous platform for the production of linear polyketide homologs utilizing advanced synthetic substrates was developed. Through the use of our engineered strain of *Escherichia coli* we envisioned the production of gephyronic acid-myriaporone hybrids, as well as novel structural analogs. It is our hope that such analogs will provide insight into the pharmacophoric relationship between the two classes of molecules, as well as the potential evolutionary link between the two producing organisms. Initial trials utilizing advanced synthetic substrates were successful in producing a novel analog of gephyronic acid. Production of this analog has revealed a significant revision in the currently accepted biosynthesis of gephyronic acid, and provides evidence for an unreported protein-protein interaction involved in polyketide production. Current experiments with modified feeding substrates are ongoing to confirm our initial results as well as determine the substrate tolerance of the biosynthetic enzymes.

Poster Presentation

Are allozymes found in two species of butterflies leading to differential enzymatic performance and affecting species' ranges?

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Advisor: Jessica Hellmann, Dept. of Biological Sciences

Lactate dehydrogenase (LDH) is an important enzyme involved in glycolysis that may be thermally sensitive in many organisms including two related species of butterflies: *Papilio glaucus* and *Papilio canadensis*. There is a lone single nucleotide polymorphism (SNP) that is believed to lead to different allozymes in these two species. In previous studies we found that the SNP responsible for the different allozymes has shifted further north. We have also looked at the coding sequence and found that this SNP leads to different enzyme activities in fish that helps them adapt to different thermal environments which seems to suggest this may be a case of convergent evolution. Yet it is important to show a causative relationship that it is the warm-adapted version of the Ldh gene that provides an advantage under warmer conditions. We are looking for this causative relationship by performing two related experiments: a thermal stability experiment and a thermal gradient experiment. In our thermal stability experiment, the two versions of the enzyme will be denatured at an extreme temperature over a range of times. The expectation is that if one allozyme is heat-adapted, it will denature less quickly. The thermal gradient experiment, meanwhile, determines the enzyme activity of each allozyme at a range of temperatures that includes the normal range of both species. Our hypothesis based on similar research in fish is that the northern-based *P. canadensis* will have lower K_m values at each temperature compared to *P. glaucus* but that at their normal living temperatures, the K_m values will be very similar. This is because we believe the different allozymes to be thermally adapted for each species. Showing this causative relationship combined with the shift of the allozymes north may indicate that the allozymes are being selected for their differential enzymatic performance in response to climate change, as well as explain their current distribution in the two species.

Poster Presentation

A dissociation between diurnal cycles in locomotor activity, feeding behavior and hepatic PERIOD2 expression in chronic alcohol-fed mice

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Advisor: Giles Duffield, Dept. of Biological Sciences

Chronic alcohol consumption contributes to fatty liver disease. Our recent studies reveal that the hepatic circadian clock is disturbed in the alcohol-induced hepatic steatosis state, and effects of chronic alcohol upon the clock itself may contribute to steatosis development (Zhou et al., 2014, Scientific Reports 4:3725). We extend these previous studies to explore the effects of chronic alcohol treatment on daily feeding and locomotor activity patterns in mice. C57BL/6J mice were maintained on a 12:12 light-dark cycle, and chronically pair-fed ad libitum for 4-weeks using the Lieber-DeCarli liquid diet, with calorie-controlled liquid and standard chow food diets as control groups. Locomotor activity was assessed by passive infrared motion, and mice on both liquid control and chow diets exhibited normal profiles of activity, characterized by a ratio of 22:78% day:night activity and a peak during the early-night. However, the pattern of activity was found dramatically altered in the alcohol fed mice, marked by a 49:51% ratio and the absence of a distinct peak. Feeding activity, measured as visits to the cage-feeder, was recorded automatically or by video monitoring and behavior scoring. While chow diet fed mice had a normal expected 24:76% ratio of feeding, and with a peak in the early-night, the pattern of feeding was found dramatically altered in both liquid diet groups: mice had a 43:57% ratio, and an absence of a distinct peak. Temporal differences were also observed between liquid diet groups during the late-day. Furthermore, cosinor analysis revealed a ~4 hr shift in the alcohol-fed group feeding rhythm. Real-time bioluminescence recording of PERIOD2::LUCIFERASE expression in cultured liver explants revealed that the molecular clock in the alcohol-fed mice and control liquid diet mice was shifted by ~12 hr, and ~6 hr, respectively. No differences were observed in suprachiasmatic nucleus explants, suggesting that changes in circadian phase in the liver were generated independently from the brain clock. These results suggest that chronic alcohol consumption and a liquid diet can differentially modulate the daily rhythmicity of locomotor and feeding behaviors; aspects that might contribute to disturbances in the circadian timing system and development of liver steatosis.

