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Combatting Antibiotic Resistance: Bioprospecting for Antimicrobial Peptides in the Deep-Sea Coral Lophelia pertusa

Bioprospecting for antimicrobial peptides (AMPs) has attracted more attention in recent years due to the growing threat of antibiotic resistant bacteria (ARB). The marine environment offers a wealth of untapped potential in the form of novel therapeutic chemical compounds. Scleractinian, or stony, corals are an order of marine organisms whose lineage may date back to the early Paleozoic Era. *Lophelia pertusa*, a member of the order Scleractinia, is a framework-builder for deep-sea coral reefs. This species is currently garnering growing interest due to its global abundance and ability to create highly biodiverse ecosystems. To isolate AMPs, samples of *L. pertusa* were crushed using liquid nitrogen. A protease inhibitor in 10 mM Tris-Cl buffer was added to create a homogenate. AMPs were then harvested from the coral homogenate using functionalized MA6A HA hydrogel microparticle beads that had an anionic charge. These particles attracted, filtered, and isolate small cationic antimicrobial peptides (CAMPs) from the coral homogenate. CAMPs were subsequently eluted, purified, and concentrated to allow for *de novo* sequencing using an Orbitrap Elite mass spectrometer equipped with electron transfer dissociation. Over 1000 peptides were isolated from these purified samples. PEAKS software was used to analyze the peptides and determine the probability of antimicrobial activity. Once available, the new draft genome of *L. pertusa* will be used in PEAKS to confirm, complete, and correct the *de novo* CAMP sequences as well as determine their origin. Putative novel CAMPs harvested from *L. pertusa* can then be synthesized, which could lead to trials that test their effectiveness against known ARB.

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Larger Meals Generate a Disproportionate Greater Cost of Digestion

Mandatory to meal digestion is the expenditure of energy stemming from the breakdown, absorption and assimilation of that meal. The magnitude of this collective energy expenditure, termed specific dynamic action (SDA), is largely a function of meal size. Predictably, any increase in meal size would generate a corresponding increase in SDA. However, unknown is the nature of this relationship. Hypothetically there are three possible scenarios: (1) increase in SDA is matched to the increase in meal size; (2) SDA increases at greater rate compared to the increase in meal size; and, (3) SDA increases at a lesser rate compared to the increase in meal size. We tested among these competing hypotheses by feeding snakes different size meals (5-25% of body mass) and quantifying for each meal size the maximum postprandial metabolism, duration of significant metabolic response, and SDA. We quantified for each of these variables a response coefficient, defined as the factorial increase of that response with a doubling in demand (i.e. meal size). For four species of pythons (*Python molurus, P. sebae, P. reticulatus, Morelia viridis*), four species of boas (*Boa constrictor, Eunectes murinus, Eryx colubrinus, Epicrates cenchria*), and the colubrid *Pantherophis guttata* the response coefficient for maximum postprandial metabolism averaged 1.41 (1.23-1.70) and for duration averaged 1.47 (1.15-2.13). The response coefficient for SDA averaged 2.35 (1.85-2.90). For these snakes, a doubling in meal size resulted on average in a 41% increase in peak postprandial metabolism and a 47% increase in duration that combined to generate a 135% increase in SDA. These findings support the second scenario that with an increase in relative meal size, snakes spend a disproportionately greater amount of energy in digesting and assimilating larger meals.

61-2 CAVIEDES-VIDAL, E*; BRUN, A; MAGALLANES, ME; BARRET-WILT, GA; KARASOV, WH; Consejo Nacional de Investigaciones Científicas y Técnicas - Universidad Nacional de San Luis, Universidad Nacional de San Luis, Consejo Nacional de Investigaciones Científicas y Técnicas, University of Wisconsin-Madison; *enrique.caviedes@gmail.com*

Dietary Adaptation to High Starch Involves Increased Abundance of α-Glucosidase and its mRNA

Dietary flexibility in digestive enzyme activity is widespread in vertebrates, but mechanisms are poorly understood. Fragmentary evidence indicates that laboratory rats modulate intestinal α-glucosidase (AG) activity mainly by relying on rapid increase in enzyme transcription followed by translation and translocation to the intestine's apical, brush border membrane (BBM). We performed the first unified study of this overall process, relying on activity, transcriptomic and proteomic data from the same animals. We used as our model nestling house sparrows (Passer domesticus), which increase their intestinal AG activity as they switch naturally from low starch insect diet to higher starch seed diet. Twenty-four hours after a switch to a high starch diet, intestinal AG activity and mRNA were increased. The protein sucrase-isomaltase (SI), which is responsible for all maltase and sucrase activity, was the only hydrolase increased in the BBM, and its abundance and activity were positively correlated. This is the first demonstration that birds may rely on rapid increase in enzyme abundance when adjusting to high starch diet.

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PEACH: The Physiology Exoplanet Astroecology model for Characterizing Habitability

A primary objective of astrobiology is to identify habitable exoplanets. Here, I apply an integrative approach between astrophysics, climate modeling, and ecophysiology to explore the relationship between alien environments and terrestrial life. I discuss the development of a novel system to be used as a tool to assess the habitable regions on exoplanet surfaces. In this model, simulated exoplanet environments are convolved with a real biological layer. Exoplanet environments are simulated using the climate model, Resolving Orbital and Climate Keys of Earth and Exoplanet Environments (ROCKE-3D, Way et al. 2018). ROCKE-3D is a fully-coupled 3-dimensional oceanic-atmospheric general circulation model (GCM) featuring interactive atmospheric chemistry, aerosols, the carbon cycle, vegetation, oceans, sea ice, and land surface components. The GCM output is coupled in the astroecology model with empirically-derived thermal performance curves of 1,627 cell strains representing extremophiles from all six Kingdoms, termed the biokinetic spectrum for temperature (Corkrey et al. 2016). The spectrum arises from a meta-analysis of cellular growth rate as a function of temperature. In this agent-based model, created with the software NetLogo, the survivability of an organism is determined by its thermal response to simulated temperatures. This model can be applied to predict exoplanet conditions compatible with terrestrial-based thermophysiology, as well as surface maps highlighting potentially habitable regions. Life, however, is dependent upon multiple variables including the presence of liquid water, nutrient content, and an energy source. Caveats of the methodology and application of results are discussed with implications for observable biosignatures.