2nd Annual Wyoming INBRE
Networks for Biomedical Research Excellence Conference

April 27th-29th, 2017

University of Wyoming, Laramie UW Conference Center (UWCC) and Marion H. Rochelle Gateway Center (MHRGC), Laramie, WY

This project is supported in part by a grant from the National Institute of General Medical Sciences (2P20GM103432) from the National Institutes of Health. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.
**Wyoming INBRE Administration**

*State EPSCoR/IdEA Chair*
- William Gern PhD, Vice President for Research and Economic Development, University of Wyoming

*Administrative Core*
- R. Scott Seville PhD, Wyoming INBRE Principal Investigator/ Program Director, Professor of Zoology and Physiology, University of Wyoming at Casper
- Florence Teulé-Finley PhD, Wyoming INBRE Program Coordinator, Biology Program, University of Wyoming at Casper
- Annie Bergman PhD, Wyoming INBRE Program Manager, University of Wyoming
- Laurie Jo Kempert, Wyoming INBRE Fiscal Manager, College of Health Sciences, University of Wyoming
- Angela Reddick, Staff, University of Wyoming at Casper

*Bioinformatics Core*
- Naomi Ward PhD, Core Director, Associate Professor of Molecular Biology, University of Wyoming
- Nicolas Blouin PhD, Research Scientist, University of Wyoming
- Vikram Chhatre PhD, Research Scientist, University of Wyoming
- Kayleigh Holmes, Staff, Departments of Molecular Biology and Botany, University of Wyoming

*Developmental Research Projects Program*
- David Fay PhD, Core Director, Professor of Molecular Biology, University of Wyoming

*Outreach and Education Core*
- R. Scott Seville PhD, Core Director, Professor of Zoology and Physiology, University of Wyoming at Casper
- Jennifer Forrester, PhD, Assessment Coordinator, Associate Professor of Elementary and Early Childhood Education, University of Wyoming at Casper

*Wyoming INBRE Research/ Education Network Primarily Undergraduate Institution (PUI) Project Leaders*
- Dagmara Motriuk-Smith PhD, Casper College and University of Wyoming at Casper
- Steve McAllister MS, Central Wyoming College
- Chris Wenzel MS, Eastern Wyoming College
- Ami Wangeline PhD and Zachary Roehrs PhD, Laramie County Community College
- Eric Atkinson MS, Northwest College
- Rob Milne MS, Northern Wyoming Community College District, Sheridan and Gillette Colleges
- Bud Chew PhD, Western Wyoming Community College
Wyoming INBRE External Advisory Committee (EAC)
- John Sladek PhD and EAC Chair, retired Professor of Neurology, Pediatrics and Neuroscience, University of Colorado School of Medicine
- Carolyn Bohach PhD, University Distinguished Professor, University of Idaho and Idaho INBRE Principal Investigator and Director
- Thomas Gorell, PhD, retired Associate Vice President for Administrative Services and Professor of Biology, Colorado State University
- Chuck Henry PhD, Department Chair and Professor of Chemistry at Colorado State University
- David Pollock PhD, Associate Professor of Biochemistry and Molecular Genetics, University of Colorado School of Medicine.
- Douglas Seals PhD, College Professor of Distinction in Integrative Physiology, University of Colorado Boulder.
- George Seidel PhD, Colorado State University Distinguished Professor

Wyoming INBRE Statewide Steering Committee (SSC)

Representatives from the University of Wyoming
- Brent Ewers PhD, Wyoming EPScOR Program Director
- Steve Barrett PhD, Professor and Associate Dean, College of Engineering
- Diane Boyle, PhD, Professor Fay Whitney School of Nursing
- Qian-Quan Sun PhD, Professor of Zoology and Physiology and UW Neuroscience Center

Representatives from the Network Primarily Undergraduate Institutions (PUIs)
- Steve McAllister MS, faculty and Project Lead, Central Wyoming College
- Kathy Wells, Dean of Health & Science, Central Wyoming College
- Chris Wenzel MS, faculty and Project Lead, Eastern Wyoming College
- Zac Roehrs PhD, faculty and Project co-Lead, Laramie County Community College
- Ami Wangelvine PhD, faculty and Project co-Lead, Laramie County Community College
- Eric Atkinson MS, faculty and Project Lead, Northwest College
- Marnee Crawford, RN, MSN, CNE, Director of Nursing & Chair of Life & Health Sciences Division, Northwest College
- Ami Erickson PhD, faculty and Project Lead, Sheridan College
- Bud Chew PhD, faculty and Project Lead, Western Wyoming Community College
- Rocky Barney PdD, faculty, Western Wyoming Community College
- Dagmara Motriuk-Smith PhD, faculty and Project Lead, UW at Casper
- Grant Wilson, Dean of School of Science, Casper College

INBRE External Review Team
- Dr. Jeff Arterburn, Regents Professor, Department of Chemistry & Biochemistry, New Mexico State University, Las Cruces, NM
- Dr. Faye Schilkey, Director, Strategic Projects & NM-IDeA Network for Biomedical Research Excellence Sequencing and Bioinformatics Core (SBC), National Center for Genomics Research, Santa Fe, NM
- Dr. Ann Bertagnolli, Montana INBRE Program Coordinator, Montana State University, Bozeman, MT
### SCHEDULE

**2ND Annual WYOMING INBRE CONFERENCE**

**APRIL 27-29, 2017**

University of Wyoming, Laramie UW Conference Center (UWCC), Marion H Rochelle Gateway Center (MHRGC), and UW Campus (Wyoming URD)

**Thursday, April 27th: UW Conference Center (UWCC) west end of Hilton Inn**

**NOTE:** Graduate students may set up posters in Salon D between 9:00 am and 4:30 pm. There will be a numbered list of posters for location. Magnets/adhesives provided.

<table>
<thead>
<tr>
<th>Time</th>
<th>Presentations</th>
<th>External Review Team</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:45-9:20 am</td>
<td><strong>Welcome</strong> – light breakfast. R. Scott Seville, Wyoming INBRE Program Director.</td>
<td></td>
</tr>
<tr>
<td>9:20-9:40 am</td>
<td><strong>Thematic Project:</strong> Anya Lyuksytova, Dept. of Molecular Biology, UW. Nonalcoholic Steatohepatitis Treatment via Micro-RNA Inhibition of Glucosyl Ceramide Synthase (GSH)</td>
<td>Administrative and Outreach and Education Cores Focus Group 9:00-10:20 am</td>
</tr>
<tr>
<td>9:40-10:00 am</td>
<td><strong>Thematic Project:</strong> Baskaran Thyagarajan, School of Pharmacy, UW. TRPV1 activation prevents high fat diet-induced non-alcoholic fatty liver disease in obesity via SiRT-1-dependent mechanisms</td>
<td></td>
</tr>
<tr>
<td>10:00-10:20 am</td>
<td><strong>Pilot Project:</strong> Carl Frick, Dept. of Mechanical Engineering, UW. Tailored Transcorneal Drainage Device Using Nano-porous Liquid-Crystalline Elastomers</td>
<td></td>
</tr>
<tr>
<td>10:20-10:40 am</td>
<td><strong>Thematic Project:</strong> Brian Cherrington, Dept. of Zoology and Physiology, UW. Epigenetic Regulation of miRNA Biogenesis in Pituitary Lactotrope Cells</td>
<td>Bioinformatics Core and DRPP Focus Group 10:20-11:40 am</td>
</tr>
<tr>
<td>10:40-11:00 am</td>
<td><strong>BREAK</strong></td>
<td></td>
</tr>
<tr>
<td>11:00 am-11:20 pm</td>
<td><strong>Thematic Project:</strong> Amy Navratil, Dept. of Zoology and Physiology, UW. Understanding Gonadotrope Regulation of Fertility</td>
<td></td>
</tr>
<tr>
<td>11:20-11:40 pm</td>
<td><strong>Thematic Project:</strong> John Oakey, Dept. of Chemical Engineering, UW. Circulating Tumor Cell Capture and Release from Degradable Hydrogel Surfaces</td>
<td></td>
</tr>
<tr>
<td>11:40-Noon</td>
<td><strong>Thematic Project:</strong> Wei Guo, Dept. of Animal</td>
<td>OPEN</td>
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<tr>
<td>Time</td>
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<td>Details</td>
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<tr>
<td>Noon-1:20 pm</td>
<td>LUNCH on own*</td>
<td>Thematic, Pilot, Collaborative Project Investigators Focus Group* with LUNCH: 12:00 – 1:20 pm</td>
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<tr>
<td>Noon-1:20 pm</td>
<td>External Advisory Committee (EAC) executive session/discussion/ INBRE Core Directors (Lunch in UWCC Board Room)</td>
<td></td>
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<tr>
<td>1:20-1:40 pm</td>
<td>Thematic Project: Guanglong He, School of Pharmacy, UW. Obesity-associated Chronic Inflammation and Myocardial Dysfunction</td>
<td></td>
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<tr>
<td>1:40-2:00 pm</td>
<td>Thematic Project: Christine Porter, Division of Kinesiology and Health, UW. Growing health from the grassroots: accomplishments on four aims I</td>
<td>Graduate Student Focus Group 1:20-2:40 pm</td>
</tr>
<tr>
<td>2:00-2:20 pm</td>
<td>Pilot Project: Jason Gigley, Dept. of Molecular Biology, UW. Heavy metal chelators and putative copper binding protein TgSco1 as novel therapeutic agents against <em>Toxoplasma gondii</em></td>
<td></td>
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<tr>
<td>2:20-2:40 pm</td>
<td>Break</td>
<td></td>
</tr>
<tr>
<td>2:40-3:00 pm</td>
<td>Pilot Project: Katie Li, Dept. of Chemical Engineering, UW. Microfluidic Production of Multimodal Therapeutic PEG Hydrogel Nanoparticles</td>
<td></td>
</tr>
<tr>
<td>3:00-3:20 pm</td>
<td>Pilot Project: Grant Bowman, Dept. of Molecular Biology, UW. Sub-Micron Scale Anatomy in Bacteria</td>
<td></td>
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<tr>
<td>3:20-3:40 pm</td>
<td>Collaborative Project: Bud Chew and Jun Ren, Dept. of Biology, Western Wyoming CC and School of Pharmacy, UW. Environmental Pollutant Acrolein Triggers Myocardial Insulin Sensitivity, Contractile Dysfunction and Apoptosis: Role of TRPV1</td>
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<tr>
<td>3:40-5:00 pm</td>
<td>EAC Focus Group 3:40-5:00 pm</td>
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<td>5:30-7:30 pm</td>
<td>Reception and Graduate Student Poster Session</td>
<td>UWCC Salon D</td>
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Friday, April 28: UW Conference Center and MHRGC
### Presentations UWCC Salon E

<table>
<thead>
<tr>
<th>Time</th>
<th>Presentations</th>
<th>External Review Team Focus Groups: UWCC Salon F/G</th>
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<tbody>
<tr>
<td>8:00 am</td>
<td>Light Breakfast</td>
<td></td>
</tr>
<tr>
<td>8:20-8:40 am</td>
<td><strong>Pilot Project:</strong> Jared Bushman, School of Pharmacy, UW. Localized Immunosuppression for Peripheral Nerve Allografts</td>
<td></td>
</tr>
<tr>
<td>8:40-9:00 am</td>
<td><strong>Collaborative Project:</strong> Baskaran Thyagarajan &amp; Steve McAllister, School of Pharmacy, UW and Dept. of Biology, Central Wyoming College Analyses of mechanisms by which TRP protein activation protects from vascular dysfunctions in metabolic syndrome</td>
<td>Primarily Undergraduate Institution Faculty &amp; Statewide Steering Committee Focus Group (with breakfast) <strong>8:20-9:40 am</strong></td>
</tr>
<tr>
<td>9:00-9:20 am</td>
<td><strong>Thematic Project:</strong> Rebecca Carron, School of Nursing, UW. Polycystic Ovary Syndrome in American Indian Women: An Exploratory Study</td>
<td></td>
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<tr>
<td>9:20-9:40 am</td>
<td>BREAK</td>
<td></td>
</tr>
<tr>
<td>9:40-10 am</td>
<td><strong>Collaborative Project:</strong> Patrick Johnson &amp; Florence Teulé-Finley, Chemical Engineering, UW and UW at Casper. Generation of Electrospun Spider Silk Nanofiber Mats for Medical Applications</td>
<td></td>
</tr>
<tr>
<td>10:00-10:20 am</td>
<td><strong>Collaborative Project:</strong> Matt Carling &amp; Eric Atkinson, Dept. of Zoology and Physiology, UW and Dept. of Biology, Northwest College. Investigating the factors that influence the distribution and impacts of diseases in wild birds</td>
<td></td>
</tr>
<tr>
<td>10:20-10:40 am</td>
<td><strong>Collaborative Project:</strong> Merav Ben-David &amp; Hayley Lanier, Dept. of Zoology and Physiology, UW and UW at Casper. Genomic assessment of the role of relatedness in spatial overlap among least chipmunks (<em>Tamias minimus</em>) in the Laramie Range</td>
<td></td>
</tr>
<tr>
<td>10:40-11:00 am</td>
<td><strong>Community College Program Report:</strong> Eric Atkinson, Northwest College. Antibiotics, birds, and Caloplaca—all the way to Zonotrichia: The ABC’s of INBRE at Northwest</td>
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</tbody>
</table>

**NOTE:** Undergraduate students may set up posters between 1:30 and 4:30 pm. There will be a numbered list of posters for location. Adhesives provided.
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>11:00 am</td>
<td>Break out for meetings</td>
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<td></td>
<td>Lunch on own for non-EAC/SSC</td>
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<tr>
<td>11:00-Noon</td>
<td>Statewide Steering Committee (SSC) Meeting</td>
<td>MHRGC Boyd Room</td>
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<tr>
<td>Noon-1:00 pm</td>
<td>EAC/SSC/ Evaluation Team Luncheon</td>
<td>MHRGC Boyd Room</td>
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<tr>
<td>1:00-2:00 pm</td>
<td>External Advisory Committee meeting</td>
<td>MHRGC Boyd Room</td>
</tr>
<tr>
<td>2:00-2:20 pm</td>
<td>Community College Program Report: Steve McAllister, Central Wyoming College.</td>
<td>MHRGC Boyd Room</td>
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<tr>
<td></td>
<td>The Central Wyoming College Undergraduate Research Program Engages Students in Diverse Research Activities</td>
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<tr>
<td>2:20-2:40 pm</td>
<td>Community College Program Report: Dagmara Motriuk-Smith, UW at Casper.</td>
<td>MHRGC Boyd Room</td>
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<td>INBRE supported research at Casper College and the University of Wyoming at Casper</td>
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<tr>
<td>2:40-3:00 pm</td>
<td>Community College Program Report: Chris Wenzel, Eastern Wyoming College.</td>
<td>MHRGC Boyd Room</td>
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<td>Denitrification Potential of Soil Microbes in the Lower North Platte River Valley, Wyoming</td>
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<tr>
<td>3:00-3:20 pm</td>
<td>Community College Program Report: Ami Wangeline &amp; Zac Roehrs, Laramie County Community College.</td>
<td>MHRGC Boyd Room</td>
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<td></td>
<td>PUI... Fertilizer for undergraduate minds and growth at Laramie County Community College.</td>
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<tr>
<td>3:20-3:40 pm</td>
<td>BREAK</td>
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<tr>
<td>3:40-4:00 pm</td>
<td>Community College Program Report: Bud Chew, Western Wyoming Community College.</td>
<td>MHRGC Boyd Room</td>
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<td>INBRE Research at Western WY Community College Provides Tremendous Student Opportunities</td>
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<tr>
<td>4:00-4:20 pm</td>
<td>Community College Program Report: Ami Erickson, Northern Wyoming Community College District- Sheridan and Gillette Colleges.</td>
<td>MHRGC Boyd Room</td>
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<td></td>
<td>Northern Wyoming Community College INBRE-Supported Research Activities</td>
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<tr>
<td>4:20-4:40 pm</td>
<td>Collaborative Project: Sadanand Dhekney &amp; Ami Erickson, Agriculture Experiment Station, UW and Dept. of Biology, Sheridan College.</td>
<td>MHRGC Boyd Room</td>
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<tr>
<td></td>
<td>Grapevine Cellular and Physiological Response to Salinity Stress</td>
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<tr>
<td>REMARKS/Move to MHRGC - R. Scott Seville, Wyoming INBRE Program Director</td>
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<tr>
<td>5:00-6:30 pm</td>
<td>Reception and Undergraduate Poster Session</td>
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2nd Annual Wyoming INBRE Conference  
April 27-29, 2017

**Marion H. Rochelle Gateway Center (MHRGC) - Legacy Hall & Atrium**

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<tr>
<th>Time</th>
<th>Location TBD</th>
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<tbody>
<tr>
<td>6:30-8:30 pm</td>
<td><strong>INBRE Banquet</strong></td>
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<td>Keynote Talk: Knockin’ on Fertility’s Door:</td>
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<td></td>
<td>Understanding Gonadotrope Function</td>
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<td></td>
<td>Dr. Amy Navratil</td>
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<td>MHRGC Salon</td>
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<td>A/B</td>
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**Saturday, April 29th**

<table>
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<tr>
<th>Time</th>
<th>Location TBD</th>
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<tbody>
<tr>
<td>12:30-2:30 pm</td>
<td>Working lunch: External Review Team</td>
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<td>Seville/Bergman</td>
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</tbody>
</table>

**Wyoming Undergraduate Research Day (URD)**

*See Undergraduate Research Day Schedule for specific student presentation rooms and times*

<table>
<thead>
<tr>
<th>Time</th>
<th>Location TBD</th>
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<tbody>
<tr>
<td>8:00-9:45 am</td>
<td><strong>INBRE Breakfast/ Community Forum</strong></td>
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<td></td>
<td>Wyoming Union Ballroom</td>
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<td></td>
<td>eRA Commons, WY INBRE Reporting, assessment, questions, programs and upcoming events</td>
</tr>
<tr>
<td>10:00 am-4:00pm</td>
<td><strong>Wyoming Undergraduate Research Day (URD)</strong></td>
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<td></td>
<td>UW Classroom Building</td>
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<tr>
<td>Noon-1:00 pm</td>
<td>LUNCH* – on your own</td>
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<td></td>
<td>Due to the high numbers of presentations there may not be a clear ‘lunch hour’</td>
</tr>
<tr>
<td>3:00-5:00 pm</td>
<td>INBRE URD Poster Session (Wyoming Union 2nd floor)</td>
</tr>
<tr>
<td>5:45-7:30 pm</td>
<td><strong>Wyoming URD Banquet and Keynote</strong></td>
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<td>(Wyoming Union Yellowstone Ballroom)</td>
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</table>
DETAILED SCHEDULE AND ABSTRACTS

ORAL PRESENTATIONS
All faculty oral presentations will be Thursday April 27th and Friday April 28th, 2017 at the UW Conference Center (UWCC; West end of Hilton Garden Inn) in Salon E.

Thursday, April 27th
UWCC Salon E

9:20-9:40 am
Thematic Project: Nonalcoholic Steatohepatitis Treatment via Micro-RNA Inhibition of Glucosyl Ceramide Synthase (GSH). Lyuksyutova, A. Department of Molecular Biology, University of Wyoming, Laramie, WY 82071; Email: alyuksyu@uwyo.edu

ABSTRACT. Metabolic syndrome occurs in 24%-27% of Americans and is associated with diseases like type 2 diabetes mellitus and atherosclerotic cardiovascular disease (ASCVD). Nonalcoholic steatohepatitis (NASH) occurs in 33% of metabolic syndrome patients and is a condition in which the liver becomes inflamed and damaged due to its high fat content. This condition can lead to fibrosis and, eventually, cirrhosis of the liver and become life threatening. Few methods of treating NASH exist, however one potential avenue of treatment is inhibition via microRNAs of a key enzyme, glucosyl ceramide synthase (GCS). High levels of GCS are associated with development of NASH, making it a prime target for inhibition. Our project has focused on creating DNA constructs using an episomal vector (EEV) with GFP fused to the GCS 3’ untranslated region (UTR) from both mice and humans as well as constructs that will contain the short sequence that encodes Mir-124, a microRNA that has a binding site in the 3’UTR of GCS. These constructs are then transfected into human or mice cells to determine if direct interaction of microRNA with the 3’UTR of GCS is responsible for the reduction in expression of GCS based on the presence of microRNA binding sites present on the 3’ UTR. The completion of this project will yield important information regarding the inhibition of GCS in mammalian cells and may lead to treatments for NASH and metabolic syndrome patients.

9:40-10:00 am
Thematic Project: TRPV1 Activation Prevents High Fat Diet-Induced Non-Alcoholic Fatty Liver Disease in Obesity via SiRT-1 Dependent Mechanisms. Baskaran, P., Zhang, Z.J., and Thyagarajan, B. School of Pharmacy, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071; Email: Baskaran.Thyagarajan@uwyo.edu

ABSTRACT. Diet-induced obesity leads to metabolic syndrome and one third of the word population is obese or overweight. Currently no effective strategy is available to counter obesity. Recent research from our laboratory and from others suggest that activation of transient receptor potential vanilloid subfamily 1 counters obesity. Our previous research work unambiguously shows that capsaicin triggers the molecular conversion of white to brute (Brown in white) phenotype by activating sirtuin-1-dependent deacetylation and interaction of peroxisome proliferator activated receptor gamma (PPARγ) and PR domain containing protein 16 (PRDM-16) via TRPV1-
dependent mechanism. This research suggests that TRPV1 activation by capsaicin (CAP) significantly enhanced the expression of thermogenic proteins including bone morphogenetic protein 8b (BMP8b), mitochondrial uncoupling protein-1 (UCP-1), PPARγ coactivator 1α (PGC-1α), sirtuin-1 (SIRT-1) and PRDM-16 in brown adipose tissue (BAT) while high fat diet (HFD)-feeding increased body weight gain by suppressing these thermogenic proteins. Capsaicin also significantly enhanced the expression of thermogenic markers and increased basal and forskolin stimulated lipolysis in BAT. Capsaicin decreased serum glucose, triglyceride and cholesterol levels and restored glucose intolerance and insulin resistance observed in HFD-fed mice. These data suggest an enhancement of plasma GLP-1 level, BAT activation and a concomitant regulation of glucose homeostasis by capsaicin. Further, the upregulation of PGC-1α, a gene that metabolically regulates mitochondrial biogenesis, by capsaicin is associated with an increased number of mitochondria in BAT. Also, capsaicin supplementation in diet increased the metabolic activity, respiratory quotient and heat production in live mice. These data provide evidence for the regulation of BAT activation and enhancement of mitochondrial biogenesis by capsaicin to increase energy expenditure and heat production to counter obesity.

10:00-10:20 am
Pilot Project: Tailored Transcorneal Drainage Device Using Nano-porous Liquid-Crystalline Elastomers. Frick¹, C., Yakacki², C., and Kahook³, M. ¹Mechanical Engineering, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071; ²Mechanical Engineering, University of Colorado-Denver, 1200 Larimer St, Denver, CO 80217; ³Ophthalmology, University of Colorado-Anschutz Medical Campus, 1675 Aurora Ct, Denver, CO 80045; Email: cfrick@uwyo.edu

ABSTRACT. The proposed research will challenge the standard approach to lowering intraocular pressure (IOP) in patients suffering from glaucoma. Glaucoma is the second leading cause of blindness worldwide and it is estimated that 70 million patients worldwide suffer from the disease. High IOP damages the optic nerve and results in vision loss. Treatment of glaucoma focuses on lowering IOP; however, a successful long-term solution remains elusive. Topical medications have limited efficacy and suffer from poor patient adherence, while surgical strategies suffer from high morbidity and limited long-term success. For example, drainage devices lower IOP by shunting aqueous humor from the anterior chamber to another compartment outside of the eye; however, these devices are prone to eventual scarring and closure of the new drainage pathway. We propose a new transcorneal drainage device that utilizes a novel material platform of functional liquid-crystalline elastomers (LCEs) to overcome the existing challenges and barriers in drainage devices. This treatment strategy would reduce IOP by directly draining aqueous humor to the tear film, bypassing the conjunctiva and tissues that commonly scar and prevent outflow. This would promote ease-of-implantation, allowing surgeons to perform the procedure with minimal training. The drainage device would consist of a LCE porous filter that has reversible shape-changing properties, which enables removal and replacement to tailor outflow and ensure long-term efficacy if the filter becomes clogged. If successful, this research could significantly alter how IOP is treated with drainage devices as well as introduce a novel, unexplored ophthalmic materials platform for future devices.
10:20-10:40 am
Thematic Project: Epigenetic Regulation of miRNA Biogenesis in Pituitary Lactotrope Cells. Cherrington, B. Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave, Laramie, WY, 82071; Email: bccherrin@uwyo.edu

ABSTRACT. During pregnancy, pituitary lactotrope cells undergo dynamic increases in size, number and connectivity. Lactotrope expansion and remodeling dramatically elevate prolactin production, which is required to initiate high volume milk production during the onset of lactation. Despite these critical physiological changes, the epigenetic mechanisms implementing lactotrope expansion and remodeling are poorly understood. Our work tests a new hypothesis that a novel histone modification controls miRNA biogenesis to regulate the transformation in lactotropes during pregnancy. Peptidylarginine deiminase (PAD) enzymes post-translationally convert arginine amino acids into non-coded citrulline residues through a reaction termed citrullination. Citrullination alters histone-DNA interactions to control gene expression. Our results demonstrate robust PAD expression and citrullinated histones in lactotrope cells from late pregnant mice. RNA-seq data generated with somatolactotrope derived GH3 cells show that histone citrullination suppresses the transcription of numerous pri-microRNAs such as let7c and miR23b, which normally prevent cell proliferation. Histone citrullination also suppresses the expression of a riboprotein termed DiGeorge Syndrome chromosomal region 8 (DGCR8). DGCR8 complexes with Drosha to form the microprocessor essential for miRNA biogenesis. Collectively, our results show that histone citrullination is a novel epigenetic mechanism controlling the transcription and processing of miRNAs in GH3 cells. Based on this scientific premise, our central hypothesis is that PAD catalyzed citrullination of histones suppresses expression and processing of miRNAs, which alleviates repression of important mRNA transcripts that control lactotrope size, number and connectivity. The central hypothesis will be tested by (1) examining how histone citrullination controls transcription of pri-miRNAs and demonstrating that miRNA programs control lactotrope transformation; (2) determining how PAD enzymes control DGCR8 expression and establishing the role of miRNA processing in lactotrope transformation. Achieving our objectives will demonstrate that PAD catalyzed histone citrullination regulates miRNA transcription and processing to transform lactotropes during pregnancy. Increasing our understanding of this novel epigenetic mechanism will provide insight for developing innovative strategies to control prolactin production and lactation in women and may also address the etiology of pituitary adenomas.

10:40-11:00 am BREAK

11:00-11:20 am
Thematic Project: Understanding Gonadotrope Regulation of Fertility. Edwards¹, B. S., Khan¹, S. A., Boehm², U., Davis³, R. J., Navratil¹, A. M. ¹Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82071; ²Department of Pharmacology and Toxicology, University of Saarland School of Medicine, D-20246 Homburg, Germany; ³Program in Molecular Medicine, University of Massachusetts Medical School, Worcester, MA 01605; ⁴Howard Hughes Medical Institute, Worcester, Massachusetts 01605; Email: anavrati@uwyo.edu
ABSTRACT. Gonadotropin releasing hormone receptor (GnRHR) activation initiates an intricate network of signaling pathways that results in the synthesis and secretion of gonadotropins, luteinizing hormone (LH) and follicle stimulating hormone (FSH), from the anterior pituitary. Previous work has highlighted an important role for the c-Jun NH2-terminal kinase (JNK) signaling cascade in regulating both GnRHR expression levels and pulsatile LH secretion; events that are essential for reproductive viability. However, whether JNK regulates fertility at the level of the pituitary in vivo is not known. To specifically address this question, we utilized Cre/loxP technology to selectively inactivate JNK 1 and JNK 2 (JNK 1/2) in gonadotrope cells of the anterior pituitary (DKO). Conditional knockout of floxed JNK 1/2 alleles in gonadotropes was accomplished using the previously described GRIC mouse strain, which coexpresses the GnRHR with Cre recombinase. qPCR analyses revealed an increase in FSHβ mRNA levels in DKO females. Consistent with elevated pituitary FSHβ transcript levels, serum FSH levels were also significantly increased in DKO females when compared to controls. Additionally, pituitary expression of GnRHR and LHβ were increased in DKO females along with serum LH levels; indicating that LH concentration may be linked to enhanced GnRHR expression. Consistent with elevated serum FSH levels, DKO females had increased ovarian weights due to enhanced folliculogenesis. Furthermore, DKO females exhibited altered estrous cyclicity marked by prolonged estrus, which resulted in significantly increased time to pregnancy compared to controls. Lastly, our results suggest that the mechanistic actions of JNK regulation of FSH is through activin signaling at the level of SMADs. Taken together, our results reveal a novel role for JNK signaling in gonadotrope regulation of FSHβ synthesis in vivo.

