Life Science Symposium
May 18th, 2018

Designed by graduate students to enhance Penn State life science collaborations for everyone.

#PSULifeSci

Life Science Symposium at Penn State

Pennsylvania State University
University Park, PA

https://sites.psu.edu/lifesciencesymposium/

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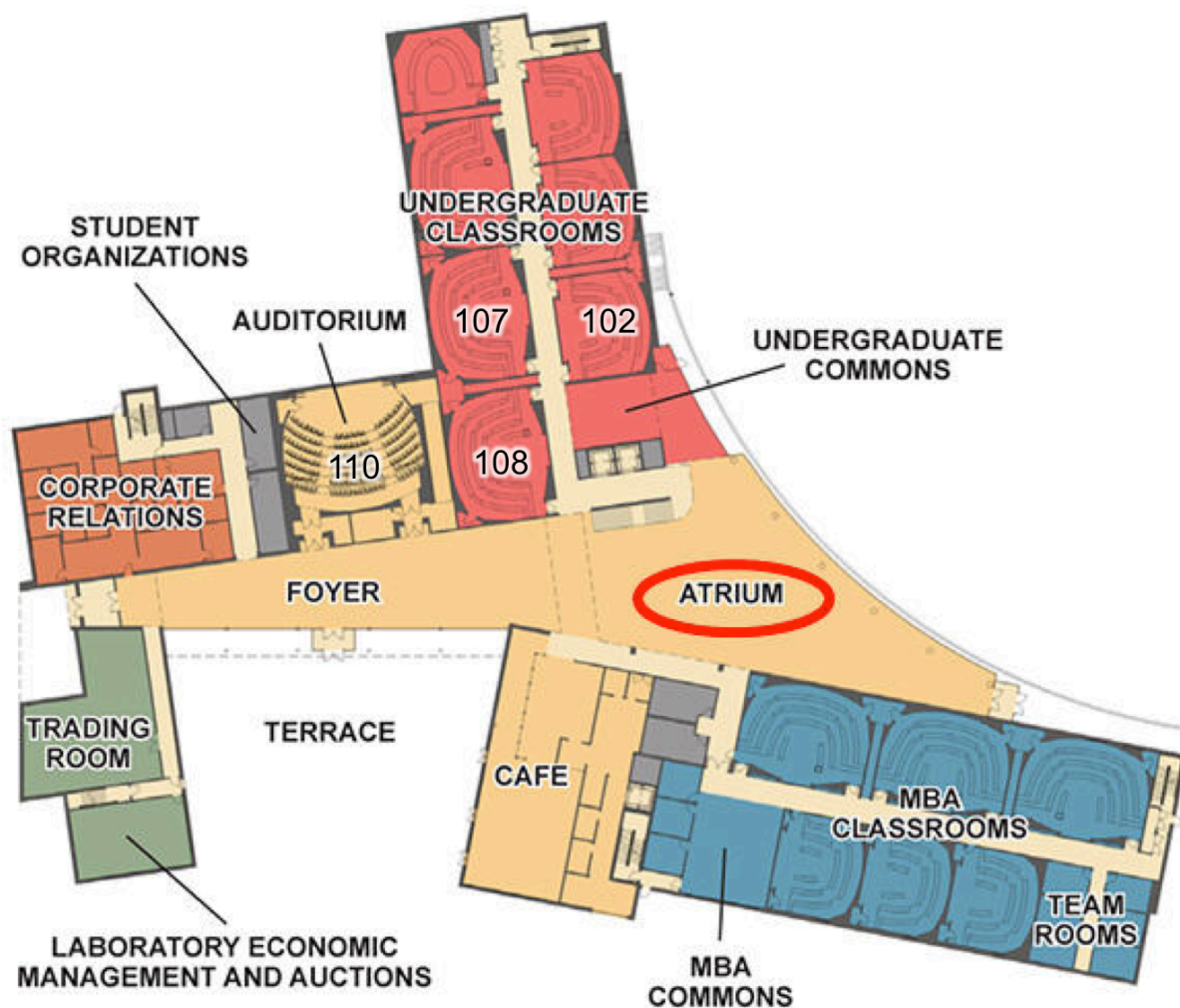PennState Huck Institutes of the Life Sciences | PennState College of Agricultural Sciences | PennState College of Nursing | PennState College of Medicine | PennState Eberly College of Science | PennState College of Health and Human Development

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Welcome

The Life Science Symposium at Penn State is a conference dedicated to promoting collaboration between, and increasing awareness of, the various branches of life science research at Penn State. The idea for the symposium was conceived in 2015 by a group of graduate students who realized that there was a lack of interaction across departments and disciplines; they recognized the need for greater collaboration and opportunities to learn about the incredible research being done at Penn State. The Life Science Symposium aims to fulfill three primary goals:
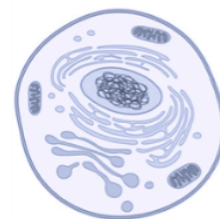
Goal 1: Foster unique research collaborations and promote networking throughout the university community in order to enhance funding possibilities and learning experiences for graduate students.

Goal 2: Increase exposure for Penn State's life science laboratories, centers, core facilities, and research opportunities in order to maximize engagement with and use of on-campus facilities.

Goal 3: Encourage meaningful dialogue and ethical understanding of our place as scientists in this world, our nation, and the surrounding community.

We wish to thank our sponsors, especially the Huck Institutes of the Life Sciences, our main contributor, along with our advisors and the university. We hope you enjoy this unique symposium!

Sincerely, The Huck Graduate Student Association Committee (HGSAC) members

Kelly Ness, *Physiology graduate student, Committee Chair*

Jasmine Caulfield, *Neuroscience graduate student, Committee Co-chair*

Di (Bruce) Chen	Genetics (MCIBS) *graduate student*
Hillary Figler	IID (MCIBS) *graduate student*
James Hester	Physiology *graduate student*
Mehreen Mughal	Bioinformatics and Genomics *graduate student*
Lila Rieber	Bioinformatics and Genomics *graduate student*
Christopher Strock	Plant Biology *graduate student*
Mackenzie Shipley	BMMB *graduate student*
Troy Ott	*Faculty Advisor*

Schedule at a Glance

Friday, May 18th

Time	Event	Location*
8:30 am	Breakfast and Registration	Atrium
9:00-9:10 am	Introduction and Welcome	Rm 110
9:15-10:15 am	**Keynote Presentation I: Dr. Nina Fedoroff**, Science Advisor at the Santa Fe Institute, Global Knowledge Initiative, and OFW Law, Washington D.C. "*Feeding 10 Billion People: is the Problem Technological or Social?*"	Rm 110
10:20-11:40 am	**Poster Session I**: Odd numbered posters *Snacks and Refreshments*	Atrium

Invited Student Talks: Session 1

11:45-12:15 pm	**Duverney Chaverra Rodriguez**: *Targeted delivery of CRISPR-associated endonuclease 9 (Cas9) into insect ovaries for heritable germ line gene editing*	Rm 107
11:45-12:15 pm	**Xuan Wang**: *Fiber resolution visualization of plant primary cell wall by fluorescently tagged cellulose binding protein*	Rm 108

Invited Student Talks: Session II

12:15-12:45 pm	**Adwitia Dey**: *A Brave Neuro World: How deciphering the novel signaling role of macrophage-associated Ron receptor tyrosine kinase activation can help us remedy the plight of neurodegeneration*	Rm 107
12:15-12:45 pm	**Hillary Figler**: *Putative microcin in ST73 E. coli strain amplifies Shiga toxin production of O157:H7*	Rm 108

12:45-2:05 pm	**Poster Session II**: Even numbered posters *Lunch Served*	Atrium
2:10-3:40 pm	**Student Research Lightning Talks**	Track A: Rm 102 Track B: Rm 107 Track C: Rm 108
3:45-4:45 pm	**Keynote Presentation II: Dr. David Titley**, Professor in the Department of Meteorology and School of International Affairs, Pennsylvania State University, "*Climate Risk and Security: People not Polar Bears (and how to talk about it)*"	Rm 110
4:45-5:30 pm	**Closing Statements and Awards** *Hors d'oeuvres served*	Atrium

*All events held at Smeal College of Business building

Track Schedule

Track A: Molecular Biology   Room 102

Time	Speaker	Field	Title
2:10-2:20 pm	James Hester	Integrative and Biomedical Physiology	Growing Oocytes Need Zinc: Zinc Deficiency in the Preantral Ovarian Follicle
2:20-2:30 pm	Di (Bruce) Chen	Computational Biology	Dynamic Landscape of Human L1 Transposition Revealed with Functional Data Analysis
2:30-2:40 pm	Faiza Siddiqui	*Postdoctoral Fellow*	Plasmodium falciparum Falcipain-2a Polymorphism in Southeast Asia and Its Potential Contribution to Artemisinin Resistance
--5 minute break--			
2:45-2:55 pm	Naomi Yamada	Molecular Biology	Characterizing protein-DNA binding event subtypes in ChIP-exo data
2:55-3:05 pm	Ehsan Mahdinia	Engineering	Vitamin K2 (Menaquinone-7) Production by *Bacillus subtilis natto* in Biofilm Reactors using a Glycerol-based Medium
--5 minute break--			
3:10-3:20 pm	Yasina Somani	Physiology and Biology	Patterns of conduit artery shear across the menopause transition
3:20-3:30 pm	Xiaoheng Cheng	Computational Biology	Detecting shared balancing selection without trans-species polymorphisms
3:30-3:40 pm	Alex Harris	MCIBS	Identifying and classifying ancestral selective sweeps from multilocus data

Track B: Nutrition Science   Room 107

2:10-2:20 pm	Anita Subramanian	Nutrition Science	Effect of Vitamin D Supplementation During Pregnancy on Blood Pressure
2:20-2:30 pm	Matt Cady	Nutritional Science	Child sex moderates the relationship between parent feeding practices and child food intake in 4-6-year-old children
2:30-2:40 pm	Bari Fuchs	Nutritional Science	Sex differences in the impact of portion size and energy density on children's neural responses to food images
--5 minute break--			
2:45-2:55 pm	Shue Huang	Nutritional Science	Alcohol consumption and risk for heart failure: a prospective cohort study and a meta-analysis
2:55-3:05 pm	Nicole Reigh	Nutritional Science	An intervention to improve eating self-regulation in children increases knowledge and energy compensation
--5 minute break--			
3:10-3:20 pm	Molly Higgins	Food Science	Topographical variation in perceived intensity of multiple bitter stimuli in humans
3:20-3:30 pm	Elizabeth Adams	Nutritional Science	Mothers vs. Fathers: Do parent's perspectives on infant feeding differ?
3:30-3:40 pm	Matt Cady	Nutritional Science	Dietary Patterns, Body Mass Index and Lifestyle Factors in Middle Childhood

Track C: Plant and Environmental Science Room 108

2:10-2:20 pm	Nathan Hepler	Plant science	CRISPR/Cas9-mediated genome editing reveals Arabidopsis thaliana expansin paralogs AtEXPA7 and AtEXPA18 function redundantly and are required for proper root hair formation.
2:20-2:30 pm	Natalie Imirzian	Ecology and Biology	Foraging dynamics in sniper alley
2:30-2:40 pm	Hannah Stewart	Entomology	Effects of immune challenge on bumblebee thermoregulatory capacity
--5 minute break--			
~~2:45-2:55 pm~~	Cancelled	Cancelled	Cancelled
2:55-3:05 pm	Nathan Johnson	Molecular Biology and Plant Science	Extensive sequence divergence of trans-species active small RNAs between the parasitic plants Cuscuta campestris and Cuscuta gronovii
--5 minute break--			
3:10-3:20 pm	Sarthok Rahman	Biology and Entomology	A Tale of two species: How different genetic mechanisms drive parallel color variation in mimetic bumble bees
3:20-3:30 pm	Ayaan Hossain	Bioinformatics and Genomics	Automated Design and Characterization of 4350 Highly Non-Repetitive E.coli Promoters using the Non-Repetitive Parts Calculator
3:30-3:40 pm	Geng-Yuan Chen	Biomedical Engineering	Contribution of kinesin-5 mediated microtubule stability reveals its functions in mitotic spindle size regulation

Student Posters

Poster Session I: Odd numbered posters (10:20-11:40 a.m.)

Atrium of Smeal College of Business Building

Poster #	Name of Presenter	Program	Title
1	Naomi Yamada	Bioinformatics and Genomics	Characterizing protein-DNA binding event subtypes in ChIP-exo data
3	Xiaoheng Cheng	MCIBS	Detecting shared balancing selection without trans-species polymorphisms
5	Debmalya Nandy	Bioinformatics and Genomics	Covariate Information Number for Feature Screening in Ultrahigh Dimension
7	Elizabeth Adams	Nutritional Science	Mothers vs. Fathers: Do parent's perspectives on infant feeding differ?
9	Bari Fuchs	Nutritional Science	Sex differences in the impact of portion size and energy density on children's neural responses to food images
11	Nicole Reigh	Nutritional Science	An intervention to improve eating self-regulation in children increases knowledge and energy compensation
13	Matt Cady	Nutritional Science	Child sex moderates the relationship between parent feeding practices and child food intake in 4-6 year-old children
15	Molly Higgins	Food Science	Topographical variation in perceived intensity of multiple bitter stimuli in humans
17	Ruth Pobee	Nutritional Science	Hemoglobin Concentration is Associated with Affective Variables in Early Pregnancy
19	Adwitia Dey*	Integrative and Biomedical Physiology	A Brave Neuro World: How deciphering the novel signaling role of macrophage-associated Ron receptor tyrosine kinase activation, can help us remedy the plight of neurodegeneration
21	June Teichmann	Food Science	Optimization of butyrate production by human fecal communities in the presence of resistant starch
23	Ehsan Mahdinia	Engineering	Vitamin K2 (Menaquinone-7) Production by *Bacillus subtilis natto* in Biofilm Reactors using a Glycerol-based Medium
25	Sabahat Gazal	VBS	AmotL1 acts as an adapter that links paramyxovirus M protein with ESCRT machinery

27	Hyunwook Lee	*Postdoctoral Fellow*	The Structure of the Transferrin Receptor:Canine Parvovirus Complex Reveals how the Interactions Control Viral Host Range
29	Latisha Franklin	BMMB	Inborn errors in purine metabolism result in neuromuscular deficits : A comparative metabolic approach
31	Lila Rieber	Bioinformatics and Genomics	Characterizing locus-specific nuclear relocalization between cell types
33	Carlene McGrady	Entomology	Pollination Services and Colony Abundance of Bombus impatiens
35	Hannah Stewart	Entomology	Effects of immune challenge on bumblebee thermoregulatory capacity
37	Seth Polydore	MCIBS	Comprehensive Analysis of RDR-independent Small RNAs in Arabidopsis thaliana
39	Jenna Reeger	Plant Biology	Rice roots for a food secure future: Investigating the physiology and genetics of rice root anatomical traits for drought tolerance
41	Dan Ye	Engineering	Resonant soft X-ray scattering reveals cellulose microfibril spacing in onion cell wall
43	Damie Pak	Biology	The role of diapause in the developmental synchrony of an agricultural pest: a case study with the tortricid pest Cydia pomonella
45	Nathan Hepler	Plant Biology	CRISPR/Cas9-mediated genome editing reveals Arabidopsis thaliana expansin paralogs AtEXPA7 and AtEXPA18 function redundantly and are required for proper root hair formation.

