

Session 1a
Room s018

<p>9:30-9:45am</p>	<p>Problem-solving performance of songbirds in urban and rural environments Kayce M. Miller, Lydia M. Hopper, Seth Magle, Jalene M. LaMontagne</p> <p>Cognitive abilities of songbirds allow them to thrive in a variety of environments, including human-dominated landscapes. Due to the pressures and opportunities of urbanization (e.g., habitat fragmentation, shifts in predators, novel food sources), it has been suggested that birds living in these landscapes are more neophilic and so better equipped to solve novel foraging problems. Currently, there are inconsistent findings on this topic and many studies are conducted in labs with wild-caught birds. Also, a binary view of urbanization (urban or non-urban) is often used, but land uses vary within urban and rural areas. We tested whether wild birds' problem-solving performance in a foraging task was affected by their habitat at local and broad scales. We conducted fieldwork in two habitat types (backyards and forests) in both urban and rural areas. We hypothesize that habitat type affects birds' problem-solving success and latency to solve. We collected >18,000 videos capturing a variety of bird species. Analyses to date show that birds living in less human-dominated landscapes are better problem-solvers, contrary to our prediction; however, we see high variability across sites.</p>
<p>9:45-10:00am</p>	<p>An experimental investigation of food unpredictability, housing and water-fasting on hematocrit levels in captive red crossbills Dawson Bradley, Rebecca Cameron and Jamie M Cornelius</p> <p>Hematocrit is the percent red blood cells in whole blood and it's fluctuation is an adaptive response to changing oxygen demands that occur during different life activities and in different environments. Because red blood cells are made from materials that can be limiting, however, it is thought that hematocrit may also reflect general body condition and access to resources. We tested the impact of hydration state, access to resources (time available to forage) and cage size (activity) on hematocrit in captive red crossbills (<i>Loxia curvirostra</i>). Cage size influenced hematocrit significantly, where birds housed in aviaries generally had higher hematocrit than those housed in small individual cages. Food manipulation successfully limited resources as evidenced by reduced mass and significantly reduced the ability of the birds to restore hematocrit following successive blood sampling. When birds were returned to ad libitum feeding schedules the birds in aviaries recovered hematocrit at the apparent expense of fat, whereas the birds in small cages recovered fat at the apparent expense of</p>

	<p>hematocrit. Together these results suggest a physiological tradeoff between investing in red blood cell development or storage of fat and reveals a potential prioritization based on activity demands when faced with a reduction of resources.</p>
<p>10:00-10:15am</p>	<p>How does predator mobility influence spillover from agricultural ditches into fields? John Woloschuk</p> <p>Spillover predation is a large-scale form of apparent competition in which predators traverse adjacent habitats to take advantage of multiple prey sources. Bats and spiders are consumers in agroecosystems and it is unclear if these same predators eating emergent insects along agricultural ditches spillover into adjacent corn fields to take advantage of crop pests. Another important question is how predator mobility and energy demand influence spillover? Here, we hypothesized that predators capable of mobility like bats and ground spiders exhibit spillover from agricultural ditches into fields while non-mobile predators like web spiders feed in one habitat at a time. Surveys were conducted at ten different farms where bats were recorded, spiders counted, and insects captured at ditches, at 100 and 200 m into adjacent corn fields to understand how active and abundant the predators were at increasing distances into the fields. Stable isotope analysis was done on ground and web spiders (collected at all distances) and bat guano collected from nearby barns. Since crop and ditch insects come from vegetative communities with relatively different photosynthetic pathways (corn=C4 & ditch plants/algae= C3), carbon isotope ratios of tissues should reflect what prey communities predators are consuming. Carbon-13 ratios from bat guano were mixed, suggesting that highly mobile predators may consume a combination of crop and ditch insects. Spiders from deep in the cornfield had high enrichment of carbon-13, showing heavy consumption of crop insects, while ratios for ground and web spiders at ditches were mixed. This indicates that ditches may support more diverse prey and vegetative communities than assumed but also that spiders, regardless of mobility, appear to capitalize on whatever prey is within their immediate vicinity.</p>
<p>10:15-10:30</p>	<p>The influence of land use history and microhabitat on ground-nesting bees Kristen Manion</p> <p>Pollinators, especially native bees, are experiencing striking declines worldwide. Approximately 80% of bee species in North American grasslands build nests in the ground. Grasslands tend to include natural or semi-natural habitat, including remnants that are unplowed parcels of pristine land, restorations that are plantings of</p>

	<p>native plants, and old fields left fallow from agriculture. However, bees may not build nests in all land types. For instance, bees may not build nests in areas of high plant diversity where they forage for resources. I ask the question: do land types differ in nesting quality for ground-nesting bees? For this study, I quantified density of ground-nesting bee nests at 8 sites, each with 3 land types, for a total of 24 locations. I placed traps used for collecting ground-nesting bees on 1,440 randomly chosen GPS coordinates, prior to bee emergence each day. I measured microhabitat data on vegetation including richness and abundance along with soil metrics including texture, slope, aspect, shade, and bare ground. To avoid data overload, I sampled all coordinates with bee nests along with 10 additional randomly chosen coordinates per location. Bee nest density differed substantially, driven by differences in both land type and site, according to a generalized linear model with a binomial distribution (p-value < 0.0001). Restorations had 9% fewer bees captured compared to remnants and old fields. Overall, I had a capture rate of 0.07% utilizing these trapping methods. Additionally, soil texture analysis suggests the majority of nests were found in sandy-loam or silty-loam soils. This evidence suggests that the three land types can support ground-nesting bees, but restorations may not provide as much habitat for ground-nesting bees. I will also present results about the relationship between the other microhabitat characteristics and nesting densities. I predict that a diverse vegetation community managed for duff and litter, a large percentage of bare ground per trap, and southeastern aspect may predict nest presence. The information from this study will improve our understanding about where native bees nest and allow land managers to make decisions to protect, conserve, and prioritize habitat suitable for ground-nesting bees.</p>
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<p>9:30-9:45am</p>	<p>Impacts of soil microbiome on invasive <i>Lonicera maackii</i> seedling success Taylor Strehl</p> <p><i>Lonicera maackii</i> (Amur Honeysuckle) is an invasive shrub that is widespread throughout the eastern United States. <i>Lonicera</i> invasion is often associated with loss of diversity and declines in overall forest health. <i>Lonicera</i>'s competitive advantage is largely attributed to its quick growth and ability to crowd out its neighbors. However, this advantage would be limited to mature plants. <i>Lonicera maackii</i> has been shown to produce root exudates and leaf litter that likely alter</p>
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	<p>the soil microbiome. Impacts on soil biota may help to explain why <i>Lonicera maackii</i> is so successful, raising the questions at the core of this study: Does the soil microbiome vary enough between <i>Lonicera maackii</i> and the native constituents to confer a competitive advantage to <i>Lonicera</i> seedlings? and Does the soil microbiome of <i>Lonicera</i> have antagonistic effects on native species? To explore these questions <i>Lonicera maackii</i> and <i>Acer negundo</i> (a common native tree) were grown in isolation and together in co-culture. For each experiment, replicates were grown in soil inoculated with either <i>Lonicera</i> or <i>Acer</i> soil. A control was grown with sterilized inoculum to account for abiotic heterogeneity. Plants were harvested, dried and weighed after three months. Biomass data revealed that the differences in the soil microbiome between <i>Lonicera maackii</i> and <i>Acer negundo</i> significantly affected plant growth. This was true both when plants were grown in isolation and in co-culture. When the plants were grown in isolation, each microbial community had either a negative or nonsignificant impact on plant growth. Interestingly, the strongest negative interactions were between each plant species and its own soil microbes, suggesting self-inhibition. When grown in co-culture, soil microbes had vastly different effects. When grown in co-culture, the relationship between each plant and microbiome varied widely from strongly antagonistic to mildly positive. The differences between plants grown in isolation and co-culture indicate that soil microbes moderated the effects of competition. When a positive plant-microbiome relationship was seen in co-culture, it much likely due to a stronger microbial inhibition of a competitor when compared to the uninoculated control. These results differ from expectations of direct microbial inhibition, yet still provide an explanation of <i>Lonicera maackii</i>'s advantages in establishment.</p>
<p>9:45-10:00am</p>	<p>Differentiating live and dead bacteria during beach monitoring with the use of propidium monoazide (PMA) and qPCR. Benjamin Giffin and Charlyn Partridge</p> <p>Exposure to unsafe recreational swimming water has been linked to an increased risk of gastrointestinal illness or skin infections. To reduce the risk of such infections, local health departments routinely monitor beaches for the presence of fecal indicator bacteria, such as <i>Escherichia coli</i> (<i>E. coli</i>). The Michigan Department of Environmental Quality, in collaboration with the United States Environmental Protection Agency, has recently implement a more rapid beach monitoring method using quantitative polymerase chain reaction (qPCR). One potential issue with this qPCR method is that it can over estimate the amount of harmful <i>E. coli</i>, by amplifying dead bacteria and environmental DNA present in the samples. We have developed a modified qPCR beach monitoring method using the DNA binding dye</p>

	<p>propidium monoazide (PMA) to reduce the overestimation of <i>E. coli</i> present in the samples. By changing the primers used during qPCR, this method could be used to target any bacteria that may be of interest to health departments or environmental researchers.</p>
<p>10:00-10:15am</p>	<p>Investigation of the role of bacterium, <i>Rhodococcus fascians</i> in fasciation of common dandelion, <i>Taraxacum officinale</i> Maria Renteria, Daniel Chaffin and Logan Minter</p> <p>In Spring 2018, a large number of specimens exhibiting fasciation, an abnormal growth pattern, were noted in dandelions, <i>Taraxacum officinale</i>. Multiple plant taxa display fasciation. Cause could be due to numerous factors, one such being a bacterial pathogen <i>Rhodococcus fascians</i>. A lab study to satisfy Koch's Postulates was conducted under greenhouse conditions. The goal was to identify the role of <i>R. fascians</i> in fasciation of <i>T. officinale</i>. Following inoculation and growth, no fasciation was observed in experimental plants, nor could the pathogen be reisolated. The same trend was observed in sweet pea seedlings for control of pathology. Field studies are continuing through Spring 2019 to examine rates of fasciation and incidence of <i>R. fascians</i> under natural conditions.</p>
<p>10:15-10:30am</p>	<p>The pollen virome: viral discovery and diversity Andrea M. Fetters, Jessica D. Stephens, Maria Teresa Sáenz Robles, Paul G. Cantalupo, Na Wei, James M. Pipas, Tia-Lynn Ashman</p> <p>Viral pathogens negatively impact their hosts and cause many important diseases worldwide. Viruses with RNA genomes are notoriously diverse, and such plant viruses threaten plant biodiversity and food security. Some RNA plant viruses even exploit the pollination process and are transported between plants by pollinators. However, pollen-associated viral taxa in wild plant species are poorly characterized. Therefore, our study aimed to determine the prevalence and diversity of plant viral communities associated with the pollen of wild plant hosts using a metagenomic approach. We extracted, sequenced, and mined the RNA using a viral detection pipeline from the pollen of 24 plant host species that represent 16 plant families growing in 4 community types. We identified at least one viral taxon in the pollen of 23 of the plant host species. These taxa span 29 viral families. Our results show that pollen-associated plant viruses are prevalent across host species, communities, and viral families, indicating that pollen is an important viral niche. This study points to the importance of identifying possible ecological correlations of pollen-associated plant viral diversity and their impact on host plant ecology and evolution.</p>

BREAK (10:30-10:45am)

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<p>10:45-11:00am</p>	<p>Changes in a pollinator food web in the face of climate change Melissa Seidel</p> <p>Understanding responses of food webs to climate change is vital, especially when those food webs influence important ecosystem services, like pollination, valued at over \$3 billion globally. Efforts at predicting these responses to climate change have historically focused on single factors and mechanisms. Studies typically investigate responses to only one factor, such as temperature or precipitation. Similarly, researchers separately examine mechanisms such as physiological performance or species interactions. However, global climate change is predicted to alter temperature and moisture simultaneously. Additionally, thermal and hydric physiological performance and species interactions are both likely mechanisms underlying food web responses to changing climate. The current lack of a synergistic, mechanistic understanding of how food webs respond to key aspects of global climate change is a major research gap. To address this critical issue our work examined multiple factors and mechanisms, including the combined effects of climate change and food web pressure, on bees. Respectively, we studied how changes in temperature and moisture may alter food web composition and stability through filtering of sensitive taxa (physiological limits) or by modifying consumption (trophic interactions). Our preliminary findings indicate that if predatory spiders are more hydrated, they expose themselves more to heat. This may influence spider consumption of bees. This work suggests that effects of factors and mechanisms acting in combination can be highly complex and impact organisms and trophic levels differently. It is apparent that multiple pressures, including climate change, impact bees. This work increases our understanding of how climate change may directly and indirectly influence insects, specifically pollinators.</p>
<p>11:00-11:15am</p>	<p>Testing the relationship between intraspecific competition and individual specialization across both behavior and diet Amaryllis Adey & Eric R. Larson</p> <p>Intraspecific variation is a key component of ecology and a driver of evolutionary processes. As population densities increase, individuals may diversify their strategies to reduce competitive pressure with conspecifics. Theoretical studies support a direct relationship between increasing population density and increasing individual</p>

	<p>specialization. However, empirical studies have not always supported these theoretical predictions, sometimes finding a unimodal relationship, with the greatest individual specialization at moderate densities and decreasing specialization at both high and low densities. One reason for this divergence between theoretical predictions and empirical evidence may be the specific metrics of specialization considered. There is potential that individual specialization measured from diet may differ from that of behavior at high relative abundances due to individuals depleting preferred food resources thereby limiting opportunity for increased dietary specialization while individuals can continue to specialize behaviorally. In this study, we tested the role of intraspecific competition on individual specialization through analysis of both behavior and diet. We conducted this study in Vilas County, Wisconsin using the invasive rusty crayfish <i>Faxonius rusticus</i> collected from six lakes across a gradient of low to high relative abundance. We conducted six behavioral assays to measure behavioral diversity between populations and used stable isotope analysis to measure dietary diversity or breadth. We then related both measures of specialization to relative abundance of <i>F. rusticus</i> in our study lakes using linear and quadratic models to represent potential relationships between individual specialization and intraspecific competition. We found that a unimodal relationship was more supported than a linear relationship between dietary diversity and <i>F. rusticus</i> relative abundance. By contrast, we found greater support for a linear relationship between behavioral specialization and relative abundance. Our results show that the specific measure of specialization can influence outcomes of comparisons between intraspecific competition and individual specialization.</p>
<p>11:15-11:30am</p>	<p>Should I stay or should I flow? The clash between temperature, stream flow and eDNA Amanda N. Curtis, Jeremy S. Tiemann, Sarah A. Douglass, Mark A. Davis and Eric R. Larson</p> <p>Environmental DNA (eDNA) has been shown to be an effective tool for detecting low abundance invasive or imperiled species. However, many unknowns related to the physical, chemical and biological aspects of the target organisms and their environment hinder the successful application of eDNA to detect new invasive or imperiled species. Here we used two local streams equipped with USGS flow gages to examine how stream flow and temperature over the course of a year influenced eDNA copy number of an invasive Asian clam (<i>Corbicula fluminea</i>). Next, we sampled eight central-Illinois streams to examine whether <i>C. fluminea</i> density was related to the amount of eDNA captured both at summer low-flows and during fall high-flow. Preliminary analyses indicate a significant positive relationship</p>

	<p>between temperature, and eDNA copy number, where eDNA copy number increased as temperature increased, which we attribute to biological activity and reproduction. Additionally, we found that as stream flow increased, eDNA copy number declined, indicating that sampling during high-flows could result in a decreased ability to detect a very abundant, invasive species. We found no significant relationship between <i>C. fluminea</i> density and eDNA copy number. Similarly to the year-long study, we found that that sampling during fall high-flow also resulted in non-detections when <i>C. fluminea</i> were present (false negatives). Our study presents novel findings that stream flow can dilute eDNA, which may have serious implications for the detection of low abundance organisms. Further, we suggest that researchers desiring to use eDNA should take into account knowledge of their biological organism and system prior to sampling efforts.</p>
<p>11:30-11:45am</p>	<p>Bioaccumulation and biomagnification of legacy pollutants in freshwater food webs using <i>Lontra canadensis</i> as a bioindicator Kathryn Mudica and Jennifer Latimer</p> <p>Water quality has improved significantly over the last forty years; however, assessing water quality alone cannot predict the ecological impacts of legacy pollution. Lingering legacy pollutants have become an inherited issue that continues to be overlooked. In order to quantify pollutant levels, research must look at the availability of pollutants to the ecology of the freshwater system. Because of long residence times, lead as well as other trace metals remain in an environment and have the potential of remaining biologically available. Once introduced into a food web, these metals bioaccumulate and biomagnify, reaching toxic levels. Due to recent reintroduction in Indiana, North American river otters provide a particularly unique study species. One issue common with endangered animal repopulation efforts is lack of thorough testing of environmental effects. Environmental pollutants have vastly changed the freshwater environments where these mammals reside. Research must include evaluation of the effect of known pollutants on a mammal. Otters exhibit several highly developed cognitive behaviors such as communal socialization and handholding, and tool use potentially effected by trace metal contamination. As a pollution sensitive, apex predator, river otters hold the potential of both biomagnification and bioaccumulation.</p>

Session 2b
Room s022

<p>10:45-11:00am</p>	<p>Influence of prior conspecific parasitism in host selection by dodder, <i>Cuscuta gronovii</i> Erika Proffitt and Logan Minter</p> <p>Cuscuta spp., commonly known as Dodder, is a vining holoparasitic plant that does not perform photosynthesis on its own but rather relies purely on a host for survival. It is understood that Cuscuta must attach to a host within 10-15 days of sprouting to survive, however, the mechanisms behind the host selection preferences are not. This study aims to investigate host selection preferences of Cuscuta seedlings when presented with plants, both preferred hosts and non-hosts, that have been subjected to prior Cuscuta parasitism and plants that have not. From this analysis, we hope to bring greater understanding to the mechanisms behind Cuscuta parasitism “choices” and how the presence of other previously established individuals influences those.</p>
<p>11:00-11:15am</p>	<p>Preliminary comparisons of wild strains and standard cultivars of Hops, <i>Humulus lupulus</i>, in Southern Ohio Haley Bigham, Brad Bergefurd, Daniel Chaffin and Logan Minter</p> <p>Common hops, <i>Humulus lupulus</i>, are an economically valuable crop used as a bittering agent in the production of beer. In recent years, a demand for locally sourced, unique, and robust growing hops has increased due to exponential increase in microbreweries. In order to meet demands for local, disease and pest resistant hops, an emphasis is placed on studying wild varieties in comparison to standard cultivars. Collection and cultivation of both standard varieties and wild isolines are being used to determine and collect morphometric data which may indicate desirable attributes for cultivation and use locally. Preliminary results of plant survival rates show that some of the wild isolines and standard cultivars propagate at similar rates when grown in a controlled setting. Comparisons will be made to predict varieties better suited to grow in Ohio conditions.</p>
<p>11:15-11:30am</p>	<p>Severe inbreeding depression is predicted by the “rare allele load” in <i>Mimulus guttatus</i> Keely E. Brown and John K. Kelly</p> <p>Most flowering plants are hermaphroditic and experience strong pressures to evolve self-pollination (automatic selection, reproductive assurance). Inbreeding depression (ID) can oppose selection for selfing, but it remains unclear if ID is typically strong enough to maintain</p>

