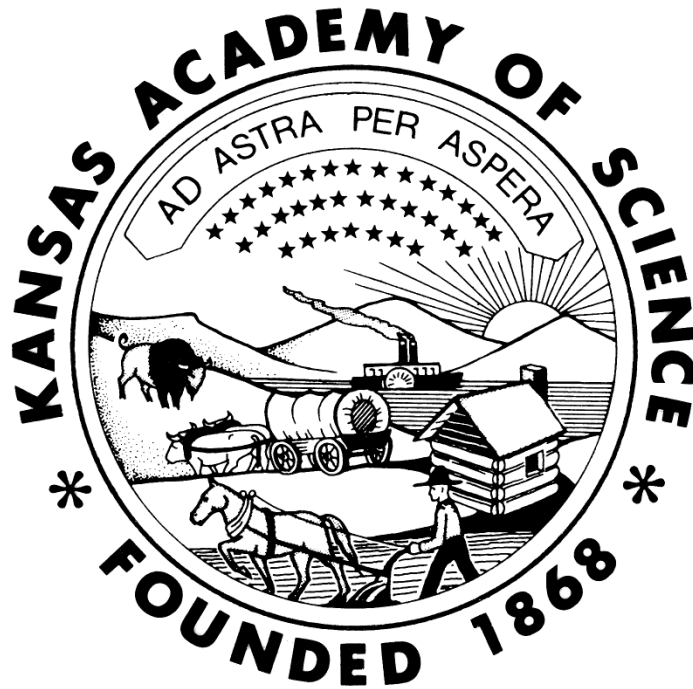


Kansas Academy of Science  
2021 Virtual Meeting



153<sup>rd</sup> Annual Meeting  
APRIL 10, 2021



## Welcome Message

Every year, scientists from across Kansas and neighboring states come together to share their scientific research as well as learn from each other through collaborative experiences. We are fortunate to have the opportunity to conduct the Kansas Academy of Science (KAS) annual meeting virtually despite the COVID-19 pandemic. As part of our virtual conference, we granted free access for KAS Members to attend the conference, which includes talks and posters.

Becoming a member of the Kansas Academy of Science includes access to the annual conference, annual fall field trip, the *Transactions of the Kansas Academy of Science* journal, a biannual newsletter, and support for the Kansas Junior Academy of Science which gives middle and high school aged students the opportunity to present their research at annual spring meetings.

If you are interested in becoming a Kansas Academy of Science Member, please fill out the following application: <http://www.kansasacademyscience.org/membership.html>

A special thank you to the organizers of this conference:

		
Dustin Wilgers McPherson College	David McKenzie Emporia State University	Kim Simons Emporia State University
		
Brian Maricle Fort Hays State University	Keri Maricle North Central Kansas Technical College	

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## Conference Overview

A video conferencing medium called Zoom will be used to host the entirety of the conference. It is highly suggested all participants ensure they have the most recent Zoom software with updates prior to the conference. All participants can download the latest version of Zoom for free by accessing the following link:

[https://zoom.us/download#client\\_4meeting](https://zoom.us/download#client_4meeting)



### *Oral Presentations*

Talks are divided into two sessions with each session having their own Zoom room. Presenters will be expected to share their screens to present their talks. A session moderator will be present for each session to facilitate the talks.

### *Poster Presentations*

There will be one poster session with each poster presenter assigned to their own breakout room within the session. Attendees will have the ability to move between breakout rooms to view posters and visit with presenters. Presenters will be expected to share their screens with their poster displayed. Presenters are also expected to share their posters to meeting coordinators ahead of time to allow an opportunity for attendees and judges to view posters.

## Schedule Overview

Saturday, April 10<sup>th</sup>

- 8:00 – 8:40 Oral Presentation Technology Check
- <https://mcphersoncollege.zoom.us/j/92146502567?pwd=WTZJcU9LV0NCbjl6cWpBMWcvWDFsQT09>
  - Meeting ID: 921 4650 2567
  - Passcode: 554716
- 8:00 – 8:40 Poster Presentation Technology Check
- <https://mcphersoncollege.zoom.us/j/96461729554?pwd=NzJlNSStLRG9VRzM2aXdKK29SelpYZz09>
  - Meeting ID: 964 6172 9554
  - Passcode: 904865
- 8:50 – 9:00 President's Welcome
- <https://mcphersoncollege.zoom.us/j/94216144503?pwd=TnRYWE9adGtDajZlZnVDdnpXd09kUT09>
  - Meeting ID: 942 1614 4503
  - Passcode: 477752
- 9:00 – 10:45 Oral Presentation Room A
- <https://mcphersoncollege.zoom.us/j/99257687560?pwd=MIU5bGRCSXBWdlEwNjNNMExsVTFFQT09>
  - Meeting ID: 992 5768 7560
  - Passcode: 775085
- 9:00 – 10:30 Oral Presentation Room B
- <https://mcphersoncollege.zoom.us/j/97889751207?pwd=L250djVhTjNvRGFKY2ZTU3JKVVZzUT09>
  - Meeting ID: 978 8975 1207
  - Passcode: 546588
- 11:00 – 12:00 Poster Presentations
- <https://mcphersoncollege.zoom.us/j/97706682488?pwd=WERKTjRnTEtsaWt4QTg0RjRLTXBUQT09>
  - Meeting ID: 977 0668 2488
  - Passcode: 706606

12:00 – 1:00

KAS Business Meeting

- <https://mcphersoncollege.zoom.us/j/94577873341?pwd=OWxlalBDcG9GUdRWWEt5RGdEZG02Zz09>
- Meeting ID: 945 7787 3341
- Passcode: 205127

**Oral Presentations**  
**Concurrent Sessions from 9:00 – 10:45 AM on Saturday, April 10<sup>th</sup>**

Italics indicates presenting author  
Designations: Undergraduates (1) and Graduates (2)

Room A: Natural Sciences and Physical Sciences

- Session Moderator: Dustin Wilgers

- 9:00      *Aguirre-Mendez, C.<sup>1</sup>, Chen, Y.<sup>2</sup>, and Terada, T.<sup>2</sup>* **1. Department of Physical Sciences, Emporia State University. 2. Arizona State University.**  
ARGUMENTATIVE WRITING TO PROMOTE NONSCIENCE MAJOR STUDENTS' LEARNING IN AN INTRODUCTORY CHEMISTRY COURSE.
- 9:15      *Gunther, S. (1) and Hoffman, B.* **Department of Natural and Applied Sciences, Park University.**  
PRELIMINARY ANALYSIS OF THE DENTAL ULTRASTRUCTURE OF THE STINGRAY *DASYATIS* FROM THE PUNGO RIVER FORMATION (MIOCENE OF NORTH CAROLINA).
- 9:30      *Hoffman, B. and Hageman S.* **Department of Natural and Applied Sciences, Park University.**  
COMPARISON OF CUTTING EDGES OF THE FOSSIL SHARKS *SQUALICORAX CURVATUS*, *GALEOCERDO ADUNCUS*, AND *PHYSOGALEUS CONTORTUS*.
- 9:45      *Sun, M.<sup>1,2</sup> and Sellens, C.<sup>1</sup>* **1. Department of Physical Sciences, Emporia State University. 2. Master Science of Forensic Program, Emporia State University.**  
IS THE LABEL CLAIMED CONTENT OF CBD IN CBD OILS AND EDIBLES CORRECT?
- 10:00     *d'Assignies, W. (2).* **Department of Physics and Astronomy, University of Kansas and Ecole Normale Supérieure, Paris, France.**  
ANOMALOUS COUPLING: THE SEARCH FOR NEW PARTICLES AT THE LHC.
- 10:15     *Alcerro, L. (2).* **Department of Physics and Astronomy, University of Kansas.**  
LEPTON NUMBER VIOLATION AND NEUTRINOS NATURE.
- 10:30     *Lindsey, C. (2) and Royon, C.* **Department of Physics and Astronomy, University of Kansas.**  
UNDERSTANDING PROTONIC STRUCTURE USING THE LHC.

Room B: Biological Sciences

- Session Moderator: Keri Maricle

- 9:00      **Schowengerdt, J. (1) and Conard, J. Department of Natural Science, Sterling College.**  
THE INFLUENCE OF DRONE PRESENCE ON PRAIRIE DOG BEHAVIOR.
- 9:15      **Janke, S. (1). Department of General Education, North Central Kansas Technical College.**  
LITTLE MASK: FOSTERING SCIENTIFIC LITERACY IN CHILDREN.
- 9:30      **Rogers, J. (1) and Hong, W-F. Department of Natural Science and Mathematics, Sterling College.**  
STUDIES OF MELANIN-LIKE PRODUCING *BACILLUS VALLISMORTIS* AND EXTRACTION OF MELANIN-LIKE PIGMENT.
- 9:45      **Skinner, N. (2) and Jensen, W. Department of Biological Sciences, Emporia State University.**  
GEOGRAPHIC PATTERNS OF MELANISM IN FOX SQUIRRELS (*SCIURUS NIGER*) IN EAST-CENTRAL KANSAS.
- 10:00     **Wertz, B. (2), Moyer, M., Kostner, D., White, T., Abernathy, O., and Kobayashi, Y. Department of Biological Sciences, Fort Hays State University.**  
EFFECTS OF FOOD INTAKE AND FOOD EXPOSURE ON EXPRESSION OF TWO DOPAMINE RECEPTORS (DR), TYROSINE HYDROXYLASE (TYRH), AROMATIC L-AMINO ACID DE CARBOXYLASE (AAAD), AND CATECHOL-O-METHYLTRANSFERASE (COMTA) MRNA IN THE BRAIN OF CHANNEL CATFISH.
- 10:15     **Thompson, J. (2) and Jensen, W. Department of Biological Sciences, Emporia State University.** DO BEHAVIORAL TENDENCIES PRESENT REPRODUCTIVE TRADEOFFS IN DICKCISSELS?