*Selected for an Invited Student Talk

Poster Session II: Even numbered posters (12:45-2:05 p.m.)

Atrium of Smeal College of Business Buidling

Poster #	Name	Program	Title
2	Di (Bruce) Chen	Genetics (MCIBS)	Dynamic Landscape of Human L1 Transposition Revealed with Functional Data Analysis
4	Alex Harris	MCIBS	Identifying and classifying ancestral selective sweeps from multilocus data
6	Tyler Garner	Integrative and Biomedical Physiology	Zip9 genetic regulation during embryonic development
8	James Hester	Integrative and Biomedical Physiology	Growing Oocytes Need Zinc: Zinc Deficiency in the Preantral Ovarian Follicle
10	Yasina Somani	Kinesiology	Patterns of conduit artery shear across the menopause transition
12	Matt Cady	Nutritional Science	Dietary Patterns, Body Mass Index and Lifestyle Factors in Middle Childhood
14	Anita Subramanian	Nutritional Science	Effect of Vitamin D Supplementation During Pregnancy on Blood Pressure
16	Juliana Fritts	Food Science	Spice it up! Results of a school-based intervention to increase vegetable intake among rural adolescents
18	Sixtus Aguree	Nutritional Science	Plasma Volume, Hydration and Complete Blood Count Across the Menstrual Cycle: Preliminary Results
20	David Narvaiz	*Undergraduate at Lamar University*	A survey of seasonal persistence of common bacterial and viral pathogens in Jefferson County Beaches
22	Hillary Figler*	Immunology and Infectious Disease (MCIBS)	Investigation for bacteriocin encoding genes in ST73 Escherichia coli strain 0.1229
24	Faiza Siddiqui	*Postdoctoral Fellow*	Plasmodium falciparum Falcipain-2a Polymorphism in Southeast Asia and Its Potential Contribution to Artemisinin Resistance
26	Santosh Panthi	VBS	Delivery of Functional Proteins into Mammalian Cells via Paramyxovirus-like Particles
28	Geng-Yuan Chen	Biomedical Engineering	Contribution of kinesin-5 mediated microtubule stability reveals its functions in mitotic spindle size regulation

30	Markus Kastner	*Postdoctoral Fellow*	Human mitochondrial transcription investigated by in-vitro transcription assays and high-resolution Atomic Force Microscopy
32	Nathan Johnson	Plant Biology	Extensive sequence divergence of trans-species active small RNAs between the parasitic plants Cuscuta campestris and Cuscuta gronovii
34	Jonathan Maturano	*Undergraduate at Rowan University*	Comparison of Detection Modes for Segmented Flow Droplets
38	Karly Regan	Entomology	Arthropod Response to Organic Cover Crop-Based Reduced-Tillage Cropping Systems
40	Imtiaz Ahmad	*Postdoctoral Scholar*	Harnessing nature: The multi-functional role of Metarhizium as a plant protectant
42	Catherine Herzog	Biology	Management practices and age cohorts that contribute to increased Peste des petits ruminants seroprevalence in sheep, goats, and cattle in northern Tanzania
44	Brianna Flonc	Entomology	Can fungi make caterpillars picky eaters? Effect of endophytic Metarhizium in corn on fall armyworm (Spodoptera frugiperda) feeding behavior

*Selected for an Invited Student Talk

Keynote Speakers

Dr. Nina Fedoroff

Talk Title: *Feeding 10 billion people: is the problem technological or social?*

Time: 9:15-10:15 a.m. **Location**: Room 110

Dr. Nina Fedoroff is a molecular biologist known for her early work in plant gene cloning, mechanisms of transposable elements, her study of epigenetic mechanisms and plant stress and hormonal responses. Dr. Fedoroff joined the faculty at Penn State in 1995 as the Director of the Biotechnology Institute and the Vern M. Willaman Chair of the Life Sciences and helped to found the Huck Institutes of the Life Sciences, an umbrella program for six intercollege graduate degree programs which promotes interdisciplinary collaborations and multifaceted research.

In 2006 Dr. Fedoroff was awarded a National Medal of Science by President George W. Bush for her pioneering work on plant molecular biology, for being the first to clone and characterize maize transposons, and for her contributions to education and public policy pertaining to recombinant DNA and genetically modified plants. She served as the Science and Technology Adviser to the Secretary of State from 2006-2010 and used her platform as an advocate for the destigmatization of genetically modified foods.

Dr. Fedoroff founded the Global Knowledge Initiative (GKI), an NGO that helps connect local innovators with resources, promotes effective collaborations through skills-building and shared agendas, and promotes innovative problem solving in order to solve the world's most pressing issues. Following her appointment at the State Department, Dr. Fedoroff joined the faculty at the King Abdullah University of Science and Technology, organizing the Center for Desert Agriculture in order to address food production in arid landscapes. Dr. Fedoroff has written editorials for the New York Times, as well as a book entitled *Mendel in the Kitchen: A Scientist's View of Genetically Modified Foods*. Today, she continues her science advocacy work through writing and lecturing internationally, serving as a science adviser for GKI and OFW Law, and through public outreach events, such as her May 2017 TED Talk.

Dr. David Titley

Talk Title: *Climate Risk and Security: People not Polar Bears {and how to talk about it}*

Time: 3:45-4:45 p.m. **Location**: Room 110

Dr. David Titley is a Professor of Practice in the Department of Meteorology, the Director of the Center for Solutions to Weather and Climate Risk, and a Professor in the School of International Affairs at Penn State known for his work and advocacy of the risks of climate change as they relate to national security.

Dr. Titley began his career through the Naval Reserve Officer Training Commissioning program and served as a naval officer for 32 years before retiring at the rank of Rear Admiral. During his time in the navy, Dr. Titley served as an oceanographer and navigator, commander of the Naval Meteorological and Oceanography Command, deputy assistant chief of naval operations for information dominance, and as senior military assistant for the director in the Office of Net Assessment in the Office of the Secretary of Defense. While serving in the pentagon, Dr. Titley initiated and lead the U.S. Navy's Task Force on Climate Change.

After retiring from the navy, Dr. Titley joined the National Oceanic and Atmospheric Administration (NOAA) as the Deputy Undersecretary of Commerce for Operations, the chief operating officer position at NOAA. Dr. Titley has served as a climate change advocate and science adviser for the CNA Military Advisory Board, the Advisory Board of the Center for Climate and Security, the Science and Security Board of the Bulletin of the Atomic Scientists, and the National Academy of Science Board on Atmospheric Sciences and Climate.

Dr. Titley has spoken across the country and around the world on the importance of climate change, particularly as it relates to national security. He was invited to present on behalf of the Department of Defense at congressional hearings and the Intergovernmental Panel on Climate Change (IPCC), acting as a science liaison between the military and congress. Dr. Titley founded the Center for Solutions to Weather and Climate Risk at Penn State, which he continues to direct. He continues to advocate on behalf of climate change and military readiness in presentations at universities across the United States as well as in a TEDx talk in November 2017.

Invited Student Speakers

Duverney Chaverra Rodriguez

Time: *11:45am – 12:15 p.m.* **Location:** *Room 107*

Talk Title: *Targeted delivery of CRISPR-associated endonuclease 9 (Cas9) into insect ovaries for heritable germ line gene editing*

Duverney earned his bachelor's degree in Biology in 2004 from the University of Antioquia. He earned his master's degree in Biology in 2011 from the University of Antioquia, and his thesis was titled, "Fitness costs of lambda-cyhalotrhin resistance in the mosquito *Ae. aegypti*." Duverney received a Fullbright Doctoral Fellowship in 2013. Since coming to Penn State, Duverney has been working towards his PhD in Entomology in Jason Rasgon's lab. He intends to complete his degree this year, and his thesis is entitled, "Cas9-mediated genome editing of the mosquito germline via receptor-mediated endocytosis." During his time at Penn State, Duverney has contributed as a co-author on two published manuscripts and currently has a first-author publication in the revision process.   *Abstract pg. 34*

Xuan Wang

Time: *11:45am – 12:15 p.m.* **Location:** *Room 108*

Talk Title: *Fiber-resolution visualization of plant primary cell wall by fluorescently tagged cellulose binding protein*

Xuan earned his bachelor's degree from the University of Minnesota (Duluth), double majoring in Chemistry and Cell and Molecular Biology, Biochemistry and Molecular Biology. He started at Penn State in 2013 working towards a PhD in Plant Biology with Daniel Cosgrove. Xuan received a James B. and Viola M. Bartoo Graduate Fellowship in 2013, a Huck Graduate Research Innovation Grant in 2016, and a Huck Institutes Graduate Travel Award in 2018. Xuan has presented oral and poster presentations at the annual CLSF retreat in State College since 2016. He has also contributed to two co-authored publications in 2018, one that has been published and one that has been submitted. Xuan is also the first author on one publication that is currently in preparation.   *Abstract pg. 36*

Adwitia Dey

Time: *12:15 – 12:45 p.m.*   **Location:** *Room 107*

Talk Title: *A Brave Neuro World: How deciphering the novel signaling role of macrophage-associated RON receptor tyrosine kinase activation can help us remedy the plight of neurodegeneration*

Adwitia earned her bachelor's degree from the University of Toronto (St. George) in 2011, double majoring in Human Biology and Animal Physiology. She received her master's degree from the University of Western Ontario in 2013 in Kinesiology/Integrated Physiology. Since 2013, she has been working toward her PhD in Physiology in Pamela Hankey-Giblin's lab. Her dissertation is entitled, "Elucidating the role of Ron receptor tyrosine kinase signaling in CNS health and disease." Since her time at Penn State, Adwitia has made numerous oral and poster presentations, and she is a co-author and first author on many publications. Following graduation, Adwitia will begin a postdoctoral fellowship with Mel Feany at Harvard Medical School.   *Abstract pg. 26*

Hillary Figler

Time: *12:15 – 12:45 p.m.*   **Location:** *Room 108*

Talk Title: *Putative microcin in ST73 E. coli strain amplifies Shiga toxin production of O157:H7*

Hillary received her bachelor's degree in Microbiology in 2014 from the University of Rochester. She started at Penn State in 2014 working towards her PhD in Immunology and Infectious Disease with Edward Dudley. She is the recipient of a USDA National Needs Fellowship and Graham Scholarship, and she received a Huck Graduate Research Innovation Grant. Hillary was a member of the Molecular, Cellular and Integrative Biosciences Graduate Student Association from 2015-2017, and she has been a member of the Huck Graduate Student Advisory Committee since 2015. Hillary has also contributed as a co-author to two publications, one of which is published and one that is in preparation. She is also the first-author on a manuscript published in 2016.   *Abstract pg. 29*

Attendee abstracts

Computational Biology & Statistics

Characterizing protein-DNA binding event subtypes in ChIP-exo data
Naomi Yamada, William Lai, Nina Farrell, Franklin Pugh, and Shaun Mahony
Regulatory proteins associate with the genome either by directly binding cognate DNA motifs or via protein-protein interactions with other regulators. Each recruitment mechanism may be associated with distinct motifs and may also result in distinct characteristic patterns in high-resolution protein-DNA binding assays. For example, the ChIP-exo protocol precisely characterizes protein-DNA crosslinking patterns by combining chromatin immunoprecipitation (ChIP) with 5' → 3' exonuclease digestion. Since different regulatory complexes will result in different protein-DNA crosslinking signatures, analysis of ChIP-exo tag enrichment patterns should enable detection of multiple protein-DNA binding modes for a given regulatory protein. However, current ChIP-exo analysis methods either treat all binding events as being of a uniform type or rely on motifs to cluster binding events into subtypes. Results: To systematically detect multiple protein-DNA interaction modes in a single ChIP-exo experiment, we introduce the ChIP-exo mixture model (ChExMix). ChExMix probabilistically models the genomic locations and subtype membership of binding events using both ChIP-exo tag distribution patterns and DNA motifs. We demonstrate that ChExMix achieves accurate detection and classification of binding event subtypes using in silico mixed ChIP-exo data. We further demonstrate the unique analysis abilities of ChExMix using a collection of ChIP-exo experiments that profile the binding of key transcription factors in MCF-7 cells. In these data, ChExMix detects cooperative binding interactions between FoxA1, ER-alpha, and CTCF, thus demonstrating that ChExMix can effectively stratify ChIP-exo binding events into biologically meaningful subtypes.
Student Research Lightning Talks: Track A   *Poster #: 1*

Dynamic Landscape of Human L1 Transposition Revealed with Functional Data Analysis
Di (Bruce) Chen, Marzia Cremona, Zongtai Qi, Robi Mitra, Francesca Chiaromonte, and Kateryna Makova
The Long Interspersed Elements-1 (L1s) are among the most active human Transposable Elements (TEs) and constitutes over 17% of the human genome. Characterizing the transpositional activity of L1s and their interactions with the genomic landscape is critical for understanding genome evolution and function. However, to date, the dynamics of L1 integration and fixation has not been studied comprehensively. We performed a genome-wide investigation of L1 transposition using three large datasets of de novo, polymorphic, and fixed, human-specific L1s. We then measured 50 genomic features at high resolution in the flanking regions of these elements and in L1-free control regions, and used Interval-Wise Testing (IWT), a novel Functional Data Analysis method, to contrast their landscapes at multiple scales and identify signatures of L1 integration and fixation. Our results suggested that de novo, polymorphic, and fixed L1s in the human genome are characterized by unique genomic landscapes, with different features acting at specific locations and scales. While L1 integrations tend to occur in regions with high GC-content, open chromatin and elevated gene expression levels, fixed L1s prefer regions with low exon content and transcriptional repression. The genomic feature signals near polymorphic L1s are similar to fixed L1s, yet the comparison with control via IWT shows less significance. These findings confirm that the genome-wide distribution of L1 elements is far from random, and suggest the role of genomic features in both insertion and fixation preferences. As the next step in our analysis, we are using multiple Functional Logistic Regression to quantify the joint effects of the genomic features selected by IWT. Here for the first time we investigate L1 transposition on the genome-wide scale and in the evolutionary

framework, while considering interactions with an extensive range of genomic features. This study sheds light on the dynamics of TE landscape and will advance our understanding of the structure, evolution and function of the human genome.