11:20-11:40 am
Thematic Project: Circulating Tumor Cell Capture and Release from Degradable Hydrogel Surfaces. Oakey¹, J.;¹Department of Chemical Engineering, University of Wyoming, 1000 E University Ave, Laramie, WY 82071; Email: joakey@uwyo.edu

ABSTRACT. Circulating tumor cells (CTCs) represent a high value clinical target with applications in diagnostic and therapeutic oncology, as well as basic cancer biology. For these cells to realize their clinical potential, they must be isolated at high yields and purity from whole blood. Given that they occur rarely (~1 in 109 cells), this challenge is exacerbated by the need to process large quantities of sample. High-throughput microfluidic devices have recently been shown to be quite promising for the task of isolating and purifying CTCs, but have difficulty providing cells in a viable state. This project describes the development of a high throughput microfluidic rare cell capture and release device that can be applied to the isolation of viable circulating tumor cells (CTCs) from clinical whole blood samples. Central to this technology is the introduction of sacrificial capture surfaces fabricated from antibody-conjugated photo-degradable hydrogels. These surfaces are fabricated by mold-polymerizing a photo-degradable hydrogel capture surface within a microfluidic flow chamber. Following capture and device flushing, cells can be individually released from the device by a short exposure to low-intensity UV light, degrading the gel’s photocleavable crosslinks. As the gel is fluidized, degradation products and cells may be gently eluted from the device and captured. In the second year of this project, this platform has been validated with cell
lines spiked into buffy coat and whole blood for clinical testing and applications in understanding cancer cell biology.

11:40-Noon
Thematic Project: Molecular Mechanism(s) of RBM20 in the Regulation of Cardiac Gene Splicing in Heart Failure. Guo¹, W., and Chew², B. ¹Department of Animal Science, University of Wyoming, 1000 E. University Ave. Laramie WY 82071; ²Western WY College, 2500 College Dr. Rock Springs, WY 82901; Email: wguo3@uwyo.edu
ABSTRACT. Heart failure (HF) is a serious, chronic condition that gradually deteriorates over time. The onset and development of HF are unpredictable and present individual variation possibly due to unclear etiology for HF progression. Muscle is one of the highest tissues undergoing gene splicing which has been found associated with the development of HF. Recently, a splicing factor, RNA binding motif 20 (RBM20), has been identified and associated with HF progression. Our data indicated that RBM20 deficiency could trigger HF development in rats. However, the detailed molecular mechanism of how RBM20 deficiency can lead to HF is poorly defined. RBM20 has been found regulating about 30 genes among which titin is a major target of RBM20. Titin is a giant sarcomeric protein responsible for ventricular wall stiffness. Abnormal titin splicing has been associated with HF. Therefore, titin could be a major linker for RBM20-induced HF. However, how RBM20 regulates titin splicing still remains elusive. In this project, we hypothesize that RBM20-regulated titin splicing is through cooperation with other splicing factors and RBM20 posttranslational modifications via Akt kinase. To test this hypothesis, we propose to do next generation sequencing analysis, mass spectrometry analysis and in vitro splicing assay. Currently, we have done next generation sequencing analysis, and also made progress on mass spectrometry which we have purified RBM20 and sent it out for both top-down and bottom-up mass spectrometry analysis. For in vitro splicing assay, we have found that mutations on potential phosphorylation sites of RBM20 could interrupt titin minigene splicing. These preliminary data have been wrapped up for grant proposal development. Our plan is to submit a R01 in June 2017 by using these preliminary data. This work is supported by the NIH NIGMSP20GM103432.

Noon-1:20 pm LUNCH- not provided

Noon-1:20 pm INBRE External Advisory Committee/INBRE Core Directors Luncheon and Discussion UWCC Board Room

1:20-1:40 pm
Thematic Project: Obesity-associated Chronic Inflammation and Myocardial Dysfunction. Peterson, M. R., Haller, S. E., and He, G. School of Pharmacy, University of Wyoming College of Health Sciences, Laramie, WY 82071; Email: ghe@uwyo.edu
ABSTRACT. Childhood obesity and its persistence into adulthood is associated insulin resistance and glucose intolerance with dire consequences on cardiovascular system. Therefore, research strategies that focus on the mechanisms underlying obesity-associated systemic insulin resistance and cardiovascular dysfunction are much needed. Obesity is accompanied with a low-grade chronic inflammation. The infiltrated
macrophages release pro-inflammatory cytokines with detrimental effects on the target cells/organs. Our approach is to dissect obesity-induced inflammatory pathways and their potential impact on cardiovascular function.

The pro-inflammatory protein caspase recruitment domain-containing (CARD)9, which is exclusively expressed in immune cells such as macrophages, plays a critical role in the innate immune responses against infection. As a central regulatory protein in macrophages, CARD9 integrates a cascade of immune signaling pathways, leading to activation of downstream transcription factors and induction of pro-inflammatory cytokines. Whether or not CARD9 plays a role in obesity-induced chronic inflammation and cardiac dysfunction is not known. It has also been demonstrated that inflammatory cytokines induced cardiomyocyte contractile dysfunction via suppression of PGC1α, a master transcriptional regulator of mitochondrial biogenesis. Given the chronic inflammation associated with obesity, we postulated that macrophage-expressed CARD9 might be involved in obesity-induced cardiovascular dysfunction. Therefore, we hypothesize that CARD9 signaling is responsible for obesity-induced insulin resistance and myocardial dysfunction in a paracrine manner. To test our hypothesis, we employed a CARD9 KO mouse model fed with a Western diet to determine whether or not obesity activates the CARD9 signaling to induce insulin resistance and suppress PGC1α-regulated mitogenesis leading to cardiac dysfunction. Our research indicated that deletion of CARD9 reconciled obesity-induced systemic insulin resistance and glucose intolerance. We also demonstrated that CARD9 knockout ameliorated obesity-induced cardiac dysfunction.

In conclusion, CARD9 knockout improved glucose tolerance and insulin response in WD-fed mice, and ameliorated obesity-induced cardiac dysfunction after 16-week WD feeding.

1:40-2:00 pm
Thematic Project: Growing Health from the Grassroots: Accomplishments on Four Aims. Porter¹, C.M., Spoonhunter², T., Wechsler¹, A., and others³. ¹Division of Kinesiology & Health, University of Wyoming, 1000 E. University Ave, Laramie, WY, 82071; ²American Indian Studies, Central Wyoming College, 2660 Peck Ave., Riverton, Wyoming 82501; ³Collaborators: Feeding Laramie Valley, Blue Mountain Associates, Eastern Shoshone Tribal Health, Northern Arapaho Tribal Health, and Drs Mary Anne Purtsner and Jenifer Jo Thomas in the UW School of Nursing; Email: christine.porter@uwyo.edu

ABSTRACT. Alison Sage, former director of Northern Arapaho Tribal Health said, “we need to put health back in the hands of the people.” This practical and ethical theory, that putting community health in communities’ hands will improve public health, guides all four aims of our thematic project. One, we prepared for and supported what has, thanks to INBRE’s support, become our highly successful first year of the R01-funded project “Growing Resilience: an RCT on the health impact of gardens with Wind River Indian Reservation.” Two, we gathered foundational qualitative data and insights on how to improve nursing with, by and for Native American communities. Three, we have supported multiple cohorts of Native American potential and current higher education students in exploring health and biomedical career and action pathways. We are integrating this now with a “health track” in this years’ inaugural Native American
Summer Institute for Wind River high school students organized by the UW Office of the President. We have also just secured five years of EPSCoR funding [news that is EMBARGOED FOR NOW] to expand that program into STEM more generally and having also been invited to apply for NSF INCLUDES funding. Four, we are preparing for our final year of feasibility piloting in “Gardens for Health & Healing” (GH&H). Last year we fielded an RCT design with 10 people struggling with multiple chronic conditions with, as in Growing Resilience, new home gardening as the intervention. Quantitative results (which will be shared in this presentation) were promising, but asking people in such ill health to wait for intervention help was problematic. In 2017, with an eye on Robert Wood Johnson Foundation “Culture of Health” funding, we are recruiting 20 people where 10 will be randomized to “usual treatment” of home gardens and 10 to the intervention of coached and supported goal setting and designing their own health intervention to meet those goals. Porter is also exploring similar action-research design ideas with a team interested in supporting veteran health at UW.

2:00-2:20 pm
Pilot Project: Heavy Metal Chelators and Putative Copper Binding Protein TgSco1 as Novel Therapeutic Agents Against Toxoplasma gondii. Denton, S.L., and Gigley, J.P. ¹Department of Molecular Biology, University of Wyoming, 1000 E. University Ave. Laramie, WY 82071; Email: jgigley@uwyo.edu

ABSTRACT. The obligate intracellular parasite Toxoplasma gondii can attack and invade any nucleated cell of warm-blooded animals and can never be cleared. All nutrients sequestered by the parasite are derived from the host, including essential ions such as heavy metals copper, iron, and magnesium. In both the host and the parasite cell biology, these metals are primarily used as cofactors in evolutionarily conserved processes such as, respiration, oxidative stress responses, and protein-protein interactions. In addition, the metals are involved in higher eukaryote processes such as signal peptide processing and angiogenesis. Limiting the availability of these ions could alter the course of the infection in the host environment, parasite biology, or host-parasite interactions. Heavy metal chelators such as, D-Penicillamine Trientine and Tetraethylene pentamine (TEPA) are used as therapies to treat heavy metal toxicity and genetic diseases but the effects of these drugs on infectious disease is largely unknown. We hypothesize a drug treatment of the above chelators for a T. gondii infection will alter the kinetic of infection. Our data reveals that transition metal chelation in vitro and in vivo may slow the growth and replication of the parasite without showing significant toxicity to drug treatment alone. We also knocked out in the parasite a putative copper binding mitochondrial protein TgSco1 and have determined it is essential for growth and replication of the parasite further supporting a role for heavy metals in parasite success. Our future studies aim to dissect the mechanism(s) by which transition metals impact T. gondii infection and identify feasibility for therapeutic approaches based on limiting heavy metal acquisition by the parasite.

2:20-2:40 pm BREAK
2:40-3:00 pm
Pilot Project: Microfluidic Production of Multimodal Therapeutic PEG Hydrogel Nanoparticles. Li, D. Department of Chemical Engineering, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071; Email: dli1@uwyo.edu
ABSTRACT. Many classes of nanoparticles have been designed with cancer-specific therapeutic applications in mind. Nanoparticles allow chemotherapeutic molecules to be protected against dispersion, biotransformation and clearance within the body via steric encapsulation. Nanoparticles provide a drug carrier that exists in a narrow size range (10-400nm) that is optimal for passage from the circulation across the endothelium into the tumor interstitium. The function of these particles can include the localized delivery of an imaging dye, the targeted delivery of a chemotherapeutic molecule, or a metallic nanoparticle for hyperthermic treatment. Natural and synthetic polymer-based hydrogels are ideal candidates for therapeutic drug delivery because they provide biopassivity and ease of functionalization with antibodies, nucleic acid and peptide sequences. Additionally, hydrogels can be fabricated into particles and loaded with pharmacological compounds, which can be released upon polymer degradation. Block copolymer hydrogels can be engineered to erode isotropically, displaying bulk degradation profiles, and the cue to which they degrade may be designed to suit particular applications. Despite the broad diversity of techniques by which polymer hydrogels may be customized, there exist no reliable methods to prepare PEG particles on nanometer length scales with narrow size distributions and well defined loading. This limitation arises from the bulk emulsion techniques used to prepare most hydrogel nanoparticles. Photopolymerizable hydrogels represent a more versatile encapsulation vehicle as they can be physically and structured, and functionalized via orthogonal additions. To date, however, photopolymerizable nanoparticle fabrication has been limited by competitive reactions with oxygen that overwhelm polymerization. Recently, funding from a bridge-year INBRE pilot project allowed us to successfully develop a platform to address this critical challenge by fabricating nano-scale, biodegradable polyethylene glycol (PEG) particles with narrow size distribution. Monodisperse PEG hydrogel-based nanoparticles are a compelling delivery vehicle because they can be far more easily designed and tuned to specific therapeutic needs than existing nanomaterials. Further, this microfluidic processing approach is superior to existing techniques due to its exquisite control over particle size and uniformity and facile tunability of the macromolecular network. Here we propose to exploit the strengths of PEG-based materials and continuous microfluidic nanoparticle production to produce multimodality nanoparticle (MMNPs) carriers for applications in cancer diagnostics and therapeutics.

3:00-3:20 pm
Pilot Project: Sub-Micron Scale Anatomy in Bacteria. Holmes, J.A., Mushnikov, N., Wang, H., and Bowman, G.R. Department of Molecular Biology, University of Wyoming, Laramie, WY 82071. Email: gbowman2@uwyo.edu
ABSTRACT. Despite being the simplest living organisms on our planet, bacteria have highly organized anatomies. Among the most prominent anatomical features are large macromolecular complexes at cell poles, which contribute to cell cycle regulation, chromosome segregation, and host-pathogen interactions. In those bacterial species that place a polar complex at only one of the two cell poles, the resulting asymmetric
cell division produces daughter cells with different polar signaling regimes, a basic form of multicellularity. My laboratory seeks to understand the rules for assembly and maintenance of these complex structures, and how the physical characteristics of the structures relate to the activities of the individual components within them. A recent discovery was that a polymeric scaffolding protein that is responsible for creating polar structures contains large regions of structural disorder, and that the disordered regions act as low-affinity binding sites that recruit a select group of proteins from the general cytoplasm. According to our model, this polar scaffolding protein creates a three-dimensional structure that works something like a sponge, with the additional feature of a selective filter that retards the passage of the select group of binding partner proteins. Currently, we are interested in how the geometry of these 'polar sponges' relates to the entrapment of molecules coming from the cytoplasm, and how the disordered regions within the scaffolding protein achieve broad yet specific binding affinity. Other ongoing projects ask how the polar scaffolding protein and its select group of binding partners change across evolutionary time, and whether this scaffolding protein can serve as the basis for establishing polar signaling networks and programmable multicellularity in naïve species.

3:20-3:40 pm
Collaborative Project: Environmental Pollutant Acrolein Triggers Myocardial Insulin Sensitivity, Contractile Dysfunction and Apoptosis: Role of TRPV1. Chew¹, B., Ma², S., and Ren², J. ¹Department of Biology, Western Wyoming Community College, 2500 College Drive, Rock Springs, WY 82901; ²University of Wyoming College of Health Sciences, Laramie, WY 82071; Email: bchew@westernwyoming.edu

ABSTRACT. Recent evidence suggests that air pollution is associated with an overtly increased prevalence of cardiometabolic diseases although the connection between the two has not been clearly explored. This study was designed to examine the effect of an environmental pollutant α,β-unsaturated aldehyde acrolein on myocardial insulin sensitivity and contractile function. Our results revealed that in vitro short-term exposure of acrolein (25 μM) provoked overt myocardial inflammatory response, apoptosis and dampened insulin signaling manifested as accumulation of the cytokines TNF-α and NFκB as well as reduced insulin-stimulated glucose uptake. These responses were accompanied with compromised cardiomyocyte function including depressed cardiomyocyte contractile capacity, prolonged duration of relaxation, decreased intracellular Ca²⁺ release and slowed intracellular Ca²⁺ clearing. Activation of TRPV1 was enhanced in response to aldehyde exposure. Interestingly, acrolein-induced pro-inflammatory response, loss of insulin sensitivity and cardiomyocyte contractile function were significantly attenuated or mitigated by the TRPV1 antagonist capsazepine. Inhibition of TRPV1 protected against the acrolein cytotoxicity. Taken together, our data suggest a role of α,β-unsaturated aldehydes as the main causative agents in environmental pollutant-induced cardiometabolic diseases via TRPV1-dependent mechanism.

3:40-5:00 pm BREAK (INBRE EAC only focus group in UWCC Salon F/G)
Pilot Project: Localized Immunosuppression for Peripheral Nerve Allografts.
Bushman, J., Houck, B. J., Dhunghana, S., Wupu, O. School of Pharmacy, University of Wyoming College of Health Sciences, Laramie, WY 82071; Email: jbushman@uwyo.edu

ABSTRACT. Peripheral nerves (PNs) branch from the spinal cord and extend axons large distances to their targets. It is therefore not surprising PN injury is a significant aspect of trauma and disease, and is often the limiting component of functional recovery. Segmental PN defects are treated via an autograft or bioengineered options, where bioengineered options are significant inferior to autograft in terms of regeneration. Allografts promote functional recovery equal to or better than autografts, yet are not widely used due to serious concerns over the side effects of systemic immunosuppression (SIS). Given that PN allografts only require temporary SIS to be successful, we hypothesize that it is possible to sufficiently suppress the immune response against the allograft locally to enable full functional regeneration using allografts. We have developed a therapeutic regimen for localized immunosuppression (LIS), delivering immunosuppressive agents only to the allograft environment. In an animal model of PN injury and allograft placement. We observed equal regeneration with allografts and LIS as compared to an autografted nerve without evidence of rejection or sensitivity at the site of implantation. The potential implications of these findings are that (i) allografts may be used clinically to replace the need for harvesting autografts after PN injury, (ii) LIS regimen avoids the risks and pitfalls of SIS previously used for allografting of PNs, and (iii) allografts offer superior regeneration over bioengineered options for PN regeneration. Further experiments will probe the limits of LIS for PN allografting.

Collaborative Project: Analyses of Mechanisms by which TRP Protein Activation Protects from Vascular Dysfunctions in Metabolic Syndrome.
Thyagarajan¹, B., Nazminia¹, K., Chakraborty¹, S., Schilling², K., McAllister², S., and Baskaran¹, P.
¹Molecular Signaling Laboratory, School of Pharmacy, College of Health Sciences, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071; ²Central Wyoming College, 2660 Peck Avenue, Riverton, WY 82501; Email: Baskaran.Thyagarajan@uwyo.edu

ABSTRACT. Non-alcoholic fatty liver disease (NAFLD) is a major health concern of modern world. It is caused principally due to consuming fat rich food accompanied by sedentary lifestyle. NAFLD is characterized by the accumulation of fat (> 5%) in liver. NAFLD is comorbidity of obesity and is often associated with obesity-related health
issues like insulin resistance, diabetes, hyperlipidemia, hyperglycemia etc. Previous research has established a protective role of transient receptor potential vanilloid-1 (TRPV1) activation in obesity and metabolic dysfunction. Herein, we present evidence of effect of TRPV1 activation in countering NAFLD. In this study, we used wild type (WT) and TRPV1−/− mice fed with normal chow diet (NCD), high fat diet (HFD; 60% calories from fat), HFD + capsaicin (CAP, an agonist of TRPV1; 1.33 mg/kg). Our data show that CAP significantly decreased the accumulation of triglycerides, inflammatory cytokines like Tumor Necrosis Factor α (TNFα), Interleukin (IL)-1β, IL-6, C-Reactive Protein (CRP) in the plasma and liver of WT but not in TRPV1−/− mice. CAP also suppressed hepatic steatosis and fat accumulation in the liver. HFD suppressed the expression of TRPV1, and metabolically important proteins peroxisome proliferator activated receptor α (PPARα), uncoupling protein-1 (UCP1) and irtuin-1 (Sirt1) in the liver and CAP antagonized this. Also, CAP increased the phosphorylation of 5’-adenosine monophosphate activated kinase and caused an interaction between PPARα and sirtuin-1. This was associated with a concomitant increase in the expression of SiRT-1, deacetylation of PPARα and an enhancement of UCP-1 expression in the liver of WT but not in TRPV1−/− mice. Based on these results, we hypothesize that TRPV1 activation counters NAFLD by promoting a SiRT-1-PPARα-UCP-1 dependent mechanism.

9:00-9:20 am
Thematic Project: Polycystic Ovary Syndrome in American Indian Women: An Exploratory Study. Boyle¹ D., Alvero² R., Kooienda¹ S., Gilman-Kehrer¹ E., Womack-Shultz³ T, Felton¹ A, Carron¹ R. ¹Fay W. Whitney School of Nursing, University of Wyoming (Dept. 3065), 1000 East University Avenue, Laramie, WY 82071-2000; ²Warren Alpert School of Medicine, Brown University, 222 Richmond St, Providence, RI 02903; ³Central Wyoming College, 2660 Peck Avenue, Riverton, WY 82501; Email: rcarron@uwyo.edu

ABSTRACT. Background: Polycystic ovary syndrome (PCOS) is the most common endocrine disorder in reproductive-aged women affecting about 6-15% of women. PCOS symptoms and problems vary by culture. However, PCOS in American Indian women is not well described in regard to symptoms and problems as well as the effects of cultural and spiritual practices for self-management. The purpose of this project is to examine PCOS in Eastern Shoshone and Northern Arapaho women on the Wind River Indian Reservation (WRIR).

Methods: Eastern Shoshone (ES) and Northern Arapaho (NA) women with suspected PCOS aged 18-40 will be recruited. PCOS will be confirmed by the Rotterdam criteria. Participants then will be interviewed regarding symptoms and problems, the role of cultural, social, and spiritual practices for self-care management, and the role of health care providers in meeting the health care needs of the women. Participants also will complete the Short Form 12 quality of life survey and the Diabetes Risk Test. Further, a biomedical profile will be compiled and the prevalence of PCOS on the WRIR will be determined. A project at Central Wyoming College will recruit a sample of American Indian and non-American Indian women without PCOS and interview them with similar interview questions with “health” substituted for “PCOS.” Participants also will complete the same surveys.
Results/Implications: Ten American Indian women with documented PCOS have been recruited and interviewed. Preliminary results indicate that women are concerned about fertility and weight issues. The results from this study will provide evidence-based cultural specific information about PCOS in ES and NA women with clinically confirmed PCOS. The results from this study will enable health care providers to address the PCOS needs of ES and NA women better.

9:20-9:40 am  
**BREAK**

9:40-10:00 am  
Collaborative Project: **Generation of Electrospun Spider Silk Nanofiber Mats for Medical Applications.** Koratala¹, M., McInroy¹, A., Aikey², T., McCurdy¹, H., Teulé-Finley², F., and Johnson¹, PA. ¹ Department of Chemical Engineering, University of Wyoming, 1000 E. University Ave, Laramie, Wyoming. 82071; ²Department of Zoology and Physiology, University of Wyoming at Casper, 125 College Drive, Casper, Wyoming. 82601; Email: pjohn27@uwyo.edu

**ABSTRACT.** Spider silk is a natural material made up strictly of proteins. Spider silk’s durability, elasticity, and biocompatibility make it suitable for a broad range of medical applications such as sutures and wound dressings. Dragline silk of the Golden Orb Weaving Spider is composed of two proteins, major ampullate spidroin #1 and #2 (Masp1 and Masp2). Dragline silk by weight is stronger than steel and has elongation greater than 35%. Flagelliform silk has an extremely high extensibility of 200%. Flag/MaSp2 chimeric proteins named as A1S820 and Y1S820 has Flag-like repeating amino acid sequence that is responsible for elasticity and MaSp2-like alanine linker that is responsible for strength. The objective of this study is to develop and characterize (MaSp2, A1S820 and Y1S820) recombinant spider silk fiber mats for wound healing applications. Procedure: Electrospinning of non-woven randomly oriented nanofibers resembling extracellular matrix (ECM) structure makes them suitable for regeneration of ECM in wound healing applications. As the yield of spider silk protein is low, we have electrospun Bovine Serum Albumin (BSA) scaffolds as a template to develop experiments. The Teulé-Finley laboratory produced and purified 100mg quantities of the recombinant proteins and recently delivered them to the Johnson Laboratory. Mechanical and physical properties analysis will be performed on the recombinant silk fiber mats. To test the biocompatibility of the material, cell attachment and growth on the nanofiber scaffolds will be conducted. NIH 3t3 Fibroblasts, human vascular endothelial cells (HUVEC’s), keratinocytes will be seeded onto the fiber mats to understand the cell viability and proliferation on the RGD modified recombinant spider silk fiber mats.

10:00-10:20am  
Collaborative Project: **Investigating the Factors that Influence the Distribution and Impacts of Diseases in Wild Birds.** Carling¹, M., and Atkinson², E. ¹Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071. ²Biology Department, Northwest College, 231 West 6th Street, Powell, WY 82345. Email: mcarling@uwyo.edu

**ABSTRACT.** Both environmental heterogeneity and changing climate can impact disease dynamics in wild birds. To better understand these impacts, we have taken a
two-pronged, field-work intensive integrative approach that relies heavily on undergraduate participation. One prong, which uses detailed studies of the Dark-eyed Junco (*Junco hyemalis*) suggests that disease state (i.e., infected with malaria or not) varies between elevations (higher prevalence at the low elevation site). Interestingly, malaria prevalence does not influence any measure of aerobic performance (RMR, SMR, scope) at either elevation. However, there is a significant, positive relationships between hemoglobin and both SMR and scope in birds sampled at our low elevation site (~2070m). At the high elevation site (~2865m), there is no significant relationship between hemoglobin and any of the aerobic performance measures. The other prong, which employs a more general survey of disease state in individuals of multiple species across heterogeneous landscapes, suggests relative low prevalence of malaria; >30% of screened individuals, which is lower than we have found in our focused studies of *J. hyemalis*. In our broad survey, prevalence of West Nile Virus is even lower (~10%). Importantly, both components of our work involve significant contributions from undergraduates. Thus far, 12 students (eight from Northwest College, four from the University of Wyoming) have been trained in myriad field-work, lab-work and analytical techniques and at least two will likely attend the annual conference of the American Ornithological Society in July 2017.

10:20-10:40 am
Collaborative Project: Genomic Assessment of the Role of Relatedness in Spatial Overlap among Least Chipmunks (*Tamias minimus*) in the Laramie Range.
Lanier¹, H. C., and Ben-David², M. ¹Department of Zoology and Physiology, University of Wyoming at Casper, 125 College Drive, Casper, WY 82601; ²Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071; Email: bendavid@uwyo.edu

ABSTRACT. This project is a research and teaching collaboration among investigators and students from the University of Wyoming (UW) main campus, University of Wyoming at Casper (UWC) and Casper College (CC). Building on a long-term educational study of least chipmunks (*Tamias minimus*), conducted in the Medicine Bow National Forest, we harness molecular biology and bioinformatics techniques to address fundamental questions in spatial ecology and to train undergraduate students in genomics, biomedical, and wildlife techniques and analyses. Since 2006, the UW Wildlife Ecology and Management class (ZOO 4300/5300) at UW (Laramie) has been studying population dynamics in least chipmunks through annual trapping and radio-tracking. These radio-telemetry studies suggest intra-sexual segregation among females. In contrast, males exhibited higher home-range overlap with females and other males. Such spatial distribution is uncommon among the Sciuridae, in which females usually exhibit higher home-range overlap. Using these early findings the students are addressing the question whether chipmunks that exhibit higher overlap are more closely related to each other using a combination of genomic analyses and radio-telemetry. Through the work of students in ZOO 4300/5300 in fall 2016, we fitted 22 individuals with radio-collars and tracked them from September through October. We also collected blood samples from these individuals as well as all other trapped chipmunks (*n = 35*). Marissa Dyck, the UW undergraduate researcher leading the telemetry effort, quantified home range size and overlap from the 2016 data. DNA is currently extracted from
chipmunk blood samples at UWC. Reduced-representation genomes (ddRADseq) will be sequenced for each individual. The resulting data will be cleaned, aligned, and analyzed using bioinformatics approaches. Undergraduate researchers, as well as students in courses at UW and UWC, and throughout the state, will benefit through direct participation (wildlife biology techniques, DNA extraction, processing of next-generation sequencing data) or through indirect involvement (e.g., data analysis, class modules on population genomics). Our goal is to target external funding sources to continue this educational collaboration in the future.