## Poster Presentations

Breakout Rooms with Presenters from 11:00 AM – 12:00 PM on Saturday, April 10<sup>th</sup>

Italics indicates presenting author

Designations: Undergraduates (1) and Graduates (2)

<u>Room</u>	<u>Presentation</u>
1	<b><i>Butenas, A.</i><sup>1</sup> (2), <i>Rollins, K.</i><sup>1</sup>, <i>Williams, A.</i><sup>1</sup>, <i>Hammond, S.</i><sup>1</sup>, <i>Parr, S.</i><sup>1</sup>, <i>Ade, C.</i><sup>1</sup>, <i>Hageman, K.</i><sup>2</sup>, <i>Musch, T.</i><sup>1,2</sup>, and <i>Copp, S.</i><sup>1</sup> 1. Department of Kinesiology, Kansas State University. 2. Department of Anatomy and Physiology, Kansas State University. THROMBOXANE A<sub>2</sub> RECEPTORS CONTRIBUTE TO THE EXAGGERATED EXERCISE PRESSOR REFLEX IN RATS WITH HEART FAILURE.</b>
2	<b><i>Fay, S.</i><sup>1,2</sup> (1) and <i>Maricle, B.</i><sup>1</sup> 1. Department of Biological Sciences, Fort Hays State University. 2. Kansas Academy of Mathematics and Science, Fort Hays State University. EFFECTS OF SOIL MICROBIAL ADDITIVES ON GROWTH IN PEA PLANTS.</b>
3	<b><i>Gaede, J.</i> (1), <i>Parris, M.</i>, and <i>McLoud, J.</i> Department of Biological Sciences, Tabor College. TESTING SPECIES THRESHOLD FOR DNA BARCODING REGION IN COMMON AIRBORNE FUNGI: USING AN ECOLOGICAL METAGENOMICS WORKFLOW WITH QIIME 2.</b>
4	<b><i>Galliard, M.</i><sup>1</sup>, <i>Olson, B.</i><sup>2</sup>, <i>Gray, M.</i><sup>2</sup>, and <i>Johnson, L.</i><sup>2</sup> 1. Department of Biological Sciences, Fort Hays State University. 2. Division of Biology, Kansas State University. SITE AND ECOTYPE GENE EXPRESSION DIFFERENCES OF AN ECOLOGICALLY-DOMINANT PRAIRIE GRASS <i>ANDROPOGON GERARDII</i> ACROSS THE GREAT PLAINS' CLIMATE GRADIENT.</b>
5	<b><i>Gehin, A.</i> (1) and <i>Stump, L.</i> (1). Science Division, Johnson County Community College. DIMENSIONS 2C US-CHINA: MICROBE ECO-EVOLUTIONARY FEEDBACKS AS DRIVERS OF PLANT COEXISTENCE AND DIVERSITY GRADIENTS: UPDATE OF PROGRESS AT THE JCCC SITE.</b>
6	<b><i>Goins, S.</i> (1) and <i>Ghosh, A.</i> Department of Biology, Pittsburg State University. SURVEILLANCE STUDY ON <i>CULEX</i> SP. IN SOUTHEAST KANSAS AND PREVALENCE OF WEST NILE VIRUS IN THE MOSQUITO POPULATION.</b>

<u>Room</u>	<u>Presentation</u>
7	<b>Johnson, M. (1) and McLoud, J. Department of Biological Sciences, Tabor College.</b> DEEP SEQUENCING OF <i>HANNAELLA COPROSMAE</i> TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION.
8	<b>Jones, R. Physical Sciences Department, Emporia State University.</b> EXPERIMENTS WITH THE A.S.A. H. AI.
9	<b>Knight, C. (1) and McLoud, R. Department of Biological Sciences, Tabor College.</b> DEEP SEQUENCING OF MULTIPLE GENES TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION.
10	<b>Krueger, C. (1) and Maricle, B. Department of Biological Sciences, Fort Hays State University.</b> EFFECTS OF SULFIDE ON GROWTH AND CHLOROPHYLL IN WHEAT AND CORN.
11	<b>Neuhauser, K.R.<sup>1</sup> and Neuhauser, K.J.<sup>2</sup> 1. Department of Geosciences, Fort Hays State University. 2. Division of Water Resources, Kansas Department of Agriculture.</b> A SMOKY HILL TRAIL 1867 MASSACRE.
12	<b>Neuhauser, K.R. Department of Geosciences, Fort Hays State University.</b> ELECTRICAL RESISTIVITY SURVEY OF A SUSPECT DNAPL SPILL: STILLWATER, OKLAHOMA.
13	<b>Neuhauser, K.R. Department of Geosciences, Fort Hays State University.</b> A GEOLOGIC HOAX IN WESTERN KANSAS – QUICK, GET MARSHALL DILLON AND HEAD TO CASTLE ROCK.
14	<b>Primrose, M. (1) and McLoud, J. Department of Biological Sciences, Tabor College.</b> DEEP SEQUENCING OF <i>EPICOCCUM NIGRUM</i> TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION.
15	<b>Ranabhat, N.<sup>1</sup> (2), Bruce, M.<sup>1</sup>, Fellers, J.<sup>2</sup>, and Rupp, J.<sup>1</sup> 1. Department of Plant Pathology, Kansas State University. 2. USDA-ARS, Kansas State University.</b> WHEAT STREAK MOSAIC VIRUS PREVALENCE IN KANSAS WINTER WHEAT FIELDS.

<u>Room</u>	<u>Presentation</u>
16	<b>Ratcliffe, A. (2), Tong, J., Hoang, A., and Schneegurt, M. Department of Biological Sciences, Wichita State University.</b> STUDIES OF SALINOTOLERANT BACTERIA AT THE GREAT HYDROSTATIC PRESSURE WITHIN EUROPA AND THE ICY OCEAN WORLDS.
17	<b>Skinner, N. (2) and Gress, J. Department of Biological Sciences, Emporia State University.</b> STATUS OF ALFALFA WEEVILS IN KANSAS.
18	<b>Travis, A. (1), Ingram, A., and McCloud, J. Department of Biological Sciences, Tabor College.</b> DEEP SEQUENCING OF <i>CLADOSPORIUM VELOX</i> TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION.
19	<b>Wiest, T. (1), Gress, J., and Rutherford, N. Department of Biological Sciences, Emporia State University.</b> RT-QPCR ANALYSIS OF ANTIOXIDANT GENE REGULATION OF <i>APIS MELLIFERA</i> IN RESPONSE TO COUMAPHOS, IMIDACLOPRID, AND CANNABIDIOL.
20	<b>Yutzy, A. (1), Wertz, B., Kostner, D., and Kobayashi, T. Department of Biological Sciences, Fort Hays State University.</b> RELATIONSHIP BETWEEN TRANSPORT PROTEIN PARTICLE COMPLEX 11 (TRAPPC11) MESSENGER RNA (MRNA) EXPRESSION AND FOOD INTAKE IN CHANNEL CATFISH.
21	<b>Alexander, J. (1), Schmidt, C., Noland, M., and Greer, M. Department of Biological Sciences, Fort Hays State University.</b> PRELIMINARY ASSESSMENT OF THE AQUATIC TURTLE COMMUNITY AT THE STERNBERG NATURAL AREA.
22	<b>Carte, M.<sup>1</sup> (2), Chen, F.<sup>2</sup>, Clark, B.<sup>3</sup>, and Schneegurt, M.<sup>1</sup> 1. Department of Biological Sciences, Wichita State University, 2. Jet Propulsion Laboratory, 3. Space Science Institute.</b> ENRICHMENT OF THE MICROBIAL COMMUNITY OF A SPACECRAFT ASSEMBLY FACILITY IN EXTREME BRINES RELEVANT TO MARS.
23	<b>Howell, S.P. (1), Kilmer, B., and Schneegurt, M. Department of Biological Sciences, Wichita State University.</b> ABUNDANCE, ISOLATION, AND CHARACTERIZATION OF HALOTOLERANT MICROBES FROM COMMON OLIGOSALINE SOILS IN KANSAS.