	<p>outcrossing. To measure the full cost of sustained inbreeding on fitness, and its genomic basis, we planted highly homozygous, fully genome-sequenced inbred lines of yellow monkeyflower (<i>Mimulus guttatus</i>) in the field next to outbred plants from crosses between the same lines. The cost of full homozygosity is severe: 65% for survival, 86% for lifetime seed production. Accounting for the unmeasured effect of lethal and sterile mutations, we estimate that the average fitness of fully inbred genotypes is only 3-4% that of outbred competitors. The genome sequence data provides no indication of simple overdominance, but the number of rare alleles carried by a line is a significant negative predictor of growth rate in the greenhouse. These findings are consistent with a deleterious allele model for ID. High variance in rare allele load among lines and the genomic distribution of rare alleles both suggest that migration might be an important source of deleterious alleles to local populations.</p>
<p>11:30-11:45am</p>	<p>Morphological reevaluation of the <i>Trifolium depauperatum</i> species complex Lydia Tressel</p> <p>The plant family Fabaceae is known for its economic importance, including important crop plants. Among important crops is the well-known clover genus, <i>Trifolium</i>, encompassing about 230 species (Zohary and Heller 1984; Ellison et al. 2006), that likely is Mediterranean in origin. <i>Trifolium depauperatum</i> Nutt., commonly known as cowbag clover or dwarf sack clover, is native to western North and South America, and has been found in British Columbia, Washington, Oregon, Idaho, California, Mexico, and Chile. <i>Trifolium depauperatum</i> has not been studied in detail and encompasses a great deal of morphological variation. The most recently published names associated with the <i>T. depauperatum</i> species complex include <i>T. depauperatum</i> var. <i>depauperatum</i>, <i>T. depauperatum</i> var. <i>amplectens</i>, <i>T. depauperatum</i> var. <i>truncatum</i>, and <i>T. hydrophilum</i> (Vincent and Isely 2012). Herbarium specimens of the <i>Trifolium depauperatum</i> species complex collected throughout western North and South America were studied. Specimens representing the known geographical range of the species complex were examined in order to understand the range of morphological characteristics based on geographic location. Data for 41 characters were analyzed using the statistical program NTSYS (Rohlf 2000). Analyses of the data show that there are four clusters of OTU's, which correspond to the four currently recognized taxa.</p>

Session 3a
Room s018

<p>9:00-9:15am</p>	<p>Can a large generalist herbivore mediate negative density dependent tree seedling mortality? Stephen Murphy</p> <p>The Janzen-Connell hypothesis (JCH) predicts that host-specific natural enemies drive negative conspecific density interactions in plant populations. These interactions are expected to promote species coexistence and diversity by keeping abundant populations in check and offering a fitness advantage to rare species. While multiple natural enemies have been implicated in JCH dynamics, large mammalian herbivores, such as white-tailed deer (<i>Odocoileus virginianus</i>), have received little attention. While this may be because deer are often considered generalist feeders, they are also known to prefer certain species over others. Using data on approximately 15,000 tree seedlings collected in southwestern Pennsylvania, we show clear evidence for negative density-dependent seedling growth and survival. By erecting exclusion fences around half of the sampling plots, we also show that deer impact mortality of specific species more than others. Using a generalized linear mixed model, we test the significance of a fencing by neighborhood density interaction term to determine whether CNDD is mediated by white-tailed deer. Importantly, we show for two species (<i>Prunus serotina</i> and <i>Fraxinus americana</i>) that CNDD occurs only when deer are allowed access to seedling plots. These data suggest that large mammalian herbivores such as deer may be important drivers of CNDD in forest communities.</p>
<p>9:15-9:30am</p>	<p>Synchrony of Mast Seeding Patterns in a Boreal Forest Community Jillian A. Sterman, Abigail C. Leeper, Jalene M. LaMontagne</p> <p>Mast seeding is the synchronous and highly variable production of seed crops over time by a population of plants. Evolutionarily, one of the leading hypotheses for mast-seeding is the predator-satiation hypothesis, whereby seed predator populations are typically low due to the lack of seed, and are then satiated by a huge pulse of seed production during a mast year. Typically, mast seeding studies are done on one plant species, and there is a lack of understanding of the level of synchrony of mast seeding patterns at the community level. To determine if mast seeding patterns are synchronous in a boreal-forest community, we quantified relative seed production from 2013-2018 for six tree species in the Huron Mountains, Michigan. Six to nine 0.5m² seed traps were randomly located within each of four</p>

	<p>sites. Seeds were collected in the spring each year and were counted, identified to species, and massed. Spearman rank correlations were used to determine the synchrony of seed production between species within a site. The two inland sites showed moderate synchrony across species ($r_s \sim 0.5$), and synchrony was weak and non-significant within the two shore sites. Variation across species may influence the effectiveness of masting as a mechanism of predator satiation.</p>
<p>9:30-9:45am</p>	<p>Synchrony and Variation in Mast Seeding White Spruce: A Genetic Approach Evan S. Cowles and Jalene M. LaMontagne</p> <p>Mast seeding is a common reproductive strategy defined as the synchronous production of a highly variable seed crop over time by a population of perennial plants. However, while mast seeding can be observed on a population level, there are high levels of individual variation in any given year. White spruce, <i>Picea glauca</i>, is the dominant species of the boreal forest and a mast seeding species. Cone counts, to determine synchrony, and needle samples, for genetic analysis, will be collected. RADSeq, restriction site associated DNA sequencing, is a next-generation, reduced representation method of DNA sequencing that makes large repetitive genomes, such as white spruce, 20 Gb, more accessible. We hypothesize that synchrony and individual variation observed in mast seeding white spruce seed cone production is affected by genetic relatedness. We predict that trees with similar patterns of annual seed cone production, synchronous, will exhibit higher genetic relatedness. Through my research, genetic structure of a population of 350 white spruce near the southern range limit in the Huron Mountains, MI will be assessed. Furthermore, it may be possible to identify genes associated with mast seeding.</p>
<p>9:45-10:00am</p>	<p>How effective are ant mutualists at protecting Karner Blue Butterflies (<i>Lycaeides Melissa samuelis</i>) under warming? & How do Alle.. Preston Thompson</p> <p>Research was conducted at the Toledo Zoo greenhouse (Toledo, OH). I manipulated temperature and presence of Allegheny mound ant tending for 17 mesocosms placed in the Toledo Zoo greenhouse. An Allegheny ant mound was placed in the center of 17 mesocosms and was approximately .1m away from each mesocosm. Mesocosms were subjected to greenhouse temperature (hereafter ambient temperature) or elevated temperature via infrared lamps. KBB measurements included survivorship, time to pupation, time from pupation to adult eclosion, vertical placement (cm)-measured by a straight-line distance from potted lupine soil surface of KBB larvae, and</p>

	<p>larvae location within mesocosm. To investigate how the Allegheny mound ant presence influences vegetation and insect composition, I collected data within the Oak Openings region. For the duration of the study I collected data from two locations within the Oak Openings Region: Oak Openings Metropark butterfly meadow, which is mostly comprised of sandy soil, low laying vegetation and tree saplings and Girdham Road Forest, which is a secondary forest mostly comprised of sandy soil, maple trees and oak trees. Data were collected once per week for each location. For each location 10 Allegheny ant mounds were randomly selected for a total of 20 ant mounds. For each sampling location (20 x 50 cm) the following data were collected: Visual obstruction reading of vegetation using the Robel Pole method (Smith, 2008), community composition of vegetation, presence of cottonwood trees (<i>Populus</i>) due to their relationship with aphid communities, number of cottonwood trees, height of cottonwood trees, presence of Allegheny mound ants, number of Allegheny mound ants, behavior of Allegheny mound ants, and plants of interest.</p>
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Session 3b
Room s022

<p>9:00-9:15</p>	<p>Context dependency of belowground effects on plant-pollinator interactions and fecundity in a tallgrass prairie species Savannah Fuqua</p> <p>Reproduction of most flowering plants depends on pollination by animals. Plant-pollinator interactions can be influenced by the diversity of the resident plant community, but recent studies have highlighted the potential importance of soil-borne microbial communities in affecting pollinator behavior. It is currently unknown to what extent these changes in pollinator behavior result in a change in individual plant fecundity. In a tall grass prairie species, I tested whether plant-soil microbial interactions mediate plant-pollinator interactions, and thus indirectly affect plant fecundity, and whether the diversity of resident plant community alters these relationships. To untangle direct and indirect effects of above- and belowground interactions that influence plant fecundity, measured as the number of seeds produced per flower, I performed pollination manipulations and pollinator observations in experimental plant communities that varied in the number of plant species (1, multiple species) and in the composition of soil microbial communities (with, without live soil microbes). I found that soil microbes negatively affected the number of seeds produced by both manually and naturally pollinated flowers in <i>Rudbeckia hirta</i> when individuals were grown in monocultures.</p>
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	<p>However, manually pollinated flowers in polycultures produced equal numbers of seeds when grown in either soil condition. Naturally pollinated flowers did not show a significant effect of diversity when grown in live soil. Pollinator visitation did not significantly differ between soil treatments in polyculture, but was significantly reduced in monocultures with live soil microbes. These results suggest that the negative effects of soil microbes on individual fecundity in polyculture are not caused by a change in pollinator behavior. Rather, the lower fecundity of naturally pollinated flowers compared to manually pollinated flowers in polyculture could indicate an increase in pollen limitation in these conditions. Our results indicate that soil microbes can lead to changes in pollinator behavior, but these changes do not have straightforward effects on fecundity.</p>
<p>9:15-9:30</p>	<p>Gene Expression of Corn Earworm (<i>helicoverpa zea</i>) when infected with <i>pseudomonas aeruginosa</i> bacteria Bayan Aljamal</p> <p>The Corn Earworm, <i>Helicoverpa zea</i> (Boddie), is the second most serious economic pest of agricultural crops in North and South America. In order to study the immune response of <i>H. zea</i> to infection by various pathogens we infected them with <i>Pseudomonas aeruginosa</i> bacteria. <i>Pseudomonas aeruginosa</i> is a pathogenic pest because of their ability to produce extracellular enzymes and toxins that destroy the physical barriers and infect host cells. This study examined <i>H. zea</i>'s immune response to infection as well as provide information on how to overcome their defense system for the development of biocontrol methods. One of the main focus of this experiment is to compare the growth, survival, and gene expression of <i>H. zea</i> when it consumed a diet treated with <i>P. aeruginosa</i> or bacteria-free diet for 72 hours. Larvae that fed on the diet containing <i>P. aeruginosa</i> had a statistically significant increase in mortality compared with control. Microarray analysis was done to measure the expression level of larvae that fed on <i>P. aeruginosa</i> diet and bacteria-free diet. The expression of 3397 genes was significantly different between the two treatment groups. Out of this total, ~31% of the genes (1067 genes) have unknown functions, and ~ 69% of the genes (2290 genes) have known functions. The main categories that had significantly different gene expression were categorized according to their specific major functions including, but not limited to, encoding for metabolism, digestive, immune system, and cell growth. Caterpillars infected with <i>P. aeruginosa</i> showed a significantly different gene expression pattern compared to control. This research determined the immune reaction of <i>H. zea</i> in response to bacterial infection. This information will be useful in figuring out how to make <i>H. zea</i> more susceptible and increasing control of this pest.</p>

<p>9:30-9:45</p>	<p>Promises and pitfalls of using vaguely georeferenced occurrence records in biodiversity modeling David Henderson, Stephen J. Murphy, Kelley Erickson and Adam B. Smith</p> <p>We are currently in the midst of a data revolution in biodiversity monitoring. Data on species occurrences and environmental gradients are becoming increasingly available, and statistical tools for analyzing these data are maturing rapidly. Despite these advances, wide variation in data quality requires that researchers utilize extensive data cleaning protocols, including removing records with poor spatial resolution (i.e., vaguely georeferenced; e.g. county-level records). While utilizing only those data that meet strict quality standards is well-justified, the effects of removing records on biodiversity models (e.g., species distribution models) has not been examined. Here, we explore potential biases that arise via commonly used data cleaning protocols for biodiversity modelling. Specifically, we compare species distribution models that use both accurate and vague records to models that use accurate records only. We use the common and widely distributed plant genus <i>Asclepias</i> spp., where as many as 64% of records were vaguely georeferenced. We find that the predicted spatial area of models using accurate records was 0.5 to 0.98 of that of models that used accurate+vague records. Our results indicate that data cleaning has a large impact on species range models, suggesting that more attention should be given to decisions involving the removal of poorly georeferenced occurrence records.</p>
<p>9:45-10:00am</p>	<p>How does changes in soil phosphorus influence understory plant nutrient concentrations in a lowland tropical rainforest? Ashley Wojciechowski, Meghan Midgley, Amayrani Sanchez, Mary Ashley Tenedor , Andrea Vincent and Silvia Alvarez-Clare</p> <p>Soil phosphorus for plant use is considered scarce across tropical soils, but recent studies based on adult tree measurements have found that nutrient limitation, even in P-poor tropical forests, is species-dependent. We leveraged a long-term (12-years), large-scale (30x30m plots) fertilization experiment in Costa Rica to investigate how N and P fertilization influenced soil nutrients and plant tissue (C, N and P) concentrations in two abundant tree seedlings (a legume tree and an arborescent palm) and three understory plants (a fern, a palm, and a forb). In soils, we could not detect evident increase in nitrate concentrations after twelve years of fertilization, but there was almost a three-fold increase of Mehlich extractable P. In plants, we found that overall foliar N did not increase with N fertilization, but foliar P increased 17.8% with P fertilization especially due to a strong response from the forb. From the seedlings, the legume had higher N and P</p>

	<p>concentrations than the palm in both stem and root tissues regardless of fertilization. In conclusion, the studied species responded differently to soil P availability. This study can help us better predict how tropical forests will respond to changes in soil nutrient availability with future anthropogenic alterations.</p>
<p>10:00-10:15am</p>	<p>Winter climate change, snow depth, and prescribed fire affect prairie plant persistence and growth Jonathan Henn, Laura Ladwig and Ellen Damschen</p> <p>The winter season is warming faster than any other season in temperate and polar regions, resulting in an overall loss of snow. In temperate grasslands (prairies), the loss of snow can substantially change the temperatures which organisms experience during winter as soils are exposed to more extreme cold conditions. Fire is another important factor affecting community composition in prairies. The timing of fire relative to winter could have an important interactive effect with lower snow cover. Specifically, burning accumulated litter prior to winter leaves plant seeds, buds, and roots even more exposed to extreme cold temperatures. Here we pair long-term (60 year) observations of prairie and savanna plant community change across a gradient of winter climate change with a field experiment manipulating snow depth and fire timing to better understand the consequences of winter climate change on prairie plant communities. Over the past 60 years, warming winter temperatures were related to increased extinction probabilities for spring-blooming species, but not summer-blooming species. Also, fire had substantial positive effects in preventing plant extinction. Following the first two years of experimental treatments, reductions in snow depth cause colder and more variable soil temperatures but did not significantly affect plant growth. Also, burning prior to winter results in colder soil temperatures when snow depth is reduced. However, fire promoted plant growth for most species. Overall, these results suggest that winter climate has important effects on prairie plant health and that even though snow manipulations affected temperature dynamics in the soil, prairie plants are relatively resilient to these changes for now. Prescribed fire has very important effects on prairie plant dynamics and might counteract the potentially negative effects of future snow loss.</p>

Poster Abstracts

1	<p>Dung Beetle Resource Preference Within a Landscape Matrix Sheryl Hosler</p> <p>The reintroduction of large grazing herbivores has been recognized as an important management technique for restored tallgrass prairies, with priority being placed on the reintroduction of American bison to these areas to serve in their role as ecosystem engineers. However, there are many technicalities that make it difficult for land managers to consider bison a feasible option for their projects, so domestic cattle have been considered as an alternative. Restoration management must consider all trophic levels in an ecosystem, including mutualists that may have co-evolved with these large grazing herbivores. I tested whether the dung beetles in a restored tallgrass prairie community showed preference for bison dung over the dung of several common domestic agricultural animals using a series of pitfall traps baited with various types of dung. The dung beetle community in this prairie seems to be dominated by a generalist species, most likely due to the loss of bison in many parts of their historic range. However, at least once bison dung specialist still remains in this prairie community, signaling that preferential reintroduction of bison over domestic cattle in prairie restorations will promote diversity within the decomposer community.</p>
2	<p>Seed predation in tallgrass prairies changes throughout the year and is affected by litter cover Genevieve Anderegg, Jonathan Henn and Ellen Damschen</p> <p>Tallgrass prairie is one of the most threatened habitats in the Midwestern United States, with less than 1% of original native prairie remaining in small and isolated patches. Small mammal seed predators are important aspects of these communities, as they influence plant recruitment and structure by consuming seeds and plant matter. However, there has been little to no research on the effects of varying levels of plant litter longitudinally throughout all seasons on seed predation intensity. We seek to measure the impact of management decisions like burn timing and mowing on rodent seed predation in a restored tallgrass prairie. Seed predation was quantified monthly (June-May) with a giving up density model using native <i>Sorghastrum nutans</i> seeds in plots that were subjected to either a spring burn, fall burn, fall mow, or unmanipulated control to alter plant litter levels. We found that seed predation was lowest during the summer and increased into the fall. Burning and mowing resulted in significant reductions ($p < 0.001$) of seed predation during a time when seed predation was otherwise very high in the control plots. This informs how prairie restoration and management decisions like prescribed fire timing and mowing affect seed predation intensity in restored prairies.</p>
3	<p>Body shape diversity in dogfish sharks (Elasmobranchii: <i>Squaliformes</i>) Phillip Sternes and Kenshu Shimada</p> <p><i>Squaliformes</i> (dogfish sharks) is a large elasmobranch order with six families (Centrophoridae, Dalatiidae, Etmopteridae, Oxynotidae, Somniosidae, and Squalidae) and over 100 species. A previous study suggested that all squaliforms share one basic body plan unlike most other shark orders that exhibit body</p>

	<p>shape diversity. We used landmark-based geometric morphometrics to investigate if Squaliformes is indeed represented by only one body plan. We examined the outline of all extant squaliform species in lateral view and conducted three separate analyses: (1) a full body analysis (precaudal body + caudal fin), (2) precaudal body analysis, and (3) caudal fin analysis. Our results indicate each family represents its own body plan. Centrophoridae has the most generalized body form within Squaliformes characterized by a moderately narrow body with the first dorsal fin just above the pectoral fin origins. Etmopteridae, Squalidae, Somniosidae, and Oxynotidae are similar to Centrophoridae, but each family tends to have a slightly different first dorsal fin position and body depth from others. Dalatiidae shows the greatest body form variation within Squaliformes. Our study shows that, whereas the caudal fin is more morphologically conservative than the precaudal body in Squaliformes, the entire shark order is indeed represented by only one basic body plan.</p>
4	<p>Effects of urbanization on stress responses in Eastern Garter Snakes Elizabeth Rock, Jeffrey Bartman, Jamie Cornelius and Katherine Greenwald</p> <p>Urbanization affects both abiotic and biotic component of the environment. Altering landscapes from natural states to urban states results in changes to microclimate, input of pollutants, and disruption of ecosystem function, all of which may increase stress on organisms in these areas. Stress metrics of individual animals may be an indicator of how likely a population is to persist, which can inform our understanding of species living in urban environments. Corticosterone (CORT) is a hormone produced in response to life history circumstances, daily demands, and stressful events. Chronic or long-term stress stimuli can alter the baseline status of CORT in the blood. This study will measure physiological stress response (CORT levels) and physical health metrics (body condition) in Eastern Garter Snakes (<i>Thamnophis sirtalis</i>) along an urban-rural gradient, with the goal of assessing whether the magnitude of this effect varies over time (e.g., decreased HPA axis sensitivity). <i>T. sirtalis</i> is a generalist species commonly found across the eastern United States in a variety of habitats, ranging from meadows to urban areas. We predict that snakes in urban areas will have increased CORT when compared to rural snakes. We further predict that snakes with higher baseline CORT will have poorer body conditions related to urban stressors.</p>
5	<p>Structural Approach to Understanding Restoration Management Effects on Prairie Community Composition Rebecca Stelzer, Nick Barber and Holly Jones</p> <p>In a prairie community, species diversity and richness can be influenced by bison and fire. Burning the prairie in the spring may increase the abundance and diversity of grass species but decrease the diversity and richness of forbs. Having bison graze on the site after it is burned can increase the species diversity and richness of the flowering plants because bison graze mostly on the grass. This study looks at understanding restoration management effects on the prairie community composition by using data from Robel pole measurements and PAR</p>