10:40–11:00 am
Northwest College Program Report: Antibiotics, Birds, and Caloplaca - all the Way to Zonotrichia: The ABC’s of INBRE at Northwest College. Atkinson¹, E.C., Childs², A., Cuddy², M. Dickerson¹, J.W., Kimble¹, E., and Udodong², U. ¹Biology Department, Northwest College, 231 W. 6th Street, Powell, WY 82435. ²Chemistry Department, Northwest College, 231 W. 6th Street, Powell, WY 82435. Email: eric.atkinson@nwc.edu

ABSTRACT. At Northwest College, INBRE supported undergraduate research, exploration, and mentoring span topics including novel antibiotic research, characterization of bactericidal compounds, rotifer endocrine disruption, and avian disease. Our broadening trend continues with extensions to water quality assessment through which we work to meet our program goals: 1) enhance opportunities for Wyoming community college undergraduates to better understand (and ultimately participate in) the field of biomedical research; and, 2) develop a pipeline of students with an interest in biomedical science who would then go on to complete their baccalaureate degrees and/or graduate degrees at UW. In 2015, we initiated a 2-credit class (BIOL 2465 - Research Problems in Biology) to partner with our INBRE program providing transcript documentation of research participation. To date, we have enrolled 30 students. In 2017, our INBRE program will be graduating 8 students with AS degrees. Two additional students have been ‘entrained’ by the excitement of our young INBRE researchers and will attend and present their non-INBRE supported research at UGRD. Once again, INBRE students have been recognized by faculty as “Outstanding Chemistry” and “Outstanding Biology” students. Further directions of our students is variable, with one already accepted to Michigan State University College of Human Medicine, another transferring to Purdue University, 2 actively applying to medical schools, 1 applying to graduate schools in wildlife biology, and 3 transferring to UW where they hope to continue as part of UW INBRE. All in all, these students have blossomed through the opportunities afforded them by INBRE. Our 5 supported and 2 informal faculty mentors have guided 15 students within our program during 2016/2017. Previous participants have matriculated into graduate/professional schools including UW School of Pharmacy, WWAMI (UW), Northern Michigan University, as well as the Peace Corps serving in Ghana. In addition to WY INBRE events, 3 students attended professional meetings, (1 presenting at the 12th Annual Academic Surgical Congress and 2 attending the ASM Microbe Conference) . Additionally, we were awarded SPREM support in FY 2015/2016 to remodel a computer lab turning it into our new Molecular Techniques Lab. We occupied this space in Fall 2016 with high daily student use.
Central Wyoming College Program Report: The Central Wyoming College Undergraduate Research Program Engages Students in Diverse Research Activities. McAllister1, S., Kapp2, K., Klancher2, J., Spoonhunter2, T., and Womack-Shultz1, T. 1Division of Health Science and Public Safety, Central Wyoming College, 2660 Peck Avenue, Riverton, WY 82501; 2Division of Arts and Sciences, Central Wyoming College, 2660 Peck Avenue, Riverton, WY 82501. Email: smcallis@cwc.edu

ABSTRACT. Five INBRE supported faculty continued to engage undergraduate students in a wide variety of research projects this year. Associate Professor Jacki Klancher led the fourteen-day Central Wyoming College Interdisciplinary Climate Change Expedition which collected data measuring ice depth of the Dinwoody glacier using ground penetrating radar, performed broad scale high elevation water sampling to test for E. coli and collected snow samples to analyze black carbon. INBRE funds supported travel and transport costs for this expedition and the purchase of i-Pad minis to collect GPS data points using ESRI collector software. Professor Kirsten Kapp received a SPREM grant to support her sabbatical for the spring semester. This allowed her to focus more exclusively on her research analyzing microplastics in the Snake River and incorporating DNA barcoding into her biology curriculum. Kirsten and her INBRE supported student traveled to Boise to speak about their work at the Annual Idaho Water Quality Workshop. As a result of her research experience with INBRE, Kirsten’s student will be interning with WY DEQ-Lander this summer. Professor Tara Womack-Shultz is a co-collaborator on a project investigating the cultural influences on American Indian women with Polycystic Ovarian Syndrome. Her team has been conducting interviews of subjects which include a demographic survey and a diabetes risk assessment. Dr. Tarissa Spoonhunter is a co-collaborator on a mentor program for college age adults to gain interest in the biomedical fields of research. Program workshops focused on tribal health and wellness for mentors and mentees and the tribal community. Tribal health incorporates a holistic view of wellness for the Wind River Indian Reservation. Workshop topics were: Research in Native American Communities, Institutional Review Boards, Addiction is not a Disease, Food is Medicine, Northern Arapaho Suicide Prevention and White Buffalo Recovery, and Language and Wellness. The mentorship also included a student focusing on Lifestyle Balance. Steven McAllister is a co-collaborator on a project investigating the ability of capsaicin to protect against the effects of obesity. He also received SPREM funding to bring inquiry-
based activities into the major’s biology courses at CWC. His team is also studying West Nile virus in Fremont County.

2:20-2:40 pm  
**Casper College/UW Casper Program Report: INBRE-Supported Research at Casper College and the University of Wyoming at Casper.** Motriuk-Smith, D., Chase, J., Lanier, H., Teulé-Finley, F., Seville, R.S.  
*University of Wyoming at Casper, University of Wyoming, 125 College Drive, Casper, WY 82601; Department of Biology, Casper College, 125 College Drive, Casper, WY 82601; Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071; Email: motriuk@uwyo.edu*

**ABSTRACT.** The goal of the INBRE supported research is to train undergraduate students in conducting biomedical research. Students receiving the INBRE internship were engaged in diverse biomedical research projects ranging from studying antibiotic resistance genes in the environment, electrospinning spider silk nanofiber mats from recombinant spider silk-like proteins, morphology and phylogeny of parasites, and developing an assay for screening the interaction of an intrinsically disordered protein with its binding partners. In addition, numerous ecology projects such as mammalian, avian, and invertebrate habitat diversity, molecular and morphological identification were investigated. Our students learned biological, molecular, and fieldwork techniques. They participated in writing and editing abstracts and papers, and in preparation of presentations for conferences. During the FY 2016/2017 sixteen students were awarded the INBRE internship and were mentored by four faculty members. Four students co-authored presentations at one regional and one national conference. Two students co-authored one peer-reviewed paper. Two faculty members received two Wyoming INBRE Scaled Participatory Research and Education Model grants (SPREM) and two faculty members received Wyoming INBRE UW - Wyoming Community College Collaborative Grant awards. Three faculty members were developing collaborative projects with UW-Laramie faculty located at three separate academic departments.

2:40-3:00 pm  
*Department of Biology, Division of Science and Mathematics, Eastern Wyoming College, 3200 West C Street, Torrington, WY 82240; Department of Ecosystem Science and Management, College of Agriculture and Natural Resources, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071; Email: chris.wenzel@ewc.wy.edu*

**ABSTRACT.** Soils and groundwater in east central Goshen County, Wyoming have been documented to have high nitrate levels since the 1950’s (Rapp et al., 1997; Parks, 1991). EPA studies have indicated that nitrates are harmful to both human and animal health at concentrations above established limits. The focus of this study is to document the extent to which the presence of nosZ, narG, nirK, and nirS gene-containing bacteria, reduce soil nitrate levels and subsequent groundwater nitrate levels by the natural process of denitrification. In addition, nitrous oxide (N2O) emissions have been assayed to further assess denitrification activity. Thus far, DNA and RNA have been extracted
from soil bacteria, and molecular techniques are being used to amplify the gene fragments and to quantify presence of nitrate reducing soil microorganisms. Student engagement has remained steady since the study began in 2013.

3:00-3:20 pm

Laramie County Community College Program Report: PUI... Fertilizer for Undergraduate Minds and Growth at Laramie County Community College.
Wangeline, A.L., and Roehrs, Z.P. School of Math and Sciences, Laramie County Community College, 1400 E College Dr., Cheyenne, WY 82007; Email: awangeli@lccc.wy.edu; zroehrs@lccc.wy.edu

ABSTRACT. The mission of the Laramie County Community College (LCCC) IDeA Networks for Biomedical Research Excellence (INBRE) research group is to improve the access of students to authentic research experiences. We attempt to accomplish this through a myriad of channels on which we will report our activities and successes over the previous year (May 2016 – April 2017). During this period 19 students participated in INBRE supported research, with 3 graduating and 1 continuing research at University of Wyoming (UW) as a Wyoming INBRE Transition Fellow. Eleven INBRE supported students presented 7 posters and 5 oral presentations at the 1st Annual Wyoming INBRE Conference, 2016 Undergraduate Research Day, Wyoming INBRE Fall 2016 Retreat and 96th Annual Meeting of the American Society of Mammalogists. We continue our collaborations with faculty at UW, Colorado State University and University of Northern Colorado as well as with Laramie County Conservation District, U.S. Park Service and National Center for Genomic Resources. We have a new faculty member in the research group (Dr. Courtney Springer) and hope to bring more LCCC faculty on board. We received two SPREM grants this year; one for improvements to our molecular lab and one for a new Adjunct Faculty member (Dr. M. Susan Marion) to develop a motion capture lab for studying movement kinematics. With the completion of a new research classroom (partly supported by Wyoming INBRE), Dr. Wangeline’s return to faculty life, and Dr. Roehrs return from Texas, we look forward to renewed focus on our mission this coming year.

3:20-3:40 pm	BREAK

3:40-4:00 pm

Western Wyoming Community College Program Report: INBRE Research at Western WY Community College Provides Tremendous Student Opportunities.
Chew, B. Western Wyoming Community College, 2500 College Drive, Rock Springs, WY 82901; Email: bchew@westernwyoming.edu

ABSTRACT. INBRE research at WWCC is designed to expose promising freshman and sophomore students to undergraduate research, to encourage students to consider a career that includes research, to enhance students’ opportunities in a competitive world, and to further scientific knowledge through presentation and publication of research work. Currently, 12 students participate in INBRE funded research; topics include evolutionary biology/ecology, and cardiovascular physiology. Three faculty members have established INBRE research programs. WWCC currently has 5 INBRE Transition Fellows at the University of Wyoming; at least 4 current INBRE students will apply for a
Transition Fellowship for Fall, 2017. Research at WWCC would not be possible without the WY INBRE grant. The opportunities presented by INBRE have allowed the college to recruit and retain better faculty members; students involved in INBRE research at WWCC become better, more confident students, while not only developing enhanced lab/field skills, but also responsibility, perseverance, and leadership skills.

4:00-4:20 pm
Northern Wyoming Community College District- Sheridan and Gillette Colleges
Program Report: INBRE-Supported Research Activities. Ami Erickson1, Sherri Adams2, Rachel Kristiansen1, and Rob Milne1, 1Department of Natural Science, Sheridan College, 3059 Coffeen Ave, Sheridan, WY 82801
2Department of Natural Science, Gillette College, 300 West Sinclair, Gillette, WY 82718; Email: amie@sheridan.edu
ABSTRACT. Northern Wyoming Community College has participated in Wyoming INBRE since its origin. During this time many faculty and community college undergraduate students have had the chance to conduct research and attend conferences, accumulating a variety of science skills and experiences. During the past few years, five tracks of research have been developed by our participating NWCCD science instructors. These tracks are: 1) plant stress physiology and development; 2) biometal redox and leaching; 3) massage effects on brain wave patterns; 4) snake venom protein anticoagulation; and 5) subbituminous coal carbon characteristics. This year we have had nine students actively involved in one or more of these tracks. Specific projects include examining 1) grape somatic embryo shoot and root germination exposed to increasing levels of NaCl; 2) the effects of different water quality variables on plant growth, nutrient status and physiology; 3) the leaching of biometals exposed to “body-like” solutions; 4) the isolation of anticoagulation proteins from snake venom to be incorporated into degradable polymers; and 5) the development of a FIFR spectroscopy method to examine coal carbon characteristics. Research projects and student experiences will be discussed.

4:20-4:40 pm
Collaborative Project: Grapevine Cellular and Physiological Response to Salinity Stress. Dhekney2, S., and Erickson1, A. 1Department of Plant Sciences, University of Wyoming, 3401 Coffeen Avenue, Sheridan WY 82801; 2Department of Natural Science, Sheridan College, 3059 Coffeen Ave, Sheridan, WY 82801; Email: amie@sheridan.edu
ABSTRACT. The goal of this project is to increase our understanding of Vitis (grape) response to drought and salinity stress, which can be potentially applied to improve grapevine salinity stress tolerance via precision breeding technology. To optimize protocols for screening response of various grapevine species and cultivars to salt stress under in vitro conditions, we are developing a procedure to screen grape somatic embryos. This method will be used to screen genetically modified embryogenic cultures that carry genes inserted for salinity tolerance. The genes of interest are involved in Na+ and K+ intracellular homeostasis. The SOS2 and AVP 1 genes were isolated from V. rupestris ‘Richter’ RNA by RT-PCR. PCR products obtained after amplification of cDNA sequences were then inserted into a binary vector.
under control of a constitutive promoter and the neomycin phosphotransferase II (npt II) gene that was used as a selectable marker. The binary vectors were inserted into Agrobacterium EHA 105 using the freeze-thaw method. Embryogenic cultures of Thompson Seedless’ and tobacco leaf discs were co-cultivated with the Agrobacterium containing the SOS2 gene. Transgenic embryos and plants were recovered following selection on medium containing kanamycin. Transgenic plants will be hardened, transferred to a greenhouse and screened for salt and drought tolerance. Additionally, transgenic plants harboring the AVP1 gene will also be produced for screening against drought and salinity tolerance.

5:00-6:30 pm  RECEPTION AND UNDERGRADUATE POSTER SESSION, Marion H. Rochelle Gateway Center, Salon A/B

6:30-8:30 PM  BANQUET AND KEYNOTE TALK

Knockin’ on Fertility’s Door: Understanding Gonadotrope Function. Navratil, Amy M. Department of Zoology and Physiology, University of Wyoming, Laramie, WY, 82071. Email: anavrati@uwyo.edu

ABSTRACT. The anterior pituitary is the body’s master gland. It contains 5 different endocrine cell types, one of which are gonadotrope cells. A primary role of gonadotrope cells is to coordinate pulsatile release of luteinizing hormone (LH). In females, a large acute surge in LH is obligatory for inducing ovulation and is mandatory for fertility in all mammals. My seminar will tell the story of how gonadotrope cells synthesize and secrete LH to regulate reproduction. First, I will discuss how gonadotrope cells activate intracellular signaling pathways, focusing on calcium, to induce epigenetic regulation of LH synthesis. More specifically, I focus on how a family of calcium dependent enzymes termed peptidylarginine deiminases (PADs), are critical for modifying histones to unspool DNA and ultimately increase LH gene expression prior to ovulation. After discussing LH synthesis, I next will detail how highly dynamic gonadotrope cells undergo directed mobilization towards vascular elements to facilitate LH secretion into peripheral circulation. Understanding mechanisms that regulate LH synthesis and secretion is critical both to our basic understanding of mammalian reproduction and for new clinical approaches for fertility management.
Saturday, April 29th
Wyoming Union Ballroom, University of Wyoming

8:00-9:45 am  INBRE Network Breakfast and Community Forum- Wyoming INBRE updates on eRA Commons, Wyoming INBRE Reporting, assessment, programs and upcoming events, question and answer session.

10:00-4:00 pm  Wyoming Undergraduate Research Day/ Wyoming INBRE Oral Presentation Sessions, UW Classroom rooms 215 and 219

3:00-5:00 pm  Poster Session- Wyoming Union 2nd Floor

5:45-7:30pm  Wyoming URD Banquet and Keynote Talk, Wyoming Union Ballroom

POSTER ABSTRACTS

GRADUATE STUDENT/POSTDOCTORAL RESEARCHER

The graduate poster session will be held on Thursday April 27th 2017 from 5:30-7:30PM at the University of Wyoming Conference Center (UWCC; West end of Hilton Inn) Salon D. All graduate student presenters must set up their posters between 3-5PM on Thursday April 27th.

GP01: Remotely Controlled Listerial Bactodrones as Anticancer Therapy. Abrar, R. and Gomelsky, M. Department of Molecular Biology, University of Wyoming, Laramie, WY 82071

ABSTRACT. Immunosuppression in tumor microenvironment (TME) is a major challenge for developing cancer immunotherapy, and myeloid derived suppressor cells (MDSCs) are major contributors to the immunosuppression. MDSCs are a heterogeneous population of immature granulocytes, macrophages and dendritic cells. Attenuated, nonvirulent, strains of Listeria monocytogenes (Lm) injected into bloodstream efficiently infect MDSCs. Because MDSCs are attracted to primary tumors and metastases, Lm is delivered there too. Lm spreads from MDSCs to the tumor cells via a cell-to-cell transfer. Immunosuppression helps Lm survive and thrive within the TME, whereas it is destroyed in the healthy tissues. Selective accumulation in tumors makes Lm an attractive delivery platform for anticancer therapies.

Cyclic dimeric GMP (c-di-GMP) is a bacterial second messenger that activates the STING pathway of the innate immune system. c-di-GMP activates tumor-associated antigen-specific T cells at low doses and induce immunogenic tumor cell death at higher doses. A combination of one high followed by multiple low doses of c-di-GMP has been shown to greatly reduce the number of metastases and inhibit growth of the primary tumor mouse cancer models. Both Lm and c-di-GMP target MDSCs, reprogramming them into IL-12 production that stimulates naïve and mature T cells to attack and destroy tumors.
The goal of this project is to engineer and test Lm for intratumoral delivery of c-di-GMP and other tumor-destroying drugs. We intend to remotely control the release of c-di-GMP by engineered Lm to avoid immune system overstimulation, which may result in cytokine storm. c-di-GMP release will be controlled optogenetically, via light within the near-infrared window (NIRW). Such light penetrates deep into mammalian tissues. We have engineered a robust NIRW light-activated c-di-GMP synthase (diguanylate cyclase) that produces c-di-GMP upon NIRW light irradiation. The gene encoding this synthase will be inserted in Lm and delivered to tumors. The effect of the genetically delivered light-activated release of c-di-GMP will be tested in murine tumor models. We expect that remotely controlled Lm (listerial bactodrone) that delivers innate immune system stimulant, c-di-GMP, for regulated intratumoral release will enhance efficacy and improve safety of this anticancer immunotherapy.

GP02: Capsaicin Stimulates Brown Adipose Tissue Activation and Enhances Mitochondrial Biogenesis. Baskaran, P., Zhang, Z.J., and Thyagarajan, B. School of Pharmacy, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

ABSTRACT. Diet-induced obesity leads to metabolic syndrome and one third of the world population is obese or overweight. Currently no effective strategy is available to counter obesity. Recent research from our laboratory and from others suggest that activation of transient receptor potential vanilloid subfamily 1 counters obesity. Our previous research work unambiguously shows that capsaicin triggers the molecular conversion of white to brute (Brown in white) phenotype by activating sirtuin-1-dependent deacetylation and interaction of peroxisome proliferator activated receptor gamma (PPARγ) and PR domain containing protein 16 (PRDM-16) via TRPV1-dependent mechanism. This research suggests that TRPV1 activation by capsaicin (CAP) significantly enhanced the expression of thermogenic proteins including bone morphogenetic protein 8b (BMP8b), mitochondrial uncoupling protein-1 (UCP-1), PPARγ coactivator 1α (PGC-1α), sirtuin-1 (SIRT-1) and PRDM-16 in brown adipose tissue (BAT) while high fat diet (HFD)-feeding increased body weight gain by suppressing these thermogenic proteins. Capsaicin also significantly enhanced the expression of thermogenic markers and increased basal and forskolin stimulated lipolysis in BAT. Capsaicin decreased serum glucose, triglyceride and cholesterol levels and restored glucose intolerance and insulin resistance observed in HFD-fed mice. These data suggest an enhancement of plasma GLP-1 level, BAT activation and a concomitant regulation of glucose homeostasis by capsaicin. Further, the upregulation of PGC-1α, a gene that metabolically regulates mitochondrial biogenesis, by capsaicin is associated with an increased number of mitochondria in BAT. Also, capsaicin supplementation in diet increased the metabolic activity, respiratory quotient and heat production in live mice. These data provide evidence for the regulation of BAT activation and enhancement of mitochondrial biogenesis by capsaicin to increase energy expenditure and heat production to counter obesity.

GP03: Differences in Excitation and Inhibition in Thalamocortical Circuits via CRACM in a Freeze Lesion Model of Focal Cortical Dysplasia. Burns, D., and Sun,
Q.Q. Departments of Zoology & Physiology and Neuroscience, University of Wyoming, 1000 E. University Ave., Laramie, WY, 82070

ABSTRACT. Background: The thalamus is a deep brain structure known as a relay station for most information coming and going to/from the cortex. Malformations of cortical development (MCD) have been highly correlated with development of epilepsy, cognitive disabilities, and psychiatric disorders. Focal cortical dysplasia (FCD) is a type of MCD. The epileptogenesis brought about by FCD and other MCDs is still not fully understood, and a better understanding may lead to better treatments and outcomes.

Objective: To determine how thalamic projections into the barrel cortex would be changed, and to what degree, following freeze lesion (FL) treatment, which mimics FCD, and what effect this has on the ratio of excitation/inhibition induced potentials within the circuit(s).

Methods: CD1 mice were either freeze lesion treated or sham treated at postnatal day 0-1. They were then injected with an AAV containing Channelrhodopsin-2 (ChR2) at ~1 month old. At ~2 months old they were euthanized and brains were removed and sectioned. 300μm slices were cut and those containing the expressed virus were kept and used for electrophysiological optogenetic recording. Channelrhodopsin-2-assisted circuit mapping (CRACM) was then carried out on patched cells in or around the barrel cortex (layer 4 or 5a). In the FL treated mice, recordings were carried out “near” and “far” from the FL microgyrus.

Results: Preliminary results suggest that there is a difference between control and FL treated mice with respect to the excitatory and inhibitory components of the thalamocortical circuits. The balance between excitation and inhibition is altered in FL mice, with hyperexcitability developing, and this disruption may contribute to epileptogenesis.

Conclusion: Damage to axons and cortical circuits can lead to a many pathological problems, such as epilepsy, schizophrenia, and depression. CRACM is a very powerful tool for studying neuronal circuitry and how it changes in diseased states, allowing for a better understanding of what goes wrong and potentially how to correct it.

GP04: Homotypic Interaction of a Dynamic Cell Surface Receptor Governs Bacterial Kin Recognition. Cao, P., and Wall, D. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071

ABSTRACT. Kin recognition in microbes allows close relatives to cooperate and confers advantages to organisms living in complex environments. In a soil-dwelling bacterium, Myxococcus xanthus, individuals use a polymorphic cell surface receptor called TraA to identify kin. Upon physical contact, cells recognize siblings bearing compatible receptors and undergo outer membrane exchange (OME). OME involves bidirectional transfer of large quantities of cellular goods between cells and provides a platform for coordinating social interactions. We previously showed that TraA requires the partner protein TraB to function in cell-cell adhesion and OME. Notably, the TraA/B-dependent adhesion is traA allele-specific, where the polymorphisms within TraA govern the binding selectivity between cells. In addition, we revealed the malleable nature of TraA, and strikingly, we identified a single residue switch within TraA that governs recognition specificity. That is, amino acid substitutions at this position reprogram the specificity of recognition. Here we sought to elucidate the molecular
basis of OME. To directly visualize recognition between cells, we created functional mCherry and msfGFP fusions to TraA. Interestingly, we found that TraA foci formed along junctions when cells physically interact. Such foci formation requires cell-cell contact and the presence of compatible TraA receptors in both cells. We then mixed cells bearing TraA-mCherry with cells bearing TraA-msfGFP. Notably, co-localization of TraA-mCherry and TraA-msfGFP foci was observed along cell-cell junctions, suggesting that TraA receptors from the neighboring cells directly interact. We also found that the transfer of fluorescently-labeled OM cargo occurs where TraA foci form. We conclude that TraA receptors from adjacent cells interact in a homotypic manner and bring the opposing membranes into close proximity, which in turn leads to transient membrane fusion junctions that allow the bidirectional exchange of OM components between cells.

GP05: TRPV1 Activation Induces Mitophagy to Prevent Non-Alcoholic Fatty Liver Disease. Chakraborty, S., Baskaran, P. and Thyagarajan, B. Molecular Signaling Laboratory, School of Pharmacy, College of Health Sciences, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

ABSTRACT. Non-alcoholic fatty liver disease (NAFLD), a comorbidity associated with obesity, is a growing health concern all over the world. Currently twenty five percent of US population has NAFLD. Other than diet control, no effective pharmacotherapy is available to treat NAFLD. Our laboratory is research is geared to evaluate the effect of activation of transeience receptor potential vanilloid subfamily 1 by capsaicin (CAP) in the prevention of NAFLD. Previous research has revealed that NAFLD causes mitochondrial dysfunction and accumulation of damaged mitochondria in the liver cells. Here we evaluated the effect of CAP on mitophagy signaling stimulated by TRPV1 activation. We analysed the expression levels of proteins involved in various stages of mitophagy in the liver samples of normal chow diet (NCD), high fat diet (HFD) and HFD + CAP (1.33 mg/kg body weight)-fed wild type and TRPV1-/- mice. HFD supressed the expression unc51 like autophagy activating kinase-1 (ULK1, a protein of autophagy induction complex) and the phosphorylation of ULK1 in liver of WT mice and CAP reversed this. Also, CAP increased the expression of Beclin-1, Autophagy-related protein-7(Atg7), Light Chain 3(LC3B) I and II (components of initiation and elongation complex of autophagosome formation) in the liver of HFD-fed WT but not in TRPV1-/- mice. Expression of Parkin was also increased in CAP-fed group. Our preliminary findings suggest that CAP can promote mitophagy to prevent NAFLD. Further studies are in progress to analyse the mechanisms involved in TRPV1-activation-stimulated mitophagy.

GP06: Using Microfluidic Encapsulation of Xenopus laevis Embryonic Cytoplasm to Identify Nuclear Size Scaling Mechanisms. Chen1, P., Nelson2, K.M., Oakey2 J. and Levy1, D.L. 1Department of Molecular Biology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071; 2Department of Chemical & Petroleum Engineering, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. Early Xenopus laevis embryogenesis is characterized by dramatic reductions in nuclear size. Between fertilization and the midblastula transition (stage 8), there is an ~4-fold reduction in the volume of individual nuclei, and an additional ~4-fold reduction from the MBT to gastrulation (stages 10-12). The regulatory mechanisms
responsible for these nuclear size reductions are poorly understood. While cytoplasmic factors, including importin \( \alpha \) and PKC, have been implicated in regulating nuclear size, the contribution of cytoplasmic volume to nuclear size scaling during embryogenesis has not been tested. To investigate this question, we couple \( X. \textit{laevis} \) embryo extracts with microfluidic devices that allow us to generate cytoplasmic droplets of defined size and shape. We isolate embryonic cytoplasm containing endogenous embryonic nuclei from stage 10 embryos, and then encapsulate single nuclei in extract droplets of differing volumes and shapes. Nuclei are visualized by uptake of GFP-NLS or mCherry-NLS, and we quantify changes in nuclear size over time. We find that nuclei in droplets expand to a new steady-state size after \(~3 \) hours. In droplets ranging in volume from \( 0.02 \text{ nl} - 0.5 \text{ nl} \), nuclear volume increases by 1.4- to 3-fold, with larger increases occurring in larger droplets. These data indicate that the volume of embryonic cytoplasm is limiting for nuclear growth. However, in droplets greater than \(~0.5 \text{ nl} \), the increase in nuclear volume reaches a threshold of \(~3 \)-fold. Also, in droplets similar in size to stage 8 blastomeres (\(~0.8 \text{ nl} \)), the nuclei do not reach the average size of nuclei present in stage 8 embryos. Furthermore, when gastrula-stage nuclei are treated with stage 5 embryo extract, the average nuclear volume increases \(~4.5\)-fold in gastrula-cell-sized droplets (\(~0.08 \text{ nl} \)). These results suggest that cytoplasmic composition also contributes to nuclear size scaling. Additionally, nuclei exhibit similar growth trends in spherical and flattened droplets of comparable volume, indicating droplet shape minimally influences nuclear growth. When embryo extract is treated with a dominant negative importin \( \beta \) binding domain fragment, nuclei fail to grow in both small and large droplets, indicating nuclear import is necessary for observed nuclear growth.

GP07: Characterization of Transcriptional and Posttranscriptional Processing of \( \text{Rbm20} \). Chen, Z., Zhu, C., Sun\(^1\), M. and Guo, W. Department of Animal Science, University of Wyoming, Laramie, WY82071

ABSTRACT. Introduction: RNA binding motif 20 (Rbm20), a recently cloned muscle tissue specific splicing factor, is associated with dilated cardiomyopathy (DCM). With RBM20 specific antibody, the western blot indicated Rbm20 may have distinct splicing variants. We hypothesize that Rbm20 expresses different isoforms which may play distinct role in the development of DCM and heart failure. This study is to investigate the transcriptional and posttranscriptional regulation of Rbm20 in rats.