<u>Room</u>	<u>Presentation</u>
24	<p><b>Tran, M. (1), Brunt, D., Camden, W., Dille, J., Rogers, C., and Schneegurt, M. Department of Biological Sciences, Wichita State University.</b>            CHARACTERIZATION OF BACTERIAL KERATINASES FROM THE FEATHERS OF WILD DARK-EYED JUNCOS (<i>JUNCO HYEMALIS</i>) IN KANSAS.</p>
25	<p><b>Zbeeb, H.<sup>1</sup>(1), Joad, M.<sup>1</sup>, Zayed, H.<sup>1</sup>, Mahdi, A.<sup>1</sup>, Luhring, T.<sup>1</sup>, Chen, F.<sup>2</sup>, Clark, B.<sup>3</sup>, and Schneegurt, M.<sup>1</sup> 1. Department of Biological Sciences, Wichita. State University, 2. Jet Propulsion Laboratory, 3. Space Science Institute.</b>            INTERACTIONS BETWEEN BACTERIAL GROWTH AND THE PHYSICAL QUALITIES OF IONS AND SALTS OVER A WIDE CONCENTRATION RANGE.</p>

## Abstracts

**Aguirre-Mendez, C.<sup>1</sup>, Chen, Y.<sup>2</sup>, and Terada, T.<sup>2</sup>** **1. Department of Physical Sciences, Emporia State University. 2. Arizona State University.** ARGUMENTATIVE WRITING TO PROMOTE NONSCIENCE MAJOR STUDENTS' LEARNING IN AN INTRODUCTORY CHEMISTRY COURSE. The purpose of this study is to examine the impact of argumentative writing assignments on nonscience major students' chemistry conceptual understanding. The participants of this study consisted of 163 students in the treatment group and 77 of the control group. A comparison of the pre- and posttest results indicated that students who engaged in argumentative writing tasks performed better than students who did not. Another result indicates that the most students are exposed to argumentative writing, the better the quality of the writing assignments. The results also indicate that mostly students' perception of the writing assignment were positive regarding their content knowledge and argumentative understanding. Students also value the integration of simulation to promote their engagement in the process of argumentation. Implication for instructors and students of the implementation of this instructional strategy will be discussed.

**Alcerro, L. Department of Physics & Astronomy, The University of Kansas.** LEPTON NUMBER VIOLATION AND NEUTRINOS NATURE: The existence of neutrinos was proposed by Wolfgang Pauli as a “ghost” particle to explain the beta decay. To date, there are many questions that prevail in the Standard Model of particle physics regarding the neutrino sector: Are neutrinos Dirac or Majorana particles? What is the mechanism associated with the generation of their masses? Why the dramatic difference between their masses and those of other charged fermions? In this talk I will give a glimpse to neutrino physics and its connection between lepton number violation. Then I will present the current status of the searches for the nature of neutrinos, such as neutrinoless double beta decay and other alternative channels that have been explored.

**Alexander, J., Schmidt, C., Noland, M., and Greer, M. Department of Biological Sciences, Fort Hays State University.** PRELIMINARY ASSESSMENT OF THE AQUATIC TURTLE COMMUNITY AT THE STERNBERG NATURAL AREA. Starting in the spring of 2020 aquatic turtle surveys took place in the section of Chetolah Creek that runs through the Sternberg Museum Natural Area owned and maintained by Fort Hays State University's Sternberg Museum of Natural History. Surveys consisted of five three-foot diameter hoop nets baited with a mix of sardines and cream corn. Nets were deployed for three consecutive days every other week until 10-23-20. A total of 64 individuals were captured and implanted with Passive Integrated Transponder (PIT) tags for individual recognition with 23 total recaptures. Three of the known four species were captured (Snapping Turtle *Chelydra serpentina*, Painted Turtle *Chrysemys picta*, and Pond Slider *Trachemys scripta*). This project joined a number of established long-term projects aimed at monitoring responses of biotic communities to prairie restoration activities. Included in these projects are: small mammal, terrestrial herpetofauna, insect, soil microbe, fish, and vegetation research components.

**Butenas, A.<sup>1</sup>, Rollins, K.<sup>1</sup>, Williams, A.<sup>1</sup>, Hammond, S.<sup>1</sup>, Parr, S.<sup>1</sup>, Ade, C.<sup>1</sup>, Hageman, K.<sup>2</sup>, Musch, T.<sup>1,2</sup>, and Copp, S.<sup>1</sup>** 1. Department of Kinesiology, Kansas State University. 2. Department of Anatomy and Physiology, Kansas State University. THROMBOXANE A<sub>2</sub> RECEPTORS CONTRIBUTE TO THE EXAGGERATED EXERCISE PRESSOR REFLEX IN RATS WITH HEART FAILURE. Thin fiber skeletal muscle afferents are stimulated during exercise which contributes to reflex increases in sympathetic nerve activity (SNA). This reflex, termed the exercise pressor reflex (EPR), is exaggerated in patients with heart failure which contributes to an exaggerated increase in SNA during exercise. Increased responsiveness of these thin fiber afferents during skeletal muscle contraction produced partially by cyclooxygenase (COX) products of arachidonic metabolism contributes importantly to the exaggerated increase in SNA in HF-rEF. We investigated the role played by one of the major receptors for products of COX metabolism present on the sensory endings of muscle afferents, namely thromboxane A<sub>2</sub> receptors (TxA<sub>2</sub>-Rs), in the exaggerated reflex increases in SNA in HF-rEF rats. We tested the hypothesis that injection of the TxA<sub>2</sub>-R antagonist daltroban (80µg) into the hindlimb arterial supply would reduce the reflex increase in renal SNA (RSNA) to 30 seconds of electrically-induced 1 Hz hindlimb muscle contractions in decerebrate, unanesthetized HF-rEF rats, but not sham controls. Ejection fraction was significantly lower in HF-rEF (47±3%) compared to sham (84±1%, p<0.01). We found that hindlimb arterial injection of daltroban reduced the RSNA response to contraction in HF-rEF (n=8; peak ΔRSNA pre: 155±51; post: 43±13%; P=0.02), but not in sham (n=10; peak ΔRSNA pre: 64±17; post: 63±15%; P=0.99) rats. These data suggest that TxA<sub>2</sub>-Rs on the sensory endings of thin fiber muscle afferents contribute to the exaggerated EPR in HF-rEF. Our data enhance the understanding of the sympathetic adjustments to exercise in the ~6 million Americans with HF-rEF.

**Carte, M.<sup>1</sup>, Chen, F.<sup>2</sup>, Clark, B.<sup>3</sup>, and Schneegurt, M.<sup>1</sup>** 1. Department of Biological Sciences, Wichita State University, 2. Jet Propulsion Laboratory, 3. Space Science Institute. ENRICHMENT OF THE MICROBIAL COMMUNITY OF A SPACECRAFT ASSEMBLY FACILITY IN EXTREME BRINES RELEVANT TO MARS. Spacecraft are assembled in clean rooms to reduce microbial contamination that could confound life detection missions. Mars' near-surface is hyperarid and rich in dry hygroscopic sulfate and (per)chlorate salts that can absorb humidity and deliquesce at certain times to produce dense brines, with extremely low water activity that preclude microbial growth. Here we challenge the microbial community in samples from the Jet Propulsion Laboratory Spacecraft Assembly Facility (JPL SAF) with the extreme chemical conditions of brines relevant to Mars. Wipe samples from JPL SAF floors were enriched in SP medium with 50% MgSO<sub>4</sub> or 20% NaClO<sub>3</sub> (w/v). Samples were taken weekly for a month and then after six months to follow changes in the SAF microbial community. Metagenomic DNA extracts of community enrichments were examined by Illumina sequencing of 16S rRNA gene sequences using bacterial and fungal primers. Culturable microbial diversity in six-month enrichment cultures was characterized and appeared limited, dominated by *Oceanobacillus* and *Staphylococcus*. A succession of bacterial and fungal species was observed over the six-month incubation; Firmicutes dominated the cultures early, with increases in Actinobacteria observed over time, along with increased overall diversity. Ascomycota dominated the fungal communities. Basidiomycota were common early in the incubation, but nearly disappeared by four weeks. The microbes persisting from the JPL SAF microbial community in aged cultures, enriched at extreme salinities, are arguably the most capable organisms of subsequently surviving and proliferating at the near-surface of Mars. Supported by NASA ROSES (09-PPR09-0004/14-PPR14-2-0002); NIH KINBRE, (P20GM103418); University of Kansas, Genome Sequencing Core.

**d'Assignies, W. Department of Physics and Astronomy, University of Kansas and Ecole Normale Supérieure, Paris, France.** ANOMALOUS COUPLING: THE SEARCH FOR NEW PARTICLES AT THE LHC. With the development of quantum mechanics (physics of the infinitely small) during the last century, physicists have been able to explore a new world: the particles' one. In this world, everything is strange and non-intuitive, but physicists and mathematicians have developed a very complex theory: the Standard Model, which gives incredible agreement with observations. Today, a major source of research is the search for a theory of everything: the unification of general relativity and quantum mechanics, string theory for example, which may have a special property known as supersymmetry, implies the existence of many new particles that could be created in a particle collider, such as the Large Hadron Collider (LHC) at CERN. Some mysteries of the Universe, such as dark matter, which represents 80% of the matter in the Universe, but that has never been observed directly, could also be elucidated by searching for them at the LHC. In this talk, I will present a visual approach to particle physics with simple drawings: Feynman diagrams. These diagrams help us describe how elementary particles interact with each other. I will highlight the astonishing accuracy of the current theory in contrast with LHC measurements. This will illustrate the level of difficulty in trying to change the current theory to a more general one. I will also present a path we are following at the University of Kansas to try to find a signature of these new particles at the LHC: the investigation of anomalous couplings with protons collision.