	<p>Light level percentages. Bison play a more significant role than fire, but both bison and fire influence the composition of the prairie. When bison and fire were used on a site the vegetation density of that site was lower than if bison and fire were not used. It is important to have plant density and diversity in the prairie community to support the small mammal and insect communities.</p>
6	<p>A new skeleton of an ichthyodectiform fish (Osteichthyes: <i>Actinopterygii</i>) from the Upper Cretaceous Woodbine Formation of Texas Riley Hacker and Kenshu Shimada</p> <p>DMNH 20149 is a 96-million-year-old fossil skeleton of a nearly complete, articulated bony fish housed in the Perot Museum of Nature and Science in Dallas, Texas, USA. It was found from the Arlington Member of the Woodbine Formation (mid-Cenomanian) in Denton County, Texas, where it was a nearshore environment along the southeastern shoreline of the Western Interior Seaway. The specimen presently exposes the right lateral side and measures about 39 cm and 50 cm in standard length and total length, respectively, and about 11 cm in maximum body depth with a fusiform body plan. The vertebral column is nearly complete with a total vertebral count of at least 49, but no more than 55. The overall skeletal characteristics, including the total vertebral count, suggest that it belongs to an extinct actinopterygian order Ichthyodectiformes. DMNH 20149 possesses a triangular dentary that is typically found in Jurassic ichthyodectiforms, unlike Cretaceous forms characterized by a rectangular dentary. The exact taxonomic identity of DMNH 20149 within Ichthyodectiformes remains uncertain at the present time, but another notable feature is its toothlessness, making the fossil fish to superficially resemble the extant Atlantic tarpon, <i>Megalops atlanticus</i> (Actinopterygii: Elopiformes).</p>
7	<p>Peculiar dental pattern of the Late Cretaceous durophagous shark, <i>Ptychodus marginalis</i> Amanda Alt and Kenshu Shimada</p> <p><i>Ptychodus</i> (Elasmobranchii: Ptychodontidae) is a Cretaceous shark genus that had specialized dentitions suited for crushing shelled animals. UNSM 1196 and 123608 are associated dental remains of <i>P. marginalis</i> housed in the University of Nebraska State Museum, Lincoln, Nebraska. Their locality data are missing, but they most certainly came from the upper part of the Greenhorn Limestone in southeastern Nebraska, where it was the middle of the Western Interior Seaway during the Late Cretaceous. The combination of data from these specimens reveal that, in <i>P. marginalis</i>, the upper dentition consisted of one medial tooth row and possibly as many as 13 lateral tooth rows on each side, whereas the lower dentition consisted of one medial tooth row and up to only about six tooth rows on each side. Unlike <i>P. decurrens</i>, <i>P. mortoni</i>, and <i>P. occidentalis</i> that have flat tooth plates, UNSM 1196 and 123608 show that teeth of <i>P. marginalis</i> in both the upper and lower dentitions were arranged in a whorl. Although the arrangement of each tooth whorl on the jaw cartilage and the functional significance of the unique whorl pattern need further investigation, UNSM 1196</p>

	<p>and 123608 are important to discern the paleobiology and paleoecology of <i>P. marginalis</i>.</p>
8	<p>Pollen in The Bank: Does pollen removal and deposition by four native bee taxa differ in a prairie perennial? Evan X. Jackson, Zeke Zelman and Jennifer L. Ison</p> <p>Pollination failure is a major problem for many natural plant populations and has been exacerbated by habitat fragmentation and declines in pollinator populations. This study measured pollinator visitation and per visit pollen removal and deposition, across common pollinator taxa to provide insight into pollination failure in the focal population of the native composite <i>Echinacea angustifolia</i>, in the Western Minnesota prairie. We collected samples of male and female phase florets from <i>E. angustifolia</i> flowerheads, before and after observed pollinator visits during the summer of 2018. In the fall at the College of Wooster, the number of pollen grains in these samples were quantified to determine how much pollen each taxon of pollinator removes and deposits per visit. These observed visits provided a measure of each pollinator taxon's relative visitation to the population. We found that the composite specialist <i>Andrena rudbeckiae</i> removes more grains of pollen per visit than the other common pollinator taxa in the study area; namely, male <i>Melissodes</i> sp., <i>Augochlorella</i> sp., and 'small black bees,' a wide taxonomic group comprising a variety of species mostly in the Halictidae. Pollen limitation in the population could be driven by frequent male <i>Melissodes</i> sp. visitation late in the season; based on the per visit removal of male <i>Melissodes</i> sp. and number of visits observed in this study. These results combine to contribute to our understanding of pollination failure and pollen limitation in small fragmented flowering plant populations, and the selective pressures that pollinators exert on these population.</p>
9	<p>Little Cost of Reproduction in the Long-Lived Perennial, <i>Echinacea angustifolia</i> Tristram O. Dodge, Michael J. LaScaleia, Lea K. Richardson and Stuart Wagenius</p> <p>Landscape fragmentation, changing fire frequency, and decreased pollinator abundance are exacerbating pollen limitation in tallgrass prairies. However, according to the cost of reproduction hypothesis, present pollen limitation might lead to increased growth or fitness of perennial plants in years following pollen limitation. To address how present pollen availability affects tallgrass prairie plants' future outlook, we compared important growth and fitness traits of <i>Echinacea angustifolia</i> (Asteraceae), a long-lived, self-incompatible, iteroparous forb. Beginning in 2012, <i>Echinacea</i> (n=58) were randomly assigned to one of three groups: pollen addition, pollen exclusion, and an open pollinated control. In contrast to the cost of reproduction hypothesis, we found that the pollen exclusion and the pollen addition treatments had mixed effects on future growth and fitness in <i>Echinacea</i>, compared to the open control. Pollen exclusion did not affect <i>Echinacea</i> in consistent or predictable ways, suggesting that current pollen limitation will not enhance <i>Echinacea</i> growth or fitness in future years. Lack of pollination treatment effects could be because <i>Echinacea</i> is not resource limited or because seed production is inexpensive compared to generation of the large</p>

	<p>floral reproductive structure and achenes. Future studies should quantify the extent of pollen limitation in <i>Echinacea</i> and in other threatened tallgrass prairie species.</p>
10	<p>What to eat when you live in manure: wasps that parasitize filth flies Elizabeth Taylor and B. H. King</p> <p>Parasitoid wasps are an important component of the rich invertebrate communities in decaying organic matter at livestock facilities. However, little is known about what adult parasitoids eat there. Most parasitoid wasps in the world parasitize herbaceous insects, so nectar from flowers is readily available. But what do adult parasitoids in large accumulations of manure eat? The present study examined feeding by adult <i>Spalangia cameroni</i>, a species which burrows through manure, where it finds the pupal stage of filth flies to parasitize. Feeding on host fluids occurs in many parasitoid wasps, including <i>S. cameroni</i>. In the laboratory these wasps also readily feed on honey or a sucrose solution, which increase their longevity. We are looking at three potential non-floral food sources: milk, manure, and sorghum silage compared to water and honey. Parasitoids were food-deprived for two days and then placed into an 8 oz jar with the potential food source and water provided ad libitum. Mortality was checked every 24 hours. Later tests will examine longevity with dandelions, buckwheat, and sweet alyssum. Knowing what these parasitoids eat may allow food supplementation, which may help the parasitoids control pest flies.</p>
11	<p>How many pollen grains does it take to set a seed in <i>Echinacea angustifolia</i>? Mia Stevens, Nate Scheerer and Jennifer L. Ison</p> <p>Over 90% of flowering plants rely on insect pollinators for sexual reproduction. Pollination biologists often quantify pollinator effectiveness by counting the number of pollen grains a pollinator deposits on a plant's stigma in a single visit. However, flowers in one of the biggest plant families, Asteraceae, are uniovulate, meaning that there is just one ovule per style. Therefore, it theoretically only takes one viable pollen grain to fully set seed in an ovary, so this standard method of quantifying pollinator effectiveness may not be appropriate for members of the Asteraceae. In our study, our objectives were to determine how many pollen grains are necessary to set a seed in <i>Echinacea angustifolia</i>, a species in the Asteraceae. We performed 60 hand crosses at varying levels of pollen deposited. Each cross consisted of nine total styles of which three were removed before the cross to get estimates of self-pollen deposition and six styles were crossed with pollen from other flowering individuals. Styles were then collected and stained using fuchsin gel and number of pollen grains presented were counted using a compound microscope. The achenes, fruits, from the crosses were x-rayed to determine if a seed was present. Preliminary data shows that seed set varies based on by pollen grains deposited. These data will aid in advancing our understanding of pollinator effectiveness in uniovulate plants. By increasing our understanding of pollinator efficiency in the Asteraceae, we can better predict the consequences of pollinator declines in fragmented habitats, such as the North American tallgrass prairie.</p>

12	<p>Hydraulic Traits in Epiphytic <i>Elaphoglossum</i> ferns from Puerto Rico Mary Pitts, Gary K. Greer and Jennifer Winther</p> <p>Tropical rainforests have the highest biodiversity of plants and animals in the world including the largest and most diverse community of epiphytes. To further our understanding of hydraulic traits that potential causes niche differentiation in these epiphytic communities, we conducted an anatomical study of eight species of the epiphytic fern <i>Elaphoglossum</i>. We collected our samples from the lower-trunk community in El Yunque National Forest, Puerto Rico. Hydraulic traits (including xylem diameter, parenchymatous path length, and meristele area) in the lamina, stipe, and rhizome were measured in each of the eight species based on sectioned plant material. Preliminary results show that hydraulic traits in the lamina and stipe for all species are similar; however, there was considerable variation in rhizome traits for all species.</p>
13	<p>Native <i>Echinacea angustifolia</i> has depressed viability relative to non-native <i>E. pallida</i> and reciprocal hybrids (<i>E. angustifolia</i> x <i>E. pallida</i>) in a fragmented prairie habitat Riley Thoen, Pamela Kittelson, Sanjive Qazi, Stuart Wagenius</p> <p>Introduced plants can alter population dynamics of native congeners and facilitate change to community structure. This is exacerbated if the introduced species and its native congener are able to form hybrids. The long-lived tetraploid forb <i>Echinacea pallida</i> was introduced to severely fragmented prairie in Douglas County, MN, where it has formed hybrids with the native, diploid <i>E. angustifolia</i>. To determine viability of the native coneflower relative the introduced crosses, we measured survival and above-ground morphology of intraspecific and reciprocal interspecific crosses of <i>E. angustifolia</i> and <i>E. pallida</i> for five years. We also recorded photosynthetic rate, water use efficiency, and leaf thickness all living basal plants in 2018. <i>E. angustifolia</i> intraspecific crosses had the lowest survival, morphology, and ecophysiology values compared with all other cross types; <i>E. pallida</i> intraspecific crosses almost always had the highest values. In nearly all categories, <i>Echinacea</i> hybrids displayed intermediate phenotypes of pure <i>E. angustifolia</i> and <i>E. pallida</i>. These results suggest that the genomes of <i>E. angustifolia</i> and <i>E. pallida</i> combined in an additive manner when forming hybrids. With increased viability over the pure native cross type, plants with a non-native <i>E. pallida</i> parent may be able to harm the already-decreasing population of <i>E. angustifolia</i> in Douglas County, MN. Management should be undertaken to eliminate mating bouts of <i>E. angustifolia</i> and <i>E. pallida</i>.</p>
14	<p>Calcification level in vertebrae of thresher sharks (Lamniformes: <i>Alopiidae</i>), and its behavioral implications Luke A. Banta and Kenshu Shimada</p> <p>Thresher sharks (<i>Alopias</i>) have an exceptionally elongated caudal fin and consist of three species: <i>A. pelagicus</i>, <i>A. superciliosus</i>, and <i>A. vulpinus</i>. <i>Alopias pelagicus</i></p>

	<p>and <i>A. vulpinus</i> have a unique hunting strategy in which they come to a sudden stop near the schooling fish, allowing their elongated caudal fin to swing over the head as a whip, to stun and capture their prey. On the other hand, the exact hunting strategy remains unknown for <i>A. superciliosus</i> that has a stouter, less flexible caudal fin compared to <i>A. pelagicus</i> and <i>A. vulpinus</i>. To further decipher the hunting method of <i>A. superciliosus</i>, we examined the level of calcification in their vertebrae using computed tomography (CT) images of preserved museum specimens of each species. Our preliminary results show that the vertebrae of <i>A. superciliosus</i> are less calcified than the vertebrae of <i>A. pelagicus</i> and <i>A. vulpinus</i>. This observation suggests that the vertebrae of <i>A. superciliosus</i> are built to allow for more bending of the body that, in turn, likely indicates that <i>A. superciliosus</i> flexes its body sideways to swing its relatively stout, inflexible caudal fin laterally for hunting, rather than over the head like <i>A. pelagicus</i> and <i>A. vulpinus</i>.</p>
15	<p>Fire predictably modifies fungal community structure and successional trajectory across ecosystems Jacob Hopkins and Benjamin A. Sikes</p> <p>Fire is an increasingly common disturbance that alters ecological processes like nutrient cycling and community dynamics. The extent of fire's effect on these processes is largely governed by the amount and quality of plant fuel loads. Plant fuel loads are modified by fungi both directly through decomposition and indirectly through plant diseases and mutualisms, yet fungal roles in fire regimes are poorly understood. We hypothesized that fire would shift fungal community structure similarly across ecosystems, and that these changes would correlate with environmental factors. Following prescribed fires in a tallgrass prairie and longleaf pine savanna, we assessed both fungal communities and edaphic factors over time. Fire filtered fungal communities, making burned communities more similar to one another than unburned communities. Fire-driven shifts in communities occurred at the species level, rather than at higher taxonomic levels (phylum & class). Communities also changed with time, and fire modified this post-fire succession. Additionally, C:N ratio was a good predictor of fungal community structure. Fungal communities differed among systems (prairie and savanna), and fire impacts on those communities likewise differed. These results show that fire changes fungal community succession, which may alter fungal modification of plant fuels that are available for future fires.</p>
16	<p>How does restoration and management techniques (prescribed fire and bison grazing) affect carbon and nitrogen cycling in prairie Angelica Bautista</p> <p>As we prepare to mitigate climate change, ecologists are looking into ways of sequestering carbon in a sustainable manner. Restored prairies can be used to create carbon sinks to offset ever increasing CO₂ emissions. In this study we looked into how different restoration and management techniques affected the levels of nitrogen and carbon in prairie vegetation. Samples were collected from tallgrass prairie sites at Nachusa Grasslands. Sites at this location vary in age of</p>

	<p>restoration, presence of bison, and use of prescribed fire as restoration management techniques. Grass and forb leaf samples were collected from 15 sites. Leaf samples from 10 different species in each site were collected, weighed, and ground. Isotope analyses were performed on the ground samples to find levels of nitrogen and carbon. The presence of bison was shown to increase nitrogen levels in grasses and forbs as a result of nutrient deposition from the bison. Increase in age and use of prescribed fire resulted in an increase in carbon in both grasses and forbs.</p>
17	<p>Late Cretaceous marine vertebrate fauna from the Juana Lopez Member of the Carlile Shale in southeastern Colorado Daniela Garza, Bruce A. Schumacher, and Kenshu Shimada</p> <p>The Juana Lopez Member of the Carlile Shale is a calcarenite deposit formed along the Western Interior Seaway of North America during the Late Cretaceous approximately 90 million years ago. Rock samples were collected from a Juana Lopez locality in southeastern Colorado to examine the taxonomic composition of vertebrate fossils by dissolving the calcarenite with a weak acid. Although almost all the specimens are represented by isolated bones and teeth that are microscopic, the paleofauna is found to be taxonomically diverse. It so far includes at least seven chondrichthyan (<i>Ptychodus whipplei</i>, <i>Cretodus crassidens</i>, <i>Scapanorhynchus raphiodon</i>, <i>Squalicorax</i> cf. <i>S. falcatus</i>, <i>Rhinobatos incertus</i>, <i>Ptychotrygon</i> sp., and <i>Ischirhiza texana</i>) and six osteichthyan fishes (e.g., <i>Hadrodus</i>(?) sp., <i>Micropycnodon kansasensis</i>, <i>Pachyrhynchus</i> sp., <i>Enchodus gladiolus</i>, <i>E. petrosus</i>, and <i>E. shumardi</i>). It also includes two marine reptiles (<i>Coniasaurus</i> and <i>Plesiosauria</i>) and at least one toothed bird taxon (<i>Ichthyornis</i> sp.). Teeth of <i>Enchodus</i> spp. are the most abundant vertebrate remains. The fossil assemblage also includes multiple teeth of <i>Ichthyornis</i>, along with teeth of <i>Ptychodus whipplei</i> and <i>Scapanorhynchus raphiodon</i> commonly found in mid-Turonian nearshore deposits, suggesting that the western shoreline of the Western Interior Seaway must have been close from the location.</p>
18	<p>Pectoral fin musculature of the three species of thresher sharks (Lamniformes: Alopiidae) Cecil A. Phibbs and Kenshu Shimada</p> <p><i>Alopias</i> (thresher shark) is a shark genus with three species, <i>A. pelagicus</i>, <i>A. superciliosus</i>, and <i>A. vulpinus</i>, characterized by an exceptionally elongated caudal fin. The hunting strategy of <i>A. superciliosus</i> is uncertain. However, a unique strategy is known for the other two species where they come to a sudden stop near the schooling fish, allowing their elongated caudal fin to swing over the head to strike and capture their prey. At or immediately prior to the sudden stop, at least <i>A. pelagicus</i> is known to significantly adduct its pectoral fins. We examined the pectoral fin musculature of the three <i>Alopias</i> species to look for any differences among them that may shed light on the behavior of <i>A. superciliosus</i>. We discovered that, from the pectoral fin base, the levator pectoralis is directed anterodorsally in <i>A. pelagicus</i> and <i>A. vulpinus</i>, whereas that</p>

	<p>of <i>A. superciliosus</i> posterodorsally. In ventral view, the main depressor pectoralis is directed posterolaterally from the medial part of the pectoral girdle at higher angles (20–60°) in <i>A. pelagicus</i> and <i>A. vulpinus</i> than <i>A. superciliosus</i> (5–20°). These observations at least indicate that the pectoral fins in <i>A. superciliosus</i> must operate quite differently from <i>A. pelagicus</i> and <i>A. vulpinus</i>.</p>
19	<p>The influence of <i>Andropogon gerardii</i> (big bluestem) on beta diversity and possible combined effects with climate change Julia Armitage</p> <p>Dominant species have a large influence on the biodiversity within ecosystems by creating a biotic filter; this tends to decrease the overall species diversity due to competition, however the influence on beta diversity is not well understood. Climate change may alter the strength of this biotic filter, but effects on alpha and beta diversity are also unclear. <i>Andropogon gerardii</i>, a common dominant species in restored tallgrass prairies, suppresses alpha diversity and richness and may be better adapted than other species to climate warming. I am testing three hypotheses in field and greenhouse experiments: 1: If <i>A. gerardii</i> is a strong competitive filter, then it will reduce alpha and beta diversity. 2: If climate change is a strong environmental filter, then it will reduce alpha and beta diversity. 3: If global climate change negatively influences other species, while having little to no effect on <i>A. gerardii</i>, then we will observe even lower alpha and beta levels. Preliminary data from a 2-year-old prairie experiment shows no effect of <i>A. gerardii</i> on diversity, but I expect effects to emerge as <i>A. gerardii</i> becomes more dominant. Results from my proposed work can help resolve effects of dominant species on diversity and how climate change may disrupt these patterns.</p>
20	<p>Ecological Stoichiometry of Neotropical Fishes Along Elevation Gradients of the Andes Mountains Jessica Vaclav and Windsor Aguirre</p> <p>Phosphorus and nitrogen are typically the most common limiting nutrients in freshwater ecosystems, where fish play important roles in the cycling of these nutrients. Variation among fish families indicates there is likely significant variation in the roles that different groups of fishes play in nutrient cycling. However, there is still much to be learned about nutrient cycling in tropical aquatic ecosystems. We aim to determine how phosphorus and nitrogen contents change in Neotropical stream fishes along elevation gradients of the Andes Mountains of western Ecuador, a region with very high endemism and under severe anthropogenic pressure. To do this, we collected freshwater fishes from ten sites located between approximately 72 and 935 meters above sea level in four rivers. Total carbon and nitrogen are being measured from ground whole specimens using a CE Elantech Flash EA1112. Phosphorus is being measured using a sulfuric acid digestion of ashed fish and analyzed through colorimetry. I hypothesize that nutrient ratios will change along elevation gradients and that they will differ significantly among taxonomic families of freshwater fishes.</p>