Results: The full length of rat Rbm20 is organized in 14 exons which encode a protein of 1207 amino acids. We define this full length of RBM20 as isoform 1. RT-PCR and RACE verified six other splicing variants in rat heart tissue. The variant 2 is produced by using a different polyadenylation site that causes a shorter 3' UTR and has an alternative cleavage when compared to variant 1, while both variants 1 and 2 encode the full length RBM20 with the same amino acid sequence. The variant 3 uses an alternative exon14 at the 3' end and encodes a shorter isoform with 1184 amino acids and a distinct C-terminus when compared to isoform 1. The variant 4 introduces a stop code after exon 7 due to the use of the different 3'UTR and encodes 686 amino acids resulting in a smaller isoform defined as isoform 4. The variant 5 and -6 differ in the 5' UTR compared to variant 1 and -4, respectively. The resulting isoform 5 and -6 have a shorter N-terminus compared to isoform 1 and -4, respectively. The variant 7 represents the shortest transcript and encodes the shortest isoform 7. These isoforms were verified
with western blot indicating three protein bands which the sizes are similar to validated isoforms.

Conclusions: Taken together, we first investigated the transcriptional and posttranslational regulation of Rbm20, and found that Rbm20 gene harbors multiple isoforms in rat heart tissue. However, effect of different isoforms of Rbm20 on the regulation of gene splicing in the heart need be further studied.

This work is supported by the NIFA-USDA 1009266, NIH NIGMS20GM103432, AHA BGIA and Faculty-Grant-in-Aid from University of Wyoming.

GP08: Detection of Inattention During Different Simulated Driving Tasks Using Four Physiological Signals. Darzi1, A., and Novak1, D. Department of electrical engineering, University of Wyoming, 100 East University street, Laramie, Wyoming, 82071

ABSTRACT. Inattention during driving is a frequent cause of car accidents, and is often caused by boredom or doing multiple tasks simultaneously (e.g. using a cell phone while driving). Furthermore, factors such as lack of sleep, personality, stress level, mood and driving skill also contribute to inattention and probability of accidents. In this study, we examined whether physiological measurements can be used to automatically detect different types of inattention during driving. Twenty healthy participants performed four sessions in a driving simulator. Each session consisted of multiple scenarios that differed according to weather (sunny or snowy), driving environment (town or highway) and cell phone use (with or without a cell phone). Furthermore, two of the sessions were performed while the participant was mildly sleep-deprived, resulting in a variety of distraction levels and types. During each scenario, physiological responses (respiration rate, heart rate, skin conductance and temperature) were measured, and participants filled out the NASA-TLX workload questionnaire after each scenario. Furthermore, driver personality, stress level, and mood were assessed at the start of each session. Results showed that cell phone usage and snowy weather significantly increased driver workload and the rate of accidents. The physiological indexes also show a significant difference in different weather condition. In the future, we will also investigate the effect of personality and mood on driving performance and physiology.

GP09: Fabrication of Multimodal Biodegradable Nanoparticles for Targeted Drug Delivery. Debroy Monzón, D., Li, D., and Oakey, J. Department of Chemical Engineering, University of Wyoming, 1000 E University Ave, Laramie, WY, 82071

ABSTRACT. Degradable polymer nanoparticles have become an intensively studied platform for the delivery of drugs to treat many diseases, since they can be easily modified to enhance treatment efficacy by combining different modalities such as thermal therapy and immunotherapy. Although there are many methods for fabricating these nanoparticles, they are often batch processes that produce broad size distributions. In this project, we employ a two-level device structure to produce micro- and nano-scale droplets to obtain monodisperse particles in a continuous fashion by merging two immiscible fluid streams. This method has an advantage over traditional approaches, such as micellization, because it allows precise dose control of each substance, facile functionalization of particle surfaces, and is compatible with a variety
of chemotherapy and immunotherapy agents. Additionally, the continuous nature of the operation allows for real time variation of operating conditions to obtain a variety of products on the same device. However, some key challenges remain, particularly the generation of sub-micrometer, stable water-in-oil droplets and their polymerization in situ. To address these challenges, we take advantage of oxygen inhibition, which is often undesirable, to control particle size and final surface properties. Briefly, due to oxygen diffusion and inhibition, droplets polymerize from the core outward. The resulting unpolymerized shell’s thickness can be precisely controlled, enabling the production of nanoparticles from larger and easily produced micro-droplets. Using poly(ethylene glycol) diacrylate (PEGDA) as a model polymer platform, we embark on understanding droplet formation and photopolymerization kinetics via both modeling and experiments to achieve multimodal drug delivery vehicles.

GP10: TGRH_257440 and TGRH_285730 Are Essential for Growth of T. gondii. Denton, S. L., and Gigley, J. P. Department of Molecular Biology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. Toxoplasma gondii is one of the most successful pathogens on the planet capable of intracellular infection of virtually any animal cell. To date, no effective treatment exists for prevention of T. gondii contraction nor a cure for an existing infection, thus, once the parasite infects an individual it is present for the host’s lifetime. The acute phase of the infection occurs when the disseminating parasite rapidly replicates and destroys the host cell, potentially causing disease in the form of hydrocephaly, blindness, and death. This life stage is a cycle of active invasion, discharge of specialized secretory organelles and their regeneration, replication, and egress, requiring alternatively mandated vesicular traffic. Typically, vesicular traffic is mediated by membrane fusion events, but mechanisms regarding how membrane fusion is specifically regulated by the parasite remain largely unknown. Comparison of known proteins involved in membrane fusion in Saccharomyces cerevisiae to the putative transcriptome of T. gondii reveals two protein candidates that may have conserved function in membrane fusion, but also have domains of unknown function. CRISPR-Cas9 mediated mutation of the genomic locus of TGRH_257440 and TG_RH285730 is lethal to the parasite.

GP11: Isolation and Characterization of Regulatory T cells for Localized Immunosuppression of Allografts. Dhungana, S., and Bushman, J. School of Pharmacy, University of Wyoming, 1000 E. University Ave, Laramie, 82071

ABSTRACT. Regulatory T-cells (Tregs) potently suppress the activity of CD4+ and CD8+ effector T cells. Tregs have been successfully used to mitigate the symptoms of graft vs host disease and other autoimmune disorders and are being explored as a method to achieve long term tolerance of allografted tissue in order to minimize the need to systemic immunosuppression (SIS). We are hypothesizing that Tregs will allow for regeneration of segmental peripheral nerve (PN) defects using allografted PNs. Allografted PNs carry several advantages compared to current options for repair of segmental PN defects, but is not clinically practiced widely due to the serious side effects and risks to the patient from SIS. Our overall hypothesis is that localized application of Tregs around a PN allograft may be sufficient to prevent rejection during
the critical time frame of regeneration as well as help eliminate multiple side effect of SIS application. To prepare for in vivo studies in a rat model of PN allografting, we are isolating and characterizing Tregs from rat spleen to meet specification thresholds. Tregs are purified from spleen of rats using MACS cell separation technique and culture conditions were established to produce sufficient quantities for transplantation studies. Tregs are immunologically characterized by their antigenicity and functionally for the ability to suppress the proliferation of effector T cells. Finally, Tregs are embedded within hydrogel carriers that will be used to deliver the Tregs in vivo and the biocompatibility of the carrier is assessed.

GP12: Cardiomyocyte-Specific Deletion of Cathepsin K Protects Against Doxorubicin-Induced Cardiac Dysfunction. Guo¹, R, Hua¹, Y, Ren¹, J, Bornfeldt², K and Nair¹, S; ¹Center for Cardiovascular Research and Alternative Medicine, School of Pharmacy College of Health Sciences, University of Wyoming, Laramie, WY 82072; ²UW Diabetes Institute, Departments of Medicine, Division of Metabolism, Endocrinology and Nutrition, and Pathology, School of Medicine, University of Washington, Seattle, WA 98109

ABSTRACT. Background and objective: Doxorubicin (DOX) is an extensively used and effective anticancer chemotherapeutic agent. Although it exhibits beneficial effects against cancer, the clinical use of DOX can induce serious cardiotoxicity, the major outcome of which is cardiomyopathy followed by congestive heart failure. The cysteine protease cathepsin K is elevated in both human and animal models of heart failure. Global deletion of cathepsin K attenuates both high fat diet- and pressure overload-induced cardiac hypertrophy and contractile dysfunction, although the role of cardiac cathepsin K remains unclear. To this end, the objective of this study was to generate a cardiomyocyte-specific knockout of cathepsin K (Ctsk<sup>−/−</sup>) and to test the hypothesis that deletion of cardiac cathepsin K protects against doxorubicin-induced cardiotoxicity. Methods: Ctsk<sup>−/−</sup> mice were generated by Ctsk targeted trap-allele including both FLP-FRT and Cre-lox systems. Cre-recombinase in MYH-Cre transgenic mice recognizes LoxP sites in “floxed (flanked by LoxP)” mice, and deletes the exons from 2 to 5 of Ctsk. Protein and mRNA levels of Ctsk and exon 2 were determined by Western blot and quantitative RT-PCR respectively. Four-months-old control (fl/fl-Cre<sup>−</sup>) and Ctsk<sup>−/−</sup> (fl/fl-Cre<sup>+</sup>) mice received two injections of doxorubicin (10mg/kg, i.p. at 3-day intervals, 20mg/kg cumulative), one week following which, body and tissue weight, echocardiographic properties, cardiomyocyte contractile function and Ca<sup>2+</sup>-handling were evaluated. Cardiac structure was assessed by histomorphology. Myofibrillar and fibrotic protein markers were determined by Western blot. Results: Cathepsin K mRNA and protein were attenuated by over 80% in the hearts of the knockout mice compared to the control. Doxorubicin injections resulted in an increase in the length of individual cardiomyocytes, and exhibited cardiomyocyte contractile dysfunction, as well as impaired intracellular Ca<sup>2+</sup> homeostasis. Additionally, mice receiving doxorubicin exhibited significant increases in end-systolic and end-diastolic diameters and decreased fractional shortening and wall thickness. Interestingly, both histomorphology and Western blot showed significantly impaired cardiac sarcomere and myofibrils. These deleterious cardiac effects of doxorubicin were significantly attenuated or reversed in mice lacking cardiac cathepsin K. Conclusion: Mitigation of doxorubicin-
induced cardiac anomalies by targeted deletion of cardiac cathepsin K suggests that cathepsin K represents a novel, bona-fide, pharmacological target for cardiac toxicity and complications.

GP13: Order from Disorder: Structure and Function of the Cell Pole Organizing Protein PopZ. Holmes, J., Bowman, G. Department of Molecular Biology, University of Wyoming, 1000 E University Ave, Laramie, WY, 82071

ABSTRACT. Despite being the simplest organisms, bacteria have highly organized internal subcellular anatomies. Among the most prominent and widely observed features are multiprotein complexes at the cell poles. Some species produce scaffold-like polymer forming proteins to facilitate the formation of these structures. One such protein in Caulobacter crescentus is a 177-amino acid (aa) protein called Polar organizing protein Z (PopZ). We find that PopZ’s polar organizing activity requires self-interactions for scaffold assembly and additional direct interactions with at least eight different proteins to form a heterogeneous macromolecular complex. The binding determinants for non-self-interactions include 24 aa at the N terminus, a 32-aa region near the C-terminal homo-oligomeric assembly domain, and portions of a proline, aspartic acid, and glutamic acid (PED) rich linker region. Together, these elements are sufficient for interacting with all binding partners, even in the absence of homo-oligomeric assembly. Structural analysis of the heterogeneous protein interaction domain revealed that it is intrinsically disordered, and in this way it may be analogous to p53 and other intrinsically disordered hub proteins that organize complex signaling networks in eukaryotic cells. To improve our understanding of the structural determinants that confer PopZ binding specificity, we are creating chimeric proteins in which Caulobacter sequence is mixed with sequences from other species that exhibit overlapping but non-identical ranges of binding partner affinities. Consistent with the flexible nature of intrinsically disordered hub proteins, we are finding that most of the sequence tolerates large variation without significant effects on interaction specificity or affinity. We identified key areas of sequence dependence in amino acids that flank a short region that is predicted to form an alpha-helix during protein-protein interactions. We propose that vicinal proline residues influence a disordered region’s propensity for adopting transient secondary structure, which aids the formation of a structured protein binding interface.

GP14: Validation of a Novel Molecular Assay for the Detection of Brucella abortus Field Strain and the Deployment in Yellowstone National Park Bison Herd. Hull1, N., Robbe-Austerman2, S., Miller1, J., Amundson1, S., Laegreid1, W., Quance2, C., and Schumaker1, B.1Department of Veterinary Sciences, University of Wyoming, 1174 Snowy Range Road, Laramie, WY 82070; 2Mycobacteria and Brucella Section, United States Department of Agriculture – Animal Plant Health Inspection Service – National Veterinary Services Laboratory, 1920 Dayton Avenue, Ames, IA 50010

ABSTRACT. Brucella abortus is the etiologic agent of brucellosis. In the United States, the sole remaining reservoir is in the Greater Yellowstone Area, affecting bison and elk with spillovers into livestock.1 Current diagnostics are not ideal for eradication efforts. Bacterial culture is considered the “gold-standard” test for diagnosis.2 However, it can
take up to ten-days, is labor intensive, and presents a high risk to personnel, as brucellosis is the most common laboratory acquired infection worldwide. Only 46% of seropositive animals will produce a culture.\textsuperscript{3} \textsuperscript{4-5} Representing the most robust in-silico analysis to date, 100 whole genome sequences of brucellae were assembled and aligned to identify informative single nucleotide polymorphisms that could be exploited for a quantitative real-time polymerase chain reaction assay.

One candidate probe-set was blindly tested on tissue samples from seropositive Yellowstone National Park bison. Culture identified 17/45 (37.8%) animals as positive. Our qPCR primers-probe set identified the same 17 animals (at the tissue level) and an additional 23 animals (40/45) as positive for brucellosis. Amplicons of seropositive-culture-negative animals were sequenced. Sequence was BLAST'ed back to only \textit{B. abortus} field strain.

GP15: Natural Killer Cells in Adaptive Immunity to Toxoplasma gondii Infection. Ivanova, D. and Gigley, J. Department of Molecular Biology, University of Wyoming, Laramie, WY 82071

\textbf{ABSTRACT.} Toxoplasma gondii is a highly prevalent food-borne obligate intracellular parasitic protozoan present in 30\% of humans worldwide and is a significant health concern for immunocompromised people. Currently there is no vaccine or drug that can prevent or clear infection. Therefore, understanding how the immune system responds to infection is important for future therapy development. CD8 T cells are known to be required for long-term protective immunity against this parasite, but their responses are insufficient to clear infection. Recent reports suggest the innate immune cell known as the Natural Killer (NK) cell can develop characteristics of adaptive immune cells such as T cells and contribute to long-term immunity, however these traits can be either cell intrinsic or extrinsic depending on the disease situation. NK cells are critical for early immunity to \textit{T. gondii} via cytokine (IFN\textgamma) production but their role beyond acute infection and in long-term immunity has not been addressed. Using an attenuated parasite infection and re-challenge model we demonstrate that NK cells are critical for adaptive immune responses to secondary \textit{T. gondii} infection. They are required for survival against lethal \textit{T. gondii} reinfection. NK cells in secondary infection are recruited to the site of infection and become activated. Adoptive transfer of \textit{T. gondii} experienced NK cells into NK cell deficient animals did not convey better protection against infection than naïve NK cells. This result suggests parasite experienced NK cells may not be intrinsically different than naïve cells and rely on extrinsic factors for activation. Secondary NK cell responses are independent of CD4 or CD8 T cells and surprisingly IL-12p70 even though IL-12p70 is essential for primary NK cell responses during acute \textit{T. gondii} infection. However, in vivo blockade of IL-12p40 subunit that is shared between IL-12p70 and IL-23 negatively affected NK cell numbers and functionality during reinfection. In the future studies, we will address the mechanism by which IL-12p40 and/or IL-23 directs NK cell response to \textit{T. gondii} infection.
GP16: Cytocompatible and Versatile Microfluidic-Based Cell Encapsulation.
Zhongliang, J., and Oakey, J. Department of Chemical Engineering, University of Wyoming, 1000 E university Ave, Laramie, WY, 82071

ABSTRACT. Cell encapsulation with PEG-based hydrogel scaffolds has been demonstrated as a robust cell delivery and 3D cell culture strategy, providing alternative strategies for tissue scaffolding, regenerative medicine, and understanding cell-matrix interactions. Recent development in multiphase microfluidics has enabled the miniaturization of PEG hydrogels into hydrogel microspheres as cell-laden vehicles. However, challenges associated with the production of cell-laden microgels, that are typically negligible at bulk length scales, have not been appreciated until recently. The presence and rapid diffusion of oxygen from the ambient environment dramatically inhibits the chain-growth polymerization of polyethylene glycol diacrylate (PEGDA). Furthermore, reactive oxygen species (ROS) generated by this process can decrease cell viability. Another promising scaffold material, polyethylene glycol norbornene (PEGNB), allows orthogonal addition with high cytocompatibility. However, its step-growth kinetics are slow and is therefore challenging to polymerize within droplets flowing through microfluidic devices. Here, we introduce a microfluidic-based droplet fabrication platform with the ability to consistently generate uniform cell-laden emulsions, which can be gelled by exposure to UV light. In this work, we introduce microfluidic devices to overcome processing challenges introduced by each hydrogel forming system and favorably compare PEGNB to PEGDA as a microscale cell encapsulant. Toxicity and versatility of the platform was validated through the investigation of specific gelation parameters and the successful encapsulation of four mammalian cell types with relatively high long-term cell viability, respectively. We also found increasing monomer concentration would compromise long-term cell viability, presumably due to the increase of hydrogel stiffness does not grant sufficient oxygen and nutrient diffusion. In conclusion, we show that this PEGNB microencapsulation platform is capable of generating cell-laden hydrogel microspheres with well-controlled size distributions and high long-term cell viability. Meanwhile, it is well tolerated by most of the mammalian cells, makes it a versatile platform to be broadly applied to tissue engineering with further modifications of biological niches.

GP17: GnRH Induced Citrullination of the Cytoskeleton Is Important for LH Secretion in Gonadotrope Cells. Khan 1, S.A., DeVore 1, S.B., Edwards 1, B.S., Muth 2, A., Thompson 2 P.R., Cherrington 1, B.D. and Navratil 1, A.M. 1Department of Zoology and Physiology, University of Wyoming, 100 E. University Ave., Laramie, WY 82071; 2Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, 364 Plantation Street Worcester, MA 01605

ABSTRACT. Our recent work shows that peptidylarginine deiminase 2 (PAD2) is highly expressed in mouse gonadotropes cells during estrus, precisely when high levels of LH secretion are critical for inducing ovulation. PADs are a family of Ca 2+ dependent enzymes that catalyze the conversion of positively charged peptidyl arginines to neutrally charged citrulline, which can alter protein structure and function. Known cytoplasmic targets of citrullination include the cytoskeletal proteins, actin and tubulin. Our work and others, suggests that GnRH engagement of the cytoskeleton not only facilitates the exocytosis of LH but also organizes these cells into a favorable spatial...
orientation to achieve an increase in circulating LH *in vivo*. Thus, we hypothesized that post-translational modification of the cytoskeleton by PADs is important for modulating gonadotrope plasticity and function. To test this, we first examined if the GnRH agonist Buserelin (GnRHa) induces citrullination of the cytoskeleton in the gonadotrope derived LβT2 cell line. Using a biotin-phenylglyoxal (Biotin-PG) probe, we selectively enriched citrullinated proteins from our lysates. Western blot analysis reveals that GnRHa temporally induces citrullination of β-actin in LβT2 cells, with maximal levels occurring at 10 minutes. The rapid citrullination kinetics are consistent with actin remodeling events occurring within seconds following GnRH activation. Citrullination of actin induced by GnRHa was blunted when cells were pre-treated with a pan PAD inhibitor biphenyl-benzimidazole-Cl-amidine (BB-ClA). To identify function, imaging studies examined actin in LβT2 cells and primary mouse gonadotropes illustrate that BB-ClA attenuated GnRHa induced actin reorganization. At issue is how citrullination of actin mediates gonadotrope secretory events. To address this, pituitary primary cultures were pre-treated with BB-ClA, then received pulses of GnRHa at 30 and 60 minutes. Cell culture medium was harvested following subsequent 30 and 60 min pulses of GnRHa and LH levels were analyzed by RIA. Our results show that inhibition of PAD catalyzed citrullination results in a decrease in LH secretion following BB-ClA pre-treatment in the presence of GnRHa. Taken together, these observations suggest that GnRH induced actin citrullination is a novel post-translational mechanism that can regulate cellular architecture and LH release in gonadotrope cells.

**GP18: Preparation and Characterization of Electrospun Fiber Mats for Wound Healing Applications.** Koratala¹, M., McInroy¹, A., Aikey², T., McCurdy¹, H., Teulé-Finley², F. and Johnson¹, P.A.

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**ABSTRACT.** Spider silk is a natural material made up strictly of proteins. Spider silk’s durability, elasticity, and biocompatibility make it suitable for a broad range of medical applications such as sutures and wound dressings. Dragline silk of the Golden Orb Weaving Spider is composed of two proteins, major ampullate spidroin #1 and #2 (Masp1 and Masp2). Dragline silk by weight is stronger than steel and has elongation greater than 35%. Flagelliform is a weak silk with an extremely high extensibility of 200%. Flag/MaSp2 chimeric proteins named as A1S820 and Y1S820 has Flag-like repeating amino acid sequence that is responsible for elasticity and MaSp2-like alanine linker that is responsible for strength. The objective of this study is to develop and characterize (MaSp2, A1S820 and Y1S820) recombinant spider silk fiber mats for wound healing applications. Procedure: Electrospinning of non-woven randomly oriented nanofibers resembling extracellular matrix (ECM) structure makes them suitable for regeneration of ECM in wound healing applications. As the yield of spider silk protein is low, we are electrospinning Bovine Serum Albumin (BSA) scaffolds as a template to develop experiments. Mechanical and physical properties analysis will be performed on the recombinant silk fiber mats. To test the biocompatibility of the material, it is essential to investigate cell attachment and growth on the nanofiber scaffolds. NIH 3t3 Fibroblasts, human vascular endothelial cells (HUVEC’s),
keratinocytes will be seeded onto the fiber mats to understand the cell viability and proliferation on the RGD immobilized recombinant spider silk fiber mats.

**GP19: TRPV1 Protein Expression in Adipose Tissues Determines Metabolic Activity and Energy Expenditure.** Krishnan, V., Baskaran, P., and Thyagarajan, B. Molecular Signaling Laboratory, School of Pharmacy, College of Health Sciences, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

**ABSTRACT.** Recent research envisages a prominent role of transient receptor potential vanilloid subfamily 1 (TRPV1) channel protein in metabolic diseases. However, published literature suggests that both activation of TRPV1 and the loss of TRPV1 are implicated in antagonizing diet-induced obesity. One potential reason behind this is variations in the percentage of fat and the type of fat used in diets to cause obesity. This study evaluated the effect of feeding high fat diet (HFD; 60% calories from fat) in wild type and TRPV1−/− mice. We fed subgroups of these mice with either normal chow diet (11% calories from fat) or HFD. Mice were fed ad libitum NCD or HFD and water for 32 weeks. We monitored food/water intake and weekly weight gain and measured the respiratory quotient, heat production and locomotor activity of these mice. Also, we measured the expression of adipogenic and thermogenic genes in white (epididymal) as well as brown fat pads isolated from these NCD or HFD-fed wild type and TRPV1−/− mice. Our data show that both white and brown adipocytes of wild type mice expressed TRPV1 protein endogenously. Genetic ablation of TRPV1 significantly decreased the expression of several genes that are implicated in lipid metabolism and thermogenesis in mice that were fed NCD. This is associated with a decreased locomotor activity in TRPV1−/− mice compared to wild type. Also, high fat diet caused a more significant down-regulation of thermogenic proteins in the adipose tissues of TRPV1−/− compared to wild type mice. Also, HFD-challenge caused more significant damage to the liver of TRPV1−/− mice and caused higher lipid accumulation compared to wild type mice. Our data reveal that lack of TRPV1 strikingly increased the susceptibility to metabolic impairment when challenged with a metabolic stress like HFD compared to wild type mice. Our data suggest that the expression and activation of TRPV1 will help in shedding new light into a strategy to counter obesity by tweaking adipogenic and thermogenic mechanisms in adipose tissues.

**GP20: A NimA-kinase Pathway Controls CDC-42 Activity and Actin Organization in C. elegans Epidermis.** Lažetić, V., and Fay, D. S. Department of Molecular Biology, University of Wyoming, 1000 E University Ave, Laramie, 82071

**ABSTRACT.** During C. elegans molting the epidermal apical extracellular matrix (cuticle) is extensively remodeled. We have shown that the NimA-related kinases, NEKL-2/NEK8 and NEKL-3/NEK6/NEK7, as well as their conserved ankyrin-repeat partners, MLT-2/ANKS6, MLT-3/ANKS3 and MLT-4/INVS, are essential for molting. Both NEKLs and MLTs are expressed in the epidermal syncytia and act primarily within two complexes composed of NEKL-2–MLT-2–MLT-4 and NEKL-3–MLT-3. To understand how the NEKL–MLT network controls molting, we identified suppressors of nekl mutant molting defects. Our screen identified CDC-42, a highly conserved Rho-family GTPase, which is important for the establishment of cell polarity and for organization of the actin cytoskeleton. Notably, molting has been proposed to require
extensive reorganization of actin within the epidermis. Specifically, actin is reorganized at each molt to form a series of circumferential bundles along the apical surface of hyp7, however, the mechanisms underlying this process are unknown. We found that inhibition of NEKL-MLT activities leads to defects in the pattern of apical actin and failure to form molting-specific actin bundles. Furthermore, expression studies indicate that components of the NEKL-MLT network colocalize with actin in specific regions of the epidermis. In addition, normal localization of CDC-42 in the epidermis depends on presence of NEKL-MLT proteins, and CDC-42 partially colocalizes with MLT-2. Our findings suggest that the NEKL–MLT network may negatively regulate CDC-42 activity and that partial inhibition of CDC-42 may thus reduce defects in nekl–mlt mutants. Interestingly, we also observed that downregulation of cdc-42 on its own can lead to molting defects, suggesting that there is a tight balance between NEKL-MLT and CDC-42 activities in the epidermis. Notably, studies in mammalian cells have implicated the MLT-4 ortholog in the regulation of CDC42 activity and apical actin organization. In addition, it was independently shown that the mammalian orthologs of NEKL-3, physically associate with CDC42, however no functional connection between these proteins has been described. For the first time, our data provide in vivo evidence for a functional link between the NEKL–MLT network and regulation of the actin cytoskeleton through the CDC42 pathway.

GP21: The Role of Protein Citrullination in Lactating Mouse Mammary Epithelial Cells. Li, G., and Cherrington, B. Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave, Laramie, WY, 82071

ABSTRACT. Peptidylarginine deiminase (PAD) enzymes post-translationally convert arginine amino acids into neutral citrulline residues. Major protein targets for PAD catalyzed citrullination are arginine residues on cytoplasmic and nuclear proteins; however, the consequences of this post-translational modification on cell function are not well understood. Our previous studies show that multiple proteins including histones are citrullinated in the mouse mammary epithelial CID-9 cell line and lactation day 9 (L9) mouse mammary glands. To begin to identify these citrullinated proteins, we conducted proof-of-principle experiments using an anti-cytokeratin 8/18 and anti-citrullinated protein antibodies for co-immunoprecipitation (IP). Using this method, we identified cytokeratin 8/18 as a citrullinated cytoskeletal protein in L9 mammary glands. Based on this work, our first objective is to identify additional citrullinated cytoskeletal proteins in the lactating mouse mammary gland using an unbiased, proteomic approach. To accomplish this, citrullinated proteins in L9 mammary glands were labeled with a biotin-conjugated phenylglyoxal (Biotin-PG) probe, and purified by IP using streptavidin-agarose beads. After separating the citrullinated proteins using SDS-PAGE, gels were stained with coomassie blue and prominent bands cored. Mass spectrometry studies are currently underway to identify citrullinated proteins in cored samples. In addition to citrullinated cytoskeletal proteins, our past work shows that PADs catalyze the citrullination of histone H3 arginine residues 2, 8, 17 in CID-9 cells and L9 mammary glands. Therefore, our second objective is to determine if histone citrullination regulates expression of lactation related genes such as butyrophilin (BTN1A1), which is important for secretion of milk fat droplets. To test this, CID-9 cells were pretreated for 1 hour with
a pan-PAD inhibitor BB-Cl-amidine (BB-CIA) (2µM) followed by 5µg/ml of prolactin for 12 hours. Preliminary qPCR data reveals that BB-CIA treatment decreases \textit{BTN1A1} mRNA suggesting that histone citrullination may regulate expression of important lactation related genes. In conclusion, our work demonstrates that PAD catalyzed citrullination of cytoskeletal filaments and histones functions to regulate the synthesis and secretion of milk in the lactating mouse mammary gland.