Poster Presentation

Patterns of Contaminant Transport by Pacific Salmon in Great Lakes Tributaries

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Environmental Sciences

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Each year, introduced Pacific salmon (*Onchorhynchus* spp.) spawn and die in Great Lakes tributaries, potentially transporting various pollutants accumulated while in the lakes. The Great Lakes are known to contain contaminants including persistent organic pollutants (POPs). A previous study focused on POP transport by salmon, but not heavy metals, such as mercury. However, concerns have been raised about the impact of tissue-bound mercury on the health of fish, wildlife, and humans. Furthermore, the concentrations of contaminants in fish and other aquatic organisms can reflect local environmental conditions, but whether this is true for mercury as well as POPs is unclear. To broaden our understanding of salmon-mediated contaminant transport, we first considered whether fish were similarly contaminated with mercury as POPs. Second, we considered whether mercury concentrations differed among lake basins and between salmon and brook trout (*Salvelinus fontinalis*) collected from Lakes Superior, Michigan, and Huron tributaries. Fish tissue homogenates were sequentially analyzed for POPs and total mercury (THg) using standard analytical methods. First we found THg was significantly correlated with the three POPs analyzed for both salmon (Pearson's correlation, $p < 0.001$) and brook trout ($p < 0.05$). Next, significant differences were found in contaminant concentration, both by contaminant type (ANOVA, $p < 0.001$) and fish species ($p < 0.05$). We also found a significant difference (ANOVA, $p < 0.001$) in contaminant concentrations among lake basins for both THg and POPs. Given the presence of a correlation between THg and POP concentrations, it is possible that salmon are as important a vector for mercury as for POPs, although upstream brook trout data is necessary to confirm this. We believe that this study helps inform future research about THg concentrations in fish tissue, and especially how mercury is spread across the Great Lakes ecosystem.

Poster Presentation

Sox2 is necessary and sufficient for Müller glial proliferation in the zebrafish retina

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Zebrafish have the ability to regenerate retinal neurons following cell death. Retinal damage induces the Müller glia to dedifferentiate and proliferate to generate a population of transiently amplifying neuronal progenitor cells (NPCs), which migrate to the proper retinal layer and differentiate into the lost neurons. Several pluripotency and stem cell-associated factors are upregulated during this regenerative response, including Sox2, which encodes a member of the B1 Sox family of HMG domain transcription factors. Sox2 is a neuronal stem cell marker during vertebrate development and in neurogenic regions of the adult vertebrate brain. Our lab found that Sox2 expression increases in zebrafish Müller glia following retinal damage, and morpholino-mediated knockdown of Sox2 prevented Müller glia proliferation. To determine whether increased levels of Sox2 are sufficient to induce Müller glia proliferation, we heat-shocked the Tg(hsp70l:sox2) transgenic line to overexpress Sox2 in undamaged retinas. Western blot and immunohistochemical analysis confirmed a significant increase in Sox2 protein expression in retinal cells following heat shock. Immunohistochemistry revealed individual PCNA-positive Müller glia after 3 days of heat shock (dhs) and larger neurogenic clusters of proliferating cells at 5 dhs. No INL proliferation was observed in the heat-shocked wild-type sibling retinas. Additionally, TUNEL labeling revealed no induction in cell death in response to heat-shock or Sox2 overexpression. These data show that Sox2 expression is necessary and sufficient to induce Müller glia to reenter the cell cycle.