Detecting shared balancing selection without trans-species polymorphisms
Xiaoheng Cheng and Michael DeGiorgio

Trans-species polymorphism has been widely used as a key sign of long-term balancing selection across multiple species. However, such sites are often rare in the genome, and could result from mutational processes or technical artifacts. No methods are yet available to specifically detect footprints of trans-species balancing selection without using trans-species polymorphic sites. In this study, we developed summary- and model-based approaches that are each specifically tailored to uncover regions of long-term balancing selection shared by a set of species by using genomic patterns of intra-specific polymorphism and inter-specific fixed differences. We demonstrate that our trans-species statistics have substantially higher power than single-species approaches to detect footprints of trans-species balancing selection, and are robust to those that do not affect all tested species. We further applied our model-based methods to human and chimpanzee whole genome sequencing data, and have identified the most outstanding candidates to be the MHC locus and the malaria resistance-associated FREM3/GYPB region, consistent with previous findings. Many other outstanding candidates also involves in immunity, e.g. ABCA13 and THSD7B. Our findings echo the significance of pathogen defense in establishing balanced polymorphisms across human and chimpanzee lineages, and suggest that non-coding regulatory regions may play an important role. Additionally, we have shown that these trans-species statistics can be applied to and work well for more than two species, and have integrated them into open-source software packages for ease of use by the scientific community.

Identifying and classifying ancestral selective sweeps from multilocus data
Alexandre Harris and Michael DeGiorgio

Positive selection causes a selected variant to rise to high frequency in a population, resulting in a selective sweep of the diversity surrounding the site under selection. Accordingly, the signature of a selective sweep occurring in an ancestral population may still remain in its modern descendants. Identifying sites under selection in the ancestor is important to contextualize the timing of a sweep, but few methods exist for this. Here, we apply the theory of H12, which detects recent hard and soft sweeps from the presence of high-frequency haplotypes, to multiple samples, to identify sites under ancestral selection. Our application of H12, denoted H12anc, is distinct from other methods because it requires a minimum of only two populations, and is not confounded by independent convergent sweeps in different populations. In simulated data, we find that H12anc has high power to detect both ancestral and convergent sweeps from pairs of populations. Furthermore, we are also able to use the pooled haplotype frequencies from all sampled populations to classify ancestral sweeps specifically as hard or soft. Finally, our empirical analyses in human data recovered known and novel signatures of ancestral sweeps between pairs of human populations worldwide.

Covariate Information Number for Feature Screening in Ultrahigh Dimension
Debmalya Nandy, Francesca Chiaromonte, and Runze Li
Modern technological advances in various scientific fields generate ultrahigh-dimensional supervised data with sparse signals, i.e. a limited number of samples (n) each with a very large number of covariates (p >> n), only a small share of which is truly associated with the response. In these settings, major concerns on computational burden, algorithmic stability, and statistical accuracy call for substantially reducing the feature space by eliminating redundant covariates before the application of any sophisticated statistical analysis. Following the development of Sure Independence Screening (Fan and Lv, 2008, JRSS-B) and other model- and correlation-based feature screening methods, we propose a model-free procedure called the Covariate Information Screening (CIS). CIS uses a marginal utility built upon Fisher Information, possesses the sure screening property, and is applicable to any type of response. An extensive simulation study and an application to transcriptomic data in rats reveal CIS's comparative strengths over some popular feature screening methods. *Poster #: 5*

Zip9 genetic regulation during embryonic development
Tyler Garner and Francisco Diaz
Upregulation of translational capacity is essential during embryogenesis to meet the rising need for protein synthesis and cellular growth. Ribosomal biogenesis is therefore amplified through increased transcription of the ribosomal RNAs (rRNAs) by RNA polymerases (pol) I and III. Both RNA pols bind multiple zinc atoms which appear to be required for their catalytic activity and stability. Zinc deficiency in embryos is known to decrease overall RNA pol activity, reduce fertility, and disrupt development. Zir-,Irt-like proteins (Zip) are zinc transporter proteins that act to increase intracellular zinc concentrations. Of the fourteen known Zip proteins, Zip9 is unique in that it is coupled to G-proteins and sensitive to androgens. This study aimed to examine genetic regulation of Zip9 throughout mouse preimplantation embryonic development by comparing changes in H3K4me3, a marker of transcriptional activation, in the promoter region of Zip9 to changes in ZIP9 transcript abundance. RNA-seq and H3K4me3 CHIP-seq datasets were acquired from NCBI-GEO ascension: GSE71434. Normalized peaks per kilobase per million mapped reads (RPKM) for H3K4me3 at the Zip9 promoter were correlated with RNA-seq fragments per kilobase of transcript per million mapped reads (FPKM) in pronuclear stage 5 (PN5) zygotes, early 2-cell, late 2-cell, 4 cell, and 8 cell embryos and the inner cell mass cells of blastocyst embryos. Zip9 RNA expression was significantly correlated with promoter H3K4me3 enrichment throughout development from the PN5 zygote to inner cell mass cells. RPKM and FPKM were upregulated beginning at the 2-cell state with H3K4me3 preceding the increase in Zip9 transcript abundance. This coincides nicely with the known major embryonic genome activation in the mouse embryo which occurs at the 2-cell stage. RPKM and FPKM peaked at the 4-cell to 8-cell stage, then declined in the inner cell mass cells, indicating a possible critical period for Zip9 upregulation during early embryonic development. Further GO-term analysis of genes with significant RNA-seq correlations with Zip9 found over-representation of genes involved in rRNA synthesis and transcription by RNA pol I. These data provide novel insights of the possible role of Zip9 for ribosomal biogenesis during embryonic development. *Poster #: 6*

Human Health, Nutrition, & Physiology

Alcohol consumption and risk for heart failure: a prospective cohort study and a meta-analysis
Shue Huang, Zhe Huang, Gregory Shearer, Yuntao Wu, Aijun Xing, Shouling Wu, and Xiang Gao
Objectives: The association between alcohol consumption and risk of heart failure (HF) remains controversial. The objective of this study was to examine the association between alcohol consumption and incident HF in Chinese adults, and to conduct a meta-analysis to summarize prospective data on alcohol and HF. Methods: The prospective study included 97, 310 Chinese men and women (mean age: 51±12 yr.) from the Kailuan Study who were free of HF in 2006 (baseline) and followed up to Dec. 2015. Baseline alcohol consumption was assessed via a questionnaire, and was grouped as never drinkers, former drinkers, light (women: 0-0.4 drinks/day, men: 0-0.9 drinks/day), moderate (women: 0.5-1 drinks/day, men:1-2 drinks/day) and high (women: >1 drinks/day, men: >2 drinks/day) alcohol intake. Incident HF at follow up was defined as a first HF event, confirmed by review of medical records. Multivariable Cox proportional hazard ratio was used to examine the association between alcohol consumption and time to heart failure, adjusting for potential covariates including age, sex, education, monthly income, occupation, smoking status, physical activity, body mass index, hypertension, diabetes and total cholesterol. A meta-analysis including 13 published prospective studies on alcohol and heart failure, and this current study was conducted using random-effects models. Results: During an average of 8.8 years follow up, we documented 1597 incident HF cases. Compared with never and past drinkers, the corresponding adjusted hazard ratios (HRs) for light, moderate and high alcohol intake were 0.71 (95%CI: 0.59, 0.86), 0.84 (95%CI: 0.62, 1.13), and 0.63 (95%CI: 0.52, 0.76), respectively. In the meta-analysis including 491, 374 participants, we observed a significantly lower risk for HF among light-drinkers (pooled HR for light alcohol intake vs non-drinkers was 0.84 (95% CI: 0.80, 0.89)). In contrast, we did not find significant associations between moderate and high alcohol intake and HF risk. Conclusions: Alcohol intake was associated with a lower risk for HF incidence. Meta-analysis confirmed the lower risk of HF associated with light alcohol intake. However, because of large heterogeneity across studies, particularly for the moderate and high intake categories, results should be interpreted with caution.
Student Research Lightning Talks: Track B

Mothers vs. Fathers: Do parent's perspectives on infant feeding differ?
Elizabeth Adams and Jennifer Savage
Objectives: Parent feeding styles shape infants' early experiences with food, thus having a profound impact on infant growth. Infant feeding has traditionally been the mother's role; therefore, the majority of research on infant feeding has been conducted solely in mothers. More recently, fathers have become more involved with infant feeding. Therefore, the purpose of this exploratory analysis was to compare mothers and fathers' perception of their infant feeding responsibilities and their infant feeding style. Methods: Mother-father dyads (n=21) independently completed the Infant Feeding Style Questionnaire (IFSQ) and Who Does What (WDW) Questionnaire when their infants were 24 weeks of age. The IFSQ assessed beliefs and behaviors on pressure to 1) get infants to finish their food, 2) use of cereal when feeding, and 3) use of food to soothe a fussy infant. The WDW questionnaire measured mothers and father's perceptions of their current infant feeding responsibilities and their desired responsibility. Discrepancy scores were created by comparing current vs. desired responsibility, then categorized as 1) desired father to do more, 2) desired mother to do more, 3) content with current level of responsibility. For this pilot study, significance was set at $p < 0.1$. Results: Mothers and fathers had different perceptions on current infant feeding responsibilities. Half (50%) of mothers reported sole responsibility in deciding their infants feeding schedule, whereas only 25% of fathers reported that mothers solely decided. One-fifth (20%) of mothers reported full responsibility for infant feedings, whereas 10% of fathers reported that mothers exclusively fed their infants. Discrepancy scores for current vs. desired responsibility

revealed that almost half (47%) of fathers reported wanting a greater role in deciding their infant's feeding schedule, and 30% of mothers reported wanting fathers to have more of this responsibility. For infant feedings, 60% of fathers reported wanting to do more, and similarly, 60% of mothers reported wanting fathers to do more infant feedings. On the IFSQ, mothers and fathers responses for pressure using cereal (r=0.39, p=0.09) and food to soothe (r=0.41, p=0.07) were positively correlated, whereas pressure to finish were not correlated (p>0.1). Conclusions: There was disagreement among couples, such that a greater proportion of mothers reported sole responsibility for infant feeding; yet fewer fathers reported that mothers took full responsibility. There was agreement among couples, such that fathers reported wanting more infant feeding responsibilities, which mothers also reported wanting for fathers. Future research should explore barriers that may be limiting father's involvement with infant feeding. Mothers and fathers appear consistent with pressure using cereal and food to soothe, but not pressure to finish food. Intervention messaging should consider delivery to both mothers and fathers to promote feeding style consistency.

Student Research Lightning Talks: Track B   *Poster #: 7*

Growing Oocytes Need Zinc: Zinc Deficiency in the Preantral Ovarian Follicle
James Hester and Francisco Diaz

Objective: To evaluate the effect of zinc deficiency on oocyte development in the preantral ovarian follicle – a novel developmental stage for micronutrient investigation. Methods: Oocyte-granulosa cell complexes were collected from preantral ovarian follicles of 14 day old CD-1 mice and cultured on collagen membranes under control, zinc-deficient, or rescue conditions. Oocyte diameter was measured from brightfield images taken with an Olympus DP20 microscope digital camera. Chromatin arrangement and nucleolar development was observed after DAPI staining. Gene expression was measured with qPCR. Meiotic competence was measured by exposing cultured oocyte-granulosa cell complexes to Epidermal Growth Factor (EGF) to mimic the in-vivo ovulatory signal (maturation media). The ability of the oocytes to undergo meiotic division was assessed 24 hours after EGF treatment. Apoptosis was assessed via a TUNEL assay. Trans-zonal projections, actin-rich connections between oocyte and granulosa cells were stained and quantified with Phalloidin. Results: Zinc deficiency disrupted oocyte growth in vitro. Zinc deficient oocytes were smaller than control or rescue on day 4 (p<0.001) and 6 (p<0.05), but not day 10 of cell culture. Zinc deficiency impacted nuclear development; zinc deficient oocytes were more likely to have multiple nucleoli on day 6 (p<0.001), but not day 10 of cell culture. Differentiation of somatic cells was also impaired; zinc-deficient granulosa cell gene expression became dysregulated. The somatic cell markers lhcgr, ar, pcsk6, and fosb were elevated compared with control (p<0.05 for all). DTPA induced apoptosis in granulosa cells (TUNEL assay p<0.001). There were fewer connections between the oocyte and somatic cells (p<0.05). Preantral zinc deficiency reduced the meiotic potential of cultured oocytes. After EGF treatment, oocytes matured in zinc deficient media were less likely to resume meiosis and reach the meiotic stage required for fertilization (p<0.001). The meiotic defect was seen in zinc-deficient oocytes even when transferred to maturation media containing zinc. Conclusions: Prior to entering the pool of antral ovulatory follicles, oocytes and the surrounding somatic cells undergo a period of growth and differentiation. This phase is known as preantral oocyte development and may last 3-5 months in humans. This study shows that zinc deficiency impairs multiple preantral developmental milestones including oocyte growth, oocyte nuclear maturation, and somatic cell differentiation. Most notably, the acquisition of meiotic competence – a benchmark of oocyte fertility and viability – was severely reduced by zinc deficiency. The meiotic defect was noted in zinc-deficient cultured oocytes even when they were transferred to maturation media containing zinc, indicating a zinc requirement during development, rather than during meiotic resumption. A loss of metabolic support from the surrounding somatic cells may explain the observed oocyte deficits. These results demonstrate that zinc is required in oocyte development earlier than previously reported, and that even short periods of zinc deficiency may impact fertility months later. These results may impact our understanding of prenatal micronutrient supplementation, as well as optimal methods for in-vitro oocyte maturation.

Student Research Lightning Talks: Track A   *Poster #: 8*

Sex differences in the impact of portion size and energy density on children's neural responses to food images

BA Fuchs, TP Masterson, EJG Brian, LK English, SN Fearnbach, M Lasschuijt, SJ Wilson, BJ Rolls, AL Pearce, and KL Keller

Large portions of high energy-dense foods increase energy intake in children, which may contribute to the development of obesity. We previously used a region-of-interest analysis to demonstrate sex-differences in children's responses to food portion size (PS) and energy density (ED) in brain regions implicated in reward, valuation and emotion. To extend these findings, we conducted a whole-brain analysis to test for sex differences in neural responses to food images varied by PS and ED. In a block-design fMRI paradigm, 48 children (N=23 boys, 7-10 yrs) viewed food images at two levels of ED (high, low) and PS (large, small). Repeated measures ANOVA tested for differences in blood-oxygen level dependent responses to food cues between boys and girls. Beta values were extracted from clusters demonstrating differential activation by sex, and post-hoc analyses were run after controlling for BMIz and food image liking/wanting. Results showed sex x PS interactions in the visual cortex, fusiform gyrus, putamen, hippocampus and cingulate (all $P < 0.001$). In all regions, girls, but not boys, showed greater responses to large vs. small PS. In the putamen, these effects were driven by increased activation among girls to the large PS, high-ED cues. Boys showed an opposite response pattern in the putamen, with greater activation to smaller portions, particularly to low-ED foods. These results extend our previous findings by demonstrating that girls and boys also process food cues differently in regions implicated in visual processing and memory. Future analyses are needed to explore the etiology and behavioral implications of these differences. This work may inform the development of more effective, personalized approaches to reduce overeating in the presence of large portion sizes.