GP22: Improving MALDI-TOF Identification Capabilities Using Offline LC-MALDI-TOF. \textit{Maus}¹, A., Anders², J., Bisha², B. and Basile¹, F. ¹Department of Chemistry, University of Wyoming, 1000 E. University Ave., Laramie, WY, 82071; ²Department of Animal Science, University of Wyoming, 1000 E. University Ave., Laramie, WY, 82071

\textbf{ABSTRACT.} A well-established method for microorganism identification is MALDI-TOF-MS “fingerprinting” or “profiling”. Despite its widespread acceptance, this method still has some limitations. One limitation of particular interest in the clinical setting is the inability to differentiate between antibiotic resistant and susceptible bacteria. This issue is believed to be the result of the limited protein detection capabilities of the technique. Detection is typically limited to small ribosomal proteins below 14kDa, which are highly conserved within a species. Thus, detecting only these proteins is inadequate for identification of antibiotic resistant bacteria. To expand the detectable proteome, we have deployed offline Liquid Chromatography (LC) separation prior to MALDI-TOF-MS analysis. Our results prove that this methodology drastically increases the number of detected protein signals in both the mid mass (3k-20kDa) and high mass (20k-100kDa) regions. This technique was then applied to \textit{E. coli} isolates obtained from a concentrated animal feeding operation in an effort to identify protein biomarkers for antibiotic resistance. Prior to proteomic analysis, the resistance characteristics of these isolates was established by the disk diffusion method. Proteins were then chemically extracted from selected isolates. The proteins were separated by reversed phase LC and deposited onto the MALDI plate in discrete fractions, which underwent MALDI-TOF-MS analysis. Based on the disk diffusion results, principle component analysis was then applied to the resulting peak lists in search of biomarkers. Four protein signals were determined to be correlated to resistance to β-lactam antibiotics. The protein biomarker detected at \textit{m/z} 9355 exhibited the strongest correlation to β-lactam resistance. Bottom-up proteomic analysis of the fraction corresponding to that biomarker confidently established the presence of β-lactamase. Efforts are currently underway to determine the identity of the biomarker \textit{m/z} 9355 and its relation to β-lactamase.

GP23: A Synthetic Genetic Circuit for Programming Asymmetric Cell Division in \textit{E. coli}. Mushnikov, N., and Bowman, G. Department of Molecular Biology, University of Wyoming, 1000 E., University Ave., Laramie, WY, 82071

\textbf{ABSTRACT.} In multicellular eukaryotic organisms, asymmetrically dividing stem cells produce daughter cells with different fates and different patterns of gene expression. Cell polarity and corresponding patterns of asymmetric localization of regulatory proteins play a crucial role in this process. The prokaryotic world features its own examples of this phenomenon, such as the asymmetric cell divisions that produce differentiated cell layers in microbial biofilms. Here, the biofilm-specific gene expression is modulated by the intracellular concentration of the secondary messenger molecule c-
di-GMP. Another example is the asymmetric cell division of *Caulobacter crescentus*, which results in two morphologically distinct cells – a swarmer cell bearing a flagellum and a sessile cell bearing a stalk. Here, asymmetry is regulated by multiple proteins that are localized to one or both cell poles, including the polar scaffolding protein PopZ. In this project, we combine elements of these two systems to create a synthetic genetic circuit for creating programmable patterns of asymmetric cell division in *E. coli*. By using the polar organizing capability of PopZ, we establish an asymmetric distribution of c-di-GMP, which when coupled to a c-di-GMP dependent transcriptional regulation system results in a programmable system for producing two distinct cell types in a population of dividing cells. Our results show that a small set of components is sufficient for establishing differential control of gene expression in the context of asymmetric cell division in bacteria. Thus, seemingly complex cellular behaviors normally associated with multicellular life can be mimicked with a surprisingly simple set of genes. We also discuss strategies for future utilization, such as a stem cell – factory cell fermentation system for the production of toxic molecules.

**GP24: NLR Family, Pyrin Domain-Containing 3 Knockout Rescues Systolic Cardiac Dysfunction Induced by High-Fat Diet Feeding**. Peterson, M.R., Haller, S., Ta, T., Bosch, L., Smith, A., Sanders, A., Aquino, J., He, G. School of Pharmacy, University of Wyoming, 1000 E. University Avenue, Laramie, Wyoming 82071

**ABSTRACT.** NLR family, pyrin domain-containing 3 (NLRP3) is a pattern recognition receptor responsible for perpetuating an inflammatory response through production of pro-inflammatory cytokines IL-1β and IL-18. It has been implicated in the sustained inflammatory response in obesity and multiple cardiovascular disease conditions. In order to investigate NLRP3 as a potential therapeutic target in metabolic syndrome, C57BL/6 wild-type (WT) and NLRP3 knockout (NLRP3−/−) mice were fed a normal diet (ND; 12% fat chow) or a high fat diet (HFD; 45% fat chow) for 5 months. At 5 months, echocardiography and glucose tolerance tests (GTTS) were performed. Cardiac function assessed by fractional shortening (FS) was significantly impaired by HFD feeding in the WT group (0.335 HFD vs. 0.456 ND; p<0.05) but not in the NLRP3−/− (0.449 HFD vs. 0.492 ND; p>0.05). FS was higher in NLRP3−/−HFD than in WT-HFD (p<0.05). Two-dimensional analysis shows the FS difference between NLRP3−/−HFD and WT-HFD was primarily explained by the difference in left ventricular end-systolic dimension (0.2716 cm WT vs. 0.1883 cm NLRP3−/−; p<0.05). Glucose tolerance measured by area under the curve (AUC) was significantly impaired by HFD feeding for both WT (23183 ND vs. 57298 HFD; p<0.001) and NLRP3−/− (23197 ND vs. 44626 HFD; p<0.001), but significantly better in the NLRP3−/−HFD than in WT-HFD (p<0.01). HFD feeding increased fasting blood glucose (FBG) for both WT (97.7 mg dl−1 ND vs. 164.7 mg dl−1 HFD; p<0.01) and NLRP3−/− (80.50 mg dl−1 ND vs. 108.8 mg dl−1 HFD; p<0.05), but significantly less in NLRP3−/− mice (NLRP3−/− vs. WT; p<0.05). For GTTs, body weight was significantly higher in the WT than NLRP3−/− fed HFD (47.93 g vs. 36.5 g; p<0.001). Body weight explained 92% of variation in glucose tolerance (p<0.0001) and 69% of variation in fasting blood glucose (p<0.0001). WT-HFD averaged 1.31X heavier than NLRP3−/−HFD, while the AUC for the IGTT was 1.28X larger for the WT-HFD than NLRP3−/−HFD. Body weights were not significantly different between genotypes at the time of echo. The results suggest that knockout of NLRP3 may be protective against...
HFD induced cardiovascular dysfunction. A protective effect on glucose tolerance is not strongly supported.

**GP25: The Role of RBM20 on Skeletal Muscle Regeneration After Injury.** Rexiati, M., Sun, M., and Guo, W. *Department of Animal Science, College of Agriculture and Natural Resources, University of Wyoming, Laramie, WY82071, USA*

**ABSTRACT.** Skeletal muscle injuries are extremely common during sports or athletic endeavor and impaired muscle function or increased risk of recurring injury is accompanied after the recovery. During recovery, satellite cells, the quiescent skeletal stem cells residing in the space between basal lamina and muscle fiber membrane, orchestrate the regeneration of the myofibers. Recently, RNA binding motif 20 (Rbm20) expression is correlated with sarcomere assembly in differentiating myoblasts: Rbm20 expression peaks during differentiation and declined as the sarcomere begins to mature. We induced skeletal muscle injury by the injection of barium chloride to the rat *Tibialis anterior* and investigated the regeneration process 18 hours, 3 days, 5 days, 7 days and 14 days post-injection between wild type and Rbm20 knockout rats. We discovered impaired skeletal muscle regeneration in Rbm20 knockout rats with respect to wild type. At 5 days post injury, the Rbm20 knockout *Tibialis anterior* has lighter muscle mass compared to wild type. Moreover, we found the cross sectional areas of the wild type myofibers are larger than the Rbm20 knockout group at 5 days and 7 days post-injury. However, the regenerating myofiber numbers are similar between wild type and knockout group. Interestingly, wild type rats have significantly less fibrotic areas with regard to Rbm20 knockout group at 14 days post-injury. The finding of this study suggest that Rbm20 is a potential regulator of skeletal muscle regeneration and could serve as a novel target for improving skeletal muscle healing after injury and muscle diseases.

*Acknowledgments:* This work was supported by the NIFA-USDA 1009266, National Institutes of Health NIGMS P20GM103432, AHA BGIA and Faculty-Grant-in-Aid from University of Wyoming.

**GP26: Posttraumatic Stress and Anger: Model Evaluation in a Civilian Trauma Sample.** Ripley, A. J. & Clapp, J. D. *Psychology Department, University of Wyoming, 1000E University Ave., Laramie, WY 82071*

**ABSTRACT.** Whereas fear and anxiety are the emotions most commonly associated with posttraumatic stress disorder (PTSD), relations with anger have also received considerable interest. Chemtob, Novaco, Hamada, Gross, and Smith (1997) propose the relation between PTSD severity and subjective anger among combat veterans is mediated by specific cognitive, arousal, and behavioral processes. Proposed cognitive processes include hostile attribution bias, which is thought to increase the likelihood of responding to perceived provocation with anger. Arousal mechanisms are believed to manifest as increased cardiovascular reactivity (e.g., blood pressure, heart rate, respiration rate) to frustrating stimuli. Behavioral processes involve aggressive behavioral scripts and increased aggressive inclinations. The aim of the present research was to determine the extent to which these processes mediate relations between PTSD severity and subjective anger in survivors of non-combat trauma.
Participants (N=152) were trauma-exposed university students completing a laboratory-based anger induction procedure. Probable trauma exposure and responses to the PTSD Checklist (PCL-5) were collected during initial screening. Participants completed self-report measures of cognitive and behavioral anger processes upon presenting to the lab. Continuous blood pressure, heart rate, and respiration rate were assessed as participants were asked to ruminate on an angry memory. Subjective anger was assessed following the anger rumination task. Mediation models were used to evaluate for indirect effects of PTSD severity on subjective anger through cognitive, arousal, and behavioral processes.

Results were partially consistent with hypothesized relations proposed by Chemtob et al.’s (1997) model. PCL-5 scores predicted hostile attribution bias (α=.161, p=.047), which in turn predicted ratings of subjective anger (β=.312, p<.001), resulting in a significant indirect effect (αβ=.019, 95% CI [.004, .042]). Additionally, PTSD evidenced a marginally significant relation with aggressive behavioral scripts (α=.158, p=.052), which predicted ratings of subjective anger (β=.195, p=.018), resulting in a reliable indirect effect (αβ=.011, 95% CI [.001, .038]). Data failed to support indirect relations through cardiovascular activation.

Results provide preliminary support that anger-related processes proposed by Chemtob et al. may be similar across survivors of combat and non-combat trauma. Specifically, hostile attribution bias and aggressive behavioral scripts may mediate the relation of PTSD and subjective anger in non-combat trauma survivors.

GP27: The potential role of RBM20 in protection from obesity and diabetes in rats
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Denise De Loera¹,², Andrea Sanchez Walk¹,³, Jun Ren⁴ and Wei Guo¹
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ABSTRACT. Obesity and Diabetes are public health problems with more than one-third of US adults (35.7%) afflicted with obesity. The obesity is known to predispose to chronic diseases such as type II diabetes, non-alcoholic fatty liver disease (NAFLD), heart disease, stroke and certain types of cancers. It is postulated that the hormonal imbalance, insulin resistance and low grade inflammation are the potential risk factors for the adiposity. However, the molecular mechanisms for the progression are still unclear. It is proposed that around half of mutations linked to disease affect alternative splicing (AS) and several splicing factors (SRp20, CUG-BP1 etc.) have been found to regulate AS of obesity and diabetes genes. Recently, we found that the expression and downstream effects of RNA binding motif 20 (RBM20), a splicing factor that regulates gene AS mainly in muscle tissues, can be regulated through the PI3K/Akt/mTOR and insulin signaling. Therefore, it could not only regulate AS of cardiac proteins mastering the stiffness of ventricular wall but also play a role in the progression of obesity and/or diabetes by regulating glucose uptake via insulin signaling. In this project, we hypothesize that RBM20 regulates insulin signaling associated genes and thus influences lipid and/or glucose metabolism. To test this hypothesis, wild type (WT) (N=12) and RBM20 knockout (KO) rats (N=6) were fed high-fat diet (HFD) and normal
diet (ND) for 6 month to induce obesity type and its metabolic, oxidative, and functional complications such as diabetes. Body weight and food consumption were measured and glucose tolerance test (GTT) was performed. The results indicated that body weight of WT rats was significant higher than that of KO group and the food consumption has no significant difference between two groups. GTT showed that KO group has faster glucose uptake than the control group, suggesting active insulin and insulin receptors in KO rat skeletal muscles since RBM20 is highly expressed in muscle tissues with less or none expression in other tissues. Therefore, in the future, it would be interesting to study whether RBM20 increases insulin sensitivity in skeletal muscle by regulating alternative splicing of insulin signaling associated gene. All together, these preliminary data suggest that RBM20 could play a role in the development of obesity and/or diabetes.

This work is supported by the NIFA-USDA 1009266, NIH NIGMSP20GM103432, AHA BGIA and Faculty-Grant-in-Aid from University of Wyoming

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ABSTRACT. The evolutionary origin of endomembranes in eukaryotes is a long-standing question in cell biology. We are exploring this question in a bacterial model: members of the Planctomycete-Verrucomicrobia-Chlamydiae (PVC) superphylum. Many of these bacteria contain eukaryotic-like features atypical for prokaryotes, including morphologically complex endomembranes of unknown composition. The planctomycete Gemmata obscuriglobus has an extensive endomembrane system and is one of only a handful of bacterial species that produce membrane sterols. Eukaryotic sterols are necessary for membrane structure, dynamics, and many membrane-mediated processes. Bacteria typically contain the structurally similar hopanoids as sterol surrogates, suggesting bacterial sterols should be functionally redundant. Our goal is to elucidate the function and evolutionary origin of bacterial sterols relative to their eukaryotic counterparts. Using complementary chemical and genetic approaches, we found membrane sterols to be essential for survival in G. obscuriglobus, the first instance in a bacterium. Using time-lapse light microscopy and transmission electron microscopy, we observed a profound defect in cellular replication associated with sterol depletion, suggesting membrane sterols are essential for proper cell division in G. obscuriglobus. We used a bioinformatic approach to predict the prevalence of sterol synthesis in other members of the PVC superphylum. In candidate sterol-producing organisms, we have applied the same chemical and genetic methodology to determine sterol function. Lastly, we have conducted phylogenetic analysis to determine whether PVC sterol biosynthesis arose independently through convergent evolutionary processes, or was acquired through horizontal transfer from eukaryotic lineages.
Determining the function and evolutionary origin of bacterial sterols could provide a useful context for understanding the origin of eukaryotic endomembranes.

**GP29: A Protein of Unknown Function is Involved in Chromosome Segregation Regulation in Caulobacter.** Wang, H., and Bowman, G. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071

**ABSTRACT.** All species have mechanisms for the faithful transmission of genetic material to daughter cells. *Caulobacter* uses the Par components ParA (motor), parS (centromere), and ParB (binds to ParA and parS), as well as two additional proteins, PopZ and TipN, which are localized to the cell poles and provide spatial and temporal cues that guide centromere segregation in M phase. Chromosome replication and segregation occur precisely once per cell cycle, which raises the question of whether these processes are subject to negative regulation.

In this study, we have identified an evolutionarily conserved protein, given the name SpbR, that may play such a role. Consistent with this, SpbR overproducing cells initiate chromosome replication and segregation like wild type cells, but the travel of the centromere across the cell is severely inhibited. Fluorescent protein tagging shows that SpbR is localized to the cell poles in a PopZ-dependent manner, and a bacterial two-hybrid assay supports a direct interaction between PopZ and SpbR. Overproduction of SpbR exhibits a strong synthetic phenotype with tipN mutants, providing further evidence of interaction between SpbR and polar cues for chromosome segregation. SpbR levels are under tight cell-cycle dependent control, and the protein is rapidly degraded in G0 cells immediately after cell division. Subsequent accumulation of SpbR may help to limit the window of chromosome segregation activity to earlier stages in the cell cycle.

**GP30: Maternal Obesity Impairs Contractile Function of Cardiomyocytes in Term Fetal Sheep.** Wang, Q., Zhu, C., Sun, M., Hu, Sun, M., Ford, S. P., Nathanielsz, P. W., Ren, J., and Guo, W. 1Department of Animal Science, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071; 2Center for the Study of Fetal Programming, University of Wyoming, Laramie, WY 82071; 3School of Pharmacy, University of Wyoming, Laramie, WY 82071

**ABSTRACT.** Background: Maternal obesity (MO), in pregnancy, predisposes offspring to a higher risk of obesity, heart disease, hypertension, and vascular dysfunction, known as fetal programming. However, the effect of MO on contractile function of fetal cardiomyocytes has not been studied. We assessed contractile function in cardiomyocytes of fetuses of MO and control sheep at term.

**Methods:** From 60 days before and throughout pregnancy, Rambouillet/Columbia crossed ewes were fed either 100% of National Research Council (NRC) recommendations (control, n=8) or 150% of NRC’s recommendations (MO, n=7). At 135 day gestation (Term 150 days), pregnant ewes and fetuses underwent general anesthesia. The fetal heart was quickly removed and perfused to isolate cardiomyocytes. Contractile and intracellular Ca^{2+} properties were evaluated using an IonOptix system. Analysis by Student’s t-test: \( p < 0.05 \).

**Results:** MO elevated maternal body weight, total heart and cardiac ventricular weights and wall thicknesses \( (p < 0.05) \). Fetuses from MO ewes had greater body weight and
left ventricular weight ($p < 0.05$). LV and RV cardiomyocytes from fetuses of MO ewes showed increased cell length and decreased peak shortening. LV cardiomyocytes showed decreased sarcomere length ($p < 0.05$). MO disrupted fetal cardiomyocyte intracellular Ca$^{2+}$ homeostasis, evidenced by increased resting and peak intracellular Ca$^{2+}$ levels in LV and RV fetal cardiomyocytes ($p < 0.05$).

Conclusions: MO impairs fetal cardiac contractile function. To our knowledge this is the first study to evaluate functional properties in cardiomyocytes of fetuses of obese mothers and provides potential mechanism for programming of later life cardiac disease.

This work is supported by the NIH HD070096-01A1 from University of Wyoming.

**GP31: Deterministic Encapsulation by Microfluidic Droplet Formation.** Yao¹, J., and Oakey¹,², J. ¹Petroleum Engineering Department, University of Wyoming, 1000 E. University Ave. Laramie, WY 82071; ²Chemical Engineering Department, University of Wyoming, 1000 E. University Ave. Laramie, WY 82071

**ABSTRACT.** Microfluidic encapsulation has been established as a versatile method by which to encapsulate cells within emulsion droplets of picoliter volumes. With well-defined, uniform sizes and precise compositions, these droplets serve as excellent vehicles for quantitative cellular analysis. However, randomly positioned cells result in Poisson encapsulation statistics, and therefore inefficient encapsulation conditions. Recently, encapsulation schemes based upon upstream inertial focusing have been developed to overcome Poisson distributions. Inertial focusing is a technique by which inertial fluid forces are used to guide cells to well-defined lateral and longitudinal equilibrium positions. While efficient at deterministically encapsulating discrete numbers of cells at high rates, these approaches are limited by their inability to simultaneously and independently control cell number and volume fraction within droplets. We address this limitation with a microfluidic device that combines inertial focusing with fluid siphoning. By removing particle-free effluent from the particulate streams, interparticle spacing can be altered, allowing droplet size to be varied independently of the number of encapsulated cells. Combined with a thorough understanding of droplet formation, this approach can be used to produce droplets or hydrogel microparticles of any size, composition and cell number. This presentation will present an overview of the physics of inertial focusing and droplet formation, as well as the design and function of the integrated encapsulation device.
GP32: RBM20-Deficiency Plays a Protective Role in Angiotensin II-Induced Hypertension and Cardiac Hypertrophy. Zhu¹, C., Nair², S., and Guo¹, W.
¹Department of Animal Science, University of Wyoming, 1000 E University Ave., Laramie, WY 82071; ²School of Pharmacy, University of Wyoming, 1000 E University Ave., Laramie, WY 82071

ABSTRACT. Background: RNA binding protein 20 (RBM20) is a muscle specific splicing factor. Mutations in RBM20 have been implicated in dilated cardiomyopathy (DCM) with thinner myocardial wall and enlarged ventricular chamber. Titin, a giant sarcomere protein responsible for passive tension in muscle cell, is a major target of RBM20. Loss of function of RBM20 results in mis-splicing of titin gene which increases titin compliance in both striated and smooth muscle. Angiotensin II, the major bioactive peptide of the renin-angiotensin system, raises blood pressure mainly by causing vasoconstriction. Cardiac hypertrophy also occurs as an adaptation to hypertension and cell growth in the cardiovascular system driven by signaling pathways that activated by angiotensin II. Since RBM20-deficiency would lead to DCM and increase muscle compliance, thus RBM20-deficiency may play a negative role in cardiac hypertrophy and hypertension. Therefore, this study is to determine the role of RBM20 in angiotensin II induced hypertension and cardiac hypertrophy.

Method: Male wild type (WT) and knockout (KO) (Rbm20⁻/⁻) rats were subcutaneously implanted with osmotic minipump to continuously infuse angiotensin II at a rate of 400ng/kg/min for 28 days. Control groups of WT and KO rats were infused with saline. Blood pressure was measured by noninvasive tail-cuff system. Cardiac geometry and function were evaluated by echocardiography. Heart and aorta tissues were collected after sacrifice for protein and gene expression examination.

Results: Both systolic blood pressure and diastolic blood pressure were significantly increased with angiotensin II infusion in WT and KO rats by comparing to both control groups which have normal blood pressure. Interestingly, we found that KO rats with angiotensin II treatment had a significant lower blood pressure by comparing to treated WT rats. Left ventricle (LV) wall thickness was increased and LV chamber diameter was decreased with angiotensin II infusion in both WT and KO hearts. However, KO heart shows a resistance to angiotensin II induced hypertrophy with thinner myocardial wall and larger chamber size when compared to WT heart treated with angiotensin II. Conclusion: RBM20-deficiency plays a protective role in angiotensin II induced hypertension and cardiac hypertrophy.

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UNDERGRADUATE STUDENTS
The undergraduate poster session will be held on Friday April 28th 2017 from 5-6:30PM at the Marion H. Rochelle Gateway Center (MHRG) Legacy Hall & Atrium. All undergraduate student presenters must set up their posters between 2-4PM on Friday 28th 2017.

UP01: Neural Control of Vasopressin Release. Adriaens, D. and Flynn, F. Department Zoology and Physiology and Neuroscience Program, University of Wyoming, 1000E University Ave., Laramie, WY 82071
ABSTRACT. Vasopressin is produced by magnocellular neurons in the paraventricular (PVN) and supraoptic (SON) nuclei of the hypothalamus. These neuron’s axons project all the way to the posterior pituitary, where vasopressin is released into the bloodstream and executes its functions peripherally. Vasopressin release is mainly stimulated by hyperosmolarity and hypotension. Vasopressin stimulates the retention of water and restoration of fluid volume. This retention of water in response to hyperosmolarity directly dilutes the serum concentration of solutes and restores normal plasma osmolarity. In comparison to the variety of expressed receptors on vasopressinergic neurons, the neurokinin 3 receptor (NK3R) receptor is heavily expressed on VP neurons. Hyperosmolarity and hypovolemia activate NK3R and this activation is essential for the release of VP into the circulation. A number of studies show that following ligand binding, the NK3R are internalized to the cytoplasm and then trafficked to the cell nucleus where it affects gene expression. In spite of the significance of this receptor in the release of vasopressin we do not know the transmitter that triggers this signaling event. Two tachykinin transmitters may bind to the NK3R; neurokinin B (NKB) has the highest affinity for NK3R but a second tachykinin, Substance P (SP) will bind the receptor but with a far lower affinity than NKB. There is limited information on the innervation of NK3R expressing vasopressin neurons in the PVN and SON by NKB. The experiment was approved by UW IACUC. Male rats were sacrificed and the brains processed using immunohistochemistry to detect NKB and NK3R and then laser scanning microscopy to determine the relationship of NKB and NK3R. We are exploring the relationship between the neurotransmitter NKB and the NK3R expressing vasopressinergic neurons. That is, does NKB innervate NK3R expressing VP neurons and form traditional synapses. Alternatively, NKB terminals may not form synapses but may act in a paracrine fashion where the NKB diffuses over a distance. Preliminary data has shown that NKB immunoreactive axon terminals are in the vicinity of NK3R expressing vasopressin neurons, though, further data is currently being processed.

UP02: Exploring Sterol Function in the Bacterium Gemmata obscuriglobus. Armitage1, E., Stettner2, S., and Ward1, N. 1Department of Molecular Biology, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071
ABSTRACT. Unlike eukaryotic cells, bacterial cells generally lack membranes that enclose their nucleus, do not contain organelles, and lack cellular compartmentalization altogether. However, members of the Planctomycete-Verrucomicrobia-Chlamydiae (PVC) bacterial superphylum challenge the traditional view of eukaryotes vs. prokaryotes as they contain some of these eukaryotic-like features. A particularly interesting bacterium in this group, Gemmata obscuriglobus, has been shown to have a
complex endomembrane system, highly condensed nucleoid region, and segregated transcription and translation. *G. obscuriglobus* has also been found to produce sterols, a class of molecules that are essential for structure and function of membranes in eukaryotic cells. Sterols only have been detected in a subset of bacteria, however the function remains enigmatic. Generally, hopanoids are present in bacteria as proxies to sterols. To explore the function of sterols in *G. obscuriglobus*, our lab has developed a chemical approach using the drug terbinafine, an inhibitor of sterol biosynthesis, to begin to determine sterol function. We have shown that sterol depletion by terbinafine causes severe replication defects, suggesting sterols are necessary for survival, the first instance in a bacterium. We are conducting RNA sequencing on treated vs. untreated cells to determine the global effect of sterol depletion. This will allow for the identification of genes responding to sterol depletion, providing insight into sterol function. Then, I will conduct quantitative real time polymerase chain reactions on the best hits to verify the RNA sequencing reads. Ultimately, we will utilize a recently developed genetic approach for the planctomycetes to further elucidate the RNA sequencing best hits function in response to sterol depletion. There may be a relationship between the eukaryotic-like features of *G. obscuriglobus* and sterol synthesis, and understanding bacterial sterol function could elucidate this.

**UP03: Isolating an *Agkistrodon piscivorus piscivorus* (Eastern Cottonmouth) Venom Protein for Use in Degradable Polymer-Drug Eluting Stents (DP-DES).**
Bare, L., Johnson, C., and Milne, R. Natural Science Division, Northern Wyoming Community College District-Sheridan College, 3059 Coffeen Ave., Sheridan, WY 82801

**ABSTRACT.** Snake venom is an incredibly rich source of bioactive proteins, some of which may prove to be useful for biomedical applications. *A. p. piscivorus* venom, in particular, has both anticoagulant and coagulant proteins that can clot and thin the blood when it enters into the blood stream. The purpose of this investigation is isolating the anticoagulation protein to evaluate its incorporation in degradable polymers for drug eluting stents (DP-DES). The protein was separated by using ion exchange chromatography. The isolated protein was then combined with several different degradable polymer formulations. Details of venom isolation as well as DP-DES results will be reported.

