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SICB 2018 Annual Meeting Abstracts

4-1 DARBY, AM*; PATTON, SA; GIBBS, AG; Univ. of Nevada, Las Vegas, Nevada State College; darbya1@unlv.nevada.edu Gut Microbiome Effects on Desiccation Resistance in Drosophila melanogaster

The microbiome is the collection of microorganisms that occupy an individual's skin and intestines, and it has many potential effects on an animal's physiology. Changes in the microbiome affect an organism's ability to tolerate certain stressors such as desiccation. To our knowledge, no study has yet examined whether gut bacteria have any impact on an organism's ability to tolerate dry conditions, which is important to understand how animals may react to a drier climate. The Gibbs lab has selected for desiccation resistance in replicated populations of *Drosophila melanogaster* for over 225 generations, resulting in desiccation-selected (D) flies that survive desiccation ~50% longer than fed control (F) flies. D and F flies had similar numbers of gut bacteria. We generated axenic flies by washing embryos with bleach and rearing them on sterile media. Axenic D and F flies survived desiccation stress ~20% longer than non-sterile controls. Axenic flies did not lose water more slowly than non-sterile controls; instead they were larger and contained more water. Our results suggest that the gut microbiome may affect insect survival in arid environments. Supported by the McNair Scholars Institute at UNLV and an REU supplement to NSF award IOS-1355210.

78-2 DE MEYER, J*; BELPAIRE, C; VAN WASSENBERGH, S; HERREL, A; MAES, GE; DIRKS, RP; BOECKX, P; BERVOETS, L; COVACI, A; MALARVANNAN, G; DHAENE, J; ADRIAENS, D; Univ. of Ghent, Belgium, Institute for Forest and Nature Research (INBO), Museum National d'Histoire Naturelle, Paris, Museum National d'Histoire Naturelle, Paris, Univ. of Leuven, Belgium, Univ. of Leiden, the Netherlands, Univ. Of Antwerp, Belgium, Centre for X-ray Tomography, Ghent; *jendmeye.demeyer@ugent.be* Head Shape Dimorphism in European Eels ... the What, How and Why Story

Since the early 20th century, head shape dimorphism in European eel was documented, but it was only in the early 21st century that statistical support for the two morphotypes was provided. Most prominent at the yellow eel stage, broad-headed eels are known to feed more on harder and larger prey than their narrow-headed conspecifics, as well as they show different foraging behaviour. The onset of this dimorphism could be traced back to the earlier glass eel stage, where both phenotypic plasticity responses to different diets as well as genetic mechanisms seem to control for it. Although the underlying musculoskeletal differences in the feeding apparatus suggest that broad-heads show adaptive modifications to deal with larger and harder prey, the integration of multiple lines of evidence suggest the story is more complex, also including aspects of differential growth rates and habitat preference. Paradoxically, the adaptive benefit of broad-heads in a natural environment actually becomes maladaptive as this environment increasingly became polluted. Dimorphic bio-accumulation of especially highly lipophilic pollutants may even compromise the reproductive success of broadheads.

100-8 DEAROLF, J.L.*; MCLELLAN, W.A.; PABST, D.A.; HERMANSON, J.W.; HENDRIX COLLEGE, CONWAY, AR, UNIV. OF NORTH CAROLINA AT WILMINGTON, CORNELL UNIVERSITY, ITHACA, NY; *dearolf@hendrix.edu*

Regional variation in the fiber-type profile of the bottlenose dolphin diaphragm

Currently, the role, if any, of the primarily slow-twitch (65%) diaphragm in the explosive inhalation (< 0.03 seconds) of bottlenose dolphins, is still unknown. In other mammals, the diaphragm has been shown to exhibit regional variation in fiber-type profile, and these differences in fiber composition have been related to other functions of the diaphragm. Thus, the purpose of this study is to investigate regional variation in the fiber-type profile of the bottlenose dolphin diaphragm, in order to better understand the functions of this muscle. To achieve this goal, sections of the dolphin diaphragm from the middle (M) and lateral edge (L) of the costal region, ventral to the esophagus (E), ventral to the caval foramen (C), and near to the dorsal edge (D) were cut and stained for their myosin ATPase activities. Digital images of the stained sections were captured and printed, and the numbers of slow- and fast-twitch fibers were counted on each image. These data were used to calculate the average percentage of slow-twitch fibers in each region of the diaphragm. A mixed statistical model demonstrated that there is significant variation in fiber-type profile between the different diaphragm regions. The E region possessed significantly more slow-twitch fibers by count than the C, L, and M regions, a result that suggests this region of the diaphragm acts as a sphincter to prevent regurgitation of prey. However, overall, the diaphragm of bottlenose dolphins is composed primarily of slow-twitch fibers (range: 63% to 82%). Thus, the regions of this muscle may work together to play a role in ventilation by acting as a spring or to decouple ventilation and locomotion while these animals dive on a breath-hold.

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Chasing Diversity: Phylogenetic Assessment of Central Philippine Sea Pens

Octocorals are a diverse group of, for the most part, non-reef building corals accounting for almost 65% of global coral diversity. Sea pens are a highly specialized group of octocorals inhabiting both shallow and deep water ecosystems. The evolutionary origin of sea pens and their interspecies relationships have historically been a point of contention among zoologists, with only recent molecular methods being able to elucidate systematic relationships. Here we present a molecular analysis of six sea pen genera alongside representatives from the Calcaxonia, Scleraxonia, Holaxonia, and soft coral groups using the NADH 2, NADH 6, and msh1 mitochondrial genes. All specimens were collected in the central Philippines, which is an extremely high marine biodiversity area. We found the sea pens to be monophyletic with the calcaxonian family Ellisellidae, confirming previous studies. We also found the sea pen genera Veretillum and *Cavernulina* to be highly derived within the sea pen clade, refuting past hypotheses that Veretillid sea pens are among the least derived. Instead, our analysis shows the genus *Virgularia* with well differentiated polyp leaves to be the most basal. Because the sea pen clade is monophyletic with the Ellisellids, which inhabit shallow to mid-deep water, further studies are aimed at investigating whether the sea pens originated and diversified in the shallows and subsequently adapted to deep water ecosystems. A comprehensive sampling of both sea pens and calcaxonians from all depths is the next step in investigating the origin and radiation of sea pens, giving us valuable information about adaptations to different bathymetric environments in an age with rapidly rising sea levels.