	<p>These are the first data on the ecological stoichiometry of freshwater fishes from western Ecuador.</p>
21	<p>Lyme Disease in Migratory vs. Resident Birds Jennifer Driscoll, Tham Mana, Shane Andrews, Cassidy Hanson, Damon Roznoswki, Sean Beckman and James Marshall</p> <p>Lyme disease is a zoonotic disease caused by the bacterium <i>Borrelia burgdorferi</i> which can be transmitted when an infected black legged tick takes a blood meal from another organism, thus, becoming a vector that is capable of spreading the bacterium to other organisms. Lyme Disease is prevalent in certain parts of the Midwest where ticks infect mammals as well as birds. Small rodents, such as the white-footed mouse are commonly infected and become reservoirs that can further perpetuate the spread of the disease. Because the disease seems to be localized to certain regions in the United States, it has become increasingly important to understand how the disease may become more common in areas outside of the “hot zones” as temperatures and environments fluctuate due to climate change. Mammals as reservoirs are of minimal concern when addressing this question as they do not travel long distances, therefore the disease could stay relatively contained in the highly infected areas. Due to many species of birds’ migration patterns, it is important to understand the prevalence, and therefore, the potential for the spread of the <i>Borrelia burgdorferi</i> bacterium great distances. In this study the percentage of migratory versus resident birds who tested positive for <i>Borrelia burgdorferi</i>, were 25% and 24% respectively. While the difference between the two subsets is statistically insignificant, every infected migratory bird can potentially facilitate the spread of the disease to new locations. Current research is being conducted to understand if the same trend is seen for birds tested in 2018 or if there are any significant deviations from the previous years data.</p>
22	<p>Spatio-temporal Patterns of Brown Rat Populations and Free-Roaming Cat Populations in Chicago María Jazmín Rios, Seth B. Magle, and Jalene M. LaMontagne</p> <p>In cities, free-roaming cats are a suggested rodent population control method but the interaction between cats and rats is relatively unexplored. Programs like trap-neuter-release have become a popular method used to control rat populations across the US. I will examine the spatial and temporal patterns of the brown rat (<i>Rattus norvegicus</i>) in Chicago, Illinois, the “rattiest” city in USA, using 10 years of citizen-contributed data from the City of Chicago Bureau of Rodent Control, and Animal Control and Rescue. Rat complaints will be used as an index of rat relative abundance, as these factors are highly correlated. Free-roaming cat complaints will be used as estimated relative abundance of cats in Chicago’s 90 zip-code sites because there currently is no other more accurate way to measure cat abundance. Complaints will be categorized, mapped, and analyzed within Chicago’s 90 zip-codes. If free-roaming cats influence rat abundance, we predict</p>

	<p>that the relative abundances of these species will be synchronous but negatively correlated through space and time. We will test this prediction using multiple regression matrices including five distance matrices: human population density, cat abundance, temperature, vacancy rates, and rodenticide amounts. This study will inform us how free-roaming cats influence rat distributions in Chicago.</p>
23	<p>Borrelia Infection in Canopy and Ground Dwelling Birds in Northern Illinois Whitney Felker, Hailey Avery, Jennifer Driscoll, Tham Mana, Shane Andrews, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p> <p>Lyme disease is caused by a bacterium, <i>Borrelia burgdorferi</i>. This bacterium must have a host to survive, and the host can influence the spread of the disease. According to the Center of Disease Control and Prevention (CDC), Lyme disease is a serious disease that is affecting many people and organisms. With 30,000 cases being reported each year, it is imperative that this disease gets identified and treated as early in the cycle as possible. Small mammals are the most common host for the disease, but birds have also been infected at increasing rates. As birds can cover more area than small rodents, birds become a greater risk for disease spread through their migratory routes and home ranges. The goal of this study is to determine how birds can serve as a host for <i>Borrelia</i>, in both canopy and ground dwelling birds. Blood samples were taken from different birds in two different locations within Northern Illinois over a three-year time period (2015-2017). Polymerase Chain Reaction (PCR) assays were then conducted to see which birds were positive for the disease. We initially hypothesized ground dwelling birds would be a greater reservoir from the disease, but the data collected suggests that canopy dwelling birds are also a compatible host. There was no significant difference in Lyme infection rates between the ground and canopy dwelling birds indicating both types of birds are at risk for infection and can influence the spread of Lyme disease.</p>
24	<p>Effect of <i>Borrelia</i> infection on body mass of birds Tham Mana, Jennifer Driscoll, Shane Andrews, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p> <p>Lyme disease is an infection that cause by <i>Borrelia burgdorferi</i> and transmitted by Ixodid tick vectors. Many ticks never become infected because some hosts are highly inefficient at transmitting spirochete infections to feeding ticks. While a lot is known about the ability of mammals to infect ticks, the role of birds in <i>Borrelia</i> transmission remains less clear. It is also uncertain what effect, if any, <i>Borrelia</i> infection has on infected birds. One way to detect potential negative impacts of infection on birds is to look at various indices of body condition, under the assumption that an infection might interfere with feeding or other basic maintenance activities. We predicted that birds infected with <i>Borrelia</i> would have lower body mass than healthy birds. We caught birds during fall migration from 2015-2018, and collected blood samples and recorded body mass. We used primers for the <i>Borrelia</i> flagellin B gene to detect the presence of</p>

	<p>an infection in blood samples. According to the data, birds with and without <i>Borrelia</i> infections did not differ significantly in body mass. Although that does not mean birds are unaffected by <i>Borrelia</i> infection, we did not see evidence that birds with infection experienced any decline in condition.</p>
25	<p>Testing Parameters in Maxent for SDMs of Natural Papaya Hannah B. Scheppler, Mariana Chávez-Pesqueira and Richard C. Moore</p> <p>Maxent is a user-friendly computer program that is used for species distribution models (SDMs) based on spatially biased presence-only data. There are over ten parameters that can be overridden in Maxent models, yet there is no standard way to test what parameters are best given the specific input data. In fact, most SDM studies that use Maxent do not optimize model parameters, such as regularization multipliers or resampling strategy. Here I developed ways to test what regularization multiplier and resampling strategy to use for modeling the distribution of natural papaya, using spatially biased records collected by my lab. These strategies can be applied to any species presence-only data.</p>
26	<p>A preliminary exploration of local adaptation in common milkweed Angie Martinez, Cassandra Arratia, Andrew McCall and Emily Mohl</p> <p>Monarch butterfly (<i>Danaus plexippus</i>) populations have recently declined throughout the United States, with one of the causes being the scarcity of larval food. One of the main resources used by larvae is common milkweed, <i>Asclepias syriaca</i>. To help increase adult populations, several conservation efforts have included planting <i>A. syriaca</i> in <i>D. plexippus</i>'s adult range. This practice may introduce maladapted <i>A. syriaca</i> genotypes into native populations that are locally-adapted. There is little information on whether <i>A. syriaca</i> is actually locally-adapted. Our study is a preliminary exploration of whether local adaptation occurs in this plant. Seeds from 28 source sites across the U.S. were raised at 19 different recipient sites under greenhouse conditions. We measured leaf number, stem height, and the length of the largest leaf on each plant. There were significant effects of source and recipient site on all variables. There was a significant interaction between source and recipient site for stem height such that some source genotypes did better than others in some sites but not in others. These results suggest that there is a genetic basis for differences in growth measures and that this effect depends on the recipient site, which could lead to local adaptation in <i>A. syriaca</i>.</p>
27	<p>Lyme Disease in Birds from Urban and Rural Areas Kayla Pruitt, Jennifer Driscoll, Shane Andrews, Tham Mana, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p>

Lyme disease is a zoonotic disease that is passed between two animals via ticks. Since Lyme disease is zoonotic it is important to monitor the number of animals, besides humans, that have contracted the disease. This is especially important where birds are concerned because they can migrate much farther than any other species can and can introduce Lyme disease to areas that previously didn't have it. They can also increase the amount of Lyme disease cases in areas where some cases have been reported. This study looked at whether or not Lyme disease is more prevalent in birds around urban areas or rural areas over the past few years (2015-2017). We took blood samples from birds caught in two sites, one urban and the other rural. The urban location was the wooded areas around Rockford University in Rockford, IL, and the rural location was the Severson Dells Nature Center located southwest of Rockford. The initial prediction was that there would be more birds with Lyme disease at the rural location, since there is more suitable tick habitat. However, the results show that there is no significant difference between Lyme disease in rural and urban areas. Birds may be mobile enough to carry Lyme bacteria between areas of high and low tick density.

28 **Effects of chemical composition on plant performance and associated insect communities across *Solidago Canadensis* clones**

Bryan S. Foster, Scott J. Meiners and Thomas Canam

Competition is known to play a major role in the establishment and structure of plant communities, with many plants exhibiting allelopathy to mitigate these effects. *Solidago canadensis*, a native, perennial herb of open habitats in eastern North America, is known to exhibit allelopathic properties. *Solidago canadensis* requires pollination from insects and also supports a diverse suite of herbivores, which may also respond to plant chemistry. To relate chemical diversity/composition to ecological function, we grew 24 different clones of *Solidago canadensis*, within single-clone plots. Chemical composition of each clone was quantified via HPLC. For each clone, foliar insects were assessed three times throughout the growing season with sticky cards and three pollinator surveys were conducted. We measured biomass and stem density as measures of plant performance for each clone, as well as the biomass of non-*Solidago* species within each plot as a measure of competitive ability. NMDS ordinations were conducted on plant chemistry, foliar insects, and floral visitors. Pearson correlations were then conducted to assess relationships between chemical composition, plant performance, floral visitation, and/or foliar insect communities. Plant chemical composition varied dramatically across the 24 *Solidago canadensis* clones represented by three NMDS ordination axes. Plant performance measured by increasing stem density and decreasing light penetration were both associated with chemical NMDS axis 3. However, the biomass of associated species did not vary with plant chemistry. The foliar insect community varied little across clones and was independent of plant chemical composition, with no associations with the chemical NMDS. In contrast, floral visitors did vary across clones and were associated with chemical NMDS axis 1.

	<p>Floral visitors were also associated with the plant performance variables of above ground biomass, flower mass, and light penetration. Though foliar insects appeared to be independent of plant chemistry; plant performance and floral visitors were associated with different aspects of plant chemical composition. This suggests multiple ecological functions of plant chemistry that vary across <i>S. Canadensis</i> clones, altering their performance and associated insects. Future work will include direct competitive trials to explicitly link plant chemical composition to plant-plant interactions.</p>
29	<p>What factors drive insect pollen load quality? Nevin Cullen and Tia-Lynn Ashman</p> <p>Pollen receipt is an important component of plant fitness. Receiving pollen from a plant of a different species (heterospecific pollen) can cause declines in recipient plant fitness, with greater fitness loss associated with heterospecific pollen receipt from a closely related plant species. Occurrence of heterospecific pollen on stigmas is presumed to result from inconstant pollinator foraging behavior, however the extent of pollen diversity on pollinators and the drivers of that diversity are not well understood. We collected and characterized to species pollen carried by bees in a California serpentine wild flower community. We predicted three factors will drive diversity of pollen-loads carried by bees: diversity of flowers present, degree of specialization of the bee, and body size. We quantified floral diversity of bee-capture-sites from field surveys, calculated specialization from a plant-pollinator visitation network, and measured bee size. We modeled pollen load quality using lme4 and compared models using MuMIn in R. Bee pollen loads varied substantially in composition. We characterized pollen loads on 150 individual bees, which carried 1 to 11 pollen species, while bee species carried up to 23 species of pollen. Up to 90% of pollen on individual bees was found to be heterospecific pollen.</p>
30	<p>Learning through education: understanding selection on the flower microbiome by leveraging the classroom Rebecca A. Hayes, María Rebolleda-Gómez, Kristen Butela, Nancy Kaufmann and Tia-Lynn Ashman</p> <p>Flowers function to attract pollinators to effect plant reproduction. Several traits that function to attract pollinators may also alter the floral environment and thus impact microbes that live within them. One such trait is ultraviolet (UV) absorbing patterns on their petals. These patterns are known to guide pollinators but also reduce the UV reflectance of the floral environment. Floral microbes, which are also important in pollinator attraction and plant fitness, are assumed to be sensitive to UV exposure, but how petal UV absorbing patterns shape microbial communities is unknown. Here we developed a robust undergraduate lab curriculum to characterize the culturable petal microbiome of two co-flowering Asteraceae (<i>Helianthus tuberosus</i> and <i>Verbesina alternifolia</i>) that differ in petal UV patterns. We characterized UV patterns using a camera adapted for UV photography and isolated bacteria along the length of the petal</p>

	<p>via plating. We identified 86 putatively unique isolates via colony morphology, to be subsequently confirmed via DNA sequencing. Along with a panel of biochemical tests, we scored survival curves of isolates exposed to UV radiation. Our aim is to determine whether microbial UV tolerance relates to the location or size of petal UV patterns. In addition to teaching students hypothesis testing research design and laboratory techniques, we will leverage the contributions of the hundreds of students in the lab course to construct a uniquely large and continuously enhanced database. This data will have broad implications for understanding how floral color phenotype shapes associated microbial communities and the potential of these microbes for generating selection for petal UV phenotypes.</p>
31	<p>Evaluating the relationship between Microcystis abundance, toxicity, and environmental conditions in Muskegon and Bear Lakes Andrew Pyman and Charlyn Partridge</p> <p>Cyanobacterial blooms are becoming a greater concern in freshwater systems due to their increasing frequency and potential to produce toxic secondary compounds. Microcystis is a common bloom forming cyanobacteria that is capable of creating harmful algal blooms (HABs) through the production of the hepatotoxin, microcystin. HABs can cause many negative effects to the surrounding environment that include scums on surface waters, hypoxia, or unsafe drinking water. The goal of my project is to develop quantitative polymerase chain reaction (qPCR) methods that allow for early detection and quantification of toxic and non-toxic Microcystis strains to aid in the management of water resources. Water samples were collected from Bear and Muskegon Lakes biweekly between July and September 2017. The samples collected during the summer indicate a much higher proportion of non-toxic to toxic cells in both lakes, which is in accordance with similar findings in the literature. We are continuing to explore the relationships among our data and environmental parameters, including: temperature, nutrients, and microcystin concentrations. The development of these qPCR methods will serve as a tool for lake managers to make informed decisions regarding public and environmental health.</p>
32	<p>Ovoviviparous Lizards and Their Offspring Sarah Worthington</p> <p>Female aggression and male-like coloration are not well-studied in squamate reptiles. Female <i>Sceloporus jarrovii</i> (Yarrow's Spiny Lizards) exhibit blue ventral colorations similar to males of the same species. The ovoviviparous females are aggressive towards one another, with a peak in aggression around the parturition season in May and June. This research focuses on the mechanisms leading to and functions of female coloration, aggression, and</p>

	<p>offspring phenotype. Previous research has found changes in population levels of testosterone and corticosterone during the parturition season. We have collected ventral images, morphological data, behavioral observations, and hormone samples from females before and after birthing their offspring in a semi-natural enclosure. We have found that there is a significant effect of reproductive stage on the patch size, patch color, and corticosterone levels of post-gravid females. Offspring of these females remain near their mother immediately after birth and, in time, move away from her. Offspring will closely associate with each other longer than they will associate with their mother.</p>
<p>33</p>	<p>Does Genetic Diversity Lead to Greater Variation in Crops for Sustainable Agriculture? Jenny Trafford and Scott Meiners</p> <p>Diversity is well known in natural systems to buffer plant populations from environmental stressors, herbivores, pathogens and to promote persistence. Less well-studied is whether genetic diversity within crops also provides similar variation across individuals. Chestnut (<i>Castanea mollissima</i> and hybrids) and Hazelnut (<i>Corylus avellana</i> and hybrids) trees are potential alternative crops for sustainable agriculture in the Midwest. This study addresses whether genetically diverse varieties of these crops also possess greater variation in leaf traits (specific leaf area and water content) and growth than genetically uniform varieties. We examined variation across six experimental orchards containing replicated plantings of 5 clonally produced (no diversity) and 3 seedling lines (diverse) for each species. We calculated the coefficient of variation as a measure of variation across individuals, for each trait in each site. For both species, LWC was the least variable trait assessed while growth displayed the most variation. However, seedling and clonal lines exhibited similar ranges of variation rather than the expected higher variation in diverse seedling lines. The lack of systemic variation between the clonal lines and the seedling lines suggests that genetic diversity does not necessarily result in increased variability in these two alternative crop species.</p>
<p>34</p>	<p>Raccoon Behavior in Urban and Rural Environments Bairbre C. Connolly, Kayce M. Miller and Jalene M. LaMontagne</p> <p>Raccoons are highly adaptable mesocarnivores with flexible diets and can thrive in both urban and rural habitats. When establishing home ranges, urban raccoons prefer densely human-populated areas with an abundance of anthropogenic food. As a result of urbanization, raccoons in urban vs. rural habitats may have developed different methods of foraging or socialization, an area where little research has been done. I predict raccoons will be more frequently observed at urban than rural sites, and that urban raccoons will display lower levels of problem solving ability than rural raccoons because food is easily attainable in urbanized areas. Additionally, rural raccoons will move solitarily due to decreased abundance of resources and reduced population density. A novel feeder was erected at 20 sites in the Chicagoland area, in both</p>

	<p>urban and rural environments. A motion-activated camera was used to record behavior, and an ethogram created to catalog raccoon social behavior and problem solving ability. Problem solving ability is determined using the amount of time required for raccoons to retrieve food from the feeder as well as the behaviors used to accomplish feeding (i.e. reaching, climbing). These observations will reveal behavioral differences urban and rural raccoons may have adapted to survive.</p>
35	<p>Does urbanization influence the population trends of European Starlings, Red-headed woodpeckers, and other cavity nesting birds?</p> <p>Jessica Barton and Jalene M. LaMontagne</p> <p>Urbanization results in habitat changes which can be detrimental to the persistence of native species. European starlings (EUST) are an invasive species that benefits from urbanization, and are aggressors that may gain control over tree cavities of cavity-nesting birds, such as Red-headed woodpeckers (RHWO), which have experienced significant population declines over the past several decades. To assess whether EUST impacts are exacerbated in urban regions, we contrasted population trends of EUST and cavity-nesting bird species around Chicago, IL, with surrounding rural regions. Using data from the Christmas Bird Count (1946-2013), Breeding Bird Survey (1966-2013), and Spring Bird Count (1975-2005), we examined the relationships between EUST and cavity-nesting species with Spearman correlations and cross-correlations. Contrary to predictions, more species were positively correlated with EUST than were negatively correlated for all examined surveys, and cross-correlations displayed no evident pattern of EUST populations impacting cavity-nester populations. RHWO declined across every survey set and location, and EUST showed significant declines across three of six surveys. Population indices for EUST and RHWO were consistently lower in urban than in rural surveys. Despite their reputation, EUST have had little demonstrable impact on cavity-nesting birds within our region of study.</p>
36	<p>Comparative Analysis of Microvertebrate Sites from Late Cretaceous Hell Creek Formation</p> <p>Alysia Alfano, Megan Seckinger, James Marshall and Josh Mathews</p> <p>The Hell Creek Formation of the Western United States spans Montana, North Dakota and South Dakota. The fossil-rich mudstone and sandstone depositions are evidence of a prehistoric coastal plain ecosystem that was present 66 million years ago. Microfossils from this formation are often analyzed when determining faunal diversity and abundance. The two microsites analyzed in this study are found in southeastern Montana's Hell Creek Formation. Blair's Sandy Site, a sandstone river deposit and Scott's Microsite, a mudstone, floodplain deposit were dissimilar in their energy levels and therefore, we proposed that the differences in energy would result in different types and relative abundances of fossils. Both microsites revealed a great abundance of Amiidae fish species and ceratopsian species. The Simpson diversity index showed that the high energy river deposit had higher diversity. When organisms common to both sites were</p>