**Fay, S.<sup>1,2</sup> and Maricle, B.<sup>1</sup>** 1. Department of Biological Sciences, Fort Hays State University. 2. Kansas Academy of Mathematics and Science, Fort Hays State University. EFFECTS OF SOIL MICROBIAL ADDITIVES ON GROWTH IN PEA PLANTS. Soil bacteria are known for their benefits when rotating crops to replenish nitrogen and other helpful substances in soil, especially for legumes. In this experiment, three types of microbial additives were applied to pea (*Pisum sativum*) plants, including “Plant Probiotics,” “Quantum Organic Total Beneficial Soil and Plant Microbial Inoculant,” and “Exceed Superior Legume Inoculant.” Treatments included each additive alone, mixed together, and a control with no additive applied. There were eight replicates of each treatment, with four pea seeds in each pot. The results varied, depending on the week the plants were measured, but the tallest plants changed for each week that measurements were taken. Treatments that contained “Plant Probiotics” and “Quantum Organic Total Beneficial Soil and Plant Microbial Inoculant” had taller plants on average compared to the others. Plant biomass following six weeks of growth was not different among treatments. Leaf chlorophyll content was different among treatments during an earlier point in the experiment, but was not different at a later point. Although effects were variable, these additives did not seem to have any effects on growth in peas.

**Gaede, J., Parris, M., and McLoud, J.** Department of Biological Sciences, Tabor College. TESTING SPECIES THRESHOLD FOR DNA BARCODING REGION IN COMMON AIRBORNE FUNGI: USING AN ECOLOGICAL METAGENOMICS WORKFLOW WITH QIIME 2. Airborne fungi contribute to allergies symptoms with molecular surveillance of air samples are continuing development. In this study our team used the metagenomic bioinformatics tool Qiime 2 to analyze ribosomal deep sequence reads (~100K sequences) from multiple common airborne fungal isolates to determine if one species/isolate would produce >1 operational taxonomic unit (OTU). Qiime 2 identifies each unique DNA sequence and classifies it as a OTU for haplotypes with a DNA homology of 97 %. This 97% species cutoff limit was set using a

bacterial model and may not be representative of a fungal model; yet, the cutoff limit and Qiime 2 program is commonly used by fungal molecular ecologists. The isolates deep sequenced were: *Bullera alba*, *Cladosporium velox*, *Epicoccum nigrum*, *Hannaella coprosmae*, and *Vishiacozyma carnescens* (*Cryptococcus carnescens*) as determined by Qiime 2. The constructed phylogenetic tree displayed >1 species within clades, not every clade was a mixture of species, but every species was observed in  $\geq 2$  clades. This translates to a single species having multiple OTUs, and at least one of the OTUs shared more nucleotide similarities with another species. Results suggest that the DNA barcoding region of these common airborne fungi should not be processed with the 97% species cutoff limit that Qiime 2 used to analyze the deep sequence reads. This novel finding suggests that future investigations should use different bioinformatics tools to process the deep sequence reads of airborne fungi to determine their intra- and inter-genomic variation of the multiple loci fungal barcoding region.

**Gallart, M.<sup>1</sup>, Olson, B.<sup>2</sup>, Gray, M.<sup>2</sup>, and Johnson, L.<sup>2</sup>** **1. Department of Biological Sciences, Fort Hays State University. 2. Division of Biology, Kansas State University.** SITE AND ECOTYPE GENE EXPRESSION DIFFERENCES OF AN ECOLOGICALLY-DOMINANT PRAIRIE GRASS *ANDROPOGON GERARDII* ACROSS THE GREAT PLAINS' CLIMATE GRADIENT. Reciprocal gardens offer an opportunity to assess genetic x environment interactions. The main question is what is the extent of environment vs gene expression in conveying adaptation of dominant grass of the Great Plains, *Andropogon gerardii*, big bluestem to the sharp precipitation gradient across the Great Plains? Two ecotypes (dry ecotype from Central KS, 500 mm rainfall and wet ecotype from Illinois, 1200 mm rainfall) were reciprocally planted in Central KS and Illinois. De novo transcriptome assembly was performed using Trinity. Measurements of cover and physiological responses were also made and plants were genotyped using GBS for genetic analysis. Site and ecotype showed differential regulation of genes—that is, when sites were compared, we detected differential regulation of genes between wet and dry sites. We found differential regulation between ecotypes, regardless of site. Both site and ecotype were of similar magnitude of importance in controlling gene expression. The dry site shows reduced plant cover of the wet ecotype and the wet site shows reduced cover of the dry ecotype. Generally, the dry ecotype had a higher photosynthetic rate than the wet ecotype in Central KS. Genetic PCoA corroborates differences between ecotypes. Outlier analysis identified 64 genes differentiated among ecotypes. One gene of interest, GA1, is involved with gibberellic acid metabolism and is well known in controlling plant height. Using the power of reciprocal gardens combined with gene expression analyses and ecological response variables provide an integrative picture of how plants respond and adapt to the environment in the long term.

**Gehin, A, and Stump, L. Science Division, Johnson County Community College.** DIMENSIONS 2C US-CHINA: MICROBE ECO-EVOLUTIONARY FEEDBACKS AS DRIVERS OF PLANT COEXISTENCE AND DIVERSITY GRADIENTS: UPDATE OF PROGRESS AT THE JCCC SITE. What role does the soil play in stabilizing the diversity of plant communities? One way may be through the soil microbiome. The plant-soil feedback (PSF) theory provides a framework for understanding this dynamic. A soil organism that is encouraged by plant species A may not significantly benefit species A, but may significantly benefit plant species B, thus influencing community dynamics. This study is a collaboration to assess how strong this mechanism is in maintaining plant community diversity, and how the effect differentiates along a precipitation gradient. For the first phase of this study, three prairie plant



species, *Lespedeza capitata*, *Andropogon gerardii*, and *Silphium integrifolium* were grown in a 3:1 mixture of background soil to remnant prairie soil and transplanted to a research plot on the JCCC campus. Several research plots were established in the Midwest by partnering institutions across the precipitation gradient. During the first growing season, soil samples from the plots were analyzed for microbial composition, and plant survival and growth were measured. The second phase of the study, now in progress, entails growing all three prairie plant species in each other's soil so each plant-soil combination is represented, then reassessing the soil microbial community and plant growth/survival. Based on prior research, we expect to see arbuscular mycorrhizal fungi playing a significant role in the mediation of plant-plant interactions, and a negative feedback when plants are grown in their own soil. This study should increase our understanding of how PSF strength can differentiate along the precipitation gradient.

**Goins, S. and Ghosh, A. Department of Biology, Pittsburg State University.** SURVEILLANCE STUDY ON *CULEX* SP. IN SOUTHEAST KANSAS AND PREVALENCE OF WEST NILE VIRUS IN THE MOSQUITO POPULATION. West Nile virus (WNV) is the most common mosquito-borne disease in Kansas and the United States. *Culex* species mosquitoes are the most common carrier of WNV in the U.S. The Kansas Department of Health and Environment (KDHE) announced that Kansas and neighboring states are becoming increasingly hospitable to *Culex* mosquitoes as average temperatures rise. According to the U.S. Centers for Disease Control and Prevention (CDC), 80% of people infected with WNV show no symptoms; for the remaining 20%, symptoms can include headaches, body aches, joint pains, vomiting, diarrhea, or rash. KDHE reported 600 cases of the worst form of the disease in KS, including 30 deaths (1999-2017). KDHE recently designated different areas of the state at high and moderate risk levels for contracting WNV. Our study is aimed at sampling mosquito populations from landscaped vegetation at residential & commercial properties and wetland habitats in urban and suburban areas of southeast Kansas. The mosquitoes were identified using taxonomic keys and sexed. Total RNA will be extracted and prevalence of WNV will be determined using real-time reverse transcriptase-PCR (RT-PCR) assays. In addition to the surveillance data available from KDHE, the outcome of this study will provide unique information about viral load in these vectors and host populations and seasonal testing of the mosquito vectors will detect temporal changes in the viral load.

**Gunther, S. and Hoffman, B. Department of Natural and Applied Sciences, Park University.** PRELIMINARY ANALYSIS OF THE DENTAL ULTRASTRUCTURE OF THE STINGRAY *DASYATIS* FROM THE PUNGO RIVER FORMATION (MIOCENE) OF NORTH CAROLINA. Microstructural analysis of teeth of the common stingray genus *Dasyatis* collected from the Pungo River Formation of Aurora, North Carolina (Miocene), was completed using scanning electron microscopy to evaluate the characteristics of enameloid present. Since chondrichthyans lack true bone and few body fossils have been found, abundant tooth fossils provide the best evidence of evolutionary history. Evaluation of enameloid microstructure allows insight into forces experienced during feeding and aids in the classification of sharks and rays. Selachimorph sharks have feeding habits that require teeth with enameloid that can resist cracking as well as compressive and twisting force, leading to evolution of a triple layered enameloid. Rays typically do not experience twisting motions within their bite cycle. In this study, *Dasyatis* was found to have a single crystallite enameloid lacking evidence of bundling. Single enameloid crystallites

surround odontoblast processes at random orientations, creating pillar-like structures oriented normally to the surface. Single crystallites at the surface could inhibit crack propagation across the tooth, while the pillared structures could resist compressive forces on the tooth. These results are consistent with the hypothesis that rays branched off from selachimorpha and did not inherit triple layered enameloid. Little is currently known about the general microstructure of batoid enameloid, and conflicting results have been presented for several genera in the current literature. *Dasyatis* has been described by other studies as possessing crystallite bundling. The sources of these inconsistencies will be discussed.