Student Research Lightning Talks: Track B   *Poster #: 9*

Patterns of conduit artery shear across the menopause transition

Yasina Somani1, David Moore, Danielle Jin-Kwang Kim, Steriani Elavsky, and David Proctor

Introduction: Disturbed patterns of conduit artery shear, characterized by greater oscillatory (bi-directional) and retrograde (backward) shear are associated with endothelial dysfunction. Moreover, declines in endothelial function can take place rapidly across the menopause transition, placing women at heightened risk for development of cardiovascular disease. Methods: Conduit artery shear patterns were assessed in women at varying stages of the menopause transition. Resting brachial artery and common femoral artery mean blood velocities and diameters were measured via Doppler ultrasound in early perimenopausal, late perimenopausal, and early postmenopausal women. Results: Brachial artery oscillatory shear was significantly higher in early postmenopausal women (n=15, 0.17 ± 0.08 a.u.) than both early (n=12, 0.08 ± 0.05 a.u., p=0.002) and late (n=8, 0.08 ± 0.04 a.u., p= 0.007) perimenopausal women, and retrograde shear was significantly higher in early postmenopausal vs. early perimenopausal women (-9.74 ± 6.48 s-1 vs. -4.81 ± 3.05 s-1, p= 0.03). Femoral artery retrograde and oscillatory shear were greater, respectively, in early postmenopausal women (n=15, -6.78 ± 2.91 s-1; 0.19 ± 0.08 a.u.) than early perimenopausal women (n=14, -4.07 ± 2.21 s-1, p=0.03; 0.11 ± 0.08 a.u., p=0.01). Further, Pearson correlation analyses revealed significant associations between follicle stimulating hormone (FSH) and both retrograde and oscillatory shear, respectively, in the brachial (R=-0.37, p=0.04; R=0.5, p=0.005) and common femoral artery (R=-0.4, p=0.03; R=0.45, p=0.01). Discussion: Our findings suggest that increases to conduit artery retrograde and oscillatory shear take place during the menopause transition and these increases are associated with FSH, a marker of reproductive age.

Student Research Lightning Talks: Track A   *Poster #: 10*

An intervention to improve eating self-regulation in children increases knowledge and energy compensation

Nicole Reigh, Shelby O'Neill, Abigail Kramer, Barbara Rolls, Jennifer Savage, Susan Johnson, Barbara Lohse, Heather Toomey Zimmerman, and Kathleen Keller

The ability to respond to internal hunger and fullness signals is critical for the maintenance energy balance and, therefore, healthy body weight. However, few interventions exist to improve self-regulation of food intake. We tested the effectiveness of a laboratory-based intervention to determine if self-regulation of food intake can be improved in 4-6 year-old children. A within-subjects design was used to test children (16 boys, 12 girls) across 10 laboratory visits to assess knowledge and eating self-regulation before and after a 4-week intervention. The intervention was designed to teach children how to better respond to satiety signals and employed a virtual reality game to help children learn about digestion and the stomach-filling effects of various foods. Knowledge was assessed with 10 interview questions about digestion and satiety. Energy compensation (COMPx), which is the ability to adjust food intake in response to a previously ingested food or beverage, was assessed with a preloading protocol. This protocol measured children's intake at ad libitum meals served 20 minutes after receiving either a high- (150 kcal) or low- (3 kcal) energy beverage. COMPx was calculated as a percentage of energy consumed at the test-meal after the high- relative to the low-calorie preloads, such that a score of 100% indicates perfect COMPx and a score above or below 100% indicates undereating and overeating, respectively. Additionally, parents reported child food responsiveness (FR) and satiety responsiveness (SR) on the Children's Eating Behavior Questionnaire at baseline and at follow-up. Knowledge scores increased from 3.6 ± 1.9 to 7.0 ± 2.0 out of 10 ($P < 0.0001$). COMPx also increased from baseline (11.5 ± 110.3) to follow-up (59.2 ± 117.9) ($P < 0.05$), suggesting a shift towards perfect COMPx; however, repeated measures ANOVA showed a sex * condition interaction ($p < 0.01$). Boys significantly increased COMPx from -5.7 to 96.9% ($P<0.001$) while no change was found in girls. Repeated measures mixed models showed a FR x time interaction on COMPx ($P=0.04$); children with higher baseline FR showed greater improvements in COMPx relative to children with lower baseline FR. Further, a trend for a SR x time interaction ($P=0.06$) suggested that children with lower baseline SR showed greater increases in COMPx over time. No significant effects of covariates (BMIz, age and sex) were found. These results suggest that a virtual-reality food intake game, a cost-effective and sustainable delivery model, may improve food intake regulation, although this improvement was moderated by child sex and appetitive traits. These findings may aid in the development of targeted approaches to improve food intake self-regulation in children.

Student Research Lightning Talks: Track B　　　　　　　　　　　　　　　　*Poster #: 11*

Dietary Patterns, Body Mass Index and Lifestyle Factors in Middle Childhood

Matt Cady, Diane Mitchell, Chang Liu, and Jody Ganiban

The identification of dietary patterns via cluster analysis has become a useful method for describing dietary intake. However, little is known about how dietary patterns relate to obesity or lifestyle variables that are associated with obesity, such as physical activity, screen time, and sleep, in children. Children (n=394) aged 7-9 years were recruited from an ongoing prospective adoption study. Parents reported on child height and weight, and completed three 24-hour recalls to assess child diet, sleep, physical activity and screen time. Child dietary patterns were defined using cluster analysis on servings of food subgroups, controlling for caloric intake. Food group and nutrient intakes as well as BMI, sleep, physical activity, and screen time were compared across clusters. Two dietary patterns were identified and labelled as the Grains, Fruits and Vegetable (GFV) Cluster and the Snacks and Sweets (SS) Cluster. Children in the GFV cluster consumed significantly more whole grains, fruits, vegetables, fish, yogurt, nuts and seeds, and eggs and significantly less sweets, fried potatoes, milk, and sugar sweetened beverages (p<.05). GFV children had significantly lower BMI's, less screen time and longer night time sleep durations (p<.05) than SS children. This study identified two dietary patterns in children with one being markedly healthier than the other. Children in the healthier pattern also exhibited a lower BMI and healthier lifestyle factors.

These findings emphasize the need for obesity prevention programs that recognize that children's diets are embedded within an overall healthy behavioral lifestyle.

Child sex moderates the relationship between parent feeding practices and child food intake in 4-6-year-old children
Matt Cady, Catherine Sheehan, and Kathleen Keller

Background: Parents use a variety of practices to encourage a nutritious diet such as pressuring children to eat healthful foods and restricting their access to palatable foods. Details about how these practices relate to child food intake and the role that child sex may play in moderating this relationship remain elusive. This study examined the effect of parental feeding practices on child dietary intake and the role that child sex plays in moderating this relationship. Methods: Fifty-eight 4- to 6-year-old children and one parent took part in two 60-90 minute laboratory visits. Children consumed an ad libitum test meal while parents completed a computerized questionnaire including a food frequency questionnaire to assess child laboratory and usual food intake, respectively. The Child Feeding Questionnaire was used to assess parent feeding practices. Spearman's bivariate correlations were used to assess the relationship between feeding practices and child food intake. The effect of child sex as a moderator of parent feeding practice and child food intake was assessed using hierarchical multiple regression. Results: Restriction was not related to any aspect of test meal intake but was significantly associated with reported snack intake (r= 0.36, p<.05). Pressure to eat was significantly associated with reduced total intake (r= -0.41, p<.01) and reduced intake from high ED foods (r= -0.36, p<.05) at the test-meal. Child sex significantly moderated the effect of both feeding practices on overall lab meal intake, lab intake of high ED foods, and reported sugar-sweetened beverage (SSB) intake (p<.05). For laboratory intake, restriction was related to decreased intake in boys and increased intake in girls, but for reported usual intake of SSBs, the opposite pattern was seen. Pressure to eat was related to decreased lab intake in both sexes but this relationship was more pronounced in boys. Further, pressure to eat was related to decreased reported SSB intake in girls but increased reported SSB intake in boys. Conclusion: These findings show that child sex likely moderates the relationship between parental feeding practices and child food intake. Further research examining how to improve parent feeding practices is needed, as these practices may need to be tailored differently for boys and girls.

Effect of Vitamin D Supplementation During Pregnancy on Blood Pressure
Anita Subramanian, Jill Korsiak, Kellie Murphy, Abdullah Al Mahmud, Daniel Roth, and Alison Gernand

Objectives: To examine the effect of vitamin D supplementation during pregnancy on blood pressure across gestation. Methods: We examined longitudinal blood pressure (BP) measurements within the Maternal Vitamin D for Infant Growth trial, a randomized controlled trial of maternal vitamin D supplementation in Dhaka, Bangladesh. Women (n=1300) were enrolled at 17-24 weeks gestation and randomized to 1 of 5 vitamin D supplementation groups: placebo, 4200 IU/week, 16800 IU/week, 28000 IU/week during pregnancy and placebo from 0-6 months postpartum, or 28000 IU/week during pregnancy and 0-6 months postpartum. BP was measured using an automated digital blood pressure monitor. Two measurements were taken at least one minute apart and a third reading was taken if systolic BP (SBP) or diastolic BP (DBP) measurements differed by >10 mmHg. BP was measured at enrollment, 24 weeks, 30 weeks and weekly from 36 weeks gestation until delivery. Gestational hypertension was defined as SBP ≥140 mmHg or DBP ≥90 mmHg at any point after enrollment. Mixed effect models were used to analyze treatment effect of vitamin D on SBP or DBP across gestation; logistic regression was used to assess relative odds of gestational hypertension. Results: Among 1194 women with complete blood pressure data, the mean (SD) SBP and DBP were 98.7 (9.4) mmHg and 61.9 (7.1) mmHg at baseline; 104 (11) mmHg and 68.1 (9.1) mmHg from after enrollment until delivery. The prevalence of gestational hypertension was 5.2%. The highest dose of vitamin D increased both SBP 1.28 mmHg [95% CI (0.1,

2.3)] and DBP 1.10 mmHg [95% CI (0.1, 2.0) compared to placebo. There was no effect of vitamin D on BP across gestation for the low [SBP 1.09 (-0.1, 2.3) and DBP 0.58 (-0.4, 1.6)] and mid [SBP 0.21 (-1.0, 1.4) and DBP 0.03 (-1.0, to 1.0)] doses compared to placebo. Vitamin D did not impact the odds of gestational hypertension. <u>Conclusions:</u> In a population of women with low vitamin D status and relatively low BP, vitamin D supplementation at the tolerable upper intake level in pregnancy, but not lower doses, resulted in an increase in BP across gestation while not increasing risk of gestational hypertension. These findings do not support a beneficial role of vitamin D in reducing risk of hypertensive disorders of pregnancy.

Student Research Lightning Talks: Track B   *Poster #: 14*

Topographical variation in perceived intensity of multiple bitter stimuli in humans
Molly Higgins and John Hayes
Taste receptors are found throughout the oral cavity, including on the soft palate, pharynx, larynx, and anterior and posterior tongue. Despite widespread and persistent myths of a tongue map, all five commonly accepted taste qualities are sensed all over the tongue. However, modern psychophysical data also suggest there may be more nuanced differences in suprathreshold intensity across loci, especially for bitterness. Here, we test whether bitter stimuli matched for whole mouth intensity differ in perceived intensity across regions of the oral cavity in two experiments. Experiment 1 (n=63) consisted of a whole mouth sip and spit protocol in which participants rated the intensity of 4 intensity matched solutions – sucrose, quinine HCl, sucrose octaacetate (SOA; a GRAS bitterant), and Tetralone (from hops). After orientation to a general Labeled Magnitude Scale (gLMS), they rated overall intensity for 5 different regions: front, middle, back of tongue; roof of mouth; and lip. Temporal effects were explored by obtaining in-mouth and aftertaste ratings. In Experiment 2 (n=48), participants completed a spatial taste test by rating the intensity of Tetralone and quinine HCl after the solutions were painted onto 3 different receptor areas of the tongue (fungiform, foliate, and circumvallate papillae). Information regarding participants' beer consumption frequency and the type of beer commonly consumed (IPA, lager, etc.) was collected at the end of the testing session. In Experiment 1, as expected, the bitter stimuli were rated near moderate on gLMS for all regions that contain taste papillae; the lip, included to control for demand characteristics, showed mean intensities below weak. In ANOVA with region and bitterant (fixed) and panelists (random) for in-mouth data, we observed an interaction of bitterant by region (F(2,1813), p=0.04), suggesting intensity differed across region. This effect was driven entirely by lower ratings for Tetralone on the anterior tongue (p<0.001). Topographical variation in perceived intensity between the compounds may be due to differential expression of TAS2R1, TAS2R14, and TAS2R40 across regions in the oral cavity. An additional temporal effect was observed by comparing the in-mouth and aftertaste intensity ratings for each solution at each locus. Student's t-test results revealed significantly lower aftertaste intensity ratings for all quinine locations except the lip. Reasons for the variance in temporal ratings are unknown but suggest differences in receptor binding or affinity among bitterants. Results of Experiment 2, confirmed the bitterant by locus interaction findings from Experiment 1 as Tetralone was rated lower on the anterior tongue than quinine (p=0.006). Additionally, self-reported beer consumption data revealed a positive association between Tetralone intensity ratings for pale ale consumers and yearly pale ale intake (R2=0.31, p<0.001). This contradiction to the bitter avoidance hypothesis suggests that the bitterness in pale ales from iso-alpha-acids is reinforcing and drives consumption in those who taste Tetralone more intensely.

