Oral Presentation Abstracts for 2024 Nachusa Grasslands Science Symposium

"Fire frequency drives tradeoffs among conservation priorities in tallgrass prairie" – *Kathryn Bloodworth, PhD*, Postdoctoral Research Associate, University of Maryland (College Park)

Land management goals in tallgrass prairie are diverse and land managers need to be equipped with the knowledge of how management decisions may alter ecological factors in similar or distinct ways. We addressed this by performing a meta-analysis of 37 studies to assess the effects of fire frequency on ecological factors (*i.e.*, arthropods, birds, plants, small mammals, and soil properties) and the interactive effects of fire frequency and grazing. Fire frequency often altered the abundance and diversity of taxa. However, the directionality of the change varied among taxonomic groups. Annual fires promoted small mammal abundance but decreased plant abundance and diversity. Intermediate fire frequencies promoted plant abundance but at the cost of plant diversity, arthropod abundance, and soil total carbon and nitrogen. Finally, grazing promoted plant abundance while reducing arthropod and obligate grassland bird abundance. Our study revealed research gaps, with critical data lacking from small mammals, birds, soil properties, and eastern tallgrass prairie. Nonetheless, we were able to outline important tradeoffs associated with management strategies using fire frequency and highlight the potential for fire to be used in unison with grazing to create a more heterogeneous landscape conducive to tallgrass prairie.

"Managing to thrive: the direct and indirect impacts of tallgrass prairie management and land cover on small mammals" - *Erin Rowland-Schaefer, PhD*, Northern Illinois University

Small mammals, which sit at the center of tallgrass prairie food webs, are understood to have speciesspecific responses to tallgrass prairie management practices, but whether these responses are directly linked to management or occur indirectly is unclear. Furthermore, small mammal communities are shaped by the landscape context of prairie restorations, which are often fragmented and share edges with heavily human-modified landscapes. Using ten years of small mammal trapping data, we assessed the impacts of management and land cover on small mammals, as well as indirect effects through the mediator of vegetation. We found strong evidence for species-specific indirect relationships to prescribed fire, largely driven by the impacts of prescribed fire on vegetation structure. We found that management impacts on the plant community are consistent with the literature, and that these changes to the vegetative community in turn impact small mammals.

"Solitary bee species vary in response to tallgrass prairie restoration and management" - Bethanne Bruninga-Socolar, PhD, Assistant Professor of Biology, Albright College

Recent work shows that plant-based restorations can support high levels of bee diversity and abundance. However, the community assembly process by which bee species from a regional pool are sorted into restored habitats during colonization is not well understood. In existing restorations, understanding site-level habitat associations of individual bee species can shed light on past community assembly process and inform restoration implementation and management. We used a multi-year dataset of bee specimens collected at Nachusa Grasslands to determine how bee species are distributed among a chronosequence of 14 restored and 3 remnant sites. We used generalized linear mixed models to explore how bee species vary in their site-level abundance in response to site-level characteristics: age of restoration, flowering plant diversity, recent burn history, presence of bison, and proximity to non-prairie habitat. We collected 7,561 bees of 117 species or morphospecies in 2015-2017. We chose to analyze the 10 most abundant bee species. Our results confirm that common bee species vary: they respond positively, negatively, or not at all to site-level characteristics of restorations, as well as to ongoing restoration management. Our results contribute to a growing body of literature suggesting that maintaining large or well-connected restorations with spatiotemporal diversity in implementation and management is necessary for the maintenance of diverse and abundant bee communities.

"Effects of Ecological Gradients on Soil-Climate Interactions in Restored Midwest Ecosystems" - *Michael Yonker*, PhD candidate, Earth and Environmental Sciences, University of Illinois at Chicago. Advisor: G. McNicol, PhD

Agricultural conversion in the Midwest has contributed significantly to climate warming via emissions of greenhouse gases (GHG); however, less information is available about GHG exchanges (emissions or uptake) following ecosystem restoration, including carbon dioxide, methane, and nitrous oxide. Native Midwest landscapes consisted of wetlands, woodlands, and prairies and gently sloping topography, both of which could still influence GHG exchange via differences in vegetation, microclimate, and soil properties. Here, we quantify soil GHG emissions and uptake in distinct restored ecosystems and along gentle topographic gradients at Nachusa Grasslands using soil flux chamber methods. We explore spatiotemporal GHG patterns using soil temperature and moisture measurements. Based on two growing seasons of measurements we find strong seasonal changes in GHG emissions, with a peak in uptake of methane in woodlands during dry spells and generally very slight nitrous oxide exchanges. Transparent chamber comparisons indicate that photosynthesis in short-stature vegetation can mitigate most or all of soil carbon dioxide emissions. Overall, our results suggest that well-managed native ecosystems exhibit net uptake of GHG and support the continued restoration of native ecosystems to reverse trends of carbon loss via favorable uptake of greenhouse gases.