**UP04: Using Predictive Simulations and Genomic Variation to Understand Selection Responses.** Baker¹, L.D., Chhatre², V.E., and Lanier¹, H.C. ¹Department of Zoology & Physiology, University of Wyoming at Casper, 125 College Drive, Casper, WY 82601; ²Department of Molecular Biology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

**ABSTRACT.** In a world of rapid anthropogenic change understanding the factors that influence the pace with which a population can respond to natural selection has become a necessity for conservation. Often when considering risk of extinction, we take population size into account. However, understanding the evolutionary implications of that population size may also be important. Most mechanisms involved in evolution act within a population, such as selection, mutation, migration, and genetic drift. Notably, these processes are not static across species or populations and are often influenced by dynamic aspects such as population size. By comparing among groups that naturally
show difference in population size we can better understand the impacts of population size pressures on genetic diversity and the effectiveness of natural selection. In this comparative study of five co-distributed Alaskan mammals—Collared Pikas, Hoary Marmots, Brown Lemmings, Artic Ground Squirrels, and Singing Voles—we tested whether population size influences the ability of a population to respond to selection using genomic data and predictive simulations. Our results show species with larger population sizes display more genomic variation, suggesting that selection may be working more effectively in larger populations. Meanwhile, smaller populations are more likely to lose advantageous loci by chance alone. In conclusion, evolution is not a static process, but rather, as we found, selection response is dynamic in relation to population size.

UP05: Coal Dust Exposure and Cardiovascular and Pulmonary Dysfunction.
Bosch¹, L., Haller¹, S., Smith¹, A., Sanders¹, A., Aquino¹, J., Ta¹, T., Peterson¹, M., Lu², W., Fan², M., Fults³, S., Snider³, J., and He¹, G. ¹School of Pharmacy, University of Wyoming, 1000 E. University Avenue, Laramie, WY 82071; ²School of Energy Resources, Energy Innovation Center, 1000 E. University Avenue, Laramie, WY 82071; ³College of Engineering and Applied Science, 1000 E. University Avenue, Laramie, WY 82071

ABSTRACT. Significance: Exposure to coal mine dust has been associated with increase of respiratory and heart disease as well as overall increase mortality among coal miners. A common consequence of particulate matter exposure is the development of chronic low-grade inflammation, mainly with macrophage infiltration and continuing pro-inflammatory cytokine production, which leads to cell damage and organ dysfunction. However, a mechanistic understanding of these disease conditions associated with coal dust exposure is lacking.

Overall Objective: This project is designed: 1) to characterize the concentration and size distribution of coal dust in a custom-made aerosol exposure system; and 2) to determine the mechanistic effect of coal dust exposure on the progression of lung and heart disease in mice.

Hypothesis: Coal dust exposure induces proinflammatory cytokine production leading to exacerbation of pulmonary and heart injury through an inflammasome signaling pathway.

Experimental Design and Results: A custom-built exposure system was designed and tested for particulate matter exposure on small animals. Wild-type C57BL/6 mice were exposed to coal dust generated from water suspension of 35 mg/L for 3 hours/day and 30 days followed by transverse aortic constriction (TAC) for 10 days to study exposure effect on the exacerbation of TAC-induced cardiac hypertrophy and dysfunction as well as pulmonary fibrosis. Cardiac function was determined by P-V loop measurements followed by tissue collection on: lung lavage and inflammatory cells, heart, liver, as well as brain. Western immunoblotting analyses and ELISA assay will be performed to determine protein expressions and cytokine production on NLR family pyrin domain containing 3 (NLRP3)-associated inflammasome signaling pathway. In addition, pulmonary and cardiac fibrosis will be determined on TGFβ-Smads signaling.

Interim Conclusion: The custom-made aerosol exposure system was characterized on the size distribution and concentration of the coal dust aerosol generated from its water suspension. We expect that coal dust exposure would exacerbate pressure overload-
induced hypertrophic cardiac remodeling and pulmonary fibrosis through activated inflammasome signaling. The outcome could potentiate a therapeutic intervention targeting the NLRP3 gene to protect the miners from exposure to the hazardous mine dusts and other air pollutants in general.

UP06: Varying Water Quality Variables Effects on Plant Growth, Nutritional Status and Physiology. Brungart Rosenberg¹,², M., Praska¹, B., Erickson¹, A., and Dhekney², S. ¹Natural Science Department, Northern Wyoming Community College District-Sheridan College, 3059 Coffeen Ave, Sheridan, WY 82801; ²Department of Agriculture, University of Wyoming, ShREC, 3059 Coffeen Ave, Sheridan, WY 82801
ABSTRACT. Successful plant growth requires proper water pH, mineral levels, and conductivity. The purpose of the experiments was to identify any differences of plant growth, nutritional status and physiology when plants were watered from different water sources. Following a summer field project examining the effect of high SAR ground water on vegetable production, two greenhouse experiments were conducted comparing different water source effects on plant growth under controlled conditions. One experiment examined the effect of high SAR ground water on growth and physiology (pH 8; EC 1880 umhos/cm; Ca 174 mg/L and Na 83 mg/L) compared to city water (pH 8; EC 95 umhos/cm; Ca 5 mg/L and Na 9 mg/L). Twenty one-gallon pots containing three bean seedlings were divided with ten pots watered with groundwater and ten pots with city water. Water conductivity, SAR, and pH were measured and plant growth and physiology were evaluated. In another experiment, we attempted to determine the cause of apparent nutrient deficiency of grapevines grown in the greenhouse. Our hypothesis was that city water used to irrigate grapevines had a high pH, which interfered with nutrient uptake. Twenty grape plants showing no sign of nutrient deficiency were watered using city water (pH 7.84) or water treated by reverse osmosis (RO) (pH 7.25). Water pH and temperature were tested when the plants were watered. To assess plant nutritional level and physiological response for both experiments, photosynthetic rate, stomatal conductance, chlorophyll content, and dry weight were collected.

UP07: Evaluation and Mapping of Antibiotic Resistance Genes in the Resistome: A Metagenomics Approach. Burrough¹, H., Schimpf¹, L., Schimpf², K., Lawless², G., Quealy², L., and Chase¹, J. ¹Biology Department, Casper College, 125 College Drive, Casper, WY 82601; ²Biology Department, University of Wyoming, 1000 E University Ave, Laramie, WY 82071
ABSTRACT. The emergence and spread of antimicrobial resistance genes poses one of the most threatening health care problems to the world’s populations. Although the problem is significant, little research has been completed on antibiotic resistance and the resistome (1,2,3).
A metagenomics approach was adopted, to evaluate the presence of β-Lactamase and Klebsiella Pneumoniae Carbapenemase (KPC) genes within the environmental resistome. Various natural aquatic systems and environmental soil samples in Wyoming were analyzed utilizing this method. Samples were collected along with data on sample type, GPS location, pH and dissolved oxygen. The samples were differentially filtered to isolate eukaryote, prokaryote and bacteriophage communities. After metagenomic DNA...
Extraction, randomly amplified shotgun libraries (RASLs) were created for each sample. PCR was used to test for the presence of ß-Lactamase and KPC genes. Isolated genomic sequences revealed evidence of resistance genes within the samples. Additionally, a large proportion of the sample sites were positive for resistance genes. This evidence suggests that horizontal gene transfer of resistance genes within the environment can lead to the emergence of resistant bacterial pathogens. (3,4,5,6).

UP08: Feasibility Pilot of Using Functional & Transition Profiles to Improve Transition Planning for Those with Cerebral Palsy. Crawford, P., and Hidecker, M. J. C. Division of Communication Disorders, University of Wyoming, 1000 E. University Ave, Dept. 3311, Laramie, WY 82071

ABSTRACT. As adolescents move to adulthood, they experience additional expectations such as postsecondary training or education, employment, and independent living. Adolescents with cerebral palsy often have a more difficult time in accomplishing these tasks. With added obstacles such as motor difficulties, communicative impairments, and lack of self-efficacy, these adolescents are less likely to obtain post-secondary education, live independently, and obtain employment in the community. With improved planning in areas such as education, employment, finances, housing, and transportation, these individuals may find more success in achieving higher levels of independence.

Within the last ten years, new classification systems have been developed that may assist a team working with an individual with cerebral palsy in evaluating the individual’s current abilities and future needs. These classification systems address areas such as communication, walking (gross motor movement), and hand function. When used together, they may help individuals with cerebral palsy determine the level of assistance needed in areas of education, employment, and independent living.

The aims for this project are as follows: 1) Evaluate possible transition needs in adolescents with cerebral palsy when moving into adulthood and 2) determine usefulness of classification systems and transition profiles in discussing planning with practitioners, individuals with cerebral palsy, and their families. Researchers will collect information about the individuals using three classification systems and one transition profile. The tools will be evaluated for usefulness when discussing future needs in areas like education, employment, and independent living.

UP09: Effect of Mid-Flight Trunk Motion on Landing Mechanics. Hinshaw¹, T., Davis, D., Layer, J., and Dai, B. Kinesiology and Health Promotion, University of Wyoming, 1000 E. University Ave, Laramie, WY 82071

ABSTRACT. ACL injuries are highly prevalent and problematic in day-to-day life, and especially in an athletic domain. Often ACL tears occur when the athlete lands in a non-vertical position, rendering them unable to utilize both legs symmetrically in landing. This subsequently increases the ACL load of the landing leg, which is at least a partial cause of the injury. Mid-flight trunk motion may cause athletes to land in this non-vertical position.

The goal of the current study was to analyze the effect of mid-flight medial-lateral trunk motion on Center of Mass (COM) distribution and subsequent landing mechanics. Forty-one recreational athletes (18 males and 23 females) participated. Forty-four
markers were placed on each participant’s body and were tracked using 3D cameras. Peak Vertical Ground Reaction Force (VGRF) was measured with two force plates. Participants were instructed to jump vertically, reach straight up, left, or right, and land naturally. Each medial-lateral reach condition (left or right) produced asymmetric landing between legs, with the leg ipsilateral to reach direction landing first (mean difference of 14.0 ms reaching left and 16.7 ms reaching right). Peak VGRF was also greater for the ipsilateral leg in these conditions (2.6 times body weight for both left and right reaching conditions) compared to the contralateral leg (1.7 times body weight). These results indicate that mid-flight trunk motion can cause athletes to land in a non-vertical position, placing more stress on the leg ipsilateral to the reach direction, and increasing their risk of ACL injury in that leg.

UP10: Short-Term and Long-Term Movement Patterns among Amall Mammals in a Disturbed Habitat. Diesburg, L.M., and Lanier, H.C. Department of Zoology and Physiology, University of Wyoming at Casper, 125 College Dr., Casper, Wyoming 82601

ABSTRACT. Fires have the ability to reshape entire landscapes, changing the composition of plants species as well as the structure of the terrain. Forest fires also leave behind a large amount of coarse woody debris, i.e., downed logs, which can provide small mammals with habitat, cover from predators, and have the potential to alter movement patterns. Movement patterns are also influenced by other habitat features, such as the separation of habitat by a road. For this study I utilized capture-recapture data from burned and unburned study sites in the Yellowstone National Forest as well as genetic analyses to determine both short and long-term movement patterns relative to species, habitat (burned or unburned), and the presence/absence of a road. I focused specifically on the two most abundant species in the intermountain west: red-backed voles (Myodes gapperi) and deer mice (Peromyscus maniculatus). Capture data indicated that on average deer mice travel greater distances, and both species have greater average movements in burned areas compared to unburned areas. These results are an important complement to the results from genetic analyses, which suggest a decrease in gene flow across the road. Further analysis is needed to determine the causes of the differences between burned and unburned areas, such as diet requirements and vegetative layout. Understanding the impact fires and roadways have on small mammals will not only expand our knowledge on their ecological role but may also implicate the use of controlled burns as tools for population management.

UP11: Understanding the Role of Natural Killer Cell Cytotoxicity on Immune Exhaustion and the Quality of CD4 and CD8 Response During Chronic Infection with Toxoplasma gondii. Fatima, R., and Gigley, J. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave. Laramie, WY 82071

ABSTRACT. 30% of the world’s population is infected by Toxoplasma gondii including, more than 60 million people in the USA alone (CDC 2015). Toxoplasma poses a critical threat to individuals with a weakened immune system such as HIV/AIDS patients (Mayo Clinic 2014). In addition, severe birth defects, blindness, and abortion can occur in the fetus when the parasite is transmitted to healthy mothers who are pregnant (Sibley 2012). Thus, understanding how long term immunity protects against this parasite is
important for better therapy design.

Natural Killer cells (NK cells) are known to be important for early protection against Toxoplasma. Recently, it has been discovered that NK cells can also be detrimental to the proper function of long-term immunity against the parasite. We test what function of NK cells is required to negatively regulate the immune response resulting in parasite reactivation and death of animals. Also, we further explore how this NK cell function impacts the quality of CD4 and CD8 T cells in long term immunity to the parasite.

UP12: Investigating the Role of *ari-1* in *C. elegans*. Favela, J., Fay, D., and DiBona, K. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave., Laramie, WY, 82071

**ABSTRACT.** The attachment of one or several ubiquitin (Ub) molecules to a target protein, ubiquitination, is an important post-translational protein modification. Ubiquitination of a target protein may lead to degradation via the proteasome, translocation, or alteration of activity. This process requires an E1 (Ub-activating), E2 (Ub-conjugating) and E3 (Ub-ligase) enzyme. A *C. elegans* homolog of the highly conserved Ariadne RBR E3 (ARIH1), *ari-1* (C27A12.8) is highly expressed in muscles, neurons, and the germline, and has previously been found to function in pharyngeal development. However, deletion of *ari-1* (tm2549) did not produce any observable effect. This result is likely due to genetic redundancy as *C. elegans* possess two *ari* paralogs, C27A12.7 and C27A12.6. Recently, our lab generated a deletion in all 3 *ari* homologs (*ari3X*) using CRISPR technology. Partial sterility was observed and quantified in *ari3X* null mutants. The data indicate increased sterility of *ari3X*, compared to wild type controls. Further analyses indicate a Mog (masculinization of germline) phenotype in sterile *ari3X* mutants, resulting in increased sperm production. An RNAi screen of a known E2 partner of *ari-1*, *ubc-18*, revealed increased sterility with *fbf*(RNAi), which has been shown to function in germline development. Based off this preliminary information, *ari3X* mutants were evaluated on *fbf*(RNAi) to elucidate their role in germline development. A drastic increase in sterility due to Mog, along with an unanticipated multivulval phenotype was observed for *ari3X* mutants on *fbf*(RNAi). Taken together, these results indicate an important role for ARI-UBC-18 ubiquitination in germline development.

UP13: The Viability of Somatic Coliphage as a Water Quality Indicator. Flowers, E., and Dickerson, J. Biology Department, Northwest College, 231 W 6th Street, Powell, WY, 82435

**ABSTRACT.** Somatic coliphages are viruses that infect *Escherichia coli* and other *coliform* bacteria that live in the intestines of mammals. Recent epidemiological studies indicate that somatic coliphages have the potential to serve an indicator organism of recent fecal pollution in recreational waters. However, concerns exist that somatic coliphages, like bacterial indicators, may be able to replicate in the environment. Our study examines whether the potential for environmental replication of somatic coliphages is of enough significance to re-evaluate or exclude them from being used as a water quality indicator. Environmental coliphages and *E. coli* were isolated from mule deer (*Odocoileus hemionus*) fecal samples collected in Cody, Wyoming, using USEPA Method 1602: Male-specific (F+) and Somatic Coliphage in Water by Single Agar Layer
(SAL) Procedure, and eosin methylene blue agar, respectively. All E. coli isolates were further confirmed on nutrient agar with MUG. Isolated somatic coliphages were picked, and spot-plated onto TSA plates poured with isolated strains of E. coli. After incubation at 37°C for 24h, the formation of plaques indicated the coliphages had successfully infected and burst the E. coli cells. The percentage of coliphage isolates capable of causing infecting, and lysing E. coli collected from the same fecal sample has been calculated and is reported here.

UP14: Banging our Heads against a Cell Wall: Genomic Extraction in Filamentous Fungi. Frain, W., Carpenter, C., Reitmeyer, T., Springer, C., Wangelin, A., Roehrs, Z. Department of Natural Science, Laramie County Community College, 1400 East College Drive Cheyenne, WY 82007

ABSTRACT. Genomic research has allowed scientists to find answers to once elusive questions in the genetic code, as well as begin to manipulate useful compounds found in organisms for alternative uses (e.g. pharmaceuticals). Alternaria astragali (A3) is a fungus with an exceptional metabolic tolerance to otherwise toxic concentrations of selenium (Se). Se tolerance in A3 is hypothesized to be attributed to yet uncharacterized metabolic pathways. Further, we have isolated two anti-cancer compounds in this fungus. Mapping the A3 genome would not only provide insight into this particular species, it would also contribute to our understanding of Alternaria in general, a genus that contains many economically important plant pathogens. Historically, extraction of intact genomic DNA from some filamentous fungi has been difficult, largely due to chemical components of their cell walls, such as chitin, glucan, and cellulose. In this work, lyophilized tissue from A3 was treated with two types of chitinase (Streptomyces griseus and Trichoderma viride) and a β-glucanase (Trichoderma longibrachiatum). After cell wall digestion, the DNA was purified and isolated using a Qiagen Genomic-tip column. Fluorescence quantitation of the product verified that we had 24.9 μg of high molecular weight DNA suitable for genomic sequencing. This genetic information will provide the foundation for further research including selenic dependent gene expression of A3 and characterization of its potentially medically useful compounds.

UP15: Effects of DSM-5 Changes on ADHD Symptom Endorsement in College Students. Garner, A., Stevens, A., and Hartung, C. Department of Psychology, University of Wyoming Dept. 3415, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. In the most recent iteration of the Diagnostic and Statistical Manual of Mental Disorders (DSM-5), changes were made to the diagnostic criteria for Attention-Deficit/Hyperactivity Disorder (ADHD); among these changes were parenthetical examples of adult behavior that were added for each symptom. This was done to make the criteria developmentally appropriate for adolescents and adults. Prior research has found that the changes significantly increased the number of symptoms parents of adolescents with ADHD endorsed for their children. This study conducted a similar procedure with a community sample of college students and collateral reports from a small group of participants with ADHD and matched controls.

This study was conducted at four universities in the Western, Midwestern, and Easter United States; participants were undergraduate students (ages 18-25) who rated
themselves on the *DSM-IV* and *DSM-5* checklists, as well as the Weiss Functional Impairment Rating Scale – Self-Report (WFIRS) and the Depression Anxiety Stress Scale (DASS-21). Parents of some participants in the ADHD group within the sample were contacted with the consent of their child to provide collateral reports, completing the *DSM-IV* and *DSM-5* checklists on their child’s behaviors and the WFIRS other-report. The *DSM-IV* and *DSM-5* checklists were counterbalanced in the survey. To test the hypothesis that the changes to the *DSM* criteria would increase symptoms endorsed, a repeated measures ANOVA was conducted. The within-subjects variable was *DSM* edition, and it was found that college students endorsed significantly more symptoms, specifically inattentive symptoms, using the *DSM-5* checklist.

These findings indicate that the changes to the *DSM* criteria allow for better identification of ADHD among adolescents and adults, due to better understanding of the disorder and developmentally appropriate behavior examples. However, these changes may be overcorrecting the diagnostic system, as it is still largely based on the behavior of school-aged children with ADHD. Further findings and implications will be discussed on in the poster presentation.

**UP16: The Effect of Salinity on Grape Embryo Growth and Physiology**

Weeden¹, K., Giandonato¹, T., Brungart Rosenberg¹, M., Erickson¹, A., and Dhekney², S. ¹Natural Science Department, Northern Wyoming Community College District–Sheridan College, 3059 Coffeen Ave. Sheridan, WY 82801; ²Department of Plant Sciences, University of Wyoming, Sheridan Research and Extension Center, 3401 Coffeen Avenue, Sheridan, WY 82801

**ABSTRACT.** The growth of grape somatic embryos can be affected by elements in their surrounding environment. Improving grapevine tolerance to salinity necessitates the optimization of protocols for screening response of various grapevine species and cultivars to salt stress under in vitro conditions. We germinated Thompson Seedless somatic embryos on MS medium containing 1.0 µM BAP and varying levels of sodium chloride. The salt treatments included MS medium containing: 1) no sodium chloride (control), 2) 5 mM NaCl, 3) 10 mM NaCl, 4) 25 mM NaCl, 5) 50 mM NaCl, 6) 100 mM NaCl and 7) 200 mM NaCl. Cultures were placed in a growth room. The plates were monitored regularly, photographed, and rated on a growth scale of one to four each week for six weeks. Dry weights of embryos were collected and root samples were fixed in Histochoice and embedded in paraffin to examine root tissue development. Normal embryo growth and development was observed in the control. With added NaCl growth decreased and development of shoot and root structures were inhibited. Severe inhibition in shoot and root growth of germinated embryos was observed above 50mM NaCl concentration. The project will be repeated using Frontenac grape embryos. Once we identify the concentration of NaCl that inhibits growth and development of somatic embryos, this method will be used to screen genetically modified embryogenic cultures that carry genes inserted for salinity tolerance. Our in vitro screening technique should allow for rapid identification of embryo lines that exhibit salinity tolerance following genetic modification.
UP17: Personality and Pair Bonds: Future Research to Investigate Communication and Coordination on a Problem-Solving Task in Captive Zebra Finches. **Graham, R., Barrett, L., and Benson-Amram, S. Department of Zoology and Physiology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071**

**ABSTRACT.** Zebra finches (*Aeniopygia guttata*) exhibit consistent individual differences in behavior, also known as personality. Previous research in our lab has measured several different personality traits including aggressiveness, exploration tendency, and neophobia in a captive colony of zebra finches. This particular study will investigate whether personality of pair bond members influences the pair’s coordination on a novel problem-solving task. We plan to form pair bonds of zebra finches with similar personality types and pair bonds of zebra finches with dissimilar personality types. The paired birds will then be placed into a maze that will require them to pool their knowledge in order to find a food reward. We will also investigate whether communication plays a role in coordinated problem solving and whether personality influences how communicative mates are with each other while they are in the maze. This study is important in bringing in the potential influence of personality on cognition and fitness and why personality may be a critical component of mate choice for species where pair bonded mates exhibit a lot of coordination in parental care and foraging.

UP18: Caspase Recruitment Domain-Containing Protein 9 (CARD9) Knockout Attenuates Myocardial Ischemia and Reperfusion Injury. **Haller, S. E., Sanders, A. J., Peterson, M.R., Bosch, L. M., Smith, A., Aquino, J., Ta, T., Thomas, P., and He, G. School of Pharmacy, University of Wyoming, 1000 E. University Ave., Laramie WY 82071**

**ABSTRACT.** Ischemic heart disease is one of the leading causes of morbidity in the US. Reperfusion of the ischemic area, along with neutrophil infiltration increases the degree of injury. The adaptor protein caspase recruitment domain-containing protein 9 (CARD9) plays an important role in innate immunity, so we hypothesized that CARD9 knockout would provide some protection against ischemic and reperfusion (I/R) injury through a decrease in inflammation.

The left anterior descending (LAD) coronary artery in male C57BL/6 wild-type (WT) and CARD9−/− mice was occluded for 45 minutes, followed by reperfusion for 24-h. Area at risk (AAR) and infarct size were measured by Evans blue and triphenyltetrazolium chloride (TTC) staining. Frozen heart sections were stained with anti-mouse GR-1 antibody to detect infiltrated neutrophils. Concentrations of cytokines/chemokines TNF-α, IL-6, CXCL-1 and MCP-1 were determined in heart tissue and serum by ELISA. Western immunoblotting analyses were performed to measure the phosphorylation of p38 MAPK. Following I/R, infarct size was significantly smaller in CARD9−/− mouse hearts compared to that of WT mice. The number of infiltrated neutrophils was also significantly lower in the hearts of CARD9−/− mice compared to WT mice. Levels of TNF-α, IL-6, CXCL-1 and MCP-1 were significantly reduced in heart tissue and serum of CARD9−/− mice compared to those of WT mice. CARD9−/− mice also exhibited significantly lower levels of phosphorylated p38 MAPK compared to that of WT mice.

Our results suggest that CARD9 knockout provides protection against ischemic and reperfusion injury, possibly through reduction of acute inflammatory signaling, and reduced neutrophil infiltration.

ABSTRACT. Attempting to replicate a previous experiment, we are testing the relationship between the amictic and mictic cycles of the rotifer, *Brachionus plicatilis*, and the brine shrimp, *Artemia salina*. In 1986, not only brine shrimp, but also media conditioned by their presence, inhibited rotifers from entering mixis ($\chi^2=14.737$, d.f.=1, $p <0.001$). Many rotifers exhibit a dual life cycle, in which females generally reproduce asexually (amictic parthenogenesis) until environmental cues initiate mixis leading to the production of haploid males and haploid eggs. The union of these leads to the production of diploid resting eggs. Resting eggs are resistant to desiccation and can remain viable for many years as an evolutionarily adaptive trait in ephemeral water bodies. We are testing to see if chemicals (potentially, hormones or endocrine disruptors) produced by brine shrimp have any effect on the mictic cycle of the rotifers. We have three groups of 20 vials each: Just rotifers, rotifers with brine shrimp and rotifers in brine shrimp-conditioned (2 days) water (25 ppt Instant Ocean®). We placed 5 amictic rotifers into each 4 dram shell vials to test to see if they would undergo the mictic cycle. We let the rotifers sit for four days and then viewed the vials to determine if any rotifers have an egg.

UP20: The Geography of Birdsong Variation. Hein, L.W., and Lanier, H.C. Department of Zoology and Physiology, University of Wyoming at Casper, 125 College Drive, Casper, WY, 82601

ABSTRACT. Birdsong is known to be variable geographically in many species, and we have anecdotally observed this effect in Wyoming populations of the House Wren (*Troglodytes aedon*). This variation may be due to gradual divergence in song dialects between geographically distinct breeding populations, genetic variation among populations, or habitat-driven differentiation based on sound transmission properties of the environment. In this project, we collected 944 wren calls from three different locations around Wyoming, tested the similarity of various acoustic environments and modeled call similarity against distance and acoustic environment type. These comparisons were made using time-frequency analysis, clustering, and summary statistics. The geographic distribution of these song dialects is shown to be quite diverse, with some locations showing great consistency and others showing as much internal dialect variability as exists between locations. We found that between locations, dialects can be distinguished by differences in rate of singing, minimum pitch attained, and the proportion of the song spent in pauses between phrases. These findings may help answer important questions about population diversity, boundaries for mating, and migration patterns.

UP21: Antibiotic Resistance of *Enterococcus* spp. and *E. coli* in Mule Deer.
Hinckley, E. L., Christner, H., Flowers*, E. Dickerson, J. Biology Department, Northwest College, 231 W 6th St., Powell, WY 82435

ABSTRACT. *Enterococcus* spp. and *Escherichia coli* are bacteria found in the intestinal tract of mammals. Some strains can be harmful. Antibiotic resistance is a recent issue
as antibiotics have been introduced into the environment by humans. This study is a comparative analysis of urban and rural deer populations and its relationship to antibiotic resistance. The hypothesis is that bacteria found in the urban deer will be resistant to a greater number of antibiotics as a result of their association with human waste water, pollution, fertilizers, pesticides, etc. Fecal samples are being collected to obtain *Enterococcus* spp. and *E. coli*. These bacteria are being isolated using mEnt agar or EMB respectively. Then the isolates are confirmed with Enterococcosel broth or Nutrient agar with MUG respectively. Once *Enterococcus* spp. and *E. coli* are found, the Kirby-Bauer disk diffusion method will be used to test antibiotic resistance. Data analysis will be conducted to determine the significance of antibiotic resistance.

UP22: Searching Environmental Sources for Novel Antibiotic-Producing Bacteria. Hunt¹, J., Kimble¹, E., and Udodong², U. ¹Biology Department, Northwest College, 231 W. Sixth St., Powell, WY 82435; ²Chemistry Department, Northwest College, 231 W. Sixth St., Powell, WY 82435

ABSTRACT. Growing resistance of pathogenic bacteria to antibiotics has health, economic, and societal costs, yet most antibiotics in use today are synthetic derivatives of core classes of antibiotics created during the heyday of antibiotic development in the 1940s to 1960s. Because of the abundance of current antibiotics originally derived from soil-based bacteria (*Actinomyces*, *Streptomyces*, and *Micromonospora*, for example), we have decided to focus our search for novel sources antibiotic-producing bacteria on similar environmental sources, specifically marsh water/mud and two different compost piles. The marsh water and mud yielded several isolated bacterial colonies that had inhibitory effects against our three pathogens of interest, *S. aureus*, *E. coli*, and *P. aeruginosa*. One of the inhibitory colonies, identified by BLAST search as *S. plymuthica*, produced a pink inhibitory secondary metabolite we were able to isolate and purify using organic chemistry techniques. We hypothesize the compound is a type of prodigiosin due to its color and the fact that a different *Serratia* species, *S. marcescens* is well-known to produce prodigiosin. Further characterization of the isolate is ongoing. The two compost piles, one pig compost and the other residential compost, produced numerous inhibitory bacterial colonies, including several that inhibited *P. aeruginosa*. In addition, many of the compost-based bacterial colonies grew weakly at 37°C and strongly at 60°C, indicating they may be thermophiles, a group that is understudied in antibiotic research. Identification of these inhibitory bacteria is ongoing using genomic DNA extraction, PCR amplification of the 16S ribosomal gene, DNA sequencing, and BLAST database searches.