Student Research Lightning Talks: Track B   *Poster #: 15*

Spice it up! Results of a school-based intervention to increase vegetable intake among rural adolescents
Juliana Fritts, Maria Bermudez, Rebecca Hargrove, Laurie Alla, Clara Fort, <u>Qihan Liang</u>, Terri Cravener, Barbara Rolls, Christopher D'Adamo, John Hayes, and Kathleen Keller
Adolescents do not consume enough vegetables, thus novel approaches to increase intake within school lunch programs are needed. In phase I of this 2-part study, we hypothesized that adding herbs and spices

to common vegetables would increase students' intake compared to when served plain (with oil and salt alone). Over 32 sessions in the school cafeteria, student intake and "choice to eat again" were compared for 8 seasoned and 8 plain vegetable recipes. Intake was assessed by measuring plate waste and student reported "choice to eat again." Two-way ANOVAs testing the effect of condition (plain, seasoned) and age group (middle, high school) found that middle schoolers (11-14 y) ate more plain than seasoned broccoli (P=0.03), cauliflower (P=0.04) and corn and peas (P<0.0001). High schoolers (14-18 y) ate more plain than seasoned green beans (P=0.02) but showed a trend toward higher intake of seasoned black beans and corn (P=0.065). High schoolers also consumed more seasoned vegetables than middle schoolers. A Mantel-Haenszel test found that more students said they would eat five of the vegetables again when they were plain than when seasoned. In phase II, we tested the impact of 5 repeated exposures to 2 seasoning blends (dill and Latin) served on a variety of vegetables during school lunch, on intake and choice to eat again outcomes. Post-exposure, we saw a trend toward higher intake of seasoned broccoli (P = 0.07) and increased percentage of students reporting they would eat seasoned broccoli again (77.9 to 91.5% for middle school, 86.2 to 96.2% for high school, P=0.003). No exposure effects were seen for black beans and corn. These studies show that while younger students may initially favor plain vegetables, seasonings could boost intake long term.   *Poster #: 16*

Hemoglobin Concentration is Associated with Affective Variables in Early Pregnancy
Ruth Adisetu Pobee, Jacob Setorglo, Moses Klevor, and Laura Murray-Kolb

Introduction: Pregnancy is a risk factor to low hemoglobin and negative psychosocial wellbeing. Objective: To examine the associations between hemoglobin concentration, depressive symptoms and anxiety in early pregnancy. Methods: A longitudinal study is ongoing with the goal of determining iron status and psychosocial well-being among pregnant women in Central Region of Ghana. Initial data on 117 women in their first trimester of pregnancy (< 13 weeks) is presented. Data on sociodemographic variables, food security (8-item version of US Household Food Security Survey Module), anxiety (Beck Anxiety Inventory) and depressive symptoms (Center for Epidemiological Studies-Depression Inventory) were collected via questionnaires. Weight and height were measured to determine body mass index; hemoglobin (Hb) concentration was determined using a Hemocue and anemia was defined as Hb < 11 g/dL. Multiple linear regression models were used to determine predictors of depressive and anxiety symptoms and T-tests were run to test for significant differences between groups. Results: The mean age of participants was 27.1 ± 5.2 years, mean body mass index was 24.6 ± 4.8 kg/m2 and mean Hb was 11.2 ± 1.7 g/dL. Most of the women were married (68%) and nearly 31% were primigravida. Food insecurity (FIS) was present among 50% of the households. Using conventional cutoffs, depressive symptoms were exhibited by 49% of the women while 34% exhibited symptoms of anxiety. Anemia was present in 36% of the participants. Regression analyses revealed anxiety (beta = 0.47), hemoglobin concentration (beta = -1.01), not taking iron supplements (beta weight = 3.12), income level (beta = -3.17) and food insecurity (beta = 0.84) as significant predictors of depressive symptoms. Food insecurity (beta = -0.61) and depressive symptoms (beta = 0.66) were the only significant predictors of anxiety. Conclusions: Hb is a significant predictor of depressive symptoms and depressive symptoms are a significant predictor of anxiety in early pregnancy among women in Central Region of Ghana. We will follow these women throughout pregnancy and will track these affective variables to determine if they change as pregnancy progresses to term.   *Poster #: 17*

Plasma Volume, Hydration and Complete Blood Count Across the Menstrual Cycle: Preliminary Results
Sixtus Aguree and Alison Gernand

Background: Blood plasma is a medium for transport of several nutritional biomarkers and could have implications for various physiological conditions. Variation in the total volume of plasma can influence the concentrations of plasma biomarkers and impact the interpretation of clinical findings. Physiological changes across the menstrual cycle make it an ideal model for examining plasma volume changes across time in healthy women. The aim of this study was to examine plasma volume, hydration, hemoglobin,

hematocrit, and mean corpuscular hemoglobin (MCH) across the menstrual cycle in healthy women. Method: Women aged 18-44 years with regular menstrual cycle were recruited into a longitudinal study that involved three visits to the clinical research center. At the first visit, women self-reported their health history and socio-demographic data. Weight, blood pressure and nutritional biomarkers were measured at all three visits: early follicular phase (menses), late follicular phase (estrogen surge) and midluteal phase (progesterone surge). Each woman was provided a Clearblue Fertility Monitor to track her cycle to enable us to determine her estrogen and progesterone surge. We used ATAGO™ digital hand-held urine specific gravity clinical refractometer to measure hydration status. Indocyanine green (ICG) was used as the tracer to measure plasma volume based on dye dilution principle. Baseline blood was collected, after which subjects rested in supine position for 15 minutes, followed by ICG injection and a series of blood draws. Baseline plasma and post-injection plasma were used to measured plasma volume. Baseline whole blood samples were analyzed for complete blood count (CBC) which included hemoglobin concentration, hematocrit and MCH, using a Coulter counter. Data from eight participants were included in this analysis. Results: The mean (SD) age of participants was 25.4 (8.4) years, and BMI was 21.3 (0.6) kg/m2. Women were mostly white, single, nulliparous and college students or graduates. Mean (SD) plasma volume during menses, estrogen and progesterone surge were 2390 (934) mL, 2295 (591) mL, and 2380 (645) mL, respectively. Urine specific gravity was 1.013 (0.008), 1.012 (0.007), and 1.012 (0.009), at visits 1, 2, and 3. Hemoglobin concentrations were 12.2 (0.4) g/dL, 12.1 (0.5) g/dL and 12.2 (0.6) g/dL while that of hematocrit were 37.7 (1.6) %, 37.1 (1.7) %, and 36.7 (1.4)%, at visits 1, 2 and 3 respectively. The MCH was 29.5 (1.4) pg, 29.4 (1.3) pg, and 29.5 (1.6) pg at visits 1, 2 and 3 respectively. Conclusions: These preliminary results showed that plasma volume, hydration status, and CBC related parameters remain relatively constant across the menstrual cycle. The current ongoing study will provide further insight on how these variables change across the menstrual cycle.   *Poster #: 18*

A Brave Neuro World: How deciphering the novel signaling role of macrophage-associated Ron receptor tyrosine kinase activation, can help us remedy the plight of neurodegeneration
Adwitia Dey, Shaneice Nettleford, James Fraser, Amelia Hare, Diana Alnemri, Robert Paulson, K. Sandeep Prabhu, and Pamela Hankey-Giblin
Neurodegenerative disorders, such as Alzheimer's Disease and aging associated dementia, are the leading causes of disease burden globally and are biologically very well characterized by severe central-nervous-system(CNS) inflammation. To date, very little is known about how chronic inflammation develops in the brain, challenging neuroimmune function and in turn regulating neural disease progression. A sentinel group of immune cells, the macrophages or CNS microglia, closely regulate inflammation by taking on different states, classical activated(M1) or alternatively activated anti-inflammatory (M2). The source of inflammation in many neurodegenerative diseases, particularly Alzheimer's has been linked to a decrease in CNS M2 microglial population, associated with NLR family pyrin domain containing 3 (NLRP3) inflammasome activation and interleukin (IL)-1β accumulation in microglia. Our lab studies a transmembrane tyrosine-kinase receptor, Receptor D'Origine Nantais (Ron), which is expressed on tissue resident M2 macrophages including CNS microglia. Our recently published data confirmed that a loss of Ron responsiveness to its ligand, macrophage stimulating protein(MSP), exacerbates disease-mediated neuroinflammation in murine models of multiple sclerosis and diet induced inflammation. These results demonstrated that Ron plays a key protective role in CNS health and homeostasis. However, the underlying cellular mechanism as to how Ron signaling mediates neuroprotection remains to be characterized. Herein, the objective of this study was to evaluate and identify a novel cell signaling pathway underlying Ron mediated neuroprotection, with in vitro assays and in vivo modelling. In the in vitro studies, immortalized human microglial cells (CHME-3) were pretreated or untreated with Ron agonist MSP followed by LPS and ATP stimulation in order to assess for microglial inflammasome activation. MSP-pretreated CHME-3 cells had attenuated inflammation with significant decreases in gene expression and protein levels of interleukin-IL1β following the LPS+ATP challenge. Gene profiling with qRT-pcr revealed MSP-dependent activation of Ron attenuated NLRP3 inflammasome activation with decreased microglial expression of AIM2, NLRP3 and its adaptor ASC and NLRP3 substrates, caspase-1

and Interleukin-IL18. To confirm these in vitro results, we evaluated the role of Ron signaling in an in vivo disease model of chronic neuroinflammation, whereby Apolipoprotein E knockout (ApoE-/-) and Ron receptor ApoE double knockout (DKO) transgenic mice were developed and maintained on a high fat (60% fat) high-cholesterol diet(1.25%cholesterol) (HFHCD) for 18 weeks. DKO CNS exhibited increased protein expression of cyclooxygenase-2(COX-2) and the NLRP3 inflammasome complex. It is known that COX-2 regulates NLRP3 inflammasome-derived IL-1β accumulation, thus this observation was a pivotal confirmation of an upstream regulator in this pathway. The tissue inflammation was associated with increased gene expression of COX-2 effector inducible-nitric oxide synthase (iNOS) and NLRP3 substrates IL1β and IL18. These results elucidate a neuroprotective mechanism of CNS Ron-receptor tyrosine kinase activation induced suppression of NLRP3 inflammasome pathway, leading to decreased caspase-1 and IL-1β accumulation in microglial cells and CNS tissue proper. This is the first study to illustrate a potential mechanism underlying Ron expression in cellular neuroinflammation and has supported on-going studies into the protective role of Ron in amyloidosis and tauopathy. The targeted expansion of this population of Ron expressing M2 macrophages could then be a therapeutic approach to attenuating progressive stages of inflammation exhibited in a spectrum of neurodegenerative disease.
Selected for Invited Student Talk (Session II, 12:15 pm, Room 107)   *Poster #: 19*

Microbiology, Pharmacology, & Immunology

A survey of seasonal persistence of common bacterial and viral pathogens in Jefferson County Beaches
David Narvaiz, Carlo Vanz, Jami Brown, and Ashwini Kucknoor
Exposure to marine recreational waters carrying a variety of human pathogens has been linked to multiple adverse health outcomes. Due to this reason, the recreational marine waters are subjected to regular monitoring of indicator bacterial species (fecal coliforms) by the environmental protection agency. However, there are several other bacteria, protozoa, and viruses that are responsible for more chronic diseases. Vibrio vulnificus is responsible for seafood related infections. Open wound infections resulting from Vibrio vulnificus is a common occurrence during summer months and several cases have been reported from around the South East Texas region. Wound infection results in varied degrees of tissue damage which can require amputation. This study utilized the water samples concurrently collected for the routine beachwatch analysis run by Lamar University Beachwatch program to detect indicator organisms. Water samples were collected weekly during different seasons (spring, summer, fall) from McFadden and Sea Rim beaches in South East Texas. Nucleic acids (both RNA and DNA) were isolated from these samples. Species specific primers were used to detect the presence of Vibrio vulnificus (bacteria), Giardia (protozoa), human adenovirus, human enterovirus, and human norovirus using PCR and RT-PCR methods. The data from all the different samples will be analyzed to see any seasonal variation with the presence or absence of a given type of pathogen.   *Poster #: 20*

Optimization of butyrate production by human fecal communities in the presence of resistant starch
June Teichmann and Darrell Cockburn
A healthy gut microbiome has been linked to prevention of multiple inflammatory related diseases like inflammatory bowel disease, obesity, and colorectal cancer. One of the mechanisms at work is thought to be bacterial production of butyrate, a short chain fatty acid (SCFA) known to provide energy to colon cells and promote apoptosis in cancerous cells, among other benefits. Resistant starch (RS) is an emerging prebiotic that has been shown to modify the SCFA profile in the large intestine. This study uses a human fecal community in a batch fermentation to determine factors that maximize butyrate production in the presence of potato starch (PS), a common source of RS. A preliminary experiment was conducted where a fecal community was given one of 6 carbohydrates (glucose, maltose, amylopectin, digested PS, undigested PS, and digested PS +maltose) then analyzed 24h later via HPLC to determine the SCFA profile. We found that butyrate production was significantly higher among the PS treatments compared to the digestible carbohydrates. In addition, a significant decrease in lactate was observed and an increase in acetate. These results suggest that different fermentation pathways are activated by different carbohydrate sources. Our next experiments will test optimization of the butyrate producing pathways by supplementing our fermenter vessels with additional resistant starch degrading bacteria or purple flesh potato (PFP) polyphenols. Primary degraders are expected to perform the initial digestion of the RS, allowing butyrate producing bacteria access to easily degradable carbohydrates. Polyphenols are a compound of rising consumer interest due to their suggested health benefits. They are naturally present in potatoes and found at especially high levels in PFP. Our research on RS and how to manipulate its effect on bacterial metabolomes can eventually be used to mitigate the illness caused by diseases tied to an unhealthy gut microbiome.   *Poster #: 21*

Investigation for bacteriocin encoding genes in ST73 Escherichia coli strain 0.1229
Hillary Figler, Kakolie Goswami, and Edward Dudley

Introduction: Escherichia coli serotype O157:H7 is a food-borne pathogen. Symptoms vary greatly among individuals, even those infected with the same strain (Bell et al. 1997). Shiga toxin (Stx), one of O157:H7's main virulence factors, is encoded on a phage and released upon induction of bacterial cell lysis (Serna & Boedeker 2008), which can be caused by DNA damage and other mechanisms (Oppenheim et al. 2005). It has been shown that the production of Stx can increase depending on the other bacteria present in the environment (Gamage et al. 2003; Goswami et al. 2015). This research aims to identify novel secreted factors in ST73 strain 0.1229 that can induce Stx2 and worsen O157:H7 infections. Methods: A co-culture protocol was used where an O157:H7 strain, PA2, was grown with the whole cells (16 hours) or cell-free supernatant (8 hours) of each isolate at 37C. One step recombination was used to knock out gene(s) and regions in E. coli strain 0.1229. Whole genome sequencing was done on this isolate using both the Illumina Miseq and PacBio sequencing platforms. Annotations were completed by RAST (Aziz et al. 2008). Results: Thirteen E. coli strains were tested as a co-culture with PA2, five were able to amplify Stx2 production. Of those five, only one strain also amplified Stx2 production in a cell independent manner. This E. coli strain designated 0.1229 produced 33.7 g/mg of Stx2 when co-cultured with PA2 (compared to 6.1 g/mg for PA2 alone) and 33.96 g/mg of Stx2 when PA2 was grown in cell-free supernatant of 0.1229 (compared to 5.51 g/mg for PA2 in LB media). Putative bacteriocin producing genes for microcin B17 (MccB17) were revealed in the E. coli 0.1229 genome, however, knockouts had no differing phenotype, suggesting molecule(s) other than MccB17 are responsible for this phenotype. Treatment of the 0.1229 supernatant with Proteinase K (1mg/ml) had 20-fold decreased Stx2 amplification, suggesting protein involvement. Through sequencing, three plasmids were identified. The 96kb plasmid (p0.1229_2) carries the MccB17 operon and thus is of most interest. Conclusion: From the data, we conclude that 0.1229 produces a Proteinase K sensitive molecule that is able to induce Stx2 production of O157:H7. It is not uncommon for two bacteriocins to be carried on the same plasmid, and in that case, the genes for both tend to be close to each other (Cascales et al. 2007). Therefore, we postulate that p0.1229_2 houses the novel gene(s), presumably adjacent to the mccB17 operon.
Selected for Invited Student Talk (Session II, 12:15 pm, Room 108)   *Poster #: 22*

Vitamin K2 (Menaquinoe-7) Production by Bacillus subtilis natto in Biofilm Reactors using a Glycerol-based Medium
Ehsan Mahdinia, Ali Demirci, and Aydin Berenjian