	<p>assessed using the Rank-Order and Spearman's Correlation the sites were found to be positively correlated. This suggests that aquatic microfossils display similar levels of diversity in both high and low energy systems. Further studies may be completed to confirm the diversity of microsites with similar aquatic paleontological environments.</p>
37	<p>No evidence of pollen limitation in the long-lived perennial <i>Echinacea angustifolia</i> Michael LaScaleia & Stuart Wagenius</p> <p>Pollen limitation is the phenomenon where a plant's seed set is limited by the amount of pollen it receives. Pollen limitation can be detrimental to isolated populations of plants, as lack of pollination reduces seedling recruitment and ultimately population size. These deleterious effects of pollen limitation are well documented in annual plants, but they are less clear in long-lived perennials. While a self-incompatible plant receiving no pollen in one year will have low to no seed set for that year, it might receive more pollen the next year, ultimately demonstrating no pollen limitation. It is also possible that modest pollen limitation one year may increase lifetime seed-set in future years due to tradeoffs in resource allocation between reproduction and growth/survival from one year to the next. Here, we attempt to use the long-lived aster <i>Echinacea angustifolia</i> to determine the effects of lifetime pollen limitation in a long-lived, iteroparous perennial. We use 3 groups of <i>E. angustifolia</i> where all heads on each plant in every year had pollen excluded, added, or was unmanipulated. We find that, over the course of 7 years, <i>E. angustifolia</i> is not pollen limited, as seed set was similar between the supplemented and unmanipulated groups. Additionally, pollen limitation did not increase future reproduction investment in <i>E. angustifolia</i>. Unequivocally, some florets that receive pollen on <i>E. angustifolia</i> heads do not have resources allocated to it post-pollination, suggesting that <i>E. angustifolia</i> is either limited by resources or evolutionarily self-limits its seed set through resource allocation regulation to prevent future tradeoffs.</p>
38	<p>Segmentation patterns of the pectoral fin radials in lamnid sharks (Elasmobranchii: <i>Lamnidae</i>) Andres Lafuente S. and Kenshu Shimada</p> <p>Lamniformes (Chondrichthyes: Elasmobranchii) is a relatively small, monophyletic group of sharks consisting of fifteen extant species with diverse life styles and habitat preferences, ranging from macropredatory forms to plankton-feeding forms as well as from shallow coastal forms to deep marine forms. Lamnidae is one of the lamniform families consisting of five macropredatory species: <i>Lamna ditropis</i> (salmon shark), <i>L. nasus</i> (porbeagle shark), <i>Carcharodon carcharias</i> (white shark), <i>Isurus oxyrinchus</i> (shortfin mako shark), and <i>I. paucus</i> (longfin mako shark). In this study, we examined the skeletal patterns in the pectoral fins of these five lamnid species, particularly the segmentation patterns of their radials, based on computed tomographic imaging. In all five species, all major radials are segmented regularly into three sections:</p>

	<p>short proximal and intermediate radials and elongate distal radials. However, long distal radials in <i>C. carcharias</i> are found to be further segmented rather irregularly. Although pectoral fins with more segmented radials are said to be more flexible, the exact functional and evolutionary significance of this previously unreported irregular segmentation pattern in <i>C. carcharias</i> needs further investigation. Lamnids are relatively well-studied shark taxa, but this survey of their pectoral fin skeletons demonstrates that there are still many unknown aspects of their basic biology.</p>
39	<p>Mechanistic Modeling of Evolutionary Dynamics for Phylogenetic Inference Christina Kolbmann B.S. and April Wright</p> <p>Phylogenetic analyses that incorporate extinct data allow for more attachment points to estimate lineage relationships. The fossilized birth-death (FBD) model considers all available data points as part of the same macroevolutionary process of diversification and sampling, enabling fossil records to be fully integrated with extant data points for analysis of evolutionary history. Simulating sampling events from rich fossil records like the ant family Formicidae can be compared to fossil records with sparse data. This pipeline will serve as a subsampling scheme assessment for node age precision.</p>
40	<p>Effects of Food Source on Fatty Acid Composition in Amphipods Alissa Buchta</p> <p>In aquatic organisms, fatty acid composition can be altered by many different abiotic and biotic factors including differences in diet. We conducted an experiment to examine the constraints of the food source effect on omega-3 and omega-6 fatty acid composition a freshwater amphipod (<i>Gammarus</i>). Amphipods were raised on exclusive diets of either algae or leaf material and adults were then assayed for fatty acid composition. Fatty acid methyl ester (FAME) signatures were used to identify which fatty acids were more prevalent in both the individuals raised on algae and the individuals raised on leaf material. We found that the amphipods that had an exclusive algae diet had elevated concentration of omega-3 fatty acids and no omega-6 fatty acids present. It was also found that amphipods on an exclusive leaf material diet had a high concentration of omega-6 fatty acids present and no omega-3 fatty acids present. From the data collected it could be determined that there was a significant difference between the autochthonous and allochthonous data for both the ALA and EPA fatty acids. From the mixing model it could be determined that there is a significant difference between the autochthonous and allochthonous data for both the ALA and EPA fatty acids, indicating that wild</p>

	<p>amphipods have a more varied diet which includes other sources of fatty acids, such as diatoms.</p>
41	<p>Herbicide drift has species-specific effects on wildflowers and alters the timing and abundance of pollinator resources Veronica Iriart, Gina Baucom and Tia-Lynn Ashman</p> <p>When an herbicide volatilizes and drifts beyond the intended crop, it can cause damage to nontarget vegetation, such as the wildflower communities that pollinators forage on. Using the herbicide dicamba as a case study, we grew 11 species of wildflowers from Tennessee, an area where dicamba use is prevalent, and subjected them to dicamba drift (~1% of the field application rate) or the control (surfactant only) in a greenhouse setting to understand how herbicide drift is affecting local plant-pollinator ecology. We found that dicamba drift significantly reduced plant size in four wildflower species, <i>Erigeron annuus</i>, <i>Chenopodium album</i>, <i>Solanum ptycanthum</i>, and <i>Trifolium pratense</i>, but had no effect on <i>Abutilon theophrasti</i>, <i>Ipomoea lacunosa</i>, <i>Mollugo verticillata</i>, <i>Rumex crispus</i>, <i>Lepidium virginicum</i>, <i>Plantago lanceolata</i>, and <i>Daucus carota</i>. Dicamba drift also delayed the day of first flower by 16.7 days and reduced display size of flowers five-fold. Together, our results indicate that the use of dicamba and other volatile herbicides may be shifting wildflower communities through varying species responses to drift, and likewise threatening economically important insects by altering resource availability.</p>
42	<p>Plant chemical defenses, density dependence, and biodiversity in a temperate tree community Emily A. Dewald-Wang, Joseph A. LaManna, Brian E. Sedio, Marko J. Spasojevic and Jonathan A. Myers</p> <p>Explaining the mechanisms that maintain biodiversity is a fundamental goal of ecology. Two proposed mechanisms are intraspecific competition and specialized natural enemies, in which higher densities of conspecifics exert greater negative effects on species' fitness (conspecific negative density dependence, CNDD) than heterospecifics. Both mechanisms produce similar community- and population-level dynamics, requiring disentanglement. We examined variation in leaf chemical defenses among co-occurring tree species to elucidate whether natural enemies determine CNDD and local tree species diversity in a temperate oak-hickory forest. We collected leaves from 220 saplings across 22 tree species in a large, stem-mapped forest dynamics plot and analyzed leaf chemistry with nuclear magnetic resonance (NMR). We used species' chemical dissimilarity to test if specialized enemies increase CNDD and local tree species diversity. Interspecific chemical dissimilarity increased with the strength of species' CNDD, consistent with the hypothesis that more chemically distinct species experience stronger CNDD generated by specialized enemies. Local rarefied-species richness and Shannon's diversity increased with interspecific chemical dissimilarity, consistent with the hypothesis that specialized natural enemies increase local species diversity by limiting densities</p>

	<p>of conspecifics. Our findings suggest an important role for specialized natural enemies in determining density-dependent recruitment and spatial patterns of local biodiversity within temperate forests.</p>
43	<p>Analysis of <i>D. melanogaster</i> Survival on Dietary Sterols, Sterol Metabolism, and Ecdysteroid Production. Scott Martin, Jordan Middleton, Patrick Comerford, Robert Grebenok and Andrew Stewart</p> <p>Sterols are important for all living organisms, but are particularly important in <i>Drosophila melanogaster</i>, because they serve as the base for molting hormones (ecdysteroids). <i>Drosophila</i>, like most other insects, cannot synthesize their own sterols, so must obtain them from their diet. Previous research indicated that cholesterol was optimal, while other sterols either only supported limited growth, or were insufficient for development. Here we present the results of an extended trans-generation study, where we demonstrate that 1) two different dietary sterols (β-sitosterol & ergosterol) support superior growth and survivorship, 2) these sterols are readily taken up, and 3) are converted to ecdysteroids. While these results run counter to established dogma, they are congruent with <i>Drosophila</i> life-history and standard laboratory diets. Our hope is that by understanding sterol needs of insect models, it may be possible to genetically modify plants, in order to make them pest resistant.</p>
44	<p>Nanoplankton Ecology of the Arabian Sea Shawn Gibford and Amos Winter</p> <p>Phytoplankton is the foundational feature of all marine ecosystems and a critical component of the global biogeochemical cycle. To gain further insight into these systems it is necessary to understand the ecology of organisms that support them, in particular, the nanoplankton (5 to 20 μm) community which are comprised primarily of coccolithophores. Our research is an attempt to quantify and categorize nanoplankton by depth in the photic water column throughout the Arabian Sea and near-shore India. Local and seasonal climate anomalies control the dynamic interactions among nanoplankton and changes in their environment. Coccolithophores live in all oceanic habitats but their distribution and ecological dynamics in warmer water with lower nutrient availability such as the Indian Ocean has seldom been studied. Samples of ocean water from targeted depths from the surface to 125 m were filtered on site and shipped to Indiana State University for further examination. Nanoplankton were observed with a Scanning Electron Microscope (SEM) to be appropriately analyzed. Subsamples were taken and coated in a thin layer of gold and then viewed under the SEM. Examination occurred under magnifications from 1 to 40 kx for accurate identification and morphometric studies of species. Once the initial analysis is complete, an ecological and population distribution model is created. This project interlinks many fields of study, including ecological dynamics and</p>

	environmental change. Understanding nanoplankton community structures and dynamics is critical in the biogeochemical cycling of carbon.
45	<p>Relative sizes of olfactory, optic, and otic regions of the skull in lamniform sharks, and their ecological implications Nora Westman and Kenshu Shimada</p> <p>Lamniformes is a group of sharks (Chondrichthyes: Elasmobranchii) that display diverse habitat preferences and life history strategies, including macropredatory goblin, sandtiger, crocodile, thresher, porbeagle, mako, and white sharks and plankton-feeding megamouth and basking sharks. Based on radiographic images of museum specimens and published illustrations, we examined the proportion of the anteroposterior length of the olfactory, optic, and otic regions with respect to the neurocranial length excluding the rostrum in each extant lamniform species as proxy of relative importance of each sensory region to the ecology and lifestyle of each lamniform species. Our preliminary quantitative data suggest that plankton-feeding lamniforms have large olfactory and otic regions relative to those of macropredatory forms. Although species that are commonly caught in deep waters tend to have large optic region, the trend was found not to be universal. While exceptions do exist and the functional significance of our data need further investigation, the fact that certain neurocranial characteristics in lamniforms appear to be correlative to their ecology provides another dimension to the consideration for the evolution of lamniform sharks as well as their conservation biology if the sea-level continues to rise or types of food resources shifts due to climate change.</p>
46	<p>Mast seeding synchrony and tree fate during an insect defoliator outbreak Abigail C. Leeper and Jalene M. LaMontagne</p> <p>Mast seeding is the spatially synchronous and temporally variable production of seed crops by populations of perennial plants. The ultimate hypotheses for this reproductive phenomenon are primarily described as predator satiation or increased pollination efficiency. Based on these, asynchronous individuals are thought to have reduced fitness. Despite mast seeding being described as synchronous within populations, a large amount of individual reproductive variation has been recorded in tree populations, leading to the question of the possible benefits of asynchrony. In the event a predator is attracted to regions with synchronous reproduction, such as eastern spruce budworm (SBW), mast seeding synchrony may not be beneficial. We test the hypothesis that levels of reproductive synchrony in white spruce are related to the defoliation level by SBW. Since 2012, 308 trees have been monitored for cone production in northern Wisconsin, with 2013 identified as a mast year. In 2014, we detected a SBW outbreak, impacting at least 176 trees. Since 2014, 20% of study trees have died. Implications of population-level synchronous events and SBW defoliation will be discussed in terms of both its ecosystem and evolutionary significance.</p>
47	<p>Function of juvenile color in a cichlid fish Benjamin Prindle, Daniel Licari, Carlos David Santos and Hugo F. Gante</p>

	<p>Animals communicate using a variety of signal modalities, including visual signals. Juvenile coloration frequently differs from that of territorial adults for reasons that have been attributed to lowering adult aggressiveness, thus allowing for prolonged coexistence in the same territory. We found that adults <i>Variabilichromis moorii</i> are more aggressive to black dummies relative to yellow dummies, irrespective of dummy size. Our results suggest that 'black' is a reliable signal and point to additional hypothesis of why juvenile and adult color differs.</p>
48	<p>The Effects of <i>Alliaria petiolata</i> (Garlic Mustard) Invasion on Mycorrhizal Fungi Colonization in Areas of Conservation Efforts</p> <p>Maria L. Taylor and Andrew C McCall</p> <p><i>Alliaria petiolata</i> is an incredibly successful invasive in U.S. forest understories. One key component to its success is its release of allelochemicals, preventing mycorrhizal fungi colonization in seedlings. This study compares mycorrhizal fungi colonization percentages of <i>Acer rubrum</i> roots in areas of previous conservation efforts and current invasion throughout the Denison University Biological Reserve. Six sites, three with a history of <i>A. petiolata</i> removal and three currently invaded sites, were sampled. Within each site, ten <i>A. rubrum</i> seedlings were collected, cleared and stained. Colonization percentage was scored using the magnified intersections method. Intersections were examined for hyphae, vesicles and arbuscules. Comparing one removal site sample to one current invasion site sample revealed higher root percentage colonization in the removal site sample. Higher hyphae and vesicle percentages were seen in removal site samples, though invaded site samples showed a higher arbuscule percentage. Preliminary results indicate a positive trend in mycorrhizal associations after removal of <i>A. petiolata</i>. Going forward, genetic analysis of mycorrhizal fungi diversity and spore percentages present in soil could lend to a more complete picture of conservationist efforts. Ultimately, this study begins to document effects of mycorrhizal associations after conservation efforts have removed <i>A. petiolata</i>.</p>
49	<p>Morphometric variation of teeth in the extant megamouth shark, <i>Megachasma pelagios</i>, and its paleontological implications</p> <p>Alexandra Krak and Kenshu Shimada</p> <p><i>Megachasma pelagios</i> (Lamniformes: Megachasmidae) is a large filter-feeding fish with a dentition commonly characterized as 'homodont.' We used geometric morphometrics to investigate whether or not sufficient variation in tooth morphology exists in <i>M. pelagios</i> that may aid in reconstructing the dentition of <i>M. applegatei</i>, a fossil (late Oligocene–early Miocene) megachasmid known only from isolated teeth. We examined the upper right and lower right dental series of the holotype of <i>M. pelagios</i> where each dental series was divided into the 'mesial half' and 'distal half' to determine if teeth of the four groups can be distinguished</p>

	<p>quantitatively. Our analysis shows two distinct clusters of plots, one consisting of upper teeth, and another, lower teeth. Within each cluster, mesially-located teeth are found to be morphologically less variable than distally-located teeth. Ten randomly selected teeth of <i>M. applegatei</i> in a museum collection preliminarily plotted with teeth of <i>M. pelagios</i> not only show that the two megachasmids are morphometrically distinct, but also that teeth of <i>M. applegatei</i> exhibit a wider morphological range than those of <i>M. pelagios</i>. More remarkably, two clusters similar to those seen for <i>M. pelagios</i> are also recognized for <i>M. applegatei</i> that may reflect the difference between upper and lower teeth.</p>
50	<p>The effect of fungicide on root and leaf associated fungi in Glycine max.</p> <p>Terri Billingsley Tobias, Matthew Gooch, Winthrop Phippen and Andrea Porras-Alfaro</p> <p>The environmental impacts of traditional agriculture are a growing concern. The purpose of this project is to examine the fungal communities associated with Glycine max roots and leaves both pre and post-fungicide application using Illumina sequencing. A total of 3,627,618 sequences were generated from 71 samples of soybean roots and leaves. After quality filtering, 2,229,197 sequences were used to define Operational Taxonomic Units (OTU) resulting in 1990 OTUs. Forty-one percent of the fungal sequences belonged to the phylum Ascomycota this was followed by 6.4% in Basidiomycota. Preliminary results suggest changes in dominant fungi in roots and leaves after fungicide application. An unknown taxon of fungi in roots accounted for 43% of total fungal sequences prior to fungicide treatment. After fungicide application this taxon decreased significantly (8%) and <i>Fusarium</i> increased representing 32% of the sequences. In leaves <i>Didymella</i> (21.5%) was the most abundant fungal genus before fungicide use however after fungicide this fungal genus decreased to 1% and <i>Plectospharella</i> (10%) became the most abundant fungi. Fungal-plant interactions are a delicate and complex balance in a range of mutualistic to parasitic interactions. Understanding these interactions and the indirect impacts of fungicide on community composition will provide important insights into plant health.</p>
51	<p>Quantitative feeding patterns in <i>Daphnia magna</i> using fatty acid mixing models</p> <p>Maria Butler and Jonathan O'Brien</p> <p>We conducted a laboratory study to evaluate the effects of diet on the lipid composition of <i>Daphnia magna</i>. <i>Daphnia</i> cultures were raised under three dietary conditions: yeast pellets, algae, and a spectrum of mixed diets. After raising the <i>Daphnia</i>, we used laboratory techniques to extract the lipids and converted them to fatty acid methyl esters (FAME) to analyze the composition of fatty acids present. We then created mixing models to predict feeding composition of mixed diet cultures. We found that <i>Daphnia</i> grown under single food sources differed in percent composition of three polyunsaturated fatty acids (18:2n6, 18:3n2, and 20:5n3). We also found that a principle component axis of</p>

	fatty acid composition provided the most consistent basis for mixing model when compared with models based on single fatty acids.
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1	<p>Dung Beetle Resource Preference Within a Landscape Matrix Sheryl Hosler</p> <p>The reintroduction of large grazing herbivores has been recognized as an important management technique for restored tallgrass prairies, with priority being placed on the reintroduction of American bison to these areas to serve in their role as ecosystem engineers. However, there are many technicalities that make it difficult for land managers to consider bison a feasible option for their projects, so domestic cattle have been considered as an alternative. Restoration management must consider all trophic levels in an ecosystem, including mutualists that may have co-evolved with these large grazing herbivores. I tested whether the dung beetles in a restored tallgrass prairie community showed preference for bison dung over the dung of several common domestic agricultural animals using a series of pitfall traps baited with various types of dung. The dung beetle community in this prairie seems to be dominated by a generalist species, most likely due to the loss of bison in many parts of their historic range. However, at least once bison dung specialist still remains in this prairie community, signaling that preferential reintroduction of bison over domestic cattle in prairie restorations will promote diversity within the decomposer community.</p>
2	<p>Seed predation in tallgrass prairies changes throughout the year and is affected by litter cover Genevieve Anderegg, Jonathan Henn and Ellen Damschen</p> <p>Tallgrass prairie is one of the most threatened habitats in the Midwestern United States, with less than 1% of original native prairie remaining in small and isolated patches. Small mammal seed predators are important aspects of these communities, as they influence plant recruitment and structure by consuming seeds and plant matter. However, there has been little to no research on the effects of varying levels of plant litter longitudinally throughout all seasons on seed predation intensity. We seek to measure the impact of management decisions like burn timing and mowing on rodent seed predation in a restored tallgrass prairie. Seed predation was quantified monthly (June-May) with a giving up density model using native <i>Sorghastrum nutans</i> seeds in plots that were subjected to either a spring burn, fall burn, fall mow, or unmanipulated control to alter plant litter levels. We found that seed predation was lowest during the summer and increased into the fall. Burning and mowing resulted in significant reductions ($p < 0.001$) of seed predation during a time when seed predation was otherwise very high in the control plots. This informs how prairie restoration and management decisions like prescribed fire timing and mowing affect seed predation intensity in restored prairies.</p>
3	<p>Body shape diversity in dogfish sharks (Elasmobranchii: <i>Squaliformes</i>) Phillip Sternes and Kenshu Shimada</p> <p><i>Squaliformes</i> (dogfish sharks) is a large elasmobranch order with six families (Centrophoridae, Dalatiidae, Etmopteridae, Oxynotidae, Somniosidae, and Squalidae) and over 100 species. A previous study suggested that all squaliforms share one basic body plan unlike most other shark orders that exhibit body</p>