Poster Presentation

The Role of the Streptolysin-Associated Gene (sag) cluster in Staphylococcus aureus

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Staphylococcus aureus is an important opportunistic pathogen whose disease in humans can range from mild symptoms to fatal consequences, including sepsis, necrotizing fasciitis and especially hospital-acquired bloodstream infections. Especially relevant are antibiotic and multi-antibiotic resistant strains, termed MRSA (multiple-resistant *S. aureus*). Streptolysin S (SLS) is a powerful cytolysin produced by a similar Gram-positive opportunistic pathogen *Streptococcus pyogenes*, this gene cluster has been recently found in 2 highly virulent strains USA300 and JKD6159. The overarching goal is to determine the function of the SLS-like gene cluster as an important virulence factor in *S. aureus*. The first aim focused on assessing whether the SLS-like toxin produced by *S. aureus* strains functioned as an antimicrobial peptide by comparing strains that contain the *sag*-like cluster against strains that lack it. From these results, it was concluded that the supernatants containing SLS-like toxins did not have significant antibacterial activity against *B. subtilis* but did exhibit antibacterial activity against *E. coli*. The second aim of the project this summer involved assessing the cytotoxic potential of the SLS-like toxin against sheep red blood cells via a hemolysis assay. The data suggests that the *S. aureus* strains containing the *sag*-like cluster (JKD6159 and USA300), exhibit greater hemolysis compared to the strains that lack the *sag*-like cluster (MW2 and MRSA252). These data suggest that the *S. aureus* strains with the SLS-like toxin give it a higher hemolytic and bacteriostatic effect than strains lacking the *sag*-like cluster.

Poster Presentation

Understanding the binding mechanism of VU0404251, a positive allosteric modulator of metabotropic glutamate receptor 5 a novel target for treatment of schizophrenia and cognitive disorders

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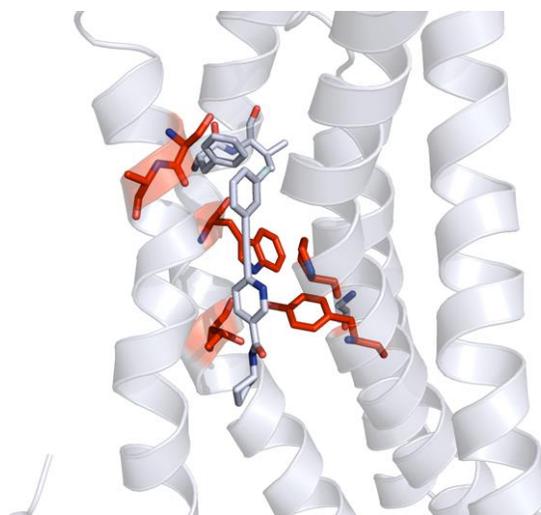
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Allosteric modulators affect the activity of G protein-coupled receptors (GPCRs) at sites that are distinct from the orthosteric binding site of the endogenous ligand. Positive allosteric modulators (PAMs) enhance the affinity and/ or efficacy of orthosteric agonists. PAMs for the GPCR metabotropic glutamate receptor 5 (mGlu5) have shown potential for treatment of cognitive disorders and schizophrenia. VU0357121 and VU03060172 are PAMs of mGlu5 at different allosteric sites. VU0404251 is a structural hybrid of VU0357121 and VU03060172, but the binding site of VU0404251 was unknown. The goal of these studies was to analyze the activity of VU0404251 in mutant and wild-type mGlu5-expressing HEK293A cells and compare this activity to that of the VU0357121 and VU03060172. Glutamate activates a cascade that causes intracellular Ca^{2+} levels to rise, so intracellular Ca^{2+} mobilization assays were performed using a Flexstation II to determine the peak response elicited by the glutamate after VU0404251 was added. The results showed that the mutant profiles with respect to affinity of VU0404251 and VU0360172 were similar with some overlap with the VU0357121 mutant profile. Interestingly two mutations had marked effects on VU0404251 cooperativity. At T780A VU0404251 behaved as a NAM. Comparisons of the VU0404251, VU0306172, and VU0357121 binding mechanisms will assist in the computational modeling of the mGlu5 receptor and promote the discovery of novel mGlu5 PAMs for the treatment of cognitive disorders and schizophrenia.



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