Vitamin K is an essential factor in human health. It improves heart health, may improve microstructure of bones and recently it was discovered that it has potent antitumor characteristics. Especially menaquinone-7 (MK-7), as the most potent form of vitamin K, has received significant attention, both medically and industrially in recent years. As menaquinones are excreted by many strains of bacteria as an electron transporter, there have been numerous studies specifically concerning MK-7 production. Among these strains, Bacillus subtilis natto seems to hold a key position. On the other hand, Bacillus subtilis, especially in static fermentations, tends to form pellicles and possibly biofilms under suitable conditions for biofilm formation, which promote MK-7 secretion but at the same time create operational and scaling up issues. In this fashion, biofilm reactors seem to be a viable strategy to create a controlled environment for the bacteria to form biofilm formations and simultaneously address operational and scaling up issues through robust agitation and aeration. Thus, in this study, most suitable Plastic Composite Support (PCS) and Bacillus strain combination was selected. Then, Biofilm reactors were constructed and through Response Surface Methodology (RSM) designs, media components and growth conditions were optimized in glycerol and glucose-based media. Furthermore, MK-7 concentrations were enhanced using fed-batch strategies to concentrations as high as 28.7±1.1 mg/L; which is quite comparable with the maximum concentrations retrievable by this strain in static fermentation in McCartney bottles.
Student Research Lightning Talks: Track A   *Poster #: 23*

Plasmodium falciparum Falcipain-2a Polymorphism in Southeast Asia and Its Potential Contribution to Artemisinin Resistance
Faiza Siddiqui, Mynthia Cabrera, Meilian Wang, Awtum Brashear, Karen Kemirembe, Zenglei Wang, Jun Miao, Thanat Chookajorn, Zhaoqing Yang, Yaming Cao, Gang Dong, Philip Rosenthal, and Liwang Cui

Falcipain-2a (FP2a; PF3D7_1115700) is a Plasmodium falciparum cysteine protease and hemoglobinase. Functional FP2a is required for potent activity of artemisinin, and in vitro selection for artemisinin resistance selected for a FP2a nonsense mutation. To investigate associations between FP2a polymorphisms and artemisinin resistance and to characterize the diversity of the enzyme in parasites from the China-Myanmar border, we sequenced the full-length FP2a gene in 140 P. falciparum isolates collected during 2004-2011. The isolates were grouped into eight different haplotype groups. Haplotype group I appeared in samples obtained after 2008, coinciding with implementation of artemisinin-based combination therapy in this region. In functional studies, compared to wild-type parasites, the FP2a haplotypes demonstrated decreased ring survival, and all haplotype groups exhibited significantly reduced FP2a activity, with group I showing the slowest protease kinetics and reduced parasite fitness. These results suggest that altered hemoglobin digestion due to FP2a mutations may contribute to artemisinin resistance.

Student Research Lightning Talks: Track A   *Poster #: 24*

AmotL1 acts as an adapter that links paramyxovirus M protein with ESCRT machinery
Sabahat Gazal, Zifei Pei, Greeshma Ray, Phuong Schmitt, and Anthony Schmitt

Enveloped viruses spread infections through particles that bud from infected cell membranes. The late steps leading up to membrane fission and particle release are accomplished in many cases through manipulation of cellular Endosomal Sorting Complex Required for Transport (ESCRT) machinery that is recruited to viral assembly sites by late domains. For many of the negative strand RNA viruses including rhabdoviruses, filoviruses, and arenaviruses, PPXY late domains within viral matrix proteins are used to recruit WW domain containing NEDD4 family E3 ubiquitin ligases for budding. Paramyxovirus matrix proteins lack the late domain sequences used by other enveloped viruses for budding, including PPXY. Nonetheless, ubiquitin and ESCRT recruitment appears to be important for budding of many paramyxoviruses. We identified angiomotin-like 1 (AMOTL1) in a screen for host factors that bind to the M protein of parainfluenza virus 5 (PIV5). This protein harbors three L/PPXY sequences, allowing it to interact with WW domain containing proteins including NEDD4 family members. We hypothesize that paramyxoviruses use AMOTL1 as a linker to indirectly recruit the same WW domain containing NEDD4 ubiquitin ligases for budding that other enveloped viruses recruit directly through their PPXY late domains. In support of this hypothesis, we found that AMOTL1 (but not AMOT or AMOTL2) could link together M proteins and NEDD4 family proteins in three-way co-IP experiments. The M-binding activity of AMOTL1 was mapped to an 83-amino acid region, and overexpression of M-binding AMOTL1derived polypeptides severely inhibited the budding of PIV5 and mumps virus. Together, these results define a novel host factor recruitment strategy used by paramyxoviruses to achieve particle release.

                                                                                         Poster #: 25

Delivery of Functional Proteins into Mammalian Cells via Paramyxovirus-like Particles
Santosh Panthi, Phuong Schmitt, Greeshma Ray, and Anthony Schmitt

Paramyxovirus nucleocapsid (N or NP) proteins encapsidate viral RNA genomes to form viral ribonucleoproteins (RNPs). Interactions between NP components of RNPs and viral matrix (M) proteins propel the generation of genome-containing infectious virus particles. M-NP interaction also stimulates efficient production of virus-like particles (VLPs) for parainfluenza virus 5 (PIV5) and mumps virus. We have previously elucidated that paramyxovirus NP proteins harbor short, DxD-containing sequences near their C-terminal ends that can be transplanted onto the C-terminal ends of foreign proteins, allowing the

foreign proteins to participate in viral assembly and package efficiently into VLPs. Using this strategy, we demonstrate here the generation of PIV5, mumps, and Nipah VLPs incorporating enzymatically active cargo proteins, including Renilla Luciferase (RLuc), superoxide dismutase (SOD), and green fluorescent protein (GFP). The cargo-loaded VLPs are capable of delivering biologically active proteins to target cells, e.g. delivery of SOD to reverse cellular oxidative stress. Also, we show that NLS (nuclear localized sequence)-bearing cargo can be successfully packaged into VLPs and subsequently delivered into the nuclei of target cells. These studies demonstrate the high degree to which paramyxovirus genome packaging interactions can be manipulated to create a flexible platform for protein delivery.

Poster #: 26

The Structure of the Transferrin Receptor:Canine Parvovirus Complex Reveals how the Interactions Control Viral Host Range
Hyunwook Lee, Heather Callaway, Colin Parrish, and Susan Hafenstein
Canine parvovirus (CPV) infects canids and can cause acute hemorrhagic enteritis and myocarditis in dogs. CPV utilizes cellular transferrin receptor (TfR) to bind, enter, and infect target cells, and species-specific binding to TfR controls viral host range. Until now, the interaction between CPV and TfR has been extensively studied by mutational and biochemical analyses, however, a structural analysis for the CPV-TfR complex has been remained at a low-resolution. To investigate the virus-receptor interaction at a high-resolution, we incubated CPV with TfR isolated from black-backed jackal and performed cryo-EM single particle analysis accompanied by a state-of-art instrumentation and technology. An icosahedral 3D reconstruction generated a near atomic resolution map for the capsid structure and allowed us to build an atomic model of the capsid. Symmetry-mismatch reconstruction and localized reconstruction methods revealed an asymmetric structure of the CPV-TfR complex and identified precise binding residues on both molecules. Unexpectedly, the purified TfR formed complexes with transferrin (Tf) molecules introduced from cell culture media and presented CPV-TfR-Tf complexes. Further analysis showed that up to twelve TfR-Tf complex molecules can bind to the viral surface and that each interaction varies slightly for the binding angle between CPV and TfR and subsequently for the binding residues. Our results summate the previous studies and provide a new insight into the host change mechanism of CPV.

Poster #: 27

Molecular Biology, Genetics, & Chemistry

Contribution of kinesin-5 mediated microtubule stability reveals its functions in mitotic spindle size regulation

Geng-Yuan Chen and William Hancock

Besides sliding apart antiparallel microtubules during spindle elongation, the mitotic kinesin-5 Eg5 promotes tubulin assembly, revealing its importance in mitotic spindle length control. Here, we characterized the Eg5-mediated microtubule dynamics with respect to tubulin-tubulin contacts. Eg5 motor acts as a "staple" to stabilize tubulin-tubulin longitudinal bonds at physiological relevant concentrations, but saturating monomeric Eg5 is sufficient to promote microtubule growth, suggesting a native tetrameric Eg5 also being a proficient microtubule polymerase. Eg5 motor domain favors tubulin straight conformation, which is opposite to depolymerizing kinesins MCAK and Kip3. Furthermore, the "intra-dimeric wedge" probes that stabilize tubulin in kinked conformation antagonize Eg5-binding in a non-competitive manner, and Eg5-tubulin complex diminishes this intra-dimeric probing. The motor affinity-driven tubulin assembly is additionally substantiated by our identification of the essential Switch-II domain that modulates gliding speed, end binding, and polymerase activities. Thus, we propose a microtubule polymerase mechanism in which Eg5 at the plus-end promotes lattice curved-to-straight transition to coalesce lateral bonds that is converse to the conventional tubulin curvature-sensing features of microtubule depolymerizing kinesins.

Student Research Lightning Talks: Track C   *Poster #: 28*

Inborn errors in purine metabolism result in neuromuscular deficits: A comparative metabolic approach

Latisha Franklin and Wendy Hanna-Rose

Errors in purine metabolism result in distinct neuromuscular phenotypes. However, the mechanism behind a perturbation to purine metabolism and the resulting suboptimal muscle function is unknown. I am using a comparative metabolic approach to bridge this gap in knowledge. Purine metabolism includes a series of catabolic and anabolic reactions in de novo synthesis, the purine nucleotide cycle (PNC), and salvage synthesis cycle to synthesize purines such as adenosine (AMP) and guanosine (GMP). These are essential components of our DNA as well as building blocks for biomolecules, such as ATP. Perturbations in purine metabolism, specifically to de novo synthesis and the PNC, result in distinct phenotypes. The conservation of purine metabolism between humans and Caenorhabditis elegans affords a powerful model organism that enables us to study, in vivo, properties of inborn errors in purine metabolism. C. elegans with impaired expression of adsl-1, a bifunctional enzyme in de novo synthesis and the PNC, results in muscle dysfunction caused by SAICAR accumulation. Interestingly, muscle dysfunction is also observed with impaired expression of adss-1, an enzyme in the PNC. Based on preliminary experiments, I hypothesize the cause of muscle dysfunction in adsl-1(RNAi) animals is distinct from that of adss-1(RNAi) animals. I use RNAi to reduce gene expression of adsl-1 and adss-1 and liquid chromatography couple to mass spectrometry to quantify metabolites present within the C. elegans. Targeted metabolic analysis of adsl-1 (RNAi) animals show no change in purine levels, while analyses of adss-1(RNAi) animals show varying amounts of purines. At the physiological level, decreased function of adss-1 results in muscle deficits with phenotypes similar to those seen in adsl-1(RNAi) animals. However, at the metabolic level, the decreased function of adss-1 reduces the formation of S-AMP and a shift in the salvage synthesis pathway increases GMP and its related substrates, while lack of adsl-1 causes increased SAICAR. I conclude the physiological effects seen in specific inborn errors of purine metabolism are caused by distinct metabolic changes. I have employed a combination of genetic manipulation using RNAi and metabolic analysis using liquid chromatography/mass spectrometry (LC/MS) as a method to characterize metabolic changes.   *Poster #: 29*

Human mitochondrial transcription investigated by in-vitro transcription assays and high-resolution Atomic Force Microscopy

Akira Uchida, Divakaran Murugesapillai, Markus Kastner, Yao Wang, Maria Lodeiro, Shaan Prabhakar, Guinevere Oliver, Jamie Arnold, L. James Maher III, Mark Williams, and Craig Cameron

Human mtDNA contains three promoters, suggesting a need for differential expression of the mitochondrial genome. Studies of mitochondrial transcription have used a reductionist approach, perhaps masking differential regulation. Here we evaluate transcription from light-strand (LSP) and heavy-strand (HSP1) promoters using templates that mimic their natural context. These studies reveal sequences upstream, hypervariable in the human population (HVR3), and downstream of the HSP1 transcription start site required for maximal yield. The carboxyterminal tail of TFAM is essential for activation of HSP1 but not LSP. Images of the template obtained by atomic force microscopy show that TFAM creates loops in a discrete region, the formation of which correlates with activation of HSP1; looping is lost in tail-deleted TFAM. Identification of HVR3 as a transcriptional regulatory element may contribute to between-individual variability in mitochondrial gene expression. The unique requirement of HSP1 for the TFAM tail may enable its regulation by post-translational modifications. *Poster #: 30*

Automated Design and Characterization of 4350 Highly Non-Repetitive E.coli Promoters using the Non-Repetitive Parts Calculator

Ayaan Hossain, Alexander Reis, Sean Halper, Daniel Cetnar, and Howard Salis

Synthetic biologists are facing new challenges as we endeavor to engineer ever larger genetic systems. Characterized genetic part toolboxes are often too small for large projects, forcing us to re-use the same or similar part in several locations. Designed constructs therefore contain repetitive DNA sequences which remain difficult to synthesize with state-of-the-art DNA synthesis approaches and are unstable in hosts with homologous recombination activity. To solve this challenge, we developed an automated design algorithm, the Non-Repetitive Parts (NRP) Calculator, to design non-repetitive sequence variants of a desired genetic part that do not share repeats above a threshold length L, dictated by the system construction and host specifications. Input to the algorithm is a constraint that ensures the design of functional non-repetitive parts, which can be a degenerate sequence, a proscribed RNA structure, and/or a quantitative model of part function. Our benchmarks show that the NRP Calculator can generate over 100,000 non-repetitive (L = 10), 100 bp long parts in less than 10 minutes. We demonstrated the NRP Calculator by designing and characterizing three large toolboxes of non-repetitive (L = 10) σ70 E. coli promoters for synthetic biology applications. The first toolbox contains 800 non-repetitive strong promoters, each with a consensus -35 and -10 hexamer, the second toolbox contains 3500 non-repetitive promoters of varied strengths, containing -35 and -10 hexamers that deviate from the consensus by 0 to 6 mismatches, and the final toolbox contains 50 weak promoters with 12 mismatches in the hexamer. We measured the transcription rates of these 4350 new promoters using chip-based oligo pool synthesis and a massively parallel reporter assay in E. coli NEB 5α, followed by DNA-Seq and RNA-Seq measurements. Overall, the Non-Repetitive Parts Calculator promises to deliver a cornucopia of rationally designed genetic parts that can all be simultaneously combined to build extremely large genetic systems, powering the future of synthetic biology.