	<p>shape diversity. We used landmark-based geometric morphometrics to investigate if Squaliformes is indeed represented by only one body plan. We examined the outline of all extant squaliform species in lateral view and conducted three separate analyses: (1) a full body analysis (precaudal body + caudal fin), (2) precaudal body analysis, and (3) caudal fin analysis. Our results indicate each family represents its own body plan. Centrophoridae has the most generalized body form within Squaliformes characterized by a moderately narrow body with the first dorsal fin just above the pectoral fin origins. Etmopteridae, Squalidae, Somniosidae, and Oxynotidae are similar to Centrophoridae, but each family tends to have a slightly different first dorsal fin position and body depth from others. Dalatiidae shows the greatest body form variation within Squaliformes. Our study shows that, whereas the caudal fin is more morphologically conservative than the precaudal body in Squaliformes, the entire shark order is indeed represented by only one basic body plan.</p>
4	<p>Effects of urbanization on stress responses in Eastern Garter Snakes Elizabeth Rock, Jeffrey Bartman, Jamie Cornelius and Katherine Greenwald</p> <p>Urbanization affects both abiotic and biotic component of the environment. Altering landscapes from natural states to urban states results in changes to microclimate, input of pollutants, and disruption of ecosystem function, all of which may increase stress on organisms in these areas. Stress metrics of individual animals may be an indicator of how likely a population is to persist, which can inform our understanding of species living in urban environments. Corticosterone (CORT) is a hormone produced in response to life history circumstances, daily demands, and stressful events. Chronic or long-term stress stimuli can alter the baseline status of CORT in the blood. This study will measure physiological stress response (CORT levels) and physical health metrics (body condition) in Eastern Garter Snakes (<i>Thamnophis sirtalis</i>) along an urban-rural gradient, with the goal of assessing whether the magnitude of this effect varies over time (e.g., decreased HPA axis sensitivity). <i>T. sirtalis</i> is a generalist species commonly found across the eastern United States in a variety of habitats, ranging from meadows to urban areas. We predict that snakes in urban areas will have increased CORT when compared to rural snakes. We further predict that snakes with higher baseline CORT will have poorer body conditions related to urban stressors.</p>
5	<p>Structural Approach to Understanding Restoration Management Effects on Prairie Community Composition Rebecca Stelzer, Nick Barber and Holly Jones</p> <p>In a prairie community, species diversity and richness can be influenced by bison and fire. Burning the prairie in the spring may increase the abundance and diversity of grass species but decrease the diversity and richness of forbs. Having bison graze on the site after it is burned can increase the species diversity and richness of the flowering plants because bison graze mostly on the grass. This study looks at understanding restoration management effects on the prairie community composition by using data from Robel pole measurements and PAR</p>

	<p>Light level percentages. Bison play a more significant role than fire, but both bison and fire influence the composition of the prairie. When bison and fire were used on a site the vegetation density of that site was lower than if bison and fire were not used. It is important to have plant density and diversity in the prairie community to support the small mammal and insect communities.</p>
6	<p>A new skeleton of an ichthyodectiform fish (Osteichthyes: <i>Actinopterygii</i>) from the Upper Cretaceous Woodbine Formation of Texas Riley Hacker and Kenshu Shimada</p> <p>DMNH 20149 is a 96-million-year-old fossil skeleton of a nearly complete, articulated bony fish housed in the Perot Museum of Nature and Science in Dallas, Texas, USA. It was found from the Arlington Member of the Woodbine Formation (mid-Cenomanian) in Denton County, Texas, where it was a nearshore environment along the southeastern shoreline of the Western Interior Seaway. The specimen presently exposes the right lateral side and measures about 39 cm and 50 cm in standard length and total length, respectively, and about 11 cm in maximum body depth with a fusiform body plan. The vertebral column is nearly complete with a total vertebral count of at least 49, but no more than 55. The overall skeletal characteristics, including the total vertebral count, suggest that it belongs to an extinct actinopterygian order Ichthyodectiformes. DMNH 20149 possesses a triangular dentary that is typically found in Jurassic ichthyodectiforms, unlike Cretaceous forms characterized by a rectangular dentary. The exact taxonomic identity of DMNH 20149 within Ichthyodectiformes remains uncertain at the present time, but another notable feature is its toothlessness, making the fossil fish to superficially resemble the extant Atlantic tarpon, <i>Megalops atlanticus</i> (Actinopterygii: Elopiformes).</p>
7	<p>Peculiar dental pattern of the Late Cretaceous durophagous shark, <i>Ptychodus marginalis</i> Amanda Alt and Kenshu Shimada</p> <p><i>Ptychodus</i> (Elasmobranchii: Ptychodontidae) is a Cretaceous shark genus that had specialized dentitions suited for crushing shelled animals. UNSM 1196 and 123608 are associated dental remains of <i>P. marginalis</i> housed in the University of Nebraska State Museum, Lincoln, Nebraska. Their locality data are missing, but they most certainly came from the upper part of the Greenhorn Limestone in southeastern Nebraska, where it was the middle of the Western Interior Seaway during the Late Cretaceous. The combination of data from these specimens reveal that, in <i>P. marginalis</i>, the upper dentition consisted of one medial tooth row and possibly as many as 13 lateral tooth rows on each side, whereas the lower dentition consisted of one medial tooth row and up to only about six tooth rows on each side. Unlike <i>P. decurrens</i>, <i>P. mortoni</i>, and <i>P. occidentalis</i> that have flat tooth plates, UNSM 1196 and 123608 show that teeth of <i>P. marginalis</i> in both the upper and lower dentitions were arranged in a whorl. Although the arrangement of each tooth whorl on the jaw cartilage and the functional significance of the unique whorl pattern need further investigation, UNSM 1196</p>

	<p>and 123608 are important to discern the paleobiology and paleoecology of <i>P. marginalis</i>.</p>
8	<p>Pollen in The Bank: Does pollen removal and deposition by four native bee taxa differ in a prairie perennial? Evan X. Jackson, Zeke Zelman and Jennifer L. Ison</p> <p>Pollination failure is a major problem for many natural plant populations and has been exacerbated by habitat fragmentation and declines in pollinator populations. This study measured pollinator visitation and per visit pollen removal and deposition, across common pollinator taxa to provide insight into pollination failure in the focal population of the native composite <i>Echinacea angustifolia</i>, in the Western Minnesota prairie. We collected samples of male and female phase florets from <i>E. angustifolia</i> flowerheads, before and after observed pollinator visits during the summer of 2018. In the fall at the College of Wooster, the number of pollen grains in these samples were quantified to determine how much pollen each taxon of pollinator removes and deposits per visit. These observed visits provided a measure of each pollinator taxon's relative visitation to the population. We found that the composite specialist <i>Andrena rudbeckiae</i> removes more grains of pollen per visit than the other common pollinator taxa in the study area; namely, male <i>Melissodes</i> sp., <i>Augochlorella</i> sp., and 'small black bees,' a wide taxonomic group comprising a variety of species mostly in the Halictidae. Pollen limitation in the population could be driven by frequent male <i>Melissodes</i> sp. visitation late in the season; based on the per visit removal of male <i>Melissodes</i> sp. and number of visits observed in this study. These results combine to contribute to our understanding of pollination failure and pollen limitation in small fragmented flowering plant populations, and the selective pressures that pollinators exert on these population.</p>
9	<p>Little Cost of Reproduction in the Long-Lived Perennial, <i>Echinacea angustifolia</i> Tristram O. Dodge, Michael J. LaScaleia, Lea K. Richardson and Stuart Wagenius</p> <p>Landscape fragmentation, changing fire frequency, and decreased pollinator abundance are exacerbating pollen limitation in tallgrass prairies. However, according to the cost of reproduction hypothesis, present pollen limitation might lead to increased growth or fitness of perennial plants in years following pollen limitation. To address how present pollen availability affects tallgrass prairie plants' future outlook, we compared important growth and fitness traits of <i>Echinacea angustifolia</i> (Asteraceae), a long-lived, self-incompatible, iteroparous forb. Beginning in 2012, <i>Echinacea</i> (n=58) were randomly assigned to one of three groups: pollen addition, pollen exclusion, and an open pollinated control. In contrast to the cost of reproduction hypothesis, we found that the pollen exclusion and the pollen addition treatments had mixed effects on future growth and fitness in <i>Echinacea</i>, compared to the open control. Pollen exclusion did not affect <i>Echinacea</i> in consistent or predictable ways, suggesting that current pollen limitation will not enhance <i>Echinacea</i> growth or fitness in future years. Lack of pollination treatment effects could be because <i>Echinacea</i> is not resource limited or because seed production is inexpensive compared to generation of the large</p>

	<p>floral reproductive structure and achenes. Future studies should quantify the extent of pollen limitation in <i>Echinacea</i> and in other threatened tallgrass prairie species.</p>
10	<p>What to eat when you live in manure: wasps that parasitize filth flies Elizabeth Taylor and B. H. King</p> <p>Parasitoid wasps are an important component of the rich invertebrate communities in decaying organic matter at livestock facilities. However, little is known about what adult parasitoids eat there. Most parasitoid wasps in the world parasitize herbaceous insects, so nectar from flowers is readily available. But what do adult parasitoids in large accumulations of manure eat? The present study examined feeding by adult <i>Spalangia cameroni</i>, a species which burrows through manure, where it finds the pupal stage of filth flies to parasitize. Feeding on host fluids occurs in many parasitoid wasps, including <i>S. cameroni</i>. In the laboratory these wasps also readily feed on honey or a sucrose solution, which increase their longevity. We are looking at three potential non-floral food sources: milk, manure, and sorghum silage compared to water and honey. Parasitoids were food-deprived for two days and then placed into an 8 oz jar with the potential food source and water provided ad libitum. Mortality was checked every 24 hours. Later tests will examine longevity with dandelions, buckwheat, and sweet alyssum. Knowing what these parasitoids eat may allow food supplementation, which may help the parasitoids control pest flies.</p>
11	<p>How many pollen grains does it take to set a seed in <i>Echinacea angustifolia</i>? Mia Stevens, Nate Scheerer and Jennifer L. Ison</p> <p>Over 90% of flowering plants rely on insect pollinators for sexual reproduction. Pollination biologists often quantify pollinator effectiveness by counting the number of pollen grains a pollinator deposits on a plant's stigma in a single visit. However, flowers in one of the biggest plant families, Asteraceae, are uniovulate, meaning that there is just one ovule per style. Therefore, it theoretically only takes one viable pollen grain to fully set seed in an ovary, so this standard method of quantifying pollinator effectiveness may not be appropriate for members of the Asteraceae. In our study, our objectives were to determine how many pollen grains are necessary to set a seed in <i>Echinacea angustifolia</i>, a species in the Asteraceae. We performed 60 hand crosses at varying levels of pollen deposited. Each cross consisted of nine total styles of which three were removed before the cross to get estimates of self-pollen deposition and six styles were crossed with pollen from other flowering individuals. Styles were then collected and stained using fuchsin gel and number of pollen grains presented were counted using a compound microscope. The achenes, fruits, from the crosses were x-rayed to determine if a seed was present. Preliminary data shows that seed set varies based on by pollen grains deposited. These data will aid in advancing our understanding of pollinator effectiveness in uniovulate plants. By increasing our understanding of pollinator efficiency in the Asteraceae, we can better predict the consequences of pollinator declines in fragmented habitats, such as the North American tallgrass prairie.</p>

12	<p>Hydraulic Traits in Epiphytic <i>Elaphoglossum</i> ferns from Puerto Rico Mary Pitts, Gary K. Greer and Jennifer Winther</p> <p>Tropical rainforests have the highest biodiversity of plants and animals in the world including the largest and most diverse community of epiphytes. To further our understanding of hydraulic traits that potential causes niche differentiation in these epiphytic communities, we conducted an anatomical study of eight species of the epiphytic fern <i>Elaphoglossum</i>. We collected our samples from the lower-trunk community in El Yunque National Forest, Puerto Rico. Hydraulic traits (including xylem diameter, parenchymatous path length, and meristele area) in the lamina, stipe, and rhizome were measured in each of the eight species based on sectioned plant material. Preliminary results show that hydraulic traits in the lamina and stipe for all species are similar; however, there was considerable variation in rhizome traits for all species.</p>
13	<p>Native <i>Echinacea angustifolia</i> has depressed viability relative to non-native <i>E. pallida</i> and reciprocal hybrids (<i>E. angustifolia</i> x <i>E. pallida</i>) in a fragmented prairie habitat Riley Thoen, Pamela Kittelson, Sanjive Qazi, Stuart Wagenius</p> <p>Introduced plants can alter population dynamics of native congeners and facilitate change to community structure. This is exacerbated if the introduced species and its native congener are able to form hybrids. The long-lived tetraploid forb <i>Echinacea pallida</i> was introduced to severely fragmented prairie in Douglas County, MN, where it has formed hybrids with the native, diploid <i>E. angustifolia</i>. To determine viability of the native coneflower relative the introduced crosses, we measured survival and above-ground morphology of intraspecific and reciprocal interspecific crosses of <i>E. angustifolia</i> and <i>E. pallida</i> for five years. We also recorded photosynthetic rate, water use efficiency, and leaf thickness all living basal plants in 2018. <i>E. angustifolia</i> intraspecific crosses had the lowest survival, morphology, and ecophysiology values compared with all other cross types; <i>E. pallida</i> intraspecific crosses almost always had the highest values. In nearly all categories, <i>Echinacea</i> hybrids displayed intermediate phenotypes of pure <i>E. angustifolia</i> and <i>E. pallida</i>. These results suggest that the genomes of <i>E. angustifolia</i> and <i>E. pallida</i> combined in an additive manner when forming hybrids. With increased viability over the pure native cross type, plants with a non-native <i>E. pallida</i> parent may be able to harm the already-decreasing population of <i>E. angustifolia</i> in Douglas County, MN. Management should be undertaken to eliminate mating bouts of <i>E. angustifolia</i> and <i>E. pallida</i>.</p>
14	<p>Calcification level in vertebrae of thresher sharks (Lamniformes: <i>Alopiidae</i>), and its behavioral implications Luke A. Banta and Kenshu Shimada</p> <p>Thresher sharks (<i>Alopias</i>) have an exceptionally elongated caudal fin and consist of three species: <i>A. pelagicus</i>, <i>A. superciliosus</i>, and <i>A. vulpinus</i>. <i>Alopias pelagicus</i></p>

	<p>and <i>A. vulpinus</i> have a unique hunting strategy in which they come to a sudden stop near the schooling fish, allowing their elongated caudal fin to swing over the head as a whip, to stun and capture their prey. On the other hand, the exact hunting strategy remains unknown for <i>A. superciliosus</i> that has a stouter, less flexible caudal fin compared to <i>A. pelagicus</i> and <i>A. vulpinus</i>. To further decipher the hunting method of <i>A. superciliosus</i>, we examined the level of calcification in their vertebrae using computed tomography (CT) images of preserved museum specimens of each species. Our preliminary results show that the vertebrae of <i>A. superciliosus</i> are less calcified than the vertebrae of <i>A. pelagicus</i> and <i>A. vulpinus</i>. This observation suggests that the vertebrae of <i>A. superciliosus</i> are built to allow for more bending of the body that, in turn, likely indicates that <i>A. superciliosus</i> flexes its body sideways to swing its relatively stout, inflexible caudal fin laterally for hunting, rather than over the head like <i>A. pelagicus</i> and <i>A. vulpinus</i>.</p>
15	<p>Fire predictably modifies fungal community structure and successional trajectory across ecosystems Jacob Hopkins and Benjamin A. Sikes</p> <p>Fire is an increasingly common disturbance that alters ecological processes like nutrient cycling and community dynamics. The extent of fire's effect on these processes is largely governed by the amount and quality of plant fuel loads. Plant fuel loads are modified by fungi both directly through decomposition and indirectly through plant diseases and mutualisms, yet fungal roles in fire regimes are poorly understood. We hypothesized that fire would shift fungal community structure similarly across ecosystems, and that these changes would correlate with environmental factors. Following prescribed fires in a tallgrass prairie and longleaf pine savanna, we assessed both fungal communities and edaphic factors over time. Fire filtered fungal communities, making burned communities more similar to one another than unburned communities. Fire-driven shifts in communities occurred at the species level, rather than at higher taxonomic levels (phylum & class). Communities also changed with time, and fire modified this post-fire succession. Additionally, C:N ratio was a good predictor of fungal community structure. Fungal communities differed among systems (prairie and savanna), and fire impacts on those communities likewise differed. These results show that fire changes fungal community succession, which may alter fungal modification of plant fuels that are available for future fires.</p>
16	<p>How does restoration and management techniques (prescribed fire and bison grazing) affect carbon and nitrogen cycling in prairie Angelica Bautista</p> <p>As we prepare to mitigate climate change, ecologists are looking into ways of sequestering carbon in a sustainable manner. Restored prairies can be used to create carbon sinks to offset ever increasing CO₂ emissions. In this study we looked into how different restoration and management techniques affected the levels of nitrogen and carbon in prairie vegetation. Samples were collected from tallgrass prairie sites at Nachusa Grasslands. Sites at this location vary in age of</p>

	<p>restoration, presence of bison, and use of prescribed fire as restoration management techniques. Grass and forb leaf samples were collected from 15 sites. Leaf samples from 10 different species in each site were collected, weighed, and ground. Isotope analyses were performed on the ground samples to find levels of nitrogen and carbon. The presence of bison was shown to increase nitrogen levels in grasses and forbs as a result of nutrient deposition from the bison. Increase in age and use of prescribed fire resulted in an increase in carbon in both grasses and forbs.</p>
17	<p>Late Cretaceous marine vertebrate fauna from the Juana Lopez Member of the Carlile Shale in southeastern Colorado Daniela Garza, Bruce A. Schumacher, and Kenshu Shimada</p> <p>The Juana Lopez Member of the Carlile Shale is a calcarenite deposit formed along the Western Interior Seaway of North America during the Late Cretaceous approximately 90 million years ago. Rock samples were collected from a Juana Lopez locality in southeastern Colorado to examine the taxonomic composition of vertebrate fossils by dissolving the calcarenite with a weak acid. Although almost all the specimens are represented by isolated bones and teeth that are microscopic, the paleofauna is found to be taxonomically diverse. It so far includes at least seven chondrichthyan (<i>Ptychodus whipplei</i>, <i>Cretodus crassidens</i>, <i>Scapanorhynchus raphiodon</i>, <i>Squalicorax</i> cf. <i>S. falcatus</i>, <i>Rhinobatos incertus</i>, <i>Ptychotrygon</i> sp., and <i>Ischirhiza texana</i>) and six osteichthyan fishes (e.g., <i>Hadrodus</i>(?) sp., <i>Micropycnodon kansasensis</i>, <i>Pachyrhynchodus</i> sp., <i>Enchodus gladiolus</i>, <i>E. petrosus</i>, and <i>E. shumardi</i>). It also includes two marine reptiles (<i>Coniasaurus</i> and <i>Plesiosauria</i>) and at least one toothed bird taxon (<i>Ichthyornis</i> sp.). Teeth of <i>Enchodus</i> spp. are the most abundant vertebrate remains. The fossil assemblage also includes multiple teeth of <i>Ichthyornis</i>, along with teeth of <i>Ptychodus whipplei</i> and <i>Scapanorhynchus raphiodon</i> commonly found in mid-Turonian nearshore deposits, suggesting that the western shoreline of the Western Interior Seaway must have been close from the location.</p>
18	<p>Pectoral fin musculature of the three species of thresher sharks (Lamniformes: Alopiidae) Cecil A. Phibbs and Kenshu Shimada</p> <p><i>Alopias</i> (thresher shark) is a shark genus with three species, <i>A. pelagicus</i>, <i>A. superciliosus</i>, and <i>A. vulpinus</i>, characterized by an exceptionally elongated caudal fin. The hunting strategy of <i>A. superciliosus</i> is uncertain. However, a unique strategy is known for the other two species where they come to a sudden stop near the schooling fish, allowing their elongated caudal fin to swing over the head to strike and capture their prey. At or immediately prior to the sudden stop, at least <i>A. pelagicus</i> is known to significantly adduct its pectoral fins. We examined the pectoral fin musculature of the three <i>Alopias</i> species to look for any differences among them that may shed light on the behavior of <i>A. superciliosus</i>. We discovered that, from the pectoral fin base, the levator pectoralis is directed anterodorsally in <i>A. pelagicus</i> and <i>A. vulpinus</i>, whereas that</p>

