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Broad patterns in the diversity of eukaryotic microbes

Microbial organisms make up the majority of organismal diversity on our planet and play a major role in biogeochemical cycling. Here we use high-throughput sequencing technology to assess broad patterns in the distribution of eukaryotic microbes across major habitat types, including soils and host-associated sites. We assess the environmental factors that drive diversity patterns across habitats. These data enable testing of the hypothesis that salinity and association with vertebrate hosts are the major drivers of diversity patterns in eukaryotic microbes as they are in bacteria and archaea. These data are also combined with community sequence data for bacteria to assess patterns of co-occurrence among taxa and gain an initial window into multilevel trophic dynamics in microbial communities.

15.4 WEIHRAUCH, D.*; FEHSENFELD, S.; MARINI, A.-M.; ZIEGLER, A.; EDWARDS, S.; MEYER, H.; SIEBERS, D.; TOWLE, D. W.; Univ. of Manitoba, Université Libre de Bruxelles, Univ. of Ulm, Appalachian State University, Univ. of Osnabrück, Alfred-Wegener-Institut f. Polar und Meeresforschung, Mount Desert Island Biological Laboratory; weihrauc@cc.umanitoba.ca

Ammonia excretion in the green shore crab *Carcinus maenas*

The passion for crabs and their capabilities for osmoregulation and ammonia excretion brought us, David Towle, me and a number of collaborators together to explore how toxic ammonia is excreted in the branchial epithelium of the green shore crab *Carcinus maenas*. Here we summarize our published and unpublished findings on ammonia excretion mechanisms in *C. maenas*. Studies were performed on animals acclimated to full strength seawater (32 ppt S.) and brackish water (10 ppt S.). Interestingly, in either environment active ammonia excretion rates were significantly lower in the osmoregulatory active, mitochondria-rich posterior gills. An Rh-like ammonia transporter cloned from *C. maenas* gills was highly expressed in the gill epithelium, here with corresponding expression levels with regard to their actual ammonia transport rates. In contrast, expression levels were found to be very low in other tissues such as the antennal gland, hypodermis, hepatopancreas and heart muscle. Long term exposure to high environmental ammonia (HEA, 1 mM NH₄Cl) caused in anterior and posterior gills of crabs acclimated to both, sea- and brackish water a significant decrease of the ammonia excretion rates. Moreover, while in seawater animals Rh-protein mRNA expression levels did not alter after short (6 hrs) and long term (14 d) HEA exposure, expression levels in the gills of brackish water acclimated crabs doubled after 14 d HEA exposure.

23.2 WEHRLE, B.A.*; ESPINOZA, R.E.; CSU Northridge; beck.wehrle.367@my.csun.edu

Why do lizards lounge? The role of social aggregations in exchanging microbial communities among hatchling Green Iguanas

Why sociality evolves is poorly understood, but both biotic and abiotic factors have been implicated. Sociality may have evolved in some herbivorous reptiles to foster the transfer of gut microbes. These endosymbionts are needed to digest plant fiber and their fermentation products can contribute substantially to their host's energy budget, but this symbiosis is poorly understood. Green iguanas (*Iguana iguana*) are herbivorous throughout life, yet hatch with sterile guts. So how do they acquire their gut microbes? Although rare in lizards, social interactions are a hypothesized route of microbe transfer via direct contact and/or eating feces of conspecifics. Early attempts (>30 years ago) to characterize this microbial community in hatchling iguanas provided crude measures of microbial turnover. Our study is the first to characterize the spatial, temporal, and social variation of these vital microbial communities using modern genomic techniques. We hypothesize that there will be microbial community variation more consistent with social transfer than individual variation. We observed and individually marked juvenile iguanas in social lounges at eight sites on and around Barro Colorado Island, Panama over two reproductive seasons. Of the 540 focal observations of hatchlings, 38% were of social aggregations (mean = 2.9 lizards/ group). Hatchlings in groups averaged 1.2 m from their nearest neighbor (range = 0–6 m), although densities varied among sites. We collected microbe samples from iguanas and their environments over the first 60 days post-hatching. Microbe-specific DNA will be isolated from samples and pyrosequenced to characterize the gut microbe communities of iguanas over space, time, and with respect to observed social interactions. We predict that microbial communities will be most similar among proximate hatchlings and will increase in diversity over time.

26.1 WEISBROD, Anat; CHIPMAN, Ariel*; The Hebrew University of Jerusalem; ariel.chipman@huji.ac.il

The origin of insect A/P axis determination pathways – insights from the holometabolous milkweed bug, *Oncopeltus fasciatus*

A key early process in development is the determination of the embryonic axes. The anterior-posterior axis in insects is determined by a series of signaling pathways and transcription factors. These are best known from the fruitfly *Drosophila melanogaster*, where the torso pathway activates a number of posterior transcription factors, while interacting diffusible factors define the anterior. We have cloned the homologues of most of the key players in axis determination from the milkweed bug *Oncopeltus fasciatus*, focusing on *huckebein*, *torsolike*, *hunchback*, *orthodenticle* and *tailless*. We then studied their expression and function, and their interaction with other early developmental pathways. Our results show that many of the pathways known to be involved in *Drosophila* axis determination have different roles in *Oncopeltus* development. We suggest that their roles in *Drosophila* are derived from the more ancestral roles still preserved in *Oncopeltus*. We use our results to discuss a model for the evolution of the axis determination process in insects.