Student Research Lightning Talks: Track C

Characterizing locus-specific nuclear relocalization between cell types

Lila Rieber and Shaun Mahony

Chromosome conformation varies in a cell-type specific manner, but the specific loci that drive this variation have not been identified. Existing methods for comparing chromosome conformation data can identify differential looping but cannot identify specific loci that relocalize within the nucleus between cell conditions. We developed a method to jointly infer 3D chromosomal structures using Hi-C data from two experiments, revealing the structural differences between the datasets. By applying the method to Hi-C data from different cell types, we quantified the degree to which cell-type-specific structural changes occurred along the A/B compartment axis, representing the nuclear interior/nuclear periphery axis. We

found that the majority of changes occurred along this axis, demonstrating the importance of lamina-associated repression in cell type identity. Focusing on changes within the A compartment, we found that loci that undergo compartment-independent changes were enriched for super-enhancers in one or both cell types. This suggests that spatial positioning is related to the cell-type-specific activity of super-enhancers.   *Poster #: 31*

Targeted delivery of CRISPR-associated endonuclease 9 (Cas9) into insect ovaries for heritable germ line gene editing
Duverney Chaverra-Rodriguez, Vanessa Macias, Grant Hughes, Sujit Pujhari, Yasutsugu Suzuki, David Peterson, Donghun Kim, and Jason Rasgon
Cas9-mediated gene editing is a powerful tool for addressing research questions in arthropods. Current approaches rely upon delivering Cas9 ribonucleoprotein (RNP) complex to arthropod eggs by embryonic microinjection. However, embryonic microinjection is challenging, is limited to a small number of species, and is inefficient even in optimized taxa. We have developed a technology termed Receptor-Mediated Ovary Transduction of Cargo (ReMOT Control) to specifically deliver Cas9 RNP to the insect germline by injection into adult females. We identified a peptide ("P2C") that mediates transduction of Cas9 RNP from the female hemolymph to the developing germline, resulting in heritable gene editing of the offspring. We demonstrate that the P2C peptide can deliver EGFP protein into the ovaries of 6 mosquito species across 3 genera. When P2C is fused to Cas9, complexed with an appropriate guide RNA, and injected into Aedes aegypti females, gene-editing efficiency is as high as 0.3 mutants per injected female. Since nutrient uptake by receptor-mediated endocytosis into the germline is conserved across oviparous animals, this technology may be widely applicable in different oviparous species if the proper ligand-receptor couple is used. Once optimized for multiple species, ReMOT Control may dramatically change the landscape of molecular entomology research, allowing easy, flexible genetic manipulation of a wide variety of vector arthropods and non-model species.
*Selected for Invited Student Talk (Session I, 11:45 am, Room 107)

A Tale of two species: How different genetic mechanisms drive parallel color variation in mimetic bumble bees
Sarthok Rahman, Li Tian, Briana Ezray, and Heather Hines
Bumble bees exhibit diverse segmental color patterns driven largely by convergence onto local mimicry patterns. To understand the genetic and developmental mechanisms underlying this adaptive diversification, we have utilized an integrative and comparative genomics approach. Utilizing state-of-the-art bioinformatic approaches such as Genome-wide Association Studies (GWAS), we have identified a narrow locus driving a red/black abdominal hair color polymorphism in the mimetic bumble bee species, Bombus melanopygus. This ~4 kilobases candidate region is located in a regulatory region of the abdominal Hox genes, abd-A and abd-B, major developmental genes that are highly evolutionarily conserved across arthropods. Results from quantitative PCR assays indicate that the expression pattern of abd-A is changed in pupal epidermal tissues to impart this color variation. Interestingly, genotyping of the same locus in co-mimicking species revealed that none of the genetic changes associated with color variation in Bombus melanopygus are correlated with the red/black color switch in other species as it suggests that they acquired the same color patterns as B. melanopygus in a convergent manner. Using independent GWAS, we discovered the possible involvement of a set of alternative loci that drive parallel color variation in co-mimicking species, Bombus bifarius. Taken together, these data suggest that varied mutations across different parts of the molecular pathway as opposed to sorting of ancestral polymorphisms might be driving this variation. Our research provides novel insights into how the genome landscape is modified under adaptive diversification as it also reveals the intricate processes involved in pigmentation and Hox gene regulation.
Student Research Lightning Talks: Track C

Extensive sequence divergence of trans-species active small RNAs between the parasitic plants Cuscuta campestris and Cuscuta gronovii
Nathan Johnson, Tamia Phifer, and Michael Axtell
Cuscuta is a genus of vine-like parasitic plants which constrict and invade the stems of host plants, forming a symplastic interface through a specialized organ called a haustorium. Water, photosynthate, protein, and nucleic acids readily transit this interface, making it a theater of competition between the host and parasite. We recently showed that Cuscuta campestris exerts influence on the host through this connection, producing a cohort of miRNAs that down-regulate target Arabidopsis thaliana genes with roles in development, defense, and the phloem. The discovery of this exciting form of parasitic effector led us to investigate if these miRNAs are produced by a second species of Cuscuta, C. gronovii. We performed sRNA sequencing on C. gronovii attachments to A. thaliana, sampling both the parasite-host haustorial interface and adjacent tissues in both plants. Analysis revealed over 200 C. gronovii small RNAs which are up-regulated in the interface. Most were 21 or 22 nucleotides in length, sizes consistent with that of most known plant microRNAs. Surprisingly, none of these haustorially-induced C. gronovii small RNAs were identical in sequence to our previously identified set of C. campestris haustorially-induced microRNAs. We identified several A. thaliana mRNAs that were targeted by induced C. gronovii small RNAs based on complementarity and induced secondary siRNA accumulation during parasitism. Verified targets of induced C. gronovii small RNAs include MPK3, which encodes a kinase implicated in plant defense responses, and MYB103, which encodes a transcription factor involved in cell-wall biosynthesis. Interestingly, one confirmed A. thaliana mRNA target was shared between C. campestris and C. gronovii: SEOR1, which encodes a P-protein which affects leakage of sugars after wounding. However, the SEOR1-targeting small RNAs from C. campestris differ substantially from those of C. gronovii in sequence. We conclude that trans-species active small RNAs are present and functional in both of the Cuscuta species we've examined to date, but that their sequences have diverged substantially. This raises the hypothesis that trans-species active small RNAs may be a common but quickly evolving feature within the Cuscuta genus.
Student Research Lightning Talks: Track C   *Poster #: 32*

Comparison of Detection Modes for Segmented Flow Droplets
Alexander Kaplintz, Jonathan Maturano, Melanie Padalino, Jeremy Decker, and James Grinias
The miniaturization of analytical methods through microfabrication techniques allows for reduced sample sizes and analysis cost. Integrating multiple laboratory functions on a single device will ultimately allow the lab to be brought to the sample, circumventing the need for conventional methodology. The goal of this project is to investigate the use of segmented droplet microfluidic techniques to achieve these benefits for targeted chemical assays. Forming segmented flow droplets is an essential step in conducting these analyses and the data collected suggests that multiple methods can be used to both effectively generate and detect droplets. An immiscible dual-phase system of an aqueous solution and perfluorodecalinoil was used in conjuction with a T-junction to form mobile droplets. Infusion and withdrawing techniques for droplet formation were studied using a syringe pump and vacuum, respectively. Fluorescence measurements using an epifluorescence microscope followed by data analysis via ImageJsoftware gave high quality results for tracking light intensity levels in droplets of rhodamineB at a wide range of concentration levels. Miniaturized absorbance detection utilizing a light emitting diode (LED) also proved successful for UV-absorbing compounds, although the detection limits were higher than with fluorescence microscopy. Implementing these methods of droplet formation and detection in future experiments will allow for efficient and successful chemical separations and bioassays for medical diagnosis.   *Poster #: 34*

Plant & Agricultural Sciences, Zoology & Ecology

Pollination Services and Colony Abundance of Bombus impatiens
Carley McGrady, James Strange, and Shelby Fleischer
Our recent work suggests that the common eastern bumble bee, Bombus impatiens, can provide up to 1,275% of required pollination services for commercially produced pumpkins in Pennsylvania. However, B. impatiens pollination activity declines as commercial pumpkin field area increases. It was previously unknown if this decline was simply a result of forager dilution across larger areas of floral resources, or instead evidence of pollinator population declines due to negative effects of agroecosystems. For eusocial bumble bees, measures of colony abundance and density can provide valuable insights unobtainable through forager census alone. In 30 commercial pumpkin fields across 3 distinct regions of Pennsylvania, we recorded the size of each field and estimated the number of colonies sending foragers into each field using genetic analysis. In a subset of 21 fields, we measured B. impatiens pollination services as the rate of bee visits to pumpkin flowers in 45 second observations. Based on these data, we found that pumpkin field area has no relationship with colony abundance, but field area does have a significant, negative effect on colony density, indicating that foragers are being diluted across larger amounts of floral resources. In an effort to maintain pollination services in managed and natural ecosystems, research and management practices are often focused on understanding and promoting colony abundance. However, the relationship between colony abundance and ecosystem services was previously unknown. We found a positive relationship between the density of colonies foraging in a given field and pollination visits provided by individual foragers. This is the first empirical evidence demonstrating that colony abundance, mediated by field size, has a direct impact on pollination services in commercial agroecosystems. Governments, NGOs and academic institutions worldwide have called for careful monitoring of native pollinators. We established a baseline for a currently common species such that subsequent researchers could track responses to environmental change and other stressors in the future. We found an average of 543.7 + 21.7 SE colonies visiting a single pumpkin field, and furthermore, average colony abundance did not change across 4 years nor 3 geographic regions, indicating an abundant and stable wild B. impatiens population in Pennsylvania.   *Poster #: 33*

*Fiber-resolution visualization of plant primary cell wall by fluorescently tagged cellulose binding protein
Xuan Wang, Sarah Kiemle, Sarah Pfaff, William Chase, Edward Wagner, Liza Wilson, and Daniel Cosgrove
Cellulose, in the form of microfibrils, bundles together and forms web-like structures serving as the foundation of plant primary cell walls. Dicot cell walls are rich in pectin and hemicellulose which fills the interfibrillar space and mediates interactions between cellulose microfibrils (CMFs). By encapsulating the plant cell, the cell wall mechanically maintains the shape of the highly turgid protoplast while allowing for substantial volume increase during cell enlargement. The dynamics of cellulose microfibril rearrangement is hypothesized to be the key regulator mediating cell expansion. Attempts have been made to investigate this mechanism by studying the architecture of plant primary cell walls, particularly the arrangement of CMFs. The use of atomic force microscopy (AFM) and scanning electron microscopy has yielded direct detection of CMF arrangement at the nanometer scale. These nanoscale assessments enable the visualization of individual CMFs and CMF bundles arranged in crossed polylamellate structures in the primary cell wall. However, these subcellular measurements often examine a small area (~1%) with respect to the whole cell, and thus, the acquired information has limited viability when attempting to predict whole-cell effects. In this study, a fluorescently-tagged cellulose binding protein, carbohydrate binding module 3 (CBM3), was tested for its ability to label CMFs for facile assessment of cellulose arrangement at the cellular scale. By binding fluorescently-tagged CBM3s to isolated onion primary wall, we were able to detect fibrillar staining pattern on the exposed cell wall surface. The

fibrillar patterning observed with CBM3 labeling was consistent with AFM-detected CMF orientation, confirming that CBM3 staining patterns are authentic detections of CMFs. Visualization of cell wall at this scale enabled us to reveal that CMFs within each cell are distributed anisotropically, yet each individual cell displays a unique, dominant CMF orientation. This result provides the first high-resolution image evidence for how CMF orientation is able to determine the shape and growing direction of plant cells. Moreover, the detection of CMFs by CBM3 is conserved among different cell types and various dicot species including cucumber hypocotyl, celery parenchyma, and Arabidopsis leaf epidermis. Interestingly, CBM3 binding to onion walls is pH-dependent, showing the highest detectable signal at pH 4 and significantly reduced CBM3 binding at pH values higher than 7.5. It is hypothesized that protonation of cell wall pectin at low pH reduces the interactions between pectin and cellulose in the wall matrix, thereby exposing cellulose surfaces for CBM3 binding. This hypothesis was partly supported by enzymatic removal of pectin which substantially enhanced CBM3 binding at neutral pH. The use of fluorescently-tagged CBM3 as a cellulose visualization probe enables the characterization of cellulose organization at the whole-cell level. This technique would be a useful approach in assessing the dynamics of CMF rearrangement during cell wall expansion in both wild-type and mutant Arabidopsis plants with disrupted cellulose organization. We also demonstrated that CBM3 being a promising molecular probe for the assessment of cellulose accessibility which may potentially benefit the study of cellulose digestibility for improved biofuel production.
Selected for Invited Student Talk (Session I, 11:45 am, Room 108)

Effects of immune challenge on bumblebee thermoregulatory capacity
Hannah Stewart and Ruud Schilder
Bumblebees are extremely important pollinators; however, their populations are in decline. One potential contributor to this decline is parasitic infection. Infections induce an immune response, which is an energetic drain on the infected organism. Energy is required for many biological processes, and when infected, many organisms demonstrate an energetic tradeoff with such processes, notably reproductive output. In the case of a bumblebee colony, only the queen acts as a reproductive unit, and reproductive tradeoffs when infected have been noted. However, the success of a colony depends on not only the queen, but also on the workers. As workers are not the primary reproductive unit, tradeoffs may manifest in other vital biological processes. Here I demonstrate a tradeoff between immune system activation and thermoregulatory capacity, a trait essential to a bee's ability to fly and forage, as well as their ability to incubate developing larvae. Immune-challenged bumblebee workers enter into heat stupor and heat-induced death quicker than healthy controls. Immune challenged bumblebees also are unable to recover from chill coma as quickly as healthy controls and have a lower resting temperature after 30 minutes of treatment. This reduced thermoregulatory capacity of worker bumblebees in the face of an immune challenge will likely negatively impact colony health.
Student Research Lightning Talks: Track C   *Poster #: 35*

Comprehensive Analysis of RDR-independent Small RNAs in Arabidopsis thaliana
Seth Polydore and Michael Axtell
Plant small RNAs modulate key physiological mechanisms through post-transcriptional and transcriptional silencing of gene expression. sRNAs fall into two major categories: those that are reliant on RNA Dependent RNA Polymerases (RDRs) for biogenesis and those that aren't. Known RDR1/2/6-dependent sRNAs include phased and repeat-associated short interfering RNAs, while known RDR1/2/6-independent sRNAs are primarily microRNAs and other hairpin-derived sRNAs. In this study, we produced and analyzed small RNA-seq libraries from rdr1/rdr2/rdr6 triple mutant plants. We found 58 previously annotated microRNA loci that were reliant on RDR1, -2, or -6 function, casting doubt on their classification. We also found 38 RDR1/2/6-independent small RNA loci that are not MIRNAs or otherwise hairpin-derived, and did not fit into other known paradigms for small RNA biogenesis. These 38 small RNA-producing loci have as of yet undescribed biogenesis mechanisms, and are frequently

located in the vicinity of protein-coding genes. Altogether, our analysis suggests that these 38 loci represent one or more undescribed types of small RNAs in Arabidopsis thaliana. *Poster #: 37*

Arthropod Response to Organic Cover Crop-Based Reduced-Tillage Cropping Systems
Karly Regan, Christina Mullen, and Mary Barbercheck