**Hoffman, B. and Hageman, S. Department of Natural and Applied Sciences, Park University.** COMPARISON OF CUTTING EDGES OF THE FOSSIL SHARKS *SQUALICORAX CURVATUS*, *GALEOCERDO ADUNCUS* AND *PHYSOGALEUS CONTORTUS*. Teeth of the Cretaceous anacoracid shark *Squalicorax curvatus* from Kansas and the Miocene sharks *Galeocerdo aduncus* and *Physogaleus contortus* from North Carolina share a common tooth design. These teeth have a strong triangular main cusp with distal heels with serrations across all cutting edges. The teeth of *Squalicorax* and *Galeocerdo* show the most commonalities, with a deep notch between the cusp and distal heel to handle high stress loads. *Galeocerdo* stands out as being the only member of this group having serrated serrations. The tooth design of *Galeocerdo* allowed it wide latitude in prey selection, while *Physogaleus* probably was limited to relatively small fish. *Squalicorax* probably had a similar prey range as *Galeocerdo*, although biased towards smaller prey. An analysis of cutting edge type, kerf, set, pitch and gullet is presented.

**Howell, S., Kilmer, B., and Schneegurt, M. Department of Biological Sciences, Wichita State University.** ABUNDANCE, ISOLATION, AND CHARACTERIZATION OF HALOTOLERANT MICROBES FROM COMMON OLIGOSALINE SOILS IN KANSAS. Halotolerant microbes that grow at NaCl concentrations approaching saturation are found in common soils with low salinity. Discrete salt phases are not obvious in oligosaline soils, but could advantage autochthonous halotolerant microbes. Allochthonous microbes within salt crystal inclusions can be transported by winds, thereby depositing hypersaline deliquescent microhabitats. We measured the abundance of microbes in common soils using most probable number analyses (MPN), where statistically valid replicates of serial dilutions are assessed for growth in liquid SP medium with 0.1, 10, or 20% (w/v) NaCl. Kansas soils were collected from oligosaline (<0.1% salinity) agricultural fields (corn, cotton, sorghum, soybean), woodland, pond margin, and prairie grassland. The abundance of microbes tolerant to 10% NaCl was on average 1.4% of the total counts at 0.1% NaCl, with sorghum fields reaching 6.3%. Only marginal growth was observed at 20% NaCl. Bacterial isolates were collected by repetitive streak-plating from hypersaline enrichment cultures of oligosaline soils and characterized by 16S rRNA gene sequencing, Gram and endospore staining, oxidase, catalase, anaerobic growth, fermentation, and enzyme tests. Isolates clustered with low G+C Gram-positive genera (*Bacillus*, *Halobacillus*, *Staphylococcus*, and *Virgibacillus*). Broad halotolerances (0.1–30% NaCl) were observed, but not halophilism. Soils were boiled to kill vegetative cells and compared by MPN with unboiled specimens. Surviving cells (endospores, spores) represented <1% of the microbes observed at 10% NaCl and ~5% of microbes at 0.1% NaCl. Halotolerant microbes in oligosaline soils are cultivable vegetative cells, not perennating structures. Supported by NASA ROSES 09-PPR09-0004/14-PPR14-2-0002); NSF GK-12 (DGE0537844); NIH KINBRE (P20GM103418).

**Janke, S. Department of General Education, North Central Kansas Technical College.** LITTLE MASK: FOSTERING SCIENTIFIC LITERACY IN CHILDREN. Guiding child development with the aim of fostering a healthy relationship with learning is as easy as piquing a child's curiosity with the appropriate age-centered interaction. The benefits of introducing an enthusiasm for learning have long been recorded, but just how that is done is not always as clear. In the case of this paper, Little Mask is a short student-made video used to hold a child's curiosity while introducing scientific information. Not all interactions require media formats, but this video is an example of the ease with which scientific information can be introduced to young children.

**Johnson M. and McLoud J. Department of Biological Science, Tabor College.** DEEP SEQUENCING OF *HANNAELLA COPROSMAE* TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION. *Hannaella coprosmae* may cause respiratory allergic reactions. Aerobiology is the beginning of the transition from classical methods to molecular methods, which include identifying fungal spore exposure through the use of DNA sequencing of a barcoding region of nuclear DNA. This study was focused on determining the intra-genomic variation of a *Hannaella coprosmae* isolate using the free bioinformatics tools from Joint Genome Institute, MAFFT, and BLAST. Environmental DNA (eDNA) is commonly analyzed with Qiime 2 in metagenomics investigations, which identifies each unique DNA sequence (of a barcoding region) and classifies the sequence as a haplotype. DNA homology of 97%, are clustered into a single operational taxonomic unit (OTU) that represents a species. Past investigation suggests that the species cutoff limit for fungi should not be 97%; therefore, the results of this investigation will identify a species limit cutoff. Our team collected air samples, and deep sequenced *Hannaella coprosmae*. Then the ~100K sequences of the barcoding region were merged with BBTools and aligned with MAFFT. Reducing repetitive sequences, the species threshold was set as 100%, 97%, 95%, and 93% and a phylogenetic tree was constructed. The OTUs were reduced from 1,426 in the 100% threshold to 33 in the 93% threshold. The 33 OTUs of the 93% threshold were aligned and identified using BLAST. Of the 33, 9 was *Hannaella coprosmae*, 4 were *Cryptococcus albidus*, 4 were *Penicillium Chrysogenum*, and 2 were *Rhizopus Oryzae*. This suggests that a threshold <93% should be used for identifying *Hannaella coprosmae* as a single species.

**Jones, R. Physical Sciences Department, Emporia State University.** EXPERIMENTS WITH THE A.S.A. H. AI. We found that: 1. If the upper layer in the initial concept hierarchy is hand coded to represent the values "lifespan" and "offspring" Asa notices the strong association with memory and learns/adds on a third value "knowledge." 2. Knowledge learned in one environment is then available for use in the next environment experienced. Some of these environments can be simulations experienced by simulated robots. The world of the simulation can, in turn, have been learned/created by Asa robots as they act in the real world. 3. We have given Asa the concepts/vocabulary of Ogden's Simplish artificial language. Stories have been translated into Simplish, Asa can read them and learn the 36 dramatic situations. 4. Concepts are defined on various different scales since there are patterns at different scales in the world. 5. As a component of each case's vector utility we can keep a running average of the dot product of the prediction vector and the next observed input vector. 6. We can use different vector utilities on different levels in the memory hierarchy. 7. We can separate training and performance phases by recording cases using one set of thresholds and then deploy the agent with a different set of thresholds.

**Knight, C. and McLoud J. Department of Biological Sciences, Tabor College.** DEEP SEQUENCING OF MULTIPLE GENES TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION. This study was focused on determining the intra-genomic variation of *Sporidiobolus pararoseus*, *Cladosporium velox*, *Epicoccum nigrum*, *Visniacozyma Carnescens*, and *Hannabella Coprosmae* using the open source bioinformatics tools from Joint Genome Institute, MAFFT, and NCBI. The aerobiology field is transitioning from gross classical analytical methods to molecular methods including: identifying presence of fungi with DNA sequencing and quantity with Real-Time PCR. Metagenomics investigations use environmental DNA (eDNA) sequencing and the Qiime 2 computer environment to identify fungi or bacteria in a micro community; this allows for identification of specific DNA sequences (haplotypes) and classification of species based on DNA nucleotide sequences. Multiple haplotypes with a DNA sequence homology of 97%, are aggregated into a single operational taxonomic unit (OTU) that represents a species. Our past lab investigations suggest that the fungal species cutoff limit of 97% homology is not accurate; therefore, the results of this investigation will identify a novel limit cutoff for specific airborne fungi. Our team collected air samples, and deep sequenced *Sporidiobolus pararoseus*, *Cladosporium velox*, *Epicoccum nigrum*, *Visniacozyma Carnescens*, and *Hannabella Coprosmae* cultures using the inter transcribed spacer of the ribosomal gene operon. Then, the paired-end DNA sequences of each culture were merged with BBTools-JGI and aligned with MAFFT. After reducing repetitive sequences, the species threshold was set as 100%, 97%, 95%, and 93% and a phylogenetic tree was constructed. Our results of the OTUs were broken down mainly into Cladosporium, Cryptococcus, Epicoccum, Hannaella corprosmensis, and Penicillium Chrysogenum.

**Krueger, C.<sup>1,2</sup>, Maricle B.<sup>1</sup>** 1. Department of Biological Sciences, Fort Hays State University, and 2. Kansas Academy of Math and Science, Fort Hays State University EFFECTS OF SULFIDE ON GROWTH AND CHLOROPHYLL IN WHEAT AND CORN. Wetland soils commonly contain hydrogen sulfide, a metabolic toxin. Sulfide is toxic to aerobic respiration and presents a significant physiological challenge for plant growth. Corn (*Zea mays*) and wheat (*Triticum aestivum*) were studied to determine the effects of sulfide on agriculturally significant plants. Three treatments of each species were watered with 0 mM, 1 mM, and 10 mM sodium sulfide. The sulfide solution was applied twice per week for five weeks. Height and chlorophyll concentration were measured weekly. Sodium sulfide substantially decreased height in corn. Wheat height was not affected. The sodium sulfide slightly decreased chlorophyll concentration in both wheat and corn. Wheat appeared to be more tolerant to the sulfide treatments than corn based on growth.

