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Dehydration causes increased reliance on protein oxidation in mice: a test of the protein-for-water hypothesis in a mammal

During fasting, animals rely on a mixture of fats, carbohydrates, and proteins that are derived solely from endogenous sources. It has long been held that endogenous proteins are spared from catabolism until the final stages of prolonged fasting, and contribute a significant proportion of energy once the other metabolic fuels have been depleted. However, evidence is mounting that protein is catabolized supplemental to fat metabolism under some circumstances. This has been shown in migratory birds that show dramatic reductions in lean mass during flights. One hypothesis to explain this seemingly maladaptive metabolic strategy is that the catabolism and oxidation of protein in situ yields five times more metabolic water than that generated through fat oxidation alone. Here we test the protein-for-water hypothesis in resting mice subjected to water deprivation during fasting while we tracked rates of protein and lipid catabolism using endogenously incorporated ¹³C-leucine and ¹³C-palmitic acid. We found no differences in instantaneous leucine oxidation; however, cumulative differences in instantaneous leucine oxidation ultimately resulted in a higher total leucine oxidation after 72h of fasting in water deprived animals. We also found that lipid oxidation was 8% higher in the hydrated mice, but the difference was not significant presumably because of a concomitant reduction in metabolic rates of the water deprived mice. Our results indicate that mammals do increase rates of protein catabolism during dehydration, but to a lesser degree than birds. The ability of mammals to produce highly concentrated urine and their lower inherent rates of protein turnover apparently preclude mammals from taking full advantage of the protein-for-water strategy during fasting under dehydrating conditions.

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Factors Influencing Settlement Patterns on the Barnacle *Chthamalus panamensis*

The gregarious settlement of dominant intertidal organisms, such as barnacles, is essential for recruitment and it's a critical determinant in the structure of the adult population. However, the recruitment density of larvae is largely dependent on physical and temporal factors, which interact dynamically in the intertidal. The barnacle, *Chthamalus panamensis*, found on the Pacific coast of Panamá is a dominant organism that has a higher settlement during neap tides than spring tides. In this study, diel cycles, substrate composition, and other physical parameters (temperature, wind direction, wind speed, and tide amplitude) were studied during the summer 2016 to understand the settlement behaviour of this species, particularly during the quarter moons. Settlement of *C. panamensis*, was higher during diurnal than nocturnal neap tides, which correlated with the warmer temperatures that occur during the day. We expected that bigger tidal amplitude and stronger inshore winds would enhance settlement rate, since this would provide transport and onshore delivery of more planktonic larvae. However, wind speed and wind direction had no significant effect on settlement, while lower tidal amplitude positively correlated with higher settlement rates. As for substrate composition, color was not a strong driving factor for substrate selection since there was no significant difference in settlement rates between the different colored plates. For substrate texture however, settlement was higher on plates with more abrasive sandpaper-like texture that had a more even microstructure. This study provides a better understanding on the settlement patterns of *C. panamensis* and the insight that is gained when considering the interactions among temporal, physical and hydrodynamic conditions that exhibit the intertidal ecosystem.

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Marine Ectoproct Communities from the Antarctic Shelf based on Sea Floor Imaging of the Ross and Weddell Seas

Benthic communities of the Antarctic shelf are comprised of a diverse assemblage of species typically dominated by invertebrates, particularly echinoderms, sponges, and ectoprocts. In some zones of the Antarctic shelf ectoproct abundance is significant, creating 'garden-like' habitats that harbor numerous other species. As the combined forces of global warming and ocean acidification threaten these communities, we sought to characterize the ectoproct gardens using direct benthic sampling (Blake Trawls) and two techniques for imaging the sea floor (YoYo camera and OFOS video systems). Blake trawls and YoYo cam transects of the Bellingshausen, Amundsen, and Ross Seas were conducted during a research cruise on the *R/V Nathaniel B. Palmer* in 2013. The OFOS imaging of the seabed in the Weddell Sea was part of the DynAMO project during the PS96 cruise of the *R/V Polarstern* in 2015-16. Species identifications of ectoproct samples were completed using SEM. The areas of ectoproct gardens were measured from the images using the Trainable Weka Segmentation plugin developed for FIJI software. Sites in the Ross Sea contained ectoproct gardens dominated by flustrid species with finely mineralized skeletons, and to a lesser extent by other lepraliomorph and umbonulomorph species having more robust mineralized skeletons. Although ectoproct gardens in Weddell Sea also contained flustrid species, ectoproct species with more heavily mineralized skeletons were more abundant. Combined with species identifications from our fixed samples, the quantification of various morphological grades of ectoprocts was facilitated by the better-resolved images created through the OFOS video system.

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Durophagy influences macroevolutionary patterns in porgies, seabreams and allies (*Sparoidea*, *Percomorpha*)

Sparoid fishes form a group of ~ 255 species currently classified in three families (Lethrinidae, Nemipteridae and Sparidae). This group of coastal, demersal fishes shows a remarkable diversity in terms of morphology (body size and shape) and ecology (diet and habitat association). Indeed, various lineages dominate fish communities in temperate soft bottom or rocky reef habitats, while others are major components of tropical coral reef ecosystems. In order to investigate the macroevolutionary pattern of this clade we generated the largest molecular phylogeny for this group, covering ~70% of the extant species diversity and time-calibrated this with seven sparoid fossils. We assembled a dataset of ~ 2300 images from the ichthyological collections of 14 major natural history museums and explored the morphospace of their overall body shape using geometric morphometric methods. We also collected data on body size and species richness from published taxonomic literature and used these data to perform phylogenetic comparative analyses on rates of lineage and phenotype evolution. Our analyses show that the major sparoid lineages all originated during the Late Cretaceous, predating the KPg extinction event. Major bursts of diversification then occurred during the Middle to Late Eocene, as well as during the Miocene, coinciding with dramatic reorganization of coastal benthic communities. We show that durophagy had an important role in driving sparoid evolutionary history. Stochastic mapping strongly suggests that ancestral sparoids were durophagous, while comparison of various models of trait evolution (Brownian motion and Ornstein-Uhlenbeck) shows that durophagy influenced both body size and shape diversification.