UP23: The Role of a Grapevine-Derived Acetolactate Synthase Gene as a Selectable Marker for Precision Breeding of *Vitis*. Jernigan, H.L., and Dhekney, S. Department of Plant Sciences, University of Wyoming, Sheridan Research and Extension Center, 3401 Coffeen Avenue, Sheridan, WY 82801

ABSTRACT. Precision breeding (PB) is a newly-enabled approach to plant genetic improvement that transfers only specific desirable traits among sexually-compatible relatives via the mitotic cell division pathway to avoid the genetic disruption imposed by meiosis. PB builds upon decades of both fundamental and applied research aimed at bypassing the disruption of sexual reproduction (meiosis) by allowing gene insertion to
be accomplished via the significantly more stable and predictable mitotic cell division pathway. Recent advances in the development of cell culture protocols for efficient plant regeneration combined with crop genome sequencing have opened new avenues for the movement of specific functional traits among sexually compatible crop cultivars. A grapevine derived MybA1 transcription factor was recently studied and characterized for its use as a reporter gene in plant transformation. We are currently studying the grape-derived tolerant acetolactate synthase gene, VvALS2f, that might potentially confer herbicide resistance and can be used as a marker gene for selection of modified events in cell culture. In the current study, the effect of different herbicides including Monument and Image, on inhibition of tobacco shoot cultures and grape embryogenic cultures will be studied to determine the optimum levels of herbicide that can be used for selection at the cell culture level. These studies will enable the use of the acetolactate synthase gene for the recovery of modified events in cell culture and regeneration of whole plants with traits of interest.

UP24: *Eimeria* in Mediterranean Geckos and Ornate Box Turtles. Kerr, C., Carmen, K., Motriuk-Smith, D., McAllister, C. T., and Seville, R. S. *University of Wyoming at Casper, 125 College Dr., Casper, WY 82601*

**ABSTRACT.** Oocysts from two different hosts, *Hemidactylus turcicus* (Mediterranean geckos) and *Terrapene ornata* (Ornate box turtles) were collected and analyzed. Samples were originally collected in Texas, Florida, Arkansas, and Mississippi and analyzed in Casper, Wyoming. Oocysts from the *H. turcicus* were identified as *Acroeimeria lineri* (*Eimeria lineri*) and *Choleoeimeria turcicus* (*Eimeria turcicus*). In five of the samples from *H. turcicus*, *A. lineri* was present. Overall, 97 oocysts were documented and measured. These oocysts had an average size of 23.95 x 18.00 µm with an average shape index (length/width) of 1.3. The sporocysts of this species measured 7.63 x 6.72 µm with an average shape index of 1.1. *C. turcicus* was also described. Sixty-six oocysts were photographed and measured. These oocysts had an average size 34.50 x 17.55 µm and an average shape index of 2.0. Sporocysts in these oocysts were 9.40 x 8.07 with a shape index of 1.2. DNA was extracted from these oocysts, but so far the results are inconclusive. A new species of *Eimeria* was described and documented from the *T. ornata* samples. Seventy oocysts were measured and had an average size of 20.6 x 13.8 µm, the shape index was 1.5. Sporocysts were ellipsoidal, 9.8 x 6.1 µm with a shape index of 1.6. Polar granules were visible in almost every oocyst, with some oocysts containing as many as 2 or 3. DNA was extracted from these samples and two unique rDNA 18S sequences were obtained. Construction of phylogenetic trees that define evolutionary relationships will be attempted in the future.

UP25: Reverse Genetic Screen in *Toxoplasma gondii*. LeFaivre, H. K., Denton, S. L., and Gigley, J. P. *Department of Molecular Biology, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071*

**ABSTRACT.** *Toxoplasma Gondii* is a eukaryotic parasite that can infect a wide array of hosts multiple times and cannot be eradicated. There are currently no treatments to eliminate this parasite fully and the effects can lead to blindness, brain inflammation, and fatality in immunocompromised patients by developing toxoplasmosis. By understanding the nature of *Toxoplasma gondii* infection, future research could lead to
possible treatments or rid the parasite from the host completely. The parasite invades a host cell by specialized organelles secreting proteins called rhoptries, micronemes, and dense granules that help facilitate the active invasion into a host cell. Mechanisms of parasitic lifestyle such as replication, immune invasion, and nutrient acquisition within the host cell are not fully characterized. To understand genes involved with these aspects of fitness, we are employing a reverse genetic screen. This is done by inducing a double stranded break at targeted sites of the genome using CRISPR-CAS9 which will cause mutations as the parasite attempts to repair the induced double stranded break. To select for these mutants, we hijack the repair mechanisms to insert a resistance cassette in place of our targeted gene, resulting in a null mutation. We assess contribution of fitness of the selected gene by monitoring growth, replication, motility, and invasion. After analysis of genes involved with parasite fitness, these gene candidates will lead to future research into the mechanisms they are involved with.

UP26: Sub-chronic Oral Safety Studies of Capsaicin. Markert, L., Zimmerman, L., Bennis, J., Frantz, J., Baskaran, P., and Thyagarajan, B. Molecular Signaling Laboratory, School of Pharmacy, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

ABSTRACT. Recent research from our laboratory demonstrate that dietary capsaicin (CAP), a selective agonist for transient receptor potential vanilloid subfamily 1 (TRPV1) protein, activates TRPV1 expressed on the membranes of white and brown adipocytes to cause browning of white adipocytes and upregulation of thermogenic gene expression. We are currently developing novel formulations of CAP for human clinical trials. Although, our sub-chronic CAP-feeding neither altered the energy intake nor any adverse reactions in mice, it is essential to demonstrate the safety of CAP in preclinical toxicological studies in mice. Keeping this goal in mind we conducted a dose response for capsaicin (0.133, 0.399, 0.665, 1.33 or 3.99 mg/kg body weight of mouse corresponding to 0.001, 0.003, 0.005, 0.01 and 0.03% of CAP in diet) to counter obesity in high fat diet-fed wild type mice. We also conducted histological studies and analyzed the plasma levels of markers metabolic, liver and kidney functions in the mice. Further, to ensure that CAP does not cause adverse reactions when in normal chow diet (NCD), we fed wild type mice a diet containing 0.01% CAP in NCD. Our data show that CAP inhibited diet-induced obesity at concentration above 0.001% (0.133 mg/kg body weight) and the theoretical EC50 of CAP is determined to 0.00157% (0.2881 mg/kg body weight). CAP did not alter food/water intake in mice in any of the concentrations used for the study. HFD feeding increased fasting plasma glucose, triglycerides and cholesterol levels and significantly elevated serum alanine aminotransferase and creatinine levels, and CAP antagonized this. HFD-induced obesity was associated with hypertension and dietary CAP prevented it at all concentrations except 0.003%. HFD feeding slightly but significantly decreased the body temperature (rectal) of mice and CAP antagonized this. Feeding CAP in NCD did not cause weight loss in mice. Analyses of histological sections revealed no pathological findings when mice were fed CAP either with NCD or HFD. Collectively, our study provides compelling preclinical data that suggest that sub-chronic oral CAP feeding is safe and does not cause any adverse effects in mice. These data are valuable for advancing the clinical uses of CAP to counter obesity in humans.
ABSTRACT. Zebra finches (Taeniopygia guttata) are often used in studies of social learning, personality, and communication. However, few studies have addressed the potential influence of an individual’s personality on their cognitive abilities, or how personality combinations can affect the success of pair-bonded mates. Our research aims to investigate these questions. We began by assessing personality in zebra finches. To evaluate an individual’s personality, we measured five different behavioral traits. These traits include: dominance, neophobia, aggressiveness, fearfulness, and obstinacy. Personality traits were tested individually and across multiple trials. Next, individuals were given a series of three problem-solving tasks with a food reward. This was used to measure an individual’s problem-solving ability. We then asked whether an individual’s personality predicted its performance on the problem-solving tasks. Future work will aim to address whether pairs of mates with similar personalities perform better than pairs of mates with dissimilar personalities on two coordinated skill-pooling maze tasks.

UP28: Effect of High Salt Diets on Reproductive Organs of the Rat. Mayer, D., and Skinner, D. Department of Zoology and Physiology, University of Wyoming, 1000 E. University Avenue, Laramie, WY 82071
ABSTRACT. Infertility rates among women all over the world are on the rise. What factors might cause this? Many differences in peoples’ physiology are due to diet. With the promotion of westernized cuisine people are consuming more salt. The negative effects of a high salt diet are understood to be harmful, but could they be responsible for the increase in infertility? Recent research has determined a high salt diet can postpone puberty in a rat significantly. Taking a closer look at the how female rats’ sexual organs are affected by a high salt diet might help us determine what is going on in humans. By looking at specific features in the ovaries of rats that have been fed different percentage salt diets, we might be able to broaden our understanding of morphological changes caused by a high salt diet.

Sprague-Dawly rats (Rattus) act as a great model of human physiology. Female rats’ completion of puberty is determined by vaginal opening. In recent research, the number of days that had passed before vaginal opening occurred was recorded in rats being fed different concentrations of salt in their food. The rats being fed higher concentrations of salt showed a delay in puberty. By taking a closer look at these rats’ ovaries, a difference could be detected. This discovery could yield a better understanding of the consequences of a high salt diet. It is important to find causes of infertility in women, and modeling using a rat is a great place to start.
UP29: Behavioral Inhibition and Posttrauma Symptomatology: The Moderating Effect of Safety Behaviors
McClure1, K. E., Ripley1, A. J., Blakey2, S. M., Kern1, S. A., Kozina1, R. M., & Clapp1, J. D. 1Department of Psychology, University of Wyoming, University of Wyoming, 1000 E. University Avenue, Laramie, WY 82071; 2Department of Psychology, University of North Carolina at Chapel Hill, 235 E Cameron Ave, Chapel Hill, NC 27514

ABSTRACT. Research demonstrates a reliable relation between activation of the Behavioral Inhibition System (BIS) and symptoms of posttraumatic stress. Behavioral inhibition involves a general sensitivity to negative outcomes and is believed to contribute to the maintenance of PTSD through increased risk of avoidance and hypervigilant behavior. Despite evidence of a relation between BIS and posttrauma symptoms, factors altering this relationship have received little attention. Anxiety-related safety behaviors (SB) are identified as actions performed by an individual intended to prevent or mitigate some feared outcome or associated distress (e.g., carrying weapons in public). The current research examined the unique and interactive associations of BIS and SB with posttrauma symptom dimensions.

Participants (N = 135; 77.0% White/non-Hispanic; 74.8% female) were undergraduates in an ongoing study examining interpersonal and functional outcomes after Criterion-A trauma. Behavioral inhibition was assessed using Carver & White’s (1994) scale. Trauma-related SB were examined using a measure targeting the frequency of actions intended to prevent feared outcomes and/or distress (e.g., travel with a “safe” person). Posttrauma symptoms were evaluated with the PTSD Checklist for DSM-5 (PCL-5). Relationships of SB and behavioral inhibition on symptom dimensions were examined with regression models controlling for gender.

Increased frequency of SB evidenced direct relations with Avoidance (p < 0.001, pr = 0.46), Cognitive Distortion (p < 0.001, pr = 0.37), and Re-experiencing (p < 0.001, pr = 0.45) clusters. An interactive effect of BIS and SB (p = 0.013, pr = 0.22) was also noted for symptoms of trauma-related Avoidance. Simple slopes indicated a reliable association of BIS and Avoidance at high levels of SB (p = 0.005, pr = 0.24). No relation was observed at low levels of SB (p = 0.534, pr = -0.06).

Results support previous findings that SB is a predictor of PTSD symptomology; however, these data suggest the influence of SB varies across symptom dimensions. SB showed a moderating effect on BIS for alterations in arousal and direct effects for other symptom clusters, suggesting the influence of SB in PTSD is complex.

UP30: Spider Silk-Like Protein Production for Biomaterial Generation. McCurdy1,2, H., Aikey2, T., Johnson1, P., and Teulé-Finley2, F. 1Department of Chemical and Petroleum Engineering, University of Wyoming, 1000 E University Avenue, Laramie, WY 82071; 2University of Wyoming at Casper, 125 College Drive, Casper, WY 82601

ABSTRACT. Spider silks have unique mechanical properties and have a wide range of potential biomedical applications including use in drug delivery, biogels, artificial tendons and ligaments, and wound dressings. The repetitive and modular nature of spider silk proteins enables genetic engineering and recombinant production of Spider Silk-Like Proteins (SSLPs). Two ~60 kDa chimeric flagelliform-dragline silk protein variants (Y1S820 and A1S820) were produced recombinantly in Escherichia coli. Silk gene expression was induced using isopropyl-β-D-1 thiogalactopyranoside (IPTG) and
the cells were harvested three hours after induction. Cell pellets were lysed to recover the total protein fraction. The SSLPs were then purified through immobilized metal (nickel) affinity chromatography (IMAC) and subjected to SDS-PAGE/Coomassie staining and Western Blot analyses. Pure SSLPs were dialyzed against a 5mM ammonium bicarbonate gradient, and lyophilized. Pure, dry SSLPs are the starting material for nanofiber mat generation by electrospinning. The chemical and mechanical properties of the electrospun SSLP mats will be tested. Cytotoxicity of these nanofiber mats will be analyzed using mammalian cell lines to determine biocompatibility.

**UP31: The Impact of *T. gondii* Infection on NK Cell Transcription Factor Usage.**
Mundhenke, T., and Gigley, J. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071

**ABSTRACT.** The parasite, *Toxoplasma gondii*, is the third world wide cause of food borne illness and possess an extreme health risk for immunocompromised individuals. Chronic infections of *T. gondii* results in immune exhaustion in which T cells become incapable of controlling the infection resulting in *T. gondii* overcoming the immune response. Natural killer (NK) cells were observed to play a role in contributing to immune exhaustion. To address why NK cells play this role in immune exhaustion, we have described the survival relationship of manipulating the NK cells through a series of survival group by the deletion of NK cells during both acute and chronic infection. Depleting the NK cells during the acute phase of infection resulted in a slight prolonged survival of the mice. The depletion of NK cells during the chronic phase of infection, however, had a much longer survival rate compared to mice that had their NK cells. Transcription factors are also of interest in how the NK cells are responding to acute and chronic infection. Transaction factors that were of interest were BLIMP, EOMES and T-Bet in which have been previously demonstrated to change during acute infection. The use of flow cytometry allowed for quantifying the transcription factors that were present in a naïve model. We directly targeted NK cells from the spleen for our baseline knowledge of transcription factors. Our naïve mice displayed high levels of EOMES and T-Bet while the BLIMP was extremely low.

**UP32: Developing an Assay for Polar Organizing Protein Z (PopZ) Mutant Screening.** Hass1, A., Paige1, L., Vigil1, D., Motriuk-Smith1, D., Holmes2, J., and Bowman2, G. 1University of Wyoming at Casper, University of Wyoming, 435 Union/University Building, Casper, Wyoming 82601; 2Department of Molecular Biology, University of Wyoming, 1000 East University Avenue, Laramie, Wyoming 82071

**ABSTRACT.** The long-standing model that protein structure is critical to function has been expanded to include intrinsically disordered proteins (IDPs). IDPs are present in all kingdoms of life, and they facilitate diverse biological functions. IDPs lack stable structures and exist as conformational ensembles, making the study of IDP structure-function relationships particularly challenging. In this project, our approach is to perform IDP structure-function analyses in a relatively efficient manner, by leveraging the inherent experimental advantages of a bacterial system. The focus of our studies is a bacterial IDP called PopZ, which is responsible for creating signaling networks at the cell poles in *Alphaproteobacteria*. In our experiments, we employ recombinant *E. coli* strains that co-express genetic variants of PopZ together with a known binding partner.
protein. Both proteins are tagged with a fluorescent protein for the purpose of subcellular localization by fluorescence microscopy. In our experiments, liquid cultures were inoculated, diluted, and recombinant protein expression was induced with IPTG and arabinose. As expected, wildtype PopZ exhibited polar localization, and the GFP-tagged binding partners, ChpT and ParB, co-localized with the polar PopZ foci. When a mutant form of PopZ was investigated in this experiment, it localized to cell poles but the binding partners failed to co-localize, indicating a defect in protein-protein interaction. These pilot experiments, together with related controls, verified the effectiveness and accuracy of the assay. They also provided information for creating detailed protocols for future PopZ mutant screening, which will be carried out in the summer of 2017 at UW-Casper.

UP33: Survey of Meso-Mammal Diversity in an Urban-Rural Interface on the High Plains. Paiz\textsuperscript{1}, D.J., Schaffer\textsuperscript{1}, F.G., IV, Wangelin\textsuperscript{1}, A.L., Lanier\textsuperscript{2}, H.C., and Roehrs\textsuperscript{1}, Z.P. \textsuperscript{1}Department of Natural Sciences, Laramie County Community College, 1400 E. College Drive Cheyenne, WY 82007; \textsuperscript{2}Department of Zoology and Physiology, University of Wyoming at Casper, 125 College Drive, Casper, WY 82601

ABSTRACT. Camera traps are a passive surveying method used to inventory and gather natural history and ecological information on vertebrates. In this study, camera traps were used to detect and obtain data on meso-mammals as a baseline survey of the Cheyenne Business Park Natural Area (CBPNA), an industrial complex on the edge of Cheyenne, Wyoming. Eight camera traps were deployed sampling forty-three 100×100 m survey grids in summer, fall, and winter 2016, with each grid surveyed by one camera for 7 days in each season, totaling 903 trap days and 879,645 photos examined. Grids were assigned to 1 of 3 habitats (prairie, riparian, or woodland). In preliminary results, riparian habitats hosted a more diverse meso-mammalian community in comparison to prairie habitats. At present, 9 mammal species badger (\textit{Taxidea taxus}), coyote (\textit{Canis latrans}), cottontail (\textit{Sylvilagus floridanus}), long-tailed weasel (\textit{Mustela frenata}), mink (\textit{Neovison vison}), mule deer (\textit{Odocoileus hemionus}), muskrat (\textit{Ondatra zibethicus}), raccoon (\textit{Procyon lotor}), and skunk (\textit{Mephitis mephitis}) have been detected on the CBPNA. Occupancy and detection probabilities will be estimated for each species in each season. Neither the mink (\textit{N. vison}) nor raccoon (\textit{P. lotor}) are well documented historically within Laramie County. While all of these species are known to be present in Laramie County, none have been documented on the CBPNA and this is the first study to estimate their abundance in southeastern Wyoming. Non-target vertebrates (e.g. birds, domestic mammals) have also been photographed and some species expected have yet to be detected on this area. Presented results consist of summer, fall and winter data, and are part of ongoing research to estimate seasonal occupancy data across the CBPNA and elucidate meso-mammal population dynamics in southeastern Wyoming.
UP34: Molecular Identification of Rhizosphere Fungi Isolated from a Selenium Rich Ecosystem. Paiz¹, D., Ridgway¹, K., Marsh¹, P., Petersen¹, A., Devilbiss², B., Wangeline¹, A., Springer¹, C., and Roehrs¹, Z. ¹Department of Natural Science, Laramie County Community College, 1400 E College Dr, Cheyenne, WY 82007; ²Department of Microbiology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. This is an ongoing study of fungal samples collected from the rhizosphere of selenium (Se) hyperaccumulator and non-accumulator plants in the north central Wind River Basin west of Lysite, WY. Development of a consistent and reliable procedure to identify these chemically diverse species proved to be challenging. Presently each sample has been assessed for Se tolerance, total phenolics, antioxidant capacity and antibiotic production. However, these isolates still require taxonomic classification. Identifying these fungi will provide insight into their phylogenetic and ecological roles in Se tolerance, host plant and fungal interactions, and impacts of environmental Se on fungal communities. To identify fungal taxa, DNA was isolated using the E.Z.N.A. SP Fungal DNA Mini Kit. Each DNA sample was amplified using standard PCR for the internal transcribed spacer region (ITS), commonly used to identify fungi. Amplified DNA was visualized and extracted using 1% agarose gels and prepared for sequencing using Quantum Prep PCR Kleen Spin Columns. The purified DNA was sequenced in both forward and reverse directions and concatenated sequences were compared to available sequence data of other fungi using BLASTN in Geneious. Using this information, we identified a sub-set of the unknown taxa minimally to genus and report preliminary results.

UP35: Fabrication and Mechanical Characterization of Thiol-ene Polymers and Thiol-acrylate Liquid Crystal Elastomers. Patel, V., Merkel, D., Cordes, A., and Frick, C. Department of Mechanical Engineering, University of Wyoming, 1000 E University Avenue, Laramie, Wyoming 82071

ABSTRACT. The purpose of the study was to synthesize and program thiol-acrylate and thiol-ene based polymeric materials. Liquid crystalline elastomers (LCEs) were formed using thiol-acrylate click chemistry. Thiol-ene polymer networks were formed by photoinitiated radical reaction. A base-catalyzed Michael addition of dithiol and tetrathiol monomers with a diacrylate mesogen is the single crosslinking mechanism to form a polydomain LCE. A room-temperature-nematic LCE exhibiting local mesogenic alignment, termed polydomain. A strained polydomain LCE with up to 45 mol% excess acrylate composition, allows a photocrosslinking reaction forming a monodomain elastomers. These polydomain and monodomain stages largely depend on the effects of increment in crosslink density, showing independent mechanical properties. To study the mechanical behavior of polydomain and monodomain LCE samples, dynamic mechanical analysis (DMA) was used to investigate linear viscoelastic region, glass transition temperature, isotropic transition temperature and thermal actuation properties. The amount of acrylate associated in LCEs changed mechanical properties of both polydomain and monodomain elastomers. Polydomain samples exhibited reduced transition temperatures, storage modulus, and high strain-to-failure with increased acrylate as a result of reduced crosslink density. On the other hand,
monodomain LCEs have higher transition temperatures, storage modulus, and reducing strain-to-failure with increased acrylate due to increased crosslink density.

A tetrathiol monomer with triene is sole crosslinking mechanism to form radical thiol-ene network polymer. The evolution of mechanical properties is analyzed as a function of UV exposure, where ultraviolet light initiates radical reaction. Thiol-ene polymers were successfully prepared through photochemical reaction with up to 80 mol% excess thiol (relative to acrylate) to form glassy polymer networks with chemically function surfaces. DMA was used to investigate the viscoelastic region and glass transition temperature. Increased thiol concentration resulted in reduced glass transition temperature.

**UP36: Effect of Neonatal Iron Supplementation on Microglial Activation in Huntington’s Disease Mice.** Realing, M., and Fox, J. Wyoming State Veterinary Laboratory, University of Wyoming, 1000 E University Ave, Laramie, WY, 82071

**ABSTRACT.** Huntington’s Disease (HD) is a neurodegenerative disorder that results from the atrophy of portions of the brain that control movement, cognition, and personality. Currently there is no therapeutic cure for HD. One change to the brain environment in HD affected individuals is neuroinflammation, this could drive HD progression, but the mechanism is not well understood. Microglial cells, the immune cells of the brain could be a main component of this neuroinflammation and can be activated by oxidative stress. The research team led by Dr. Fox has previously found that supplementation of neonatal mice with iron, worsens the effects of HD and promotes oxidative stress in brain.

The aim of this project was to understand if neonatal iron supplementation in HD mice promotes microglial activation. Findings will be relevant to understanding human HD. The initial goal of the research was to validate the microglial cell staining and analysis methods in our own laboratory. We would then utilize these techniques to assess the effect of neonatal iron supplementation in HD and wild-type mice.

**UP37: Microfluidic Devices for Cell Growth and Imaging.** Reusser, T., and Oakey, J. Department of Chemical Engineering, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071

**ABSTRACT.** The science and art of microscopy has developed to the point at which we can now image cells and their organelles on microscopic length scales. For many organisms, however, their three-dimensional structure complicates the use of modern microscopy tools. The use of microfluidic growth chambers, however, has made it possible to confine organisms within a single plane for high-resolution imaging. Microfluidic devices have been fabricated for the growth and imaging of different organisms using high-resolution microscopes and confocal microscopy. The key aspect of these devices is that they are all designed to confine growth to a single plane. Accordingly, device depth was matched to the thickness of a single cell. We are able to study the growth dynamics of species such as moss, which have never been captured because of its three-dimensional morphology. Fungus such as Ashbya can also be imaged to study cytoplasmic streaming and other processes. Microfluidic devices were also used as an in vitro mimic of fungus morphology to image cytoplasmic streaming of proteins and mRNA in a controlled environment. Finally, desiccation-tolerant green
algae found in desert crusts were grown in microfluidic devices to gather data to develop and expand models of algal growth. We are studying characteristics of this algal strain to assess how it reacts to various environmental conditions. With microfluidic devices, it appears possible to replicate key characteristics of soil in order to explore growth kinetics within and adhesion to these surrogate porous-media.

UP38: Lichen the Odds: Search for Novel Antibiotics in Lichen Secondary Metabolites. Chanthongthip¹, S., Rich¹, S.R., Kimble¹, E.J., and Cuddy², M.F.  
¹Department of Biology Northwest College, 231 West 6th Street, Powell, WY 82435; ²Department of Chemistry, Northwest College, 231 West 6th Street, Powell, WY 82435  
ABSTRACT  
There is an increasing concern about antibiotic resistance in pathogenic and potentially pathogenic bacteria. As a result, scientists are seeking novel antibiotics from environmental sources, for example, other bacteria, animals, lichen, etc… Our research focuses on some of the native lichen species in Wyoming and their ability to inhibit pathogens. We are testing the lichens’ secondary metabolites’ ability to inhibit three pathogens: Staphylococcus aureus, Escherichia coli, and Pseudomonas aeruginosa using the Kirby-Bauer disc diffusion protocol. All lichens tested, using a 50 µL dose of secondary metabolites, inhibited the growth of S. aureus. X. chlorochroa was the only lichen to inhibit Pseudomonas. These results could have possible implications for the future use of lichens in the production of antibiotics. The antibiotic-producing lichens’ secondary metabolites will be analyzed through nuclear magnetic resonance (NMR) and liquid chromatography (LC) to identify specific components that inhibit pathogens.

UP39: MicroRNA inhibition of GlcT-1 protein in Drosophila Melanogaster larvae. Rust, D. Lyuksyutova, A. Department of Molecular Biology, University of Wyoming, 1000 E. University Ave., Laramie, WY 82071  
ABSTRACT. Glucosylceramide synthase (GCS/UGCG/GlcT-1) catalyzes the formation of glucosylceramide, an important molecule in sphingolipid metabolism and obesity. Inhibition of UGCG/GCS in mice decreases liver fat content and inflammation in obese mice. Previous work suggests that microRNA’s, which are short non-coding RNA’s that silence genes upon binding to the genes mRNA transcript, are possible regulators of UGCG/GlcT-1. In order to further investigate the effects of microRNA’s on GlcT-1 in Drosophila melanogaster, we have performed qPCR in order to detect if and where, miR-190, the microRNA that regulated GlcT-1 in Drosophila, is naturally expressed. A recombinant line of mCherry expressing flies has also been established, which allows for easy determination of flies that are expressing desired traits.