Reducing tillage can benefit agroecosystems by building soil health, conserving fuel, and promoting biodiversity. In agricultural systems, arthropods can play both a negative role, as pests, and a positive role, as predators and parasites of pest arthropods. Here, we report the effects of soil and cover crop management on pest herbivores in an organic corn production system. The experiment is comprised of four management systems in a feed grain rotation that varied in preceding and in-season cover crop management and tillage. We compared cover crop mixtures of hairy vetch (Vicia villosa) and triticale (Triticale hexaploide) with red clover (Trifolium pratense) and timothy (Phleum pratense). One of the vetch/triticale systems was managed with a roller-crimper and no-till planted, while the cover crops in the other three systems were mowed and tilled in before planting corn. In the tilled hairy vetch system, and one of the red clover systems, plots were interseeded with an annual ryegrass (Lolium multiflorum) and forage radish (Raphanus sativus) mixture in early July. Crop damage from common pests was assessed shortly after corn emerged. Additionally, corn was inspected later in the season for damage from caterpillar pests including European corn borer (Ostrinia nubilalis) and corn earworm (Helicoverpa zea). The intensity of damage was similar in all systems, as was late season damage. However, the prevalence of specific types of damage varied by system early in the season. Ongoing research is investigating the arthropod predator community and its role in suppressing pest populations in these management systems. *Poster #: 38*

Rice roots for a food secure future: Investigating the physiology and genetics of rice root anatomical traits for drought tolerance
Jenna Reeger, Lauren Sarko, and Kathleen Brown

Rice feeds over half of the world's population every day, and because of its semi-aquatic nature, rice is very susceptible to yield loss under drought stress. Anatomical root traits such as metaxylem, the water conducting vessels in plants, and aerenchyma, hollow air spaces in the root cortex, could be optimized to improve drought tolerance in rice. Fewer, smaller metaxylem vessels may be beneficial under drought by reducing root hydraulic conductance and therefore increasing water use efficiency. More aerenchyma may be beneficial by decreasing the metabolic cost of root per unit length, providing roots excess energy to increase deep root growth. Studies are being conducted to determine relationships between anatomical root traits and plant performance under drought. Greenhouse drought experiments conducted on a recombinant-inbred population of rice have shown significant effects of metaxylem area (p-value < 0.001) and aerenchyma area (p-value < 0.001) when used as factors in a step-wise linear model ($R2 = 0.54$) of plant biomass under drought stress. In addition, genetic studies validating candidate genes' impacts on anatomical trait development are under way. Metaxylem area candidate genes have been identified from a genome-wide association study conducted on a subset of Rice Diversity Panel 1 (RDP1) lines and are being studied in homologous Brachypodium mutant lines. *Poster #: 39*

Harnessing nature: The multi-functional role of Metarhizium as a plant protectant
Imtiaz Ahmad, Brianna Flonc, Christina Mullen, Mary Barbercheck, Dawn Luthe, and Maria Jimenez-Gasco

Recent studies have revealed that many insect-pathogenic fungi, including Metarhizium (Hypocreales: Clavicipitaceae), are also endophytes that can benefit their host plant through plant-disease antagonism and plant growth promotion. Metarhizium is a commonly occurring insect-pathogenic fungus that can establish endophytic relationship with a variety of plants. My research focuses on the molecular and physiological aspects of plant-Metarhizium-insect interactions. Translation elongation factor (TEF) sequencing of 130 Metarhizium isolates from soil indicates that the dominant species at our research sites is M. robertsii. Moreover, in field experiments, cover crop diversity was not related to Metarhizium

species diversity. In greenhouse experiments, endophytic colonization of M. robertsii was greater in maize (90%), than in Austrian winter pea (62.5 %), canola (52 %) and cereal rye (50%) plants grown from seeds exposed to a spore suspension of M. robertsii. Re-isolation of M. robertsii from exposed plants was more frequent from roots than from leaves in all crop plants. Endophytic colonization resulted in greater plant height of maize, Austrian winter pea and cereal rye compared to control plants. Similarly, the above-ground biomass of M. robertsii-colonized maize, Austrian winter pea, and canola plants was greater than for plants grown from unexposed seed. In detached-leaf feeding bioassays, the relative growth rate of 2nd instar black cutworm (Agrotis ipsilon) was lower than when feeding on corn leaves from M. robertsii-colonized plants compared to non-treated control plants. My future research goals focus on determining the role of endophytic Metarhizium in plants on Cochliobolus heterostrophus, the causative agent of southern corn leaf blight, and the effects of endophytic M. robertsii on the regulation of gene expression in plants. These newly emerging, but not yet fully understood, ecological roles hint at the potential for the further development of Metarhizium as an inundative biopesticide and protective seed coating. *Poster #: 40*

Resonant soft X-ray scattering reveals cellulose microfibril spacing in onion cell wall
Dan Ye, Sarah Kiemle, Sintu Rongpipi, Xuan Wang, Cheng Wang, Daniel Cosgrove, Esther Gomez, and Enrique Gomez
Cellulose microfibrils are crucial for many of the remarkable mechanical properties of primary cell walls. Nevertheless, many structural features of cellulose microfibril organization in cell walls are not yet fully described. Microscopy techniques provide direct visualization of cell wall organization, and quantification of some aspects of wall microstructure is possible through image processing. Complementary to microscopy techniques, scattering yields structural information in reciprocal space over large sample areas. Using the onion epidermal wall as a model system, we introduce resonant soft X-ray scattering (RSoXS) to directly quantify the average interfibril spacing. This is achieved through the preferential binding of calcium ions to homogalacturonan in the pectin matrix, which enhances the scattering contrast between cellulose and pectin. Taking advantage of enhanced scattering contrast near the calcium L-edge, RSoXS shows the average center-to-center distance between cellulose microfibrils or microfibril bundles to be about 20 nm. *Poster #: 41*

Management practices and age cohorts that contribute to increased Peste des petits ruminants seroprevalence in sheep, goats, and cattle in northern Tanzania
Catherine Herzog, William de Glanville, Brian Willett, Tito Kibona, Isabella Cattadori, Vivek Kapur, Peter Hudson, Joram Buza, Sarah Cleaveland, and Ottar Bjørnstad
Peste des petits ruminants virus (PPRV) causes a contagious disease of high morbidity and mortality in global sheep and goat populations and has, at least following eradication of rinderpest, been shown to elicit seroconversion in cattle. PPRV, a Morbillivirus in the same genus as rinderpest virus and human measles virus, is spread by direct contact with infected hosts, aerosols, or fomites. PPRV has spread to more than 70 countries in Asia, the Middle East, and Africa. PPRV threatens 80% of the global small ruminant population of nearly 2 billion animals. Over 330 million farmers' livelihoods rely directly on small ruminants and the demand for meat and milk is expected to rise 137-177% by 2030. Globally, losses due to PPRV affect the poor, women, and children the most. We investigated PPRV age-seroprevalence data to determine the age cohort(s) responsible for PPRV transmission among sheep, goats, and cattle. To do so, we calculated the force of infection (FOI), or the per capita infection rate of susceptible hosts. FOI is the probability that an individual without disease becomes an individual with disease over a short interval of time. Serum samples and household surveys were collected in 9 agropastoral and 11 pastoral villages in the Arusha, Kilimanjaro, and Manyara regions of northern Tanzania during 2016. Of the 7,538 samples tested, the overall observed seroprevalence was 21.1% (agropastoral: 5.8% pastoral: 30.7%). Seroprevalence increased across age groups, with the oldest age groups reporting 53.6%, 46.8% and 11.6% in sheep, goats, and cattle. We calculated the force of infection

using an age-specific catalytic model and determined the age group (age determined by dentition) with the highest force of infection was aged 2-3 years for sheep and goats and 3.5-4.5 years for cattle. For females, the age groups with the highest force of infection was the same, except in cattle where under 1 year had the highest FOI and 3.5-4.5 year olds were second highest. For males, 1.5-2 years in sheep, > 5 years old in goats, and < 1.5 years in cattle had the highest force of infection. Pastoral management systems had higher FOI and a wider range of ages with a high FOI than agropastoral systems. In agropastoral systems, the highest FOI was seen in ages 2-3 years (sheep and goats) and 3.5-4.5 years (cattle). In pastoral systems, the highest FOI was in ages 2-3 years (sheep), 3-5 years (goats), and 3.5-4.5 years (cattle). By identifying age cohorts that contribute to increased PPRV transmission, management practices can be adjusted to reduce transmission. This study found widespread PPRV seroconversion in northern Tanzania among sheep, goats, and cattle, identified sex and management system as significant risk factors, and determined the age cohorts facing the highest burden of PPRV circulation. Future studies on specific management practices are needed to identify additional ecological mechanisms driving observed PPRV seroprevalence. Insights will lead to improved PPRV control strategies through feasible changes in non-vaccination practices, geographical areas and host species to target during vaccination campaigns, and more accurate calculations of herd immunity thresholds.   *Poster #: 42*

Foraging dynamics in sniper alley
Natalie Imirzian and David Hughes
When the carpenter ant Camponotus rufipes is infected with the fungal parasite Ophiocordyceps camponoti-rufipedis, infected ants are manipulated to leave their nest and die biting the underside of a leaf. Fungal infected cadavers surround the main trunk-trails of C. rufipes, forming a sniper's alley for foragers. We filmed the main trails of multiple C. rufipes nests to investigate how forager speed and movement patterns differ between beginning and peak foraging times. Using machine learning algorithms, we automated tracking of ants on these trails, providing us with a powerful dataset on undisturbed ant movement, perhaps the first such dataset obtained for a nocturnal forager outside of the laboratory. By analyzing the behavior of ants in the 'zone of fire' for infection, we can elucidate mechanisms that influence a colony's risk of infection and show how this fungus readily exploits this ant. This system demonstrates tradeoffs between consistent trail formation and disease risk, as well as reveals how parasites can take advantage of ants despite colony defenses within the nest.
Student Research Lightning Talks: Track C

The role of diapause in the developmental synchrony of an agricultural pest: a case study with the tortricid pest Cydia pomonella
Damie Pak, David Biddinger, and Ottar Bjornstad
For insect species that produce multiple generations each year, there is varying levels of developmental synchrony that can manifest into cycles with either distinct, separate generations or overlapping generations where multiple life-stages are present. To understand this population-level phenomenon, it is crucial to explore the mechanisms that have been previously proposed such as the role of seasonal disturbances, like winter, in synchronizing development each year. Specifically, our aim was to explore how diapause, a period in which development is arrested at a specific-life stage, influences the developmental synchrony across a growing season. Our focal species was Cydia pomonella, a common tortricid moth pest with diverse intergenerational dynamics and which diapause as fully-grown larvae. We developed a physiologically-structured population model consisting of the insect's life-stages (eggs, larvae, diapausing larvae, pupae, adults) and used distributed-delay equations to capture the variability in developmental periods. All vital rates such as development, survivorship, and fecundity were related to temperature with diapause induction and termination dependent on changes in photoperiod. All parameters were taken from previous laboratory works and the model was compared to pheromone trap data collected at the experimental farm site in Biglerville, PA. We found that the physiologically-structured model which incorporated diapause induction/termination better explained the dynamics of C.

pomonella than models without. With temperature data from the experimental farm site, our model closely matched the timing of the two peak flights in the reproductive adults found in the pheromone trap data. The first flights which are comprised of the overwintering generation occur in mid-May and have distinct peaks while the second flights which peak around mid-July have a less synchronous emergence. This suggests that the induction of diapause in fully-grown larvae allows C. pomonella to both survive hazardous freezing temperatures and re-synchronize their development at the end of the growing season. In conclusion, incorporating diapause into stage structured models could provide further insight into the role of both the seasonal environment and life-history on the developmental synchrony across insect pest species. *Poster #: 43*

Can fungi make caterpillars picky eaters? Effect of endophytic Metarhizium in corn on fall armyworm (Spodoptera frugiperda) feeding behavior
Brianna Flonc, Imtiaz Ahmad, Christina Mullen, and Mary Barbercheck
Organic farmers rely on naturally occurring predators and pathogens for controlling their insect pest populations. The insect-pathogenic fungus, Metarhizium, occurs naturally in soil and can infect a wide variety of insect hosts. Metarhizium was also recently found to grow in plant tissue as an endophyte that can enhance plant growth and protect them from herbivorous insects. The research goals of this study were to determine the effect of endophytic Metarhizium on: 1) corn growth across developmental stages; 2) fall armyworm relative growth rate (RGR); 3) fall armyworm feeding preference. Preliminary results showed that endophytic Metarhizium had no significant effect on corn height, dry aboveground biomass, or chlorophyll content across the V1 to V4 corn growth stages. There was also no significant difference between the average RGR of fall armyworm that fed on control corn leaves versus treated corn leaves. Furthermore, fall armyworm larvae exhibited no feeding preference for control corn leaves or treated corn leaves when presented with a choice. *Poster #: 44*

CRISPR/Cas9-mediated genome editing reveals Arabidopsis thaliana expansin paralogs AtEXPA7 and AtEXPA18 function redundantly and are required for proper root hair formation.
Nathan Hepler, Moyan Jia, and Daniel Cosgrove
Root hair formation can be divided into two distinct stages: initiation and elongation. During both of these stages, structural rearrangements occur within the cell walls of root hair-bearing epidermal cells. Wall modifying proteins are key players in this process, but the extent of their roles remains unclear. One such class of proteins believed to be critical in root hair development is expansins, the mediators of acid growth. Expression analyses in Arabidopsis thaliana (Col-0) indicate expansins AtEXPA7 and AtEXPA18, the two paralogs of clade EXPA-X, specifically localize to root hair progenitor cells and elongated root hairs. For exploring the roles of these two expansins in root hair development, we utilized CRISPR/Cas9-mediated genome editing and a polycistronic tRNA-gRNA system for simultaneously targeting both expansin loci using a single vector. Interestingly, atexpa7 and atexpa18 single knock out mutants were found to produce elongated root hairs, indicating that a single paralog is sufficient for root hair elongation. However, atexpa7/atexpa18 mutants failed to display elongated root hairs and instead exhibit only small bulges, indicative of root hair initiation but a cessation of further development. The atexpa7/atexpa18 genotype segregated with the "hairless" phenotype, confirming lack of root hair elongation is a result of EXPA-X loss. Furthermore, overall root lengths for atexpa7/atexpa18 plants were significantly reduced, which was found to be attributable to a reduced root growth rate. Complementation using either AtEXPA7 or AtEXPA18 was sufficient to restore proper root hair development in atexpa7/atexpa18 plants, further illustrating EXPA-X's importance in elongation. Surprisingly, no change in root hair density was observed for either single or double knock out plants. Taken together, these results reveal that while AtEXPA7 and AtEXPA18 together are critical for root hair elongation, they act independently from root hair initiation, suggesting additional expansins may be separately involved during the first stage of root hair growth.
Student Research Lightning Talks: Track C *Poster #: 45*

Notes