**Lindsey, C. and Royon, C. Department of Physics and Astronomy, University of Kansas.** UNDERSTANDING PROTONIC STRUCTURE USING THE LHC. At particle colliders, there exists a subset of events where the distance between the interacting particles is actually greater than the sum of their radii, yet they are still able to interact electromagnetically. These are known as ultra-peripheral collisions, and such collisions between protons and lead nuclei offer a unique probe of the parton structure of the proton. By utilizing pseudorapidity gaps (angular regions void of particles) in the final state, it is possible to isolate interactions where there is the exchange of a photon off the nucleus and a two-gluon exchange off the proton (pomeron exchange). Such collisions can be utilized to directly probe the gluonic structure of the proton with an electromagnetic probe. Events such as these have been studied at HERA, but currently there exists a gap at the LHC where we can utilize the much larger energies to get a higher resolution than

previously studied. The measurement I am working on with CMS makes a bridge between what we can do at the LHC and what will be done at a future Electron Ion Collider.

**Neuhauser, K.<sup>1</sup> and Neuhauser, K.<sup>2</sup>** 1. Department of Geosciences, Fort Hays State University, and 2. Division of Water Resources, Kansas Department of Agriculture. A SMOKY HILL TRAIL 1867 MASSACRE: An attempt to locate suspect 1867 graves at the Butterfield Overland Despatch (B.O.D.) Lookout Station near Antonino, Kansas was inconclusive. Magnetic anomalies suggest the possibility of buried bodies, but digging up graves is the jurisdiction of the Kansas State Historical Society (KSHS). Any future excavations will be determined by both the KSHS and the land owners.

**Neuhauser, K. Department of Geosciences, Fort Hays State University.** ELECTRICAL RESISTIVITY SURVEY OF A SUSPECT DNAPL SPILL: STILLWATER, OKLAHOMA: Two electrical resistivity surveys conducted for iSi Environmental (iSi) targeted a Dense Non-Aqueous Phase Liquid (DNAPL) plume near a undisclosed business in Stillwater, Oklahoma. Subsequently the anomalies provided specific zones to set up monitoring and clean-up procedures resulting in the removal of the DNAPLs.

**Neuhauser, K. Department of Geosciences, Fort Hays State University.** A GEOLOGIC HOAX IN WESTERN KANSAS – QUICK, GET MARSHAL DILLON AND HEAD TO CASTLE ROCK: Beware of things that you see –they may not be what you think. History has been replete with dupers, defrauders, jokesters, snake-oil sellers, or rascallions. What appeared to be never before observed, *in situ spherical* Fe-concretions at Castle Rock, Gove County, Kansas were actually a hoax designed by some fun-loving ‘pranksters’ to fool geologists or any other inquisitive individuals visiting the area. The spherical features were easily reproduced by this author using clay, a knife, a little palm rolling, and sun drying.

**Primrose, M. and McLoud J. Department of Biological Sciences, Tabor College.** DEEP SEQUENCING OF *EPICOCUM NIGRUM* TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION. *Epicoccum nigrum* causes hayfever, and other symptoms. Aerobiology is transitioning from classical methods to molecular methods, this includes identifying fungal spore exposure using DNA sequencing of a barcoding region. This study was focused on determining the intra-genomic variation of an *Epicoccum* isolate using the free bioinformatics tools from Joint Genome Institute, MAFFT, and BLAST. Metagenomics investigations use environmental DNA (eDNA) combined with the Qiime 2 software to determine the organisms present within a microcommunity, which identifies each unique DNA sequence (of a barcoding region) and classifies the sequence as a haplotype. Multiple haplotypes, with a DNA homology of 97%, are clustered into a single operational taxonomic unit (OTU) that represents a species. Past investigations suggest that the species range limit for fungal OTU may not be 97%; therefore, our results will identify a species OTU range for *Epicoccum nigrum*. Air samples were collected, and deep sequenced *Epicoccum nigrum*. Then the ~100K sequences of the barcoding region were merged with BBTools and aligned with MAFFT. After reducing repetitive sequences, the species threshold was set as 100%, 97%, 95%, and 93% and a phylogenetic tree was constructed. The OTUs were reduced from 15,500 in the 100% threshold to 27 in the 93% threshold. The 27 OTUs of the 93% threshold were aligned and identified using BLAST. Of the 27, 13 was *Epicoccum*, 5 were *Cladosporium*, 7 were *Cryptococcus*, and 2 were artifacts. This suggests that a threshold <93% should be used for identifying *Epicoccum nigrum* as a single species.

**Ranabhat, N.<sup>1</sup>, Bruce, M.<sup>1</sup>, Fellers, J.<sup>2</sup>, and Rupp, J.<sup>1</sup>** 1. Department of Plant Pathology, Kansas State University. 2. USDA-ARS, Kansas State University. WHEAT STREAK MOSAIC VIRUS PREVALENCE IN KANSAS WINTER WHEAT FIELDS. *Wheat streak mosaic virus* (WSMV) is a common wheat virus that causes significant yield loss in wheat production. The intermittent epidemic of this viral disease causes millions of dollars' loss. The key management strategies against WSMV is genetic resistance along with the use of good cultural practices. There are few challenges for the management of WSMV through genetic resistance. One of the important threat to durability of genetic resistance is the presence of potential new variants of the virus in the field population. The frequent monitoring and identification of field isolates of WSMV are essential to determine the population structure of the virus. A statewide survey was conducted to collect the WSMV isolates in the Kansas winter wheat fields. A total of 101 and 81 symptomatic wheat leaves were collected from 60 and 31 different counties of Kansas in 2019 and 2020 respectively. Enzyme-Linked Immunosorbent Assay (ELISA) results showed that there was a high prevalence of WSMV incidence. Out of 101 samples, 72 samples (71.3%) and out of 81, 73 samples (90.12%) were positive to WSMV. Our data from the WSMV survey and its prevalence provide the information to estimate the future incidence and potential epidemic year of the virus. The positive WSMV samples will be subjected to whole genome sequence through Nano pore sequencing technology to characterize Kansas WSMV isolates. The knowledge of WSMV prevalence and unique isolates present in the Kansas wheat fields will enable plant breeders to use relevant isolates in their future breeding program.

**Ratcliffe, A., Tong, J., Hoang, A., and Schneegurt, M.** Department of Biological Sciences, Wichita State University. STUDIES OF SALINOTOLERANT BACTERIA AT THE GREAT HYDROSTATIC PRESSURE WITHIN EUROPA AND THE ICY OCEAN WORLDS. Celestial bodies throughout the solar system have the potential to harbor life in the saltwater oceans under frozen crusts. Large icy worlds (Callisto, Europa, Ganymede, Pluto, and Titan) have deep global oceans in contact with rocky cores rich in minerals. Even modest celestial bodies (Ariel, Ceres, Enceladus, Mimas, Miranda, Oberon, and Titania) harbor at least regional oceans. The oceans of icy worlds appear to be salty, with current disagreement on their compositions and salinities. Native life or terrestrial microbes delivered as spacecraft contaminants may have to withstand hypersalinity, temperatures below 0 °C, and high physical pressure in ocean worlds. Here we measured the piezotolerances of bacteria from Hot Lake, WA and the Great Salt Plains, OK. *Halomonas* sp. str. HL12 cells held in sealed straws were exposed to hydrostatic pressures of ~8000 psi (55 MPa; 550 atm) for 48 h and culture density was determined by standard plate count. Survival relative to unpressurized controls was high, although certain experiments showed substantial (>1 log) decreases in cell numbers with pressure treatment. Note that ~30 MPa is typical at Earth's ocean floor, while 55 MPa represents a depth of 40 to 60 km in large icy moons (halfway between the ice shell and rocky core of Europa) and far greater than the ~5 MPa of the smaller icy worlds. We show here that salinotolerant, psychrotolerant, terrestrial microbes can survive the great physical pressure expected in icy ocean worlds. Supported by NASA ROSES (09-PPR09-0004/14-PPR14-2-0002); NIH KINBRE (P20GM103418).

**Rogers, J. and Hong, W-F.** Department of Natural Science and Mathematics, Sterling College. STUDIES OF MELANIN-LIKE PRODUCING BACILLUS VALLISMORTIS AND

**EXTRACTION OF MELANIN-LIKE PIGMENT.** An unidentified bacterial colony was discovered in a redworm composting box at Sterling College in Sterling, Kansas. The bacterium was isolated and sent for DNA analysis, which revealed it to be *Bacillus vallismortis*. When the phenotypical properties were compared to previously described samples found in Death Valley and China, there were slight discrepancies. Our sample released a dark brown pigment, which appeared to have inhibitory influences on the surrounding bacteria. The pigment was extracted from TSB (tryptic soy broth) using hydrochloric acid in an acidification process. This was followed by a purification process using a chloroform, methanol, and ethyl acetate wash (1:1:1). The pigment collected was tested for solubility in nine different aqueous and organic solvents. It is proposed that the pigment secreted by *Bacillus vallismortis* is melanin, therefore an IR spectroscopy will be used to confirm identification. An antibacterial study will be performed to determine if pigment produced by *Bacillus vallismortis* has antibacterial properties. It will be tested against both gram-positive and gram-negative pathogens, using ampicillin as a control.