	<p>of <i>A. superciliosus</i> posterodorsally. In ventral view, the main depressor pectoralis is directed posterolaterally from the medial part of the pectoral girdle at higher angles (20–60°) in <i>A. pelagicus</i> and <i>A. vulpinus</i> than <i>A. superciliosus</i> (5–20°). These observations at least indicate that the pectoral fins in <i>A. superciliosus</i> must operate quite differently from <i>A. pelagicus</i> and <i>A. vulpinus</i>.</p>
19	<p>The influence of <i>Andropogon gerardii</i> (big bluestem) on beta diversity and possible combined effects with climate change Julia Armitage</p> <p>Dominant species have a large influence on the biodiversity within ecosystems by creating a biotic filter; this tends to decrease the overall species diversity due to competition, however the influence on beta diversity is not well understood. Climate change may alter the strength of this biotic filter, but effects on alpha and beta diversity are also unclear. <i>Andropogon gerardii</i>, a common dominant species in restored tallgrass prairies, suppresses alpha diversity and richness and may be better adapted than other species to climate warming. I am testing three hypotheses in field and greenhouse experiments: 1: If <i>A. gerardii</i> is a strong competitive filter, then it will reduce alpha and beta diversity. 2: If climate change is a strong environmental filter, then it will reduce alpha and beta diversity. 3: If global climate change negatively influences other species, while having little to no effect on <i>A. gerardii</i>, then we will observe even lower alpha and beta levels. Preliminary data from a 2-year-old prairie experiment shows no effect of <i>A. gerardii</i> on diversity, but I expect effects to emerge as <i>A. gerardii</i> becomes more dominant. Results from my proposed work can help resolve effects of dominant species on diversity and how climate change may disrupt these patterns.</p>
20	<p>Ecological Stoichiometry of Neotropical Fishes Along Elevation Gradients of the Andes Mountains Jessica Vaclav and Windsor Aguirre</p> <p>Phosphorus and nitrogen are typically the most common limiting nutrients in freshwater ecosystems, where fish play important roles in the cycling of these nutrients. Variation among fish families indicates there is likely significant variation in the roles that different groups of fishes play in nutrient cycling. However, there is still much to be learned about nutrient cycling in tropical aquatic ecosystems. We aim to determine how phosphorus and nitrogen contents change in Neotropical stream fishes along elevation gradients of the Andes Mountains of western Ecuador, a region with very high endemism and under severe anthropogenic pressure. To do this, we collected freshwater fishes from ten sites located between approximately 72 and 935 meters above sea level in four rivers. Total carbon and nitrogen are being measured from ground whole specimens using a CE Elantech Flash EA1112. Phosphorus is being measured using a sulfuric acid digestion of ashed fish and analyzed through colorimetry. I hypothesize that nutrient ratios will change along elevation gradients and that they will differ significantly among taxonomic families of freshwater fishes.</p>

	<p>These are the first data on the ecological stoichiometry of freshwater fishes from western Ecuador.</p>
21	<p>Lyme Disease in Migratory vs. Resident Birds Jennifer Driscoll, Tham Mana, Shane Andrews, Cassidy Hanson, Damon Roznoswki, Sean Beckman and James Marshall</p> <p>Lyme disease is a zoonotic disease caused by the bacterium <i>Borrelia burgdorferi</i> which can be transmitted when an infected black legged tick takes a blood meal from another organism, thus, becoming a vector that is capable of spreading the bacterium to other organisms. Lyme Disease is prevalent in certain parts of the Midwest where ticks infect mammals as well as birds. Small rodents, such as the white-footed mouse are commonly infected and become reservoirs that can further perpetuate the spread of the disease. Because the disease seems to be localized to certain regions in the United States, it has become increasingly important to understand how the disease may become more common in areas outside of the “hot zones” as temperatures and environments fluctuate due to climate change. Mammals as reservoirs are of minimal concern when addressing this question as they do not travel long distances, therefore the disease could stay relatively contained in the highly infected areas. Due to many species of birds’ migration patterns, it is important to understand the prevalence, and therefore, the potential for the spread of the <i>Borrelia burgdorferi</i> bacterium great distances. In this study the percentage of migratory versus resident birds who tested positive for <i>Borrelia burgdorferi</i>, were 25% and 24% respectively. While the difference between the two subsets is statistically insignificant, every infected migratory bird can potentially facilitate the spread of the disease to new locations. Current research is being conducted to understand if the same trend is seen for birds tested in 2018 or if there are any significant deviations from the previous years data.</p>
22	<p>Spatio-temporal Patterns of Brown Rat Populations and Free-Roaming Cat Populations in Chicago María Jazmín Rios, Seth B. Magle, and Jalene M. LaMontagne</p> <p>In cities, free-roaming cats are a suggested rodent population control method but the interaction between cats and rats is relatively unexplored. Programs like trap-neuter-release have become a popular method used to control rat populations across the US. I will examine the spatial and temporal patterns of the brown rat (<i>Rattus norvegicus</i>) in Chicago, Illinois, the “rattiest” city in USA, using 10 years of citizen-contributed data from the City of Chicago Bureau of Rodent Control, and Animal Control and Rescue. Rat complaints will be used as an index of rat relative abundance, as these factors are highly correlated. Free-roaming cat complaints will be used as estimated relative abundance of cats in Chicago’s 90 zip-code sites because there currently is no other more accurate way to measure cat abundance. Complaints will be categorized, mapped, and analyzed within Chicago’s 90 zip-codes. If free-roaming cats influence rat abundance, we predict</p>

	<p>that the relative abundances of these species will be synchronous but negatively correlated through space and time. We will test this prediction using multiple regression matrices including five distance matrices: human population density, cat abundance, temperature, vacancy rates, and rodenticide amounts. This study will inform us how free-roaming cats influence rat distributions in Chicago.</p>
23	<p>Borrelia Infection in Canopy and Ground Dwelling Birds in Northern Illinois Whitney Felker, Hailey Avery, Jennifer Driscoll, Tham Mana, Shane Andrews, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p> <p>Lyme disease is caused by a bacterium, <i>Borrelia burgdorferi</i>. This bacterium must have a host to survive, and the host can influence the spread of the disease. According to the Center of Disease Control and Prevention (CDC), Lyme disease is a serious disease that is affecting many people and organisms. With 30,000 cases being reported each year, it is imperative that this disease gets identified and treated as early in the cycle as possible. Small mammals are the most common host for the disease, but birds have also been infected at increasing rates. As birds can cover more area than small rodents, birds become a greater risk for disease spread through their migratory routes and home ranges. The goal of this study is to determine how birds can serve as a host for <i>Borrelia</i>, in both canopy and ground dwelling birds. Blood samples were taken from different birds in two different locations within Northern Illinois over a three-year time period (2015-2017). Polymerase Chain Reaction (PCR) assays were then conducted to see which birds were positive for the disease. We initially hypothesized ground dwelling birds would be a greater reservoir from the disease, but the data collected suggests that canopy dwelling birds are also a compatible host. There was no significant difference in Lyme infection rates between the ground and canopy dwelling birds indicating both types of birds are at risk for infection and can influence the spread of Lyme disease.</p>
24	<p>Effect of <i>Borrelia</i> infection on body mass of birds Tham Mana, Jennifer Driscoll, Shane Andrews, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p> <p>Lyme disease is an infection that cause by <i>Borrelia burgdorferi</i> and transmitted by Ixodid tick vectors. Many ticks never become infected because some hosts are highly inefficient at transmitting spirochete infections to feeding ticks. While a lot is known about the ability of mammals to infect ticks, the role of birds in <i>Borrelia</i> transmission remains less clear. It is also uncertain what effect, if any, <i>Borrelia</i> infection has on infected birds. One way to detect potential negative impacts of infection on birds is to look at various indices of body condition, under the assumption that an infection might interfere with feeding or other basic maintenance activities. We predicted that birds infected with <i>Borrelia</i> would have lower body mass than healthy birds. We caught birds during fall migration from 2015-2018, and collected blood samples and recorded body mass. We used primers for the <i>Borrelia</i> flagellin B gene to detect the presence of</p>

	<p>an infection in blood samples. According to the data, birds with and without <i>Borrelia</i> infections did not differ significantly in body mass. Although that does not mean birds are unaffected by <i>Borrelia</i> infection, we did not see evidence that birds with infection experienced any decline in condition.</p>
25	<p>Testing Parameters in Maxent for SDMs of Natural Papaya Hannah B. Scheppler, Mariana Chávez-Pesqueira and Richard C. Moore</p> <p>Maxent is a user-friendly computer program that is used for species distribution models (SDMs) based on spatially biased presence-only data. There are over ten parameters that can be overridden in Maxent models, yet there is no standard way to test what parameters are best given the specific input data. In fact, most SDM studies that use Maxent do not optimize model parameters, such as regularization multipliers or resampling strategy. Here I developed ways to test what regularization multiplier and resampling strategy to use for modeling the distribution of natural papaya, using spatially biased records collected by my lab. These strategies can be applied to any species presence-only data.</p>
26	<p>A preliminary exploration of local adaptation in common milkweed Angie Martinez, Cassandra Arratia, Andrew McCall and Emily Mohl</p> <p>Monarch butterfly (<i>Danaus plexippus</i>) populations have recently declined throughout the United States, with one of the causes being the scarcity of larval food. One of the main resources used by larvae is common milkweed, <i>Asclepias syriaca</i>. To help increase adult populations, several conservation efforts have included planting <i>A. syriaca</i> in <i>D. plexippus</i>'s adult range. This practice may introduce maladapted <i>A. syriaca</i> genotypes into native populations that are locally-adapted. There is little information on whether <i>A. syriaca</i> is actually locally-adapted. Our study is a preliminary exploration of whether local adaptation occurs in this plant. Seeds from 28 source sites across the U.S. were raised at 19 different recipient sites under greenhouse conditions. We measured leaf number, stem height, and the length of the largest leaf on each plant. There were significant effects of source and recipient site on all variables. There was a significant interaction between source and recipient site for stem height such that some source genotypes did better than others in some sites but not in others. These results suggest that there is a genetic basis for differences in growth measures and that this effect depends on the recipient site, which could lead to local adaptation in <i>A. syriaca</i>.</p>
27	<p>Lyme Disease in Birds from Urban and Rural Areas Kayla Pruitt, Jennifer Driscoll, Shane Andrews, Tham Mana, Cassidy Hanson, Damon Roznowski, Sean Beckmann and James Marshall</p>

Lyme disease is a zoonotic disease that is passed between two animals via ticks. Since Lyme disease is zoonotic it is important to monitor the number of animals, besides humans, that have contracted the disease. This is especially important where birds are concerned because they can migrate much farther than any other species can and can introduce Lyme disease to areas that previously didn't have it. They can also increase the amount of Lyme disease cases in areas where some cases have been reported. This study looked at whether or not Lyme disease is more prevalent in birds around urban areas or rural areas over the past few years (2015-2017). We took blood samples from birds caught in two sites, one urban and the other rural. The urban location was the wooded areas around Rockford University in Rockford, IL, and the rural location was the Severson Dells Nature Center located southwest of Rockford. The initial prediction was that there would be more birds with Lyme disease at the rural location, since there is more suitable tick habitat. However, the results show that there is no significant difference between Lyme disease in rural and urban areas. Birds may be mobile enough to carry Lyme bacteria between areas of high and low tick density.

28 **Effects of chemical composition on plant performance and associated insect communities across *Solidago Canadensis* clones**

Bryan S. Foster, Scott J. Meiners and Thomas Canam

Competition is known to play a major role in the establishment and structure of plant communities, with many plants exhibiting allelopathy to mitigate these effects. *Solidago canadensis*, a native, perennial herb of open habitats in eastern North America, is known to exhibit allelopathic properties. *Solidago canadensis* requires pollination from insects and also supports a diverse suite of herbivores, which may also respond to plant chemistry. To relate chemical diversity/composition to ecological function, we grew 24 different clones of *Solidago canadensis*, within single-clone plots. Chemical composition of each clone was quantified via HPLC. For each clone, foliar insects were assessed three times throughout the growing season with sticky cards and three pollinator surveys were conducted. We measured biomass and stem density as measures of plant performance for each clone, as well as the biomass of non-*Solidago* species within each plot as a measure of competitive ability. NMDS ordinations were conducted on plant chemistry, foliar insects, and floral visitors. Pearson correlations were then conducted to assess relationships between chemical composition, plant performance, floral visitation, and/or foliar insect communities. Plant chemical composition varied dramatically across the 24 *Solidago canadensis* clones represented by three NMDS ordination axes. Plant performance measured by increasing stem density and decreasing light penetration were both associated with chemical NMDS axis 3. However, the biomass of associated species did not vary with plant chemistry. The foliar insect community varied little across clones and was independent of plant chemical composition, with no associations with the chemical NMDS. In contrast, floral visitors did vary across clones and were associated with chemical NMDS axis 1.

	<p>Floral visitors were also associated with the plant performance variables of above ground biomass, flower mass, and light penetration. Though foliar insects appeared to be independent of plant chemistry; plant performance and floral visitors were associated with different aspects of plant chemical composition. This suggests multiple ecological functions of plant chemistry that vary across <i>S. Canadensis</i> clones, altering their performance and associated insects. Future work will include direct competitive trials to explicitly link plant chemical composition to plant-plant interactions.</p>
29	<p>What factors drive insect pollen load quality? Nevin Cullen and Tia-Lynn Ashman</p> <p>Pollen receipt is an important component of plant fitness. Receiving pollen from a plant of a different species (heterospecific pollen) can cause declines in recipient plant fitness, with greater fitness loss associated with heterospecific pollen receipt from a closely related plant species. Occurrence of heterospecific pollen on stigmas is presumed to result from inconstant pollinator foraging behavior, however the extent of pollen diversity on pollinators and the drivers of that diversity are not well understood. We collected and characterized to species pollen carried by bees in a California serpentine wild flower community. We predicted three factors will drive diversity of pollen-loads carried by bees: diversity of flowers present, degree of specialization of the bee, and body size. We quantified floral diversity of bee-capture-sites from field surveys, calculated specialization from a plant-pollinator visitation network, and measured bee size. We modeled pollen load quality using lme4 and compared models using MuMIn in R. Bee pollen loads varied substantially in composition. We characterized pollen loads on 150 individual bees, which carried 1 to 11 pollen species, while bee species carried up to 23 species of pollen. Up to 90% of pollen on individual bees was found to be heterospecific pollen.</p>
30	<p>Learning through education: understanding selection on the flower microbiome by leveraging the classroom Rebecca A. Hayes, María Rebolleda-Gómez, Kristen Butela, Nancy Kaufmann and Tia-Lynn Ashman</p> <p>Flowers function to attract pollinators to effect plant reproduction. Several traits that function to attract pollinators may also alter the floral environment and thus impact microbes that live within them. One such trait is ultraviolet (UV) absorbing patterns on their petals. These patterns are known to guide pollinators but also reduce the UV reflectance of the floral environment. Floral microbes, which are also important in pollinator attraction and plant fitness, are assumed to be sensitive to UV exposure, but how petal UV absorbing patterns shape microbial communities is unknown. Here we developed a robust undergraduate lab curriculum to characterize the culturable petal microbiome of two co-flowering Asteraceae (<i>Helianthus tuberosus</i> and <i>Verbesina alternifolia</i>) that differ in petal UV patterns. We characterized UV patterns using a camera adapted for UV photography and isolated bacteria along the length of the petal</p>

	<p>via plating. We identified 86 putatively unique isolates via colony morphology, to be subsequently confirmed via DNA sequencing. Along with a panel of biochemical tests, we scored survival curves of isolates exposed to UV radiation. Our aim is to determine whether microbial UV tolerance relates to the location or size of petal UV patterns. In addition to teaching students hypothesis testing research design and laboratory techniques, we will leverage the contributions of the hundreds of students in the lab course to construct a uniquely large and continuously enhanced database. This data will have broad implications for understanding how floral color phenotype shapes associated microbial communities and the potential of these microbes for generating selection for petal UV phenotypes.</p>
31	<p>Evaluating the relationship between Microcystis abundance, toxicity, and environmental conditions in Muskegon and Bear Lakes Andrew Pyman and Charlyn Partridge</p> <p>Cyanobacterial blooms are becoming a greater concern in freshwater systems due to their increasing frequency and potential to produce toxic secondary compounds. Microcystis is a common bloom forming cyanobacteria that is capable of creating harmful algal blooms (HABs) through the production of the hepatotoxin, microcystin. HABs can cause many negative effects to the surrounding environment that include scums on surface waters, hypoxia, or unsafe drinking water. The goal of my project is to develop quantitative polymerase chain reaction (qPCR) methods that allow for early detection and quantification of toxic and non-toxic Microcystis strains to aid in the management of water resources. Water samples were collected from Bear and Muskegon Lakes biweekly between July and September 2017. The samples collected during the summer indicate a much higher proportion of non-toxic to toxic cells in both lakes, which is in accordance with similar findings in the literature. We are continuing to explore the relationships among our data and environmental parameters, including: temperature, nutrients, and microcystin concentrations. The development of these qPCR methods will serve as a tool for lake managers to make informed decisions regarding public and environmental health.</p>
32	<p>Ovoviviparous Lizards and Their Offspring Sarah Worthington</p> <p>Female aggression and male-like coloration are not well-studied in squamate reptiles. Female <i>Sceloporus jarrovii</i> (Yarrow's Spiny Lizards) exhibit blue ventral colorations similar to males of the same species. The ovoviviparous females are aggressive towards one another, with a peak in aggression around the parturition season in May and June. This research focuses on the mechanisms leading to and functions of female coloration, aggression, and</p>

	<p>offspring phenotype. Previous research has found changes in population levels of testosterone and corticosterone during the parturition season. We have collected ventral images, morphological data, behavioral observations, and hormone samples from females before and after birthing their offspring in a semi-natural enclosure. We have found that there is a significant effect of reproductive stage on the patch size, patch color, and corticosterone levels of post-gravid females. Offspring of these females remain near their mother immediately after birth and, in time, move away from her. Offspring will closely associate with each other longer than they will associate with their mother.</p>
33	<p>Does Genetic Diversity Lead to Greater Variation in Crops for Sustainable Agriculture? Jenny Trafford and Scott Meiners</p> <p>Diversity is well known in natural systems to buffer plant populations from environmental stressors, herbivores, pathogens and to promote persistence. Less well-studied is whether genetic diversity within crops also provides similar variation across individuals. Chestnut (<i>Castanea mollissima</i> and hybrids) and Hazelnut (<i>Corylus avellana</i> and hybrids) trees are potential alternative crops for sustainable agriculture in the Midwest. This study addresses whether genetically diverse varieties of these crops also possess greater variation in leaf traits (specific leaf area and water content) and growth than genetically uniform varieties. We examined variation across six experimental orchards containing replicated plantings of 5 clonally produced (no diversity) and 3 seedling lines (diverse) for each species. We calculated the coefficient of variation as a measure of variation across individuals, for each trait in each site. For both species, LWC was the least variable trait assessed while growth displayed the most variation. However, seedling and clonal lines exhibited similar ranges of variation rather than the expected higher variation in diverse seedling lines. The lack of systemic variation between the clonal lines and the seedling lines suggests that genetic diversity does not necessarily result in increased variability in these two alternative crop species.</p>
34	<p>Raccoon Behavior in Urban and Rural Environments Bairbre C. Connolly, Kayce M. Miller and Jalene M. LaMontagne</p> <p>Raccoons are highly adaptable mesocarnivores with flexible diets and can thrive in both urban and rural habitats. When establishing home ranges, urban raccoons prefer densely human-populated areas with an abundance of anthropogenic food. As a result of urbanization, raccoons in urban vs. rural habitats may have developed different methods of foraging or socialization, an area where little research has been done. I predict raccoons will be more frequently observed at urban than rural sites, and that urban raccoons will display lower levels of problem solving ability than rural raccoons because food is easily attainable in urbanized areas. Additionally, rural raccoons will move solitarily due to decreased abundance of resources and reduced population density. A novel feeder was erected at 20 sites in the Chicagoland area, in both</p>