"A crayfish's tale: The habitat associations for the Great Plains Mudbug (*Lacunicambarus nebrascensis*) at the Nachusa Grasslands" – *Molly Carlson, MS*, Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign

Abstract: Burrowing cravfish are among the least studied and most endangered freshwater species globally, yet they play a significant ecological role in stream, prairie, and wetland ecosystems. Limited information on them suggests that subtle variations in habitat may determine their presence. This project aimed to assess these habitat characteristics at a restored-remnant grassland. We monitored habitat variables over two field seasons. In 2022, we documented burrow abundance and factors like root biomass, water table depth, and dominant vegetation at sites with and without burrowing crayfish populations. Data from each quadrat was analyzed using Generalized Linear Mixed Models, revealing water table depth as a significant factor driving burrow presence and abundance. Root biomass and vegetation cover, while included in the final models, did not show significant influence. In 2023, we documented predation dynamics on burrowing crayfish by setting cameras at active burrow entrances across six sites identified in 2022. Cameras captured interactions with known crayfish predators for six weeks over the Spring and Summer season, but we found no significant correlation between predator abundance and crayfish populations. Vegetation height-density did not significantly affect predator detection but did decrease with increasing height-density over the growing season. These results confirm previous observations on burrowing crayfish and underscore the importance of fine-scale habitat in understanding the requirements of elusive species.

"Conserving Kittentails: an assessment of plant fitness and population genetics across a population size gradient" - *Andrew Davies,* PhD candidate, Northwestern University and Chicago Botanic Garden. Advisor: D. Meyer-Dombard. Advisor: Jeremie Fant, PhD

Rare plant species with narrow habitat requirements and small geographic ranges are categorized as threatened or endangered more than any other rarity type. Within this category of rarity, small and declining populations are predicted to experience demographic and genetic decline which can increase their extinction risk. Moreover, in small populations, it is theorized that inbreeding can lead to a further decline in plant fitness, but evidence is lacking that documents how fitness reduction can manifest at various life history stages and under environmental stress. In this study, I quantify demographic and genetic decline across a population size gradient of *Synthyris bullii* (Kittentails), a midwestern endemic that is threatened or endangered in all states it occurs. Wild remnant populations were selected in Illinois

and Indiana to test the hypothesis that compared to large populations, small populations will exhibit reductions in genetic diversity, plant size, fruit-to-flower ratio, and seed set, and increases in inbreeding. Seeds collected from a subset of populations were then grown in greenhouses at Chicago Botanic Garden to assess germination rate before being exposed to a 6-week drought treatment to better understand population level differences in stress tolerance. Results will provide insight into the mechanisms behind population decline and improve land managers' ability to prioritize and manage populations of rare species such as *S. bullii*.

"Efficacy of Predator Control as a Wildlife Management Method for Northern Illinois Raccoons" – *Jennifer Schultze*, PhD candidate, Cooperative Wildlife Research Laboratory, Southern Illinois University at Carbondale. Advisor: C. Nielsen, PhD

Raccoons (*Procyon lotor*) are mesopredators that are highly adaptable to new environments, allowing them to flourish in both urban and rural landscapes. Due to their opportunistic nature and adaptability, raccoons can negatively impact several avian and reptilian species, including the endangered Blanding's turtle (*Emydoidea blandingii*) found in Nachusa Grasslands. For raccoons, predator removal has commonly been investigated as a management strategy to increase survival of vulnerable populations, and the results suggest predator removal to be an effective approach. However, many of these studies have neglected to determine the efficacy and long-term feasibility of predator removal in mesopredator populations. Our study will analyze occupancy and abundance of raccoons before, during, and after raccoon removal through camera trap data. Preliminary results during 2022-2023 indicate mean raccoon detections and raccoon occupancy decreasing after removal. The results of this study will help determine the long-term feasibility of predator removal as a wildlife management method.

"Culture-based detection of Shiga Toxin-producing E. coli in bison" - *Ritesh Ray,* PhD candidate, Department of Biological Sciences, Northern Illinois University. Advisor: P. Singh

Escherichia coli (*E. coli*) are harmless bacteria that reside in our intestines; however, some may acquire toxins called Shiga toxins. Shiga toxin-producing E. coli (STEC) are recovered from the feces of cattle and wildlife such as white-tailed deer. Genetic relatedness with cattle and shared resources with other wildlife can transmit STEC to bison subsequently spreading it through feces. While reported to cause mild, transient diarrhea in bison calves, intervention is typically unnecessary for adults. Furthermore, the gut microbiome plays a role in preventing bacterial colonization. Therefore, the goal of this study was to detect the presence of STEC and investigate how gut microbiome composition affects colonization. For this, non-invasive bison fecal sampling was employed followed by culturing using a series of microbial enrichment and selective growth. Overall, STEC was recovered from 7.5% of samples out of 40 collected during the winter season from conservation herds. Future work on microbiome differences occurring due to STEC colonization will help to understand colonization resistance. Overall, this study highlights the potential of bison as reservoirs for environmentally acquired bacteria. Surveillance of these isolates can inform our understanding of bacterial transmission within the bison host.