**Schowengerdt, J. and Conard, J. Department of Natural Science, Sterling College.** **THE INFLUENCE OF DRONE PRESENCE ON PRAIRIE DOG BEHAVIOR.** Unmanned Aerial Vehicles (drones) are used for a variety of applications including ecological research and wildlife surveys. As drones continue to become more widely used, it is important to understand how they may influence prairie dog (*Cynomys ludovicianus*) behavior. We hypothesized that prairie dogs will react to drone flyovers by having a greater proportion of the colony exhibiting vigilant behavior. We observed the responses of prairie dogs to drone flyovers at an urban colony in Hutchinson, Kansas and a rural colony at Kanopolis Wildlife Area, Kansas. We conducted two observations of each colony in February – March 2021. During each observation, we monitored prairie dog vigilance in response to drone flyovers at various heights and speeds. In the urban colony, drone flyovers at greater heights (>20 feet) did not appear to increase vigilance of prairie dogs. However, drone flyovers at low heights (5 feet) were associated with a slight increase in vigilance in the urban colony. We observed that prairie dogs responded by sounding alarm barks and fleeing to burrows especially during low height flyovers. Drones appear to have an impact on prairie dog behavior in some situations. The specific response to drone presence may depend on whether the colony is located in an urban or rural setting.

**Skinner, N., and Gress, J. Department of Biological Sciences, Emporia State University.** **STATUS OF ALFALFA WEEVILS IN KANSAS.** The alfalfa weevil (*Hypera postica*) is one of the most damaging insect pests of alfalfa crops in Kansas and the United States causing yield losses of 10-15% annually. *H. postica* was introduced three separate times to North America and leading to the development of three strains, or subspecies: Eastern, Western, and Egyptian that differ in life history traits that can play a role in management strategies. IPM strategies exploit knowledge of the pest's biology and life history to survey its abundance and determine optimal timing of control efforts to reduce damage. The alfalfa weevil is found throughout the United States; however, it is still unknown which strains are present in Kansas. This project seeks to conduct a population genetic study and identify the strains of *H. postica* present in Kansas. Identifying the strain of weevil is important for interpreting field research results. In order to do this, we visited six alfalfa fields across the state of Kansas in the mid-spring to collect alfalfa weevil larvae. Then, we visited these six fields again in late spring to collect the adults once they were more prevalent. Using molecular genetic methods we can identify the western strain from the eastern and Egyptian strains based on a 5% sequence divergence of the mitochondrial DNA sequence, however, the

closely related eastern and Egyptian strains can only be distinguished by sequencing the mitochondrial DNA. We are currently processing 100 samples for strain identification from across Kansas.

**Skinner, N., and Jensen, W. Department of Biological Sciences, Emporia State University.** GEOGRAPHIC PATTERNS OF MELANISM IN FOX SQUIRRELS (*SCIURUS NIGER*) IN EAST-CENTRAL KANSAS. Animals with large geographic ranges often exhibit much phenotypic variability. The eastern fox squirrel (*Sciurus niger*) has a range throughout the eastern United States and exhibits geographically variable pelage colors. The melanistic phenotype is rare and has localized distributions that have been observed in rural towns throughout the fox squirrel's geographic range. Melanistic fox squirrel populations are currently known in few rural Kansas towns, such as Americus, although the geographic pattern in this phenotype has not been studied. I gathered data to determine geographic patterning of melanistic fox squirrels among 20 small towns throughout the central Flint Hills region of Kansas. I used haphazard surveys to count squirrels, per pelage phenotype, from the spring to the fall of 2019, to determine an estimated proportion of melanistic phenotypes from samples of  $\geq 10$  squirrels per town. I found that melanism was restricted to a small core of the central Flint Hills region inside the city limits of Americus and Cottonwood Falls. There were no clear longitudinal or latitudinal patterns in fox squirrel melanism. Current research is investigating the phenotypic proportions located within the Flint Hills region and how related regional melanistic populations are.

**Sun, M.<sup>1,2</sup> and Sellens, C.<sup>1</sup> 1. Department of Physical Sciences, Emporia State University. 2. Master Science of Forensic Program, Emporia State University.** IS THE LABEL CLAIMED CONTENT OF CBD IN CBD OILS AND EDIBLES CORRECT? Cannabis products are by far the most abused drugs on the illicit drug market. Several states had legalized the use of medical cannabinoids as well as the recreational use. The most common CBD products is CBD oil. Another common way of administering cannabinoids is oral route, in the form of edibles, such as baked goods, candies, gummies, chocolates, and beverages. Overdosing on cannabis might cause severe health and mental problem. On the other hand, there is possibility the labeled amounts of CBD do not reflect their real values. However, determination of cannabinoids in edibles is a problematic task due to the complexity of the involved matrices. In this study, a sensitive liquid chromatography- tandem mass spectrometry (LC-MS/MS) were developed, to determine active cannabis compounds from CBD products. CBD oils was extracted with iso-propanol and diluted with acetonitrile for further analysis. Gummy bears, cookies and chocolate bars were cut into small pieces, frozen overnight, and ground to powder. And then extracted with QuEChERS salt and analyzed with LC-MS/MS. The results show 3 out of 14 CBD oils were accurately labeled while 2 out of 5 CBD edibles were accurately labeled.

**Thompson, J. and Jensen, W. Department of Biological Sciences, Emporia State University.** DO BEHAVIORAL TENDENCIES PRESENT REPRODUCTIVE TRADEOFFS IN DICKCISSELS? Intraspecific variation in behavior can have important evolutionary and ecological consequences. Such variation might involve tradeoffs, potentially affecting some, but not all demographic parameters (e.g., components of reproductive success or survival). Using the dickcissel (*Spiza americana*) as a model organism, my project investigates how behavioral tendencies might affect multiple sources of variation in reproductive success. Specifically, my project will explore how variation in two behavioral types (boldness and activity) relate to three



components of dickcissel reproductive success: nest predation, brood parasitism, and nestling condition. By locating and monitoring nests during the breeding seasons of 2020 and 2021 from mid-May to early August each year, I will compare behavioral tendencies of individual female dickcissels to these components of reproductive success. Bolder individuals who exhibit a higher degree of conspicuous / risky behaviors in and around the nest are predicted to have either higher or lower nest depredation rates, higher brood parasitism rates, and nestlings of better condition than individuals who are less bold. Individuals who are generally more active in and around the nest are predicted to have higher nest depredation and brood parasitism rates, but nestlings who are of better condition than individuals who are less active. Boldness and activity might be positively or negatively correlated with one another, which may affect the degree with which each behavioral type affects each component of reproductive success. The observed patterns will give us a better understanding of how selection might act on certain behavioral tendencies and explain apparently maladaptive behaviors.

**Tran, M., Brunt, D., Camden, W., Dille, J., Rogers, C., and Schneegurt, M. Department of Biological Sciences, Wichita State University.** CHARACTERIZATION OF BACTERIAL KERATINASES FROM THE FEATHERS OF WILD DARK-EYED JUNCOS (*JUNCO HYEMALIS*) IN KANSAS. We collected >300 bacterial isolates from overwintering Dark-eyed Juncos (*Junco hyemalis*) in Kansas to find that ~40% appear to degrade the structural protein of feathers using extracellular keratinase enzymes. A guild of bacteria (~18% of total counts) grew significantly better on basal salt medium plates with feather meal than on agar-only plates (~8% of total counts). Of the 88 most active keratinolytic bacterial isolates, half were *Bacillus* species. Keratinolytic *Frigoribacterium*, *Methylobacterium*, *Microbacterium*, *Okibacterium*, *Pantoea*, *Sphingomonas*, *Staphylococcus*, and *Stenotrophomonas* were found. Active isolates degraded whole feathers and produced zones of clearing on milk agar plates. Our in vitro keratinase assay uses ninhydrin to quantitate amino acids released from keratin. *Bacillus licheniformis* str. ATCC 14580 was the positive control. The enzyme extract was clarified conditioned media from keratinolytic isolates induced with feather meal. Assays completed in 30 min and responses mirrored enzyme concentration. *Bacillus* sp. str. F166 was most active. *Bacillus* sp. str. F27 and F65 each performed well. We also demonstrated keratinolytic activity against alpha-keratin (wool). Juncos are long-distance migrant birds that carry bacteria that are beneficial and harmful to plants on their feathers. The abundant keratinolytic bacteria on feathers are capable of damaging them, reducing bird fitness and reproductive success. Keratinases have uses in tanning, silage, and remediation. Keratinases may be useful in the treatment of onychomycoses, actinic keratoses, and keratosis pilaris in medical and veterinary settings. Supported by NIH KINBRE (P20GM103418); Kansas NSF EPSCoR (EPS-0903806); NSF GK-12 (DGE0537844); Cohen Honors College, Wichita State University.

