9.7 VICKERS, M.E.*; ROBERTSON, M.W.; WILCOXEN, T.E.; Millikin University; *mvickers−alum@millikin.edu*
The effect of food deprivation on sexual cannibalism in an obligate predator, the jumping spider Phidippus audax (Araneae: Salticidae).
We examined the effect of food deprivation on the rate of sexual cannibalism in the jumping spider *Phidippus audax*. We separated 138 adult virgin female *P. audax* into three feeding treatments. We fed control spiders (n = 36) daily. We deprived one group of experimental spiders (n = 42) of food for 14 days, and we deprived a second group of experimental spiders (n = 59) of food for 28 days. We recorded weight loss (14−day and 28−day treatments) and survival rates, and we conducted mating trials to measure the frequency of non−aggressive and aggressive mating behaviors, mating success, and cannibalism. Food deprivation does effect *P. audax* females. Spiders deprived of food for 14 days had lower weight loss and higher survival rates than spiders deprived of food for 28 days. Food deprived spiders exhibited lower frequencies of non−aggressive behaviors than control spiders, and spiders deprived of food for 14 days exhibited a higher frequency of aggressive behaviors than control spiders. Food deprived spiders in both treatments exhibited a lower percentage of mating success, and a higher frequency of cannibalism than control spiders.

92.7 VOISIN, A−S.*; LOCREL, M.; FLAMION, E.; FALISSE, E.; FELLOUS, A.; DORTS, J.; EARLEY, R.L.; SILVESTRE, F. ; University of Namur, Belgium, University of Alabama, Tuscaloosa, USA; *anne−sophie.voisin@unamur.be*
DNA methylation in the mangrove rivulus and effects of EE2 on its developmental plasticity
The mangrove rivulus, *Kryptolebias marmoratus*, is one of the two known self−fertilizing hermaphroditic vertebrates, resulting in populations composed of distinct homozygous and isogenic strains. Despite no or low genetic diversity within a strain, this fish displays remarkable levels of phenotypic plasticity. The present study investigated developmental plasticity induced by a chronic exposure to 17−&alpha−ethynylestradiol (EE2) in rivulus, and the role of DNA methylation in driving this plastic response. Hatchlings from a single isogenic lineage were individually exposed during 28 days post hatching (dph) to solvent control, 4 and 120 ng/L of EE2, and then transferred to clean salt water until 180 dph. We aim to link global DNA methylation and methylation at specific GpG sites of selected genes to both cellular (proteome) and organismal phenotypes (hormone levels, behavior, growth, reproductive success) measured during the course of the experiment. Preliminary results show that at 28 dph, both standard length (SL; 12.6 ± 0.4 vs 13.4 ± 0.4 mm) and mass (31.9 ± 3.4 vs 37.8 ± 3.6 mg) were significantly lower in fish exposed to 120 ng/L compared to control. In the 4 ng/L group, only SL was significantly lower than control (13.0 ± 0.5 vs 13.4 ± 0.4 mm). At 56 dph, only SL of individuals exposed to 120 ng/L treatment differed from control (16.5 ± 0.4 vs 17.0 ± 0.5 mm). A first examination of global DNA methylation showed that the proportion of methylated CpG sites might be lower than what is reported in other fish species.

57.3 VOLKENBORN, N.; Stony Brook University; *nils.volkenborn@stonybrook.edu*
The "sound" of the seafloor: porewater pressure sensors as tools for studying infaunal activity
In 2005 Wethey and Woodin published the paper "Infaunal Hydraulics Generate Porewater Pressure Signals" in which they demonstrated that the sphere of influence of infaunal organisms may extend far beyond the immediate vicinity of individuals and their burrows through the propagation of porewater pressure waves. This phenomenon had been predicted from porous media flow theory but it was the first time that such pressure fluctuations in the porewater were actually measured in−situ. Since then porewater pressure dynamics have been measured in the presence of a range of large infaunal organisms including burrowing crustaceans, bivalves, and polychaetes. These measurements turned out to be highly useful to explore the frequencies and durations of behaviors such as burrowing or pumping and to link infaunal activities to biogeochemical and ecological processes in soft−sediment systems. In this presentation I will give a brief introduction to porewater pressure sensing in aquatic sediments and highlight some of the key findings and perspectives using this technology.

36.3 VOYLES, J*; RICHARDS−ZAWACKI, C; PEREZ, R; SAENZ, V; New Mexico Tech, Tulane University; *jvoyles@nmt.edu*
How does it end? Evolution of virulence in amphibian chytridiomycosis
A shift in virulence, or a transition away from the outbreak phase of a disease, toward a stable co−existence of host and pathogen can occur following the emergence of highly pathogenic infectious agents. Yet the mechanisms that underpin such transitions remain obscure. We are investigating the role of evolution in both the host and the pathogen in this process by focusing on one of the most lethal diseases of vertebrate hosts available for study, amphibian chytridiomycosis. A decade ago, the fungal pathogen *Batrachochytrium dendrobatidis* (Bd) spread through western Panama in a wave−like pattern, causing mass mortality events, dramatic declines and even local extinction of many amphibian species. However, surviving populations of some susceptible species were recently rediscovered. Although Bd is present in these persisting populations, pathogen prevalence is surprisingly low, contrary to modeling predictions. This finding suggests that there has been a shift in host−pathogen dynamics since the initial chytridiomcyosis outbreaks occurred. We collected and cryo−archived isolates during chytridomycosis outbreaks and 8−10 years following initial outbreaks. These isolates were used in laboratory infection experiments and found to be differentially pathogenic to a susceptible amphibian species. We are also currently evaluating the effectiveness of anti−microbial peptides (a component of the amphibian immune defenses) that were collected and preserved from these two time points. Understanding evolution in host−pathogen dynamics will have far−reaching implications for understanding, predicting and controlling the spread of infectious diseases and will be integral to the conservation of amphibian biodiversity in post−epidemic disease systems.