UP40: Analysis of Titin Isoform Ratio in Different Sections of the Heart of Obese Maternal and Fetal Sheep. Sanchez Walk¹, ², A., Zhu¹, C., Sun¹, M., De Loera¹, D., Ford¹, S. P. and Guo¹, W. ¹Center for the Study of Fetal Programming, Department of Animal Science, University of Wyoming, 1000 E University Ave., Laramie, WY 82071; ²Department of Molecular Biology, University of Wyoming, 1000 E University Ave., Laramie, WY 82071  
ABSTRACT. Obesity during pregnancy is a major health concern considering that 36% of women are obese in the United States. Maternal obesity (MO) predisposes offspring
to risk factors for cardiovascular disease. How MO induces cardiac dysfunction in offspring remains poorly defined. Alternative splicing (AS) has been associated with cardiac dysfunction due to developmental and environmental changes. Titin is a critical gene for cardiac development and plays a central role in cardiac muscle contractility and ventricular wall stiffness. Titin has two classes of isoforms resulting from AS. These two isoforms (N2B and N2BA) change with development and under disease condition. The normal ratio of N2B to N2BA in a healthy human heart is about 70:30. Alterations to this ratio have led to diastolic and/or systolic dysfunction. Therefore, we hypothesize that MO alters titin isoform switching in fetal hearts of obese mothers, which could be an important etiology for MO-induced cardiac dysfunction. Ewes were fed an obesogenic diet starting 60 days before conception and throughout pregnancy. At late gestation (day 135), heart tissues were collected from ewes and their fetuses. Titin ratio was examined and quantified in left ventricle, right ventricle, left atria, right atria, apex and septum. The left ventricle of fetal obese group displayed increased N2B levels. All other maternal and fetal heart tissues revealed no change of the N2B to N2BA ratio when compared to their control counterparts. Future experiments will assess RBM20 expression in these tissues, as RBM20 regulates titin isoform ratio. This work is supported by the NIFA-USDA 1009266, NIH NIGMSP20GM103432, NIH HD070096-01A1, AHA BGIA and Faculty-Grant-in-Aid from University of Wyoming

UP41: TRPV1 Activation Counters Vascular Dysfunction by Increasing PPARs, SiRT-1, PGC-1α and UCP-1 Expression in the Thoracic Aorta. Schilling1, K., Markert2, L., Watkins1, J., Kinyatta1, K., with McAllister1, S., Baskaran2, P. and Thyagarajan2, B. 1Division of Health Science and Public Safety, Central Wyoming College, 2660 Peck Avenue, Riverton, WY 82501; 2Molecular Signaling Laboratory, School of Pharmacy, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

ABSTRACT. Obesity foreshadows metabolic diseases. The imbalance between energy intake and expenditure leads to increased visceral fat accumulation causing obesity. Vascular dysfunction associated obesity causes hypertension and progressively leads to cardiovascular diseases. Recent research suggests that activating TRPV1 is a good strategy to counter obesity and metabolic complications. In this work, we evaluated a hypothesis that activation of transient receptor potential vanilloid subfamily 1 (TRPV1) expressed in the thoracic aorta vasculature suppresses the development of hypertension and vascular damage by enhancing the expression of metabolically important peroxisome proliferator activated receptors (PPARs), sirtuin-1 (SiRT-1; central cellular metabolic sensor), PPARγ coactivator 1α (PGC-1α) and uncoupling protein 1 (UCP-1). Our data show that high fat diet (HFD; 60% calories from fat) feeding caused obesity and hypertension and suppressed the expression of PPARs, SiRT-1, PGC-1α and mitochondrial UCP-1. Capsaicin (a TRPV1 agonist) supplementation reversed this. Capsaicin increased the expression of SiRT-1, PPARγ, PGC-1α and UCP-1 in the thoracic aorta of wild type mice but not TRPV1−/− mice. Further, capsaicin enhanced the expression of PKCε, which in turn enhanced the phosphorylation of PPARα. Also, capsaicin significantly decreased the elevated systolic and diastolic blood pressure (measured by non-invasive tail cuff method) in the wild type but not in the TRPV1−/− mice. Our data also show that HFD significantly suppressed the expression of TRPV1 in
the thoracic aorta and capsaicin countered this. Our data collectively suggest that the activation of TRPV1 tightly couples to a SiRT-1-PPARs and PGC-1-dependent signaling mechanism to upregulate mitochondrial UCP-1 to protect vascular damage.


ABSTRACT. Subbituminous coal is a major factor of Wyoming’s economy. However, cleaner sources of energy, such as solar energy, wind energy, and hydroelectric energy, are highly competitive towards natural gas, oil—and most importantly—coal. Coal is mostly carbon which begs the question, “What carbon materials can be extracted or produced from coal, both efficiently and economically?” to develop new markets for this resource. Discovering a second major purpose for subbituminous coal, aside from its energy uses, would boost Wyoming’s economy. A goal of this research was to establish Fourier transform infrared spectroscopy, or FTIR spectra, of known carbon materials to compare to samples of coal following experimental treatment. The known carbon materials that were tested included carbon nanotubes, graphene nanoplatelet aggregates, and graphene oxide. The subbituminous coal FTIR spectra were then analyzed and compared to spectra obtained from the known carbon materials. Throughout this research, the relationship between mass and thickness of the salt plates was also analyzed. Details of the FTIR spectra comparisons, as well as the observed salt plate relationship, will be reported.

UP43: Use of Porous Liquid-Crystalline Elastomers in Glaucoma Treatment Devices. Stowe, L., and Frick, C. Department of Mechanical Engineering, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. Glaucoma is a group of eye diseases that cause pathological changes in the retina and optic nerve with corresponding visual field loss and blindness if left untreated. The National Eye Institute concluded in 2014 that an estimated 2.7 million people in the United States are affected by this chronic illness. While there are several short-term remedies available to afflicted individuals, predictable long-term treatments for glaucoma remain elusive, especially at advanced stages. One proposed treatment plan includes surgical implantation of a glaucoma treatment device; however, current devices are prone to complications resulting in subsequent surgeries.

The proposed research explores the use of a porous liquid-crystalline elastomer (LCE) as a potential glaucoma treatment device. A transcorneal LCE filter can be designed to mitigate the risk of complication by providing a non-surgical technique to remove and replace a compromised filter, enabled by shape switching LCE properties. Similar microporous filters are commonly applied in research, pharmaceutical, and industrial settings to sterilize fluids by removal of bacteria. Additionally, the unique shape-switching abilities of LCEs combined with microporous filtration capabilities are expected to extend to applications far beyond this single device. It is the goal of this project to determine a suitable technique to create microporous LCEs suitable for use in a glaucoma treatment device. Preliminary test results are encouraging that a prototype could be developed for testing as a potential glaucoma treatment device.
UP44: **Understanding the Role of Insulin and GnRH in PCOS.** Tighe, R., Khan, S., and Navratil, A. *Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave., Laramie, Wyoming 82071*

**ABSTRACT.** It has long been established that the physiological mechanisms controlling energy balance are integrated with those that control reproduction. In humans, insulin resistance is a component of polycystic ovary syndrome (PCOS), a reproductive ovarian disorder characterized by anovulation, polycystic ovaries, high androgen levels, hyperinsulinemia, and predisposition for Type 2 diabetes. It is the most common endocrine disorder among women of fertile age, with upwards of 10% of women being affected. Although the etiology of PCOS is unclear, the syndrome is clearly associated with metabolic dysfunction in which hyperinsulinemia and peripheral insulin resistance are central features. It has been well documented that altered gonadotropin secretion is associated with the typical form of PCOS. Compared with the follicular phase of the normal menstrual cycle, women with PCOS exhibit a disproportionately high luteinizing hormone (LH) secretion with relatively constant low follicle stimulating hormone (FSH) secretion from anterior pituitary gonadotropes. Previous data from our group suggests that gonadotrope cells undergo rapid and dramatic reorganization of the actin cytoskeleton in response to gonadotropin releasing hormone (GnRH) to facilitate LH release into the periphery. What remains unclear is how GnRH and hyperinsulinemia in PCOS might work cooperatively to facilitate changes in cellular morphology and secretion of gonadotropes. Our previous data suggests that GnRH leads to the activation of the actin binding protein cortactin, which is important for actin branching. Interestingly, when there is co-treatment of GnRH and insulin, gonadotropes appear to increase the levels of phosphorylated cortactin. Taken together, we suggest that the combined effect of GnRH and insulin may be modulating the actin cytoskeleton in gonadotropes to disproportionately increase circulating concentrations of LH seen in PCOS.

UP45: **Variation in Raptor Abundance Between Urban and Rural Habitats.** Tolbert, H. N., and Lanier, H. C. *Department of Zoology & Physiology, University of Wyoming at Casper, 125 College Drive, Casper, Wyoming 82601*

**ABSTRACT.** Raptors are iconic apex predators of the prairie and grassland habitats of Wyoming. Due to extensive modification of their habitat by urbanization, these landscape changes may lead to both threats and advantages, such as human-derived food sources. This study seeks to test if (1) raptor density differs between urban and rural habitats, and (2) if this difference is due to increased food abundance in human-modified habitats. Over the summer of 2016, I used distance sampling techniques and roadkill surveys, a proxy for prey density, to examine these questions, focusing on raptors in the prairie, grassland, and riparian habitats around Casper, WY. The results indicated that raptors are less abundant in human-dominated environments, with 1.9 raptors per km² in rural habitats versus 0.7 raptors per km² in urban areas. An AIC comparison of separate urban and rural models versus a combined model strongly supported modeling the two habitats separately. There was also a significant difference between roadkill in different habitats, with an average 1 roadkill/km in rural habitats and 0.4 roadkill/km in urban zones, suggesting that prey density may be higher in rural...
areas. While raptors and roadkill were positively correlated, this correlation was suggested abundance of both is greater in rural areas. This indicates that even in a state with a small human footprint, urbanization may be negatively affecting important apex predators.


ABSTRACT. From an ongoing project, we are observing the protist malaria in House Sparrows (Passer domesticus) and House Finches (Haemorhous mexicanus) inhabiting the Greater Yellowstone Ecosystem, especially the Big Horn Basin. House Sparrows and House Finches both are resident year-round in the Big Horn Basin experiencing similar environmental conditions. Natural history between the two species is similar but House Sparrows typically nest in cavities, or woven nest balls, whereas House Finches are open cup nesters. It is hypothesized that subtle differences in natural history can influence occurrence of malaria. Previous work in our lab has shown House Finches to show significantly greater variability in West Nile Virus (WNV) titers than do House Sparrows. As both diseases are transmitted by biting dipterans, is this a pattern also shown by malaria? Malaria can weaken the bird and in severe cases cause death. The protist comes from the families of species including Haemoproteidae, Plasmodiidae, Garniidae and Leucocytozoidae. These Apicomplexans can be passed to avian species by biting midges, hippoboscid flies, female blood-sucking mosquitoes of the genera Culex, Aedes, Culiseta, and Anopheles, and blood-sucking simulid fly. We are taking blood samples from House Sparrows and House Finches caught and released at either Coons Age Farm (Belfrey, MT) or on the campus of Northwest College in Powell, WY. We made blood smears and dyed the sample with Giemsa for one hour. We observed the sample under microscopes to detect any malaria and we are also taking counts of white blood cells per field: monocytes, heterophils, eosinophils, lymphocytes, and basophils, to test the immune status against malaria.


ABSTRACT. West Nile Virus (WNV) was originally discovered in Uganda in 1937. WNV belongs to the Flaviviridae family and is in the same genus as Dengue Fever, Zika virus, and Yellow Fever. Flaviviruses are persistently emerging and of great concern globally. Individuals contracting WNV may be asymptomatic, experience mild symptoms of fever, malaise, or develop a severe disabling illness such as meningitis, encephalitis, or polio-like paralysis. WNV was first detected in the U.S. in 1999, and rapidly migrated to the West Coast over the course of ten years reaching epidemic proportions in Wyoming in 2007. The majority of these cases were found in Fremont County with 118 infected, twelve neuroinvasive cases, and one death. Its persistence in Fremont County is evident from our testing of the vector Culex tarsalis mosquitoes and from our human serosurveys in 2011 and 2012. Interestingly, our previous serosurveys in 2011 and 2012 identified three subjects with abnormally high levels of IgM antibodies.
at least five years after self-reported initial infection. This coincides with similar observations from other serosurveys. This interesting humoral response to WNV is currently of great interest. Our proposed investigation will conduct a longitudinal study to identify and track subjects infected or previously exposed to WNV with the specific goal of identifying additional subjects expressing high levels of IgM long after initial exposure. It is planned to observe the seroconversion in these subjects to gain insight into this phenomenon. We also plan to test these individuals for cryptic infection through reverse transcriptase PCR.

UP48: Denitrification Potential of Soil Microbes in the Lower North Platte River Valley, Wyoming. Wilhoit, C., Turner, D., Chavez, E., Francis, A., and Wenzel, C.R. Department of Biology, Division of Science and Mathematics, Eastern Wyoming College, 3200 West C Street, Torrington, WY 82240; Department of Mathematics, Division of Science and Mathematics, Eastern Wyoming College, 3200 West C Street, Torrington, WY 82240

ABSTRACT. Soils and groundwater in east central Goshen County, Wyoming have been documented to have high nitrate levels since the 1950’s (Rapp et al., 1957; Parks, 1991). EPA studies have indicated that nitrates are harmful to both human and animal health at concentrations above established limits. The focus of this study is to document the extent to which the presence of nosZ, narG, nirK, and nirS gene-containing bacteria, reduce soil nitrate levels and subsequent groundwater nitrate levels by the natural process of denitrification. In addition, nitrous oxide (N₂O) emissions have been assayed to further assess denitrification activity. Thus far, DNA and RNA have been extracted from soil bacteria, and molecular techniques are being used to amplify the gene fragments and to quantify presence of nitrate reducing soil microorganisms.

UP49: The Expression of Peptidylarginine Deiminase Enzymes in Uterine Tumor Cells. Williams, A., Gard, P., Young, C., and Cherrington, B. Department of Zoology and Physiology, University of Wyoming, 1000 E. University Ave, Laramie, WY, 82071

ABSTRACT. Peptidylarginine deiminase (PAD) enzymes post-translationally convert positively charged arginine amino acids into neutral citrulline residues. A major target for PAD catalyzed citrullination is arginine residues on histone tails. Citrullination of histones results in changes in chromatin organization and gene expression. There are five PAD isoforms designated PADs 1, 2, 3, 4 and 6. PADs 1-4 have catalytic activity, while PAD 6 is believed to be a structural protein limited to preimplantation embryos. PAD enzymes are highly expressed in multiple female reproductive tissues. For example, the first studies investigating this enzyme family showed strong PAD expression localized to uterine luminal and glandular epithelial cells. More recently, work from our lab demonstrated that PAD2 and 4 are highly expressed in sheep uterine epithelial cells during early pregnancy. Using a cell line derived from sheep uterine cells, we showed that PADs citrullinate histones to regulate expression of genes involved in blastocyst implantation. Based on these findings, we hypothesized that PAD enzymes are expressed in human uterine and cervical epithelial cells. To test this possibility, we first investigated if a human uterine-cervical cell line termed HeLa cells expresses PAD enzymes. HeLa cell lysates were examined by western blot analysis and probed with antibodies specific to each PAD isoform. Our results indicate that the
PAD 1-4 isoforms are all expressed in HeLa cells. Since these cells are a well characterized uterine-cervical cancer line, we next hypothesized that PAD enzymes are expressed in uterine tumors. This hypothesis was tested by examining uterine tumors with immunohistochemistry using PAD isoform specific antibodies. Our results demonstrate that PADS 2 and 4 are expressed within the uterine tumors. Since PADS 2 and 4 localize in the nucleus, we next plan to examine if they citrullinate histones in HeLa cells to regulate expression of cancer related genes. Although further investigation is clearly necessary, our findings suggests that PAD catalyzed citrullination may be an important post-translational mechanism in uterine cancer cells.

UP50: Getting Bit with West Nile Virus and Malaria. Watkins, B.R, Harakal, K., Winkler1, C.D, Russell, T., and Atkinson, E, C. Biology Department, Northwest College, 231 West 6th street, Powell, WY 82435

ABSTRACT. From an ongoing project, we are observing the protist malaria in avian communities in the Greater Yellowstone Ecosystem, especially the Big Horn Basin. House Sparrows (Passer domesticus) and House Finches (Haemorhous mexicanus) both inhabit the Big Horn Basin year-round experiencing similar environmental conditions. Natural history between the two species is similar but House Sparrows typically nest in cavities, or woven nest balls, whereas House Finches are open cup nesters. It is hypothesized that subtle differences in natural history can influence occurrence of malaria. Malaria can weaken the bird and in severe cases cause death. The protist comes from the families of species including Haemoproteidae, Plasmodiidae, Garniidae and Leucocytozoidae. These Apicomplexans can be passed to avian species by biting midges, hippoboscid flies, female blood-sucking mosquitoes of the genera Culex, Aedes, Culiseta, and Anopheles, and blood-sucking simuliiid fly. We are taking blood samples from House Sparrows and House Finches caught and released at either Coons Age Farm (Belfrey, MT) or on the campus of Northwest College in Powell, WY. We made blood smears and dyed the sample with Giemsa for one hour. We observed the sample under microscopes to detect any malaria and we are also taking counts of white blood cells: monocytes, heterophils, eosinophils, lymphocytes, and basophils, to test the immune status against malaria and West Nile Virus. Simultaneously, West Nile Virus is tested with RAMP (a specific ELISA).

UP51: Assessing the Occurrence of Microplastics in the Snake River. Yeatman, E., and Kapp, K. Department of Arts and Science, Central Wyoming College, 140 S. Glenwood Street, Jackson, WY 83002

ABSTRACT. Over the past 40 years, world production of plastic resins increased some 25-fold creating a global waste stream comprised of 60-80% plastics. Microplastics, plastic particles less than 5mm in size, are receiving increased attention as a potentially detrimental environmental contaminant. Primary sources of microplastic pollution include plastic pellets and powders produced by manufacturers for industrial sale that enter the waterway via spills, improper dumping or facility accidents and microbeads used as abrasives or exfoliant in commercial products. Secondary sources of microplastic pollution are fibers and fragments from the deterioration of larger plastics. Synthetic fibers enter our waterway as micro-sized fibers shed from laundry in our
household sewage effluent that urban wastewater treatment centers are unable to capture. Microplastics have been found throughout our oceans, but little has been done to quantify them in our freshwater systems. This study examines the Snake River for the presence of microplastics. By looking at an entire river system, we hope to identify hot spots and sources of microplastic pollution, such as wastewater treatment facilities or recreational areas. Grab samples (average volume of 1.8 liters) and volume reduced samples with a 100-micron mesh plankton net (average volume of 3,328 L) were collected throughout the summer of 2016 approximately every 50 river miles along the Snake River out to the Pacific Ocean. Grab samples were vacuum filtered through 0.45µm filters then visually inspected under a Nikon SMZ800N stereoscope with a fluorescent adapter. Suspect particles are analyzed using Raman spectrometry and/or FT-IR to confirm the type of plastic polymer. In this presentation, the results from the grab samples collected at all 28 sites will be revealed. Of the 23 grab samples visually inspected to date, 16 contained putative microplastics.

**UP52: Oral Sub-Chronic Safety Studies of Capsaicin.** Zimmerman, L., Markert, L., Bennis, J., Frantz, J., Basakran, P and Thyagarajan, B. Molecular Signaling Laboratory, School of Pharmacy, University of Wyoming, 1000 East University Avenue, Laramie, WY 82071

**ABSTRACT.** Capsaicin (CAP), a selective agonist for transient receptor potential vanilloid subfamily 1 (TRPV1) protein, activates TRPV1 expressed on the membranes of white and brown adipocytes to cause browning of white adipocytes and upregulation of thermogenic gene expression. We are currently developing novel formulations of CAP for human clinical trials. Although, our sub-chronic CAP-feeding neither altered the energy intake nor any adverse reactions in mice, it is essential to demonstrate the safety of CAP in preclinical toxicological studies in mice. Keeping this goal in mind we conducted a dose response for capsaicin (0.133, 0.399, 0.665, 1.33 or 3.99 mg/kg body weight of mouse corresponding to 0.001, 0.003, 0.005, 0.01 and 0.03% of CAP in diet) to counter obesity in high fat diet-fed wild type mice. We also conducted histological studies and analyzed the plasma levels of markers metabolic, liver and kidney functions in the mice. Further, to ensure that CAP does not cause adverse reactions when in normal chow diet (NCD), we fed wild type mice a diet containing 0.01% CAP in NCD. Our data show that CAP inhibited diet-induced obesity at concentration above 0.001% (0.133 mg/kg body weight) and the theoretical EC50 of CAP is determined to 0.00157% (0.2881 mg/kg body weight). CAP did not alter food/water intake in mice in any of the concentrations used for the study. HFD feeding increased fasting plasma glucose, triglycerides and cholesterol levels and significantly elevated serum alanine aminotransferase and creatinine levels, and CAP antagonized this. HFD-induced obesity was associated with hypertension and dietary CAP prevented it at all concentrations except 0.003%. HFD feeding slightly but significantly decreased the body temperature (rectal) of mice and CAP antagonized this. Feeding CAP in NCD did not cause weight loss in mice. Analyses of histological sections revealed no pathological findings when mice were fed CAP either with NCD or HFD. Collectively, our study provides compelling preclinical data that suggest that sub-chronic oral CAP feeding is safe and does not cause any adverse effects in mice. These data are valuable for advancing the clinical uses of CAP to counter obesity in humans.
UP53: A genetic module for programmable asymmetric cell division in bacteria. Iacovetto, R., Mushnikov, N. and Bowman, G. Department of Molecular Biology, University of Wyoming

ABSTRACT: Asymmetric cell division is a fundamental cell biological mechanism that many organisms use to achieve greater complexity. Following an asymmetric cell division, the daughter cells inherit differences that lead to distinct patterns of gene expression and different cell fates. In the bacterium Caulobacter crescentus, asymmetric cell division results in an immobile cell and a swarmer cell that produce a stalk and flagellum respectively. In another example, the differentiated cell layers of microbial biofilms are created by different intracellular concentrations of the secondary messenger molecule c-di-GMP, which regulates patterns of gene expression in the biofilm. The goal of this project was to combine elements of these two regulatory systems to create a programmable genetic module that establishes asymmetric cell division in E.coli, which normally divide symmetrically. Our results show that asymmetric cell division can be coordinated with differential control of gene expression with a surprisingly small set of regulatory components.

UP54: Accuracy of documentation and monitoring of oral chemotherapy in a small community cancer center. Zukauckas1,2 K., Holmes1,2, S., and Harshberger1,2, C. 1School of Pharmacy, University of Wyoming, Laramie, WY 82071 2Ivinson Memorial Hospital, 255 N 30th St, Laramie WY, 82072.

ABSTRACT: Newly approved oral chemotherapy agents include endocrine therapy and cytotoxic agents. These self-administered agents provide patients with convenient options and perceived benefits of less clinic visits and complications. Oral chemotherapy is only effective when patients adhere to the prescribed administration schedule and the potential for drug-drug interactions and unwanted toxicity can lead to non-adherent patients. Chemotherapy education can help identify initial potential problems, but continued monitoring and assessing patient adherence through clinic visits can lead to better efficacy, patient outcomes, and overall survival. Retrospective chart reviews were completed and de-identified prior to analysis. We evaluated oral chemotherapy patients in a small community oncology clinic over a two-month period in 2016. Documentation for adherence, chemotherapy education, monitoring parameters per package insert from manufacturers, home medication list per electronic medical record (EMR) and drug interactions were reviewed and assessed for each identified patient. Twenty of the 48 patients identified were on oral chemotherapy. Adherence to oral chemotherapy or endocrine therapy was not specifically documented in provider notes for the 48 patients. Chemotherapy education was not consistently documented in the EMR and monitoring parameters were not discussed in provider notes. Home medication lists accessible by other departments utilizing the EMR did not include these medications in >50% of the patients. Drug-drug interactions were not documented in most cases and upon review many patients had drug interactions that were category D. Medication lists were incorrectly documented. This study illustrates the difficulty of documenting patient adherence and toxicities with new oral chemotherapy agents. Currently, there is no mechanism within the EMR that requires providers to specifically question and document oral chemotherapy. EMR support will be developed for
documentation of therapy within this population of patients. Utilization of clinical oncology pharmacists is critical to provide the necessary management, monitoring, and documentation of appropriate therapy in oral chemotherapy and endocrine therapy patients.

C. UNIVERSITY OF WYOMING UNDERGRADUATE RESEARCH DAYS

The following are additional INBRE-funded research projects presented by undergraduate students (poster/UP or oral presentations/UOP) at the University of Wyoming Undergraduate Research Days on April 29th 2017 (Laramie, WY).

UP55: The Impacts of Post-Fire Succession on Native Bee Diversity within the Rocky Mountain Ecosystem. David, K., and Lanier, H. Department of Zoology, and Physiology, University of Wyoming at Casper, 125 College Dr., Casper, Wyoming 82601

ABSTRACT. Allowing natural fires to occur in our Rocky Mountain Forests may be an important factor in increasing native bee populations, as larger populations of native bees have been found in early successional stages of post-fire forests in other forest systems. Burned dead trees are important nesting sites for cavity dwelling bees and the bare ground from fires is important to ground-dwelling bees. In this work, I examined how the two recent fire disturbances on Casper Mountain (2006 and 2012) impacted native bee diversity and abundance. Since fire opens up more area for flowering plants, I hypothesize that more native bees will be found in early post-fire succession than later post-fire succession or nearby non-burned (control) areas. I tested this hypothesis by collecting native bees within the burned and non-burned areas and then counted and identified the collected specimens using morphological and molecular techniques. The total number of bees collected from Casper Mountain was 4690. Overall, bees were more abundant and more diverse in burn areas than in the control areas. This is important information for fire management practices in regards to native bee conservation.

UOP56: Examining the Networking and Behavior of Gonadotropes in Intact Mouse Pituitaries using GCamp6 Imaging. Smith, K., Navratil, A., and Asman, D. Department of Zoology & Physiology, University of Wyoming, 1000 E University Ave, Laramie, WY 82071

ABSTRACT. Pituitary gonadotropes are an integral part of the Hypothalamo-pituitary-gonadal axis. Gonadotropes synthesize and secrete luteinizing hormone (LH) and follicle-stimulating hormone (FSH) when acted upon by gonadotropin-releasing hormone (GnRH) from the hypothalamus. Activation of gonadotropes by GnRH induces a rapid biphasic elevation of intracellular calcium. The importance of calcium in gonadotropes are largely from cell culture experiments that lack any spatial resolution to address calcium activity at the population level. To address this gap in knowledge, we have taken an innovative approach of using a genetically encoded calcium indicator (GCaMP6) to detect fluctuating calcium signals within gonadotropes in vivo. Utilizing CRE/Lox technology, we have created a gonadotrope specific GCaMP6 expressing mouse that is highly responsive to GnRH. First, the pituitary was explanted from our GCamp6-positive mice and placed in oxygenated CSF where it was exposed to a pulse...
of GnRH to assess calcium kinetics. We analyzed the amplitude and frequency of Ca\(^{2+}\) transients from gonadotropes. Several gonadotropes displayed regular oscillations upon GnRH agonist application (57%), while others showed irregular oscillatory behavior (43%). Additionally, synchronization of GnRH-induced calcium transients was observed in several clusters of gonadotropes that were in proximity to one another. Gender differences in GnRH-induced gonadotrope responses were identified. The proportion of gonadotropes exhibiting increases in amplitude was significantly higher in females than males (p<0.05, \(\chi^2\)). This study, although still preliminary, shows promising steps forward in the exploration and understanding of calcium signaling within gonadotropes in response to GnRH.

**UOP57: Searching for Novel Antibiotics in Lichen Secondary Metabolites.**
Chanthongthip, S., and Kimble, E. *Department of Biology and Chemistry, Northwest College, 231 West 6th street, Powell, WY 82435*

**ABSTRACT.** Currently, an increasing concern exists about antibiotic resistance in pathogenic and potentially pathogenic bacteria. As a result, many researchers are searching for novel antibiotics from environmental sources (i.e. other bacteria, animals, lichen, etc.). Our research focuses on some of the native lichen species (*Xanthoparmelia chlorochroa* and *Caloplaca citrina*) in Wyoming and their ability to inhibit pathogens. To test the lichens’ secondary metabolites’ ability to inhibit potential infection we used three pathogens: *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa* via the Kirby-Bauer disc diffusion protocol. With a dosage amount of 50 \(\mu\)L, results showed zones of inhibition by *X. chlorochroa* on *S. aureus* (zone of 9.5 mm) and *Pseudomonas* (zone of 4.0 mm), whereas *C. citrina* extract inhibited only *S. aureus* (zone of 5.9 mm). This demonstrates significant implications for the future of lichen-derived antibiotics and their efficacy against *S. aureus* and *Pseudomonas aeruginosa*. The antibiotic-producing lichens’ secondary metabolites will be analyzed through nuclear magnetic resonance (NMR) and liquid chromatography to identify specific properties that inhibit pathogens.

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