**Travis, A.S., Ingram, A., and McLoud, J.D. Department of Biological Science, Tabor College.** DEEP SEQUENCING OF *CLADOSPORIUM VELOX* TO DETERMINE INTRA-GENOMIC VARIATION OF THE FUNGAL BARCODING REGION. *Cladosporium* is the dominant fungal spore taxa isolated in temperate regions and is allergenic to sensitized individuals, and a plant pathogen. Research has suggested there are >750 species of *Cladosporium*; this large number of species creates problems when analyzing environmental samples for *Cladosporium*. This study determined the intra-genomic variation of *Cladosporium* used BBTools from Joint

Genome Institute and MAFFT. Environmental DNA (eDNA) is commonly analyzed with Qiime 2 in metagenomics investigations, which identifies each unique DNA sequence and classifies the sequence as a haplotype. Haplotypes are reduced into an operational taxonomic unit (OTU) for sequences of 97% DNA homology. Investigations from our lab suggests a species cutoff limit for fungi should be investigated; therefore, the use of the bioinformatic tools used in this study will identify that species limit cutoff. Our team collected an air sample, and sequenced a specific fungal isolate identified as *Cladosporium velox*. Then the ~100K sequences of the barcoding region were merged with BBTools and aligned with MAFFT. After reducing repetitive sequences, the species threshold was set as 100%, 97%, 95%, and 93% and a phylogenetic tree was constructed. The OTUs were reduced from 22,145 to 22, from the 100% to 93% threshold respectively. The 22 OTUs of the 93% threshold were aligned and identified using BLAST. Of the 22, 1 was *Epicoccum*, 11 were *Cladosporium*, 4 were *Cryptococcus*, and 6 were artifacts. This suggests that a threshold <93% should be used for identifying a single species.

**Wertz, B., Moyer, M., Kostner, D., White, T., Abernathy, O., and Kobayashi, Y., Department of Biological Sciences, Fort Hays State University.** EFFECTS OF FOOD INTAKE AND FOOD EXPOSURE ON EXPRESSION OF TWO DOPAMINE RECEPTORS (DR), TYROSINE HYDROXYLASE (TYRH), AROMATIC L-AMINO ACID DECARBOXYLASE (AAAD), AND CATECHOL-O-METHYLTRANSFERASE (COMTA) MRNA IN THE BRAIN OF CHANNEL CATFISH. The dopaminergic nervous system (DNS) regulates the pathways involved in sensations of reward, pleasure, and satiety while also influencing eating behavior. Dysfunction of the DNS has been investigated extensively in humans and rodents, associating changes in feeding behavior with obesity development. However, the involvement of DNS in the regulation of food intake in channel catfish is unclear. The current study characterized tissue distribution of mRNA encoding two dopamine receptors (DR1, DR2) along with enzymes involved in dopamine synthesis (TyrH and AAAD) and an enzyme involved in dopamine clearance (COMTa). Expression of DR1, DR2, AAAD, TyrH, and COMTa mRNA was readily detectable in the brain, hypothalamus, muscle, and spleen compared to other tissues. The relationship between expression of these mRNA and food intake changes was investigated in brain samples collected from two 28-day feeding studies. In a separate study, expression of these mRNA and the timing of food exposure was investigated. The mRNA expression for DR1, DR2, AAAD, TyrH, and COMTa in the brain was not influenced by prolonged fasting, refeeding after fasting, or changes in feeding frequency ( $p>0.10$ ). The expression of DR2 mRNA tended to be lower ( $p<0.10$ ) in samples collected after food exposure. This data suggests a link between food exposure and DNS modulation in channel catfish. Further research is needed to fully elucidate the complex relationship between DNS and food intake.

**Wiest, T., Gress, J., and Rutherford, N. Department of Biological Sciences, Emporia State University.** RT-QPCR ANALYSIS OF ANTIOXIDANT GENE REGULATION OF *APIS MELLIFERA* IN RESPONSE TO COUMAPHOS, IMIDACLOPRID, AND CANNABIDIOL. Cannabidiol (CBD) is one of the main pharmacologically active phytocannabinoids of *Cannabis sativa L.* and exerts antioxidant properties. CBD may have protective antioxidant effects against the insecticides imidacloprid, a neonicotinoid and coumaphos, an organophosphate in *Apis mellifera*. Previous studies have shown that ingestion of these insecticides causes a downregulation in antioxidant genes in the gut tissue. The main objective of this study was to test comparatively the effects of CBD and these two common insecticides on honeybee worker's lifespan, mortality, and expression of antioxidant genes. To evaluate the effects of CBD on antioxidant gene

expression in the gut we exposed foraging bees to six solutions of 1 M sucrose containing 10nmol of each chemical: sugar control, imidacloprid, coumaphos, cannabidiol, coumaphos + cannabidiol, and imidacloprid + cannabidiol. 10 nmol of each chemical were added in each instance. After observing behavioral response to the treatment, we extracted RNA from their abdomens, and used RT-qPCR to assess 10 bee antioxidant genes linked to pesticide toxicity. CBD caused significant upregulation of SOD 1 & 2 genes when combined with coumaphos. CBD also caused significant upregulation of six out of the ten antioxidant genes studied when combined with imidacloprid. In 2020, Kansas had over 7,000 commercial hives producing a total of 553,000 pounds of honey worth over \$1.63 million alone not counting pollination services. Average hive losses were reported to above 20% for 2020 with pesticide stress affecting colony health in more than 25% of the hives surveyed.

**Yutzy, A., Wertz, B., Kostner, D., and Kobayashi, Y. Department of Biological Sciences, Fort Hays State University.** RELATIONSHIP BETWEEN TRANSPORT PROTEIN PARTICLE COMPLEX 11 (TRAPPC11) MESSENGER RNA (MRNA) EXPRESSION AND FOOD INTAKE IN CHANNEL CATFISH. Obesity and obesity-induced insulin insensitivity are related to non-alcoholic fatty liver disease (NAFLD) development and associated complications. In channel catfish selected for increased growth, fish develop characteristics similar to those observed during human obesity development, including increased food intake and accumulation of abdominal fats. Given that obesity leads to insulin insensitivity and NAFLD, channel catfish provide a possible model to investigate human obesity and NAFLD development. Mutation in the TRAPPC 11 gene has been linked to fatty liver development in mammals and zebrafish; however, very little is known about TRAPPC 11 expression in channel catfish. Therefore, we examined the tissue TRAPPC 11 mRNA distribution and found mRNA expression was readily detectable in the muscle, brain, and spleen. Furthermore, the relationship between food intake and TRAPPC 11 mRNA expression in the brain was also investigated using two separate 28-day feeding studies. In the first feeding study, fish received food twice (overfed) or once (control) daily, with a third group receiving food every other day (underfed). For the second study, fish were fed daily (control), did not receive food (fasted), or fasted for the first 14 days of the study and received food for the subsequent 14 days (refed). Expression of TRAPPC 11 mRNA was examined on brain samples harvested on day 28 of each study. Food intake did not influence the expression of TRAPPC 11 mRNA in the brain. Future work is underway to determine the effects of changes in food intake on the muscle TRAPPC 11 mRNA expression.

**Zbeeb, H.<sup>1</sup>, Joad, M.<sup>1</sup>, Zayed, H.<sup>1</sup>, Mahdi, A.<sup>1</sup>, Luhring, T.<sup>1</sup>, Chen, F.<sup>2</sup>, Clark, B.<sup>3</sup>, and Schneegurt, M.<sup>1</sup>** 1. Department of Biological Sciences, Wichita State University, 2. Jet Propulsion Laboratory, 3. Space Science Institute. INTERACTIONS BETWEEN BACTERIAL GROWTH AND THE PHYSICAL QUALITIES OF IONS AND SALTS OVER A WIDE CONCENTRATION RANGE. Mars' near-surface presents a hyperarid chemically harsh environment rich in salts, which seems uninhabitable by even the most extremely tolerant organisms. Dense brines have low freezing points and may remain liquid on Mars; however, brines inhibit microbial growth due to low water activity and high ionic strength. Eighteen salinotolerant bacterial isolates from environments rich in NaCl (Great Salt Plains, OK) or MgSO<sub>4</sub> (Hot Lake, WA), including *Bacillus*, *Halomonas*, *Marinococcus*, *Nesterenkonia*, *Planococcus*, and *Virgibacillus*, were grown in Salt Plains medium supplemented with salts at increasing concentrations to saturation. Over 4000 logistic growth curves from testing the anions, chloride,

nitrate, and sulfate, coupled in every combination with the cations, Mg, K, and Na, were used to estimate intrinsic rates of population increase and maximum culture densities to identify interactions with water activity, ionic strength, and degree of saturation. Strong bacterial growth was commonly observed at  $\geq 1$  M salt. Lower water activity led to lower growth rates and there were salt-specific responses from ion pairing. Greater ionic strength and degree of saturation, led to lower growth rates and again ion pairing was important. Our analyses found that ions and salts affect bacterial growth differentially across gradients of physical solution qualities. No single physical quality adequately accounted for the observed solute-specific effects on bacterial growth. Knowledge of the tolerances of terrestrial microbes to salts at extremely high concentrations sets limits for the permissible conditions of extraterrestrial habitable regions and for the risks of forward planetary contamination. Supported by NASA ROSES (09-PPR09-0004/14-PPR14-2-0002); NIH KINBRE (P20GM103418).