	<p>urban and rural environments. A motion-activated camera was used to record behavior, and an ethogram created to catalog raccoon social behavior and problem solving ability. Problem solving ability is determined using the amount of time required for raccoons to retrieve food from the feeder as well as the behaviors used to accomplish feeding (i.e. reaching, climbing). These observations will reveal behavioral differences urban and rural raccoons may have adapted to survive.</p>
35	<p>Does urbanization influence the population trends of European Starlings, Red-headed woodpeckers, and other cavity nesting birds?</p> <p>Jessica Barton and Jalene M. LaMontagne</p> <p>Urbanization results in habitat changes which can be detrimental to the persistence of native species. European starlings (EUST) are an invasive species that benefits from urbanization, and are aggressors that may gain control over tree cavities of cavity-nesting birds, such as Red-headed woodpeckers (RHWO), which have experienced significant population declines over the past several decades. To assess whether EUST impacts are exacerbated in urban regions, we contrasted population trends of EUST and cavity-nesting bird species around Chicago, IL, with surrounding rural regions. Using data from the Christmas Bird Count (1946-2013), Breeding Bird Survey (1966-2013), and Spring Bird Count (1975-2005), we examined the relationships between EUST and cavity-nesting species with Spearman correlations and cross-correlations. Contrary to predictions, more species were positively correlated with EUST than were negatively correlated for all examined surveys, and cross-correlations displayed no evident pattern of EUST populations impacting cavity-nester populations. RHWO declined across every survey set and location, and EUST showed significant declines across three of six surveys. Population indices for EUST and RHWO were consistently lower in urban than in rural surveys. Despite their reputation, EUST have had little demonstrable impact on cavity-nesting birds within our region of study.</p>
36	<p>Comparative Analysis of Microvertebrate Sites from Late Cretaceous Hell Creek Formation</p> <p>Alysia Alfano, Megan Seckinger, James Marshall and Josh Mathews</p> <p>The Hell Creek Formation of the Western United States spans Montana, North Dakota and South Dakota. The fossil-rich mudstone and sandstone depositions are evidence of a prehistoric coastal plain ecosystem that was present 66 million years ago. Microfossils from this formation are often analyzed when determining faunal diversity and abundance. The two microsites analyzed in this study are found in southeastern Montana's Hell Creek Formation. Blair's Sandy Site, a sandstone river deposit and Scott's Microsite, a mudstone, floodplain deposit were dissimilar in their energy levels and therefore, we proposed that the differences in energy would result in different types and relative abundances of fossils. Both microsites revealed a great abundance of Amiidae fish species and ceratopsian species. The Simpson diversity index showed that the high energy river deposit had higher diversity. When organisms common to both sites were</p>

	<p>assessed using the Rank-Order and Spearman's Correlation the sites were found to be positively correlated. This suggests that aquatic microfossils display similar levels of diversity in both high and low energy systems. Further studies may be completed to confirm the diversity of microsites with similar aquatic paleontological environments.</p>
37	<p>No evidence of pollen limitation in the long-lived perennial <i>Echinacea angustifolia</i> Michael LaScaleia & Stuart Wagenius</p> <p>Pollen limitation is the phenomenon where a plant's seed set is limited by the amount of pollen it receives. Pollen limitation can be detrimental to isolated populations of plants, as lack of pollination reduces seedling recruitment and ultimately population size. These deleterious effects of pollen limitation are well documented in annual plants, but they are less clear in long-lived perennials. While a self-incompatible plant receiving no pollen in one year will have low to no seed set for that year, it might receive more pollen the next year, ultimately demonstrating no pollen limitation. It is also possible that modest pollen limitation one year may increase lifetime seed-set in future years due to tradeoffs in resource allocation between reproduction and growth/survival from one year to the next. Here, we attempt to use the long-lived aster <i>Echinacea angustifolia</i> to determine the effects of lifetime pollen limitation in a long-lived, iteroparous perennial. We use 3 groups of <i>E. angustifolia</i> where all heads on each plant in every year had pollen excluded, added, or was unmanipulated. We find that, over the course of 7 years, <i>E. angustifolia</i> is not pollen limited, as seed set was similar between the supplemented and unmanipulated groups. Additionally, pollen limitation did not increase future reproduction investment in <i>E. angustifolia</i>. Unequivocally, some florets that receive pollen on <i>E. angustifolia</i> heads do not have resources allocated to it post-pollination, suggesting that <i>E. angustifolia</i> is either limited by resources or evolutionarily self-limits its seed set through resource allocation regulation to prevent future tradeoffs.</p>
38	<p>Segmentation patterns of the pectoral fin radials in lamnid sharks (Elasmobranchii: <i>Lamnidae</i>) Andres Lafuente S. and Kenshu Shimada</p> <p>Lamniformes (Chondrichthyes: Elasmobranchii) is a relatively small, monophyletic group of sharks consisting of fifteen extant species with diverse life styles and habitat preferences, ranging from macropredatory forms to plankton-feeding forms as well as from shallow coastal forms to deep marine forms. Lamnidae is one of the lamniform families consisting of five macropredatory species: <i>Lamna ditropis</i> (salmon shark), <i>L. nasus</i> (porbeagle shark), <i>Carcharodon carcharias</i> (white shark), <i>Isurus oxyrinchus</i> (shortfin mako shark), and <i>I. paucus</i> (longfin mako shark). In this study, we examined the skeletal patterns in the pectoral fins of these five lamnid species, particularly the segmentation patterns of their radials, based on computed tomographic imaging. In all five species, all major radials are segmented regularly into three sections:</p>

	<p>short proximal and intermediate radials and elongate distal radials. However, long distal radials in <i>C. carcharias</i> are found to be further segmented rather irregularly. Although pectoral fins with more segmented radials are said to be more flexible, the exact functional and evolutionary significance of this previously unreported irregular segmentation pattern in <i>C. carcharias</i> needs further investigation. Lamnids are relatively well-studied shark taxa, but this survey of their pectoral fin skeletons demonstrates that there are still many unknown aspects of their basic biology.</p>
39	<p>Mechanistic Modeling of Evolutionary Dynamics for Phylogenetic Inference Christina Kolbmann B.S. and April Wright</p> <p>Phylogenetic analyses that incorporate extinct data allow for more attachment points to estimate lineage relationships. The fossilized birth-death (FBD) model considers all available data points as part of the same macroevolutionary process of diversification and sampling, enabling fossil records to be fully integrated with extant data points for analysis of evolutionary history. Simulating sampling events from rich fossil records like the ant family Formicidae can be compared to fossil records with sparse data. This pipeline will serve as a subsampling scheme assessment for node age precision.</p>
40	<p>Effects of Food Source on Fatty Acid Composition in Amphipods Alissa Buchta</p> <p>In aquatic organisms, fatty acid composition can be altered by many different abiotic and biotic factors including differences in diet. We conducted an experiment to examine the constraints of the food source effect on omega-3 and omega-6 fatty acid composition a freshwater amphipod (<i>Gammarus</i>). Amphipods were raised on exclusive diets of either algae or leaf material and adults were then assayed for fatty acid composition. Fatty acid methyl ester (FAME) signatures were used to identify which fatty acids were more prevalent in both the individuals raised on algae and the individuals raised on leaf material. We found that the amphipods that had an exclusive algae diet had elevated concentration of omega-3 fatty acids and no omega-6 fatty acids present. It was also found that amphipods on an exclusive leaf material diet had a high concentration of omega-6 fatty acids present and no omega-3 fatty acids present. From the data collected it could be determined that there was a significant difference between the autochthonous and allochthonous data for both the ALA and EPA fatty acids. From the mixing model it could be determined that there is a significant difference between the autochthonous and allochthonous data for both the ALA and EPA fatty acids, indicating that wild</p>

	<p>amphipods have a more varied diet which includes other sources of fatty acids, such as diatoms.</p>
41	<p>Herbicide drift has species-specific effects on wildflowers and alters the timing and abundance of pollinator resources Veronica Iriart, Gina Baucom and Tia-Lynn Ashman</p> <p>When an herbicide volatilizes and drifts beyond the intended crop, it can cause damage to nontarget vegetation, such as the wildflower communities that pollinators forage on. Using the herbicide dicamba as a case study, we grew 11 species of wildflowers from Tennessee, an area where dicamba use is prevalent, and subjected them to dicamba drift (~1% of the field application rate) or the control (surfactant only) in a greenhouse setting to understand how herbicide drift is affecting local plant-pollinator ecology. We found that dicamba drift significantly reduced plant size in four wildflower species, <i>Erigeron annuus</i>, <i>Chenopodium album</i>, <i>Solanum ptycanthum</i>, and <i>Trifolium pratense</i>, but had no effect on <i>Abutilon theophrasti</i>, <i>Ipomoea lacunosa</i>, <i>Mollugo verticillata</i>, <i>Rumex crispus</i>, <i>Lepidium virginicum</i>, <i>Plantago lanceolata</i>, and <i>Daucus carota</i>. Dicamba drift also delayed the day of first flower by 16.7 days and reduced display size of flowers five-fold. Together, our results indicate that the use of dicamba and other volatile herbicides may be shifting wildflower communities through varying species responses to drift, and likewise threatening economically important insects by altering resource availability.</p>
42	<p>Plant chemical defenses, density dependence, and biodiversity in a temperate tree community Emily A. Dewald-Wang, Joseph A. LaManna, Brian E. Sedio, Marko J. Spasojevic and Jonathan A. Myers</p> <p>Explaining the mechanisms that maintain biodiversity is a fundamental goal of ecology. Two proposed mechanisms are intraspecific competition and specialized natural enemies, in which higher densities of conspecifics exert greater negative effects on species' fitness (conspecific negative density dependence, CNDD) than heterospecifics. Both mechanisms produce similar community- and population-level dynamics, requiring disentanglement. We examined variation in leaf chemical defenses among co-occurring tree species to elucidate whether natural enemies determine CNDD and local tree species diversity in a temperate oak-hickory forest. We collected leaves from 220 saplings across 22 tree species in a large, stem-mapped forest dynamics plot and analyzed leaf chemistry with nuclear magnetic resonance (NMR). We used species' chemical dissimilarity to test if specialized enemies increase CNDD and local tree species diversity. Interspecific chemical dissimilarity increased with the strength of species' CNDD, consistent with the hypothesis that more chemically distinct species experience stronger CNDD generated by specialized enemies. Local rarefied-species richness and Shannon's diversity increased with interspecific chemical dissimilarity, consistent with the hypothesis that specialized natural enemies increase local species diversity by limiting densities</p>

	<p>of conspecifics. Our findings suggest an important role for specialized natural enemies in determining density-dependent recruitment and spatial patterns of local biodiversity within temperate forests.</p>
43	<p>Analysis of <i>D. melanogaster</i> Survival on Dietary Sterols, Sterol Metabolism, and Ecdysteroid Production. Scott Martin, Jordan Middleton, Patrick Comerford, Robert Grebenok and Andrew Stewart</p> <p>Sterols are important for all living organisms, but are particularly important in <i>Drosophila melanogaster</i>, because they serve as the base for molting hormones (ecdysteroids). <i>Drosophila</i>, like most other insects, cannot synthesize their own sterols, so must obtain them from their diet. Previous research indicated that cholesterol was optimal, while other sterols either only supported limited growth, or were insufficient for development. Here we present the results of an extended trans-generation study, where we demonstrate that 1) two different dietary sterols (β-sitosterol & ergosterol) support superior growth and survivorship, 2) these sterols are readily taken up, and 3) are converted to ecdysteroids. While these results run counter to established dogma, they are congruent with <i>Drosophila</i> life-history and standard laboratory diets. Our hope is that by understanding sterol needs of insect models, it may be possible to genetically modify plants, in order to make them pest resistant.</p>
44	<p>Nanoplankton Ecology of the Arabian Sea Shawn Gibford and Amos Winter</p> <p>Phytoplankton is the foundational feature of all marine ecosystems and a critical component of the global biogeochemical cycle. To gain further insight into these systems it is necessary to understand the ecology of organisms that support them, in particular, the nanoplankton (5 to 20 μm) community which are comprised primarily of coccolithophores. Our research is an attempt to quantify and categorize nanoplankton by depth in the photic water column throughout the Arabian Sea and near-shore India. Local and seasonal climate anomalies control the dynamic interactions among nanoplankton and changes in their environment. Coccolithophores live in all oceanic habitats but their distribution and ecological dynamics in warmer water with lower nutrient availability such as the Indian Ocean has seldom been studied. Samples of ocean water from targeted depths from the surface to 125 m were filtered on site and shipped to Indiana State University for further examination. Nanoplankton were observed with a Scanning Electron Microscope (SEM) to be appropriately analyzed. Subsamples were taken and coated in a thin layer of gold and then viewed under the SEM. Examination occurred under magnifications from 1 to 40 kx for accurate identification and morphometric studies of species. Once the initial analysis is complete, an ecological and population distribution model is created. This project interlinks many fields of study, including ecological dynamics and</p>

	environmental change. Understanding nanoplankton community structures and dynamics is critical in the biogeochemical cycling of carbon.
45	<p>Relative sizes of olfactory, optic, and otic regions of the skull in lamniform sharks, and their ecological implications Nora Westman and Kenshu Shimada</p> <p>Lamniformes is a group of sharks (Chondrichthyes: Elasmobranchii) that display diverse habitat preferences and life history strategies, including macropredatory goblin, sandtiger, crocodile, thresher, porbeagle, mako, and white sharks and plankton-feeding megamouth and basking sharks. Based on radiographic images of museum specimens and published illustrations, we examined the proportion of the anteroposterior length of the olfactory, optic, and otic regions with respect to the neurocranial length excluding the rostrum in each extant lamniform species as proxy of relative importance of each sensory region to the ecology and lifestyle of each lamniform species. Our preliminary quantitative data suggest that plankton-feeding lamniforms have large olfactory and otic regions relative to those of macropredatory forms. Although species that are commonly caught in deep waters tend to have large optic region, the trend was found not to be universal. While exceptions do exist and the functional significance of our data need further investigation, the fact that certain neurocranial characteristics in lamniforms appear to be correlative to their ecology provides another dimension to the consideration for the evolution of lamniform sharks as well as their conservation biology if the sea-level continues to rise or types of food resources shifts due to climate change.</p>
46	<p>Mast seeding synchrony and tree fate during an insect defoliator outbreak Abigail C. Leeper and Jalene M. LaMontagne</p> <p>Mast seeding is the spatially synchronous and temporally variable production of seed crops by populations of perennial plants. The ultimate hypotheses for this reproductive phenomenon are primarily described as predator satiation or increased pollination efficiency. Based on these, asynchronous individuals are thought to have reduced fitness. Despite mast seeding being described as synchronous within populations, a large amount of individual reproductive variation has been recorded in tree populations, leading to the question of the possible benefits of asynchrony. In the event a predator is attracted to regions with synchronous reproduction, such as eastern spruce budworm (SBW), mast seeding synchrony may not be beneficial. We test the hypothesis that levels of reproductive synchrony in white spruce are related to the defoliation level by SBW. Since 2012, 308 trees have been monitored for cone production in northern Wisconsin, with 2013 identified as a mast year. In 2014, we detected a SBW outbreak, impacting at least 176 trees. Since 2014, 20% of study trees have died. Implications of population-level synchronous events and SBW defoliation will be discussed in terms of both its ecosystem and evolutionary significance.</p>
47	<p>Function of juvenile color in a cichlid fish Benjamin Prindle, Daniel Licari, Carlos David Santos and Hugo F. Gante</p>

	<p>Animals communicate using a variety of signal modalities, including visual signals. Juvenile coloration frequently differs from that of territorial adults for reasons that have been attributed to lowering adult aggressiveness, thus allowing for prolonged coexistence in the same territory. We found that adults <i>Variabilichromis moorii</i> are more aggressive to black dummies relative to yellow dummies, irrespective of dummy size. Our results suggest that 'black' is a reliable signal and point to additional hypothesis of why juvenile and adult color differs.</p>
48	<p>The Effects of <i>Alliaria petiolata</i> (Garlic Mustard) Invasion on Mycorrhizal Fungi Colonization in Areas of Conservation Efforts</p> <p>Maria L. Taylor and Andrew C McCall</p> <p><i>Alliaria petiolata</i> is an incredibly successful invasive in U.S. forest understories. One key component to its success is its release of allelochemicals, preventing mycorrhizal fungi colonization in seedlings. This study compares mycorrhizal fungi colonization percentages of <i>Acer rubrum</i> roots in areas of previous conservation efforts and current invasion throughout the Denison University Biological Reserve. Six sites, three with a history of <i>A. petiolata</i> removal and three currently invaded sites, were sampled. Within each site, ten <i>A. rubrum</i> seedlings were collected, cleared and stained. Colonization percentage was scored using the magnified intersections method. Intersections were examined for hyphae, vesicles and arbuscules. Comparing one removal site sample to one current invasion site sample revealed higher root percentage colonization in the removal site sample. Higher hyphae and vesicle percentages were seen in removal site samples, though invaded site samples showed a higher arbuscule percentage. Preliminary results indicate a positive trend in mycorrhizal associations after removal of <i>A. petiolata</i>. Going forward, genetic analysis of mycorrhizal fungi diversity and spore percentages present in soil could lend to a more complete picture of conservationist efforts. Ultimately, this study begins to document effects of mycorrhizal associations after conservation efforts have removed <i>A. petiolata</i>.</p>
49	<p>Morphometric variation of teeth in the extant megamouth shark, <i>Megachasma pelagios</i>, and its paleontological implications</p> <p>Alexandra Krak and Kenshu Shimada</p> <p><i>Megachasma pelagios</i> (Lamniformes: Megachasmidae) is a large filter-feeding fish with a dentition commonly characterized as 'homodont.' We used geometric morphometrics to investigate whether or not sufficient variation in tooth morphology exists in <i>M. pelagios</i> that may aid in reconstructing the dentition of <i>M. applegatei</i>, a fossil (late Oligocene–early Miocene) megachasmid known only from isolated teeth. We examined the upper right and lower right dental series of the holotype of <i>M. pelagios</i> where each dental series was divided into the 'mesial half' and 'distal half' to determine if teeth of the four groups can be distinguished</p>

	<p>quantitatively. Our analysis shows two distinct clusters of plots, one consisting of upper teeth, and another, lower teeth. Within each cluster, mesially-located teeth are found to be morphologically less variable than distally-located teeth. Ten randomly selected teeth of <i>M. applegatei</i> in a museum collection preliminarily plotted with teeth of <i>M. pelagios</i> not only show that the two megachasmids are morphometrically distinct, but also that teeth of <i>M. applegatei</i> exhibit a wider morphological range than those of <i>M. pelagios</i>. More remarkably, two clusters similar to those seen for <i>M. pelagios</i> are also recognized for <i>M. applegatei</i> that may reflect the difference between upper and lower teeth.</p>
50	<p>The effect of fungicide on root and leaf associated fungi in Glycine max.</p> <p>Terri Billingsley Tobias, Matthew Gooch, Winthrop Phippen and Andrea Porras-Alfaro</p> <p>The environmental impacts of traditional agriculture are a growing concern. The purpose of this project is to examine the fungal communities associated with Glycine max roots and leaves both pre and post-fungicide application using Illumina sequencing. A total of 3,627,618 sequences were generated from 71 samples of soybean roots and leaves. After quality filtering, 2,229,197 sequences were used to define Operational Taxonomic Units (OTU) resulting in 1990 OTUs. Forty-one percent of the fungal sequences belonged to the phylum Ascomycota this was followed by 6.4% in Basidiomycota. Preliminary results suggest changes in dominant fungi in roots and leaves after fungicide application. An unknown taxon of fungi in roots accounted for 43% of total fungal sequences prior to fungicide treatment. After fungicide application this taxon decreased significantly (8%) and <i>Fusarium</i> increased representing 32% of the sequences. In leaves <i>Didymella</i> (21.5%) was the most abundant fungal genus before fungicide use however after fungicide this fungal genus decreased to 1% and <i>Plectospharella</i> (10%) became the most abundant fungi. Fungal-plant interactions are a delicate and complex balance in a range of mutualistic to parasitic interactions. Understanding these interactions and the indirect impacts of fungicide on community composition will provide important insights into plant health.</p>
51	<p>Quantitative feeding patterns in <i>Daphnia magna</i> using fatty acid mixing models</p> <p>Maria Butler and Jonathan O'Brien</p> <p>We conducted a laboratory study to evaluate the effects of diet on the lipid composition of <i>Daphnia magna</i>. <i>Daphnia</i> cultures were raised under three dietary conditions: yeast pellets, algae, and a spectrum of mixed diets. After raising the <i>Daphnia</i>, we used laboratory techniques to extract the lipids and converted them to fatty acid methyl esters (FAME) to analyze the composition of fatty acids present. We then created mixing models to predict feeding composition of mixed diet cultures. We found that <i>Daphnia</i> grown under single food sources differed in percent composition of three polyunsaturated fatty acids (18:2n6, 18:3n2, and 20:5n3). We also found that a principle component axis of</p>

	fatty acid composition provided the most consistent basis for mixing model when compared with models based on single fatty acids.
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