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Unexpected patterns of connectivity and phylogeographic breaks in Mediterranean marine cave mysids

Habitat fragmentation is a major threat to biodiversity by reducing habitat availability and interpopulation connectivity. Submarine caves represent a naturally fragmented habitat allowing to understand how habitat fragmentation affects connectivity. We worked on the Mediterranean brooding cave-dwelling mysids *Hemimysis margalefi* and *Harmelinella mariannae* which disperse only as adults. At the Mediterranean scale, our phylogeographic study based on several mitochondrial and nuclear molecular markers revealed that *H. margalefi* is actually composed of five highly divergent lineages, likely representing as many events of ongoing allopatric speciation. Populations of the different lineages are highly structured genetically mostly according to the general current circulation and the geography of the Mediterranean, habitat fragmentation and poor dispersal abilities. However, some well-known barriers to gene flow appear to have a surprisingly reduced influence on this species. Compared to *H. margalefi*, the little-known *H. mariannae* shows far less structured populations. This is particularly puzzling since this species, considered rare, has a more fragmented habitat. At small geographical scale, the use of microsatellite markers has evidenced differences in the genetic population structuring of *H. margalefi* compared to mitochondrial data. Understanding marine population connectivity in fragmented habitats has proved more complex than previously thought and may benefit from unconventional biological models such as marine cave mysids.

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Wing shape characteristics exaggerated by RNA interference modulate aerobic performance in fruit flies

The diversity of insect wing morphology seen in nature reflects the time-integrated sum of evolutionary pressures. Extant designs represent a compromise of ecological factors including but not necessarily dominated by aerodynamic performance characteristics. Correlating wing design with flight performance usually involves crossing species boundaries and can, therefore, be confounded by phylogenetic history. Since biomechanical data sets can be technically challenging and time-consuming to obtain, implementing the comparative method is often unfeasible. One approach to this problem lies in the development of a standardized procedure for a single species that affords either discrete or continuous variation of morphological parameters that are expected, from aerodynamic theory, to play important roles in aerobatic capabilities. Aerial prowess may be crucial to individual fitness and has certainly been instrumental in the success of the insects as a class. Thus, the ability to modify experimentally wing shape alone is a powerful tool with which to investigate the underlying mechanisms of functional morphology. Here we use RNA interference to down-regulate the expression of a gene that determines wing shape in fruit flies (*Drosophila melanogaster*). The resulting phenotypes differ markedly in wing tip curvature and aspect ratio. We used stereo photogrammetry to acquire three-dimensional free flight trajectories from the range of phenotypes, calculated flight performance metrics, and found them to be significantly correlated with the modified wing morphology.

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On the flight of foraging bumblebees in the near-wake of objects

The high energy demands of a growing hive require bees to forage relentlessly, even under unfavorable weather conditions such as cool temperatures, precipitation or high winds. Bees forage in the complex environments surrounding flowering plants, bushes and trees, and the flow structures that they encounter on days with mild or strong winds can be vastly different from those encountered on calm days. Vortices shed from structures in the surrounding environment (trees, flowers, branches, etc.) can vary dramatically in size, strength and orientation, and these flow structures may influence the flight trajectories of foraging bees. Efficient flight trajectories, effective control strategies, and precise landings on nectar sources are vital to maximizing foraging success. To shed light on the interaction between bees and the wakes generated by objects in their environment, freely flying bumblebees (*Bombus impatiens*) were filmed with high speed cameras as they flew upstream in a wind tunnel at a range of freestream velocities, towards artificial flowers mounted on cylinders of varying size and orientation. Measurements of bumblebee approach trajectories were augmented with smoke flow visualization and high speed anemometry to obtain qualitative and quantitative insight into the flow structure in the vicinity of the cylinders. We found that bumblebees do employ approach patterns that depend on the geometric properties of the upstream object and its associated flow structures. This suggests that certain types of plants or particular habitats may be more challenging and/or costly for bees to forage in under adverse weather conditions.

S8-1.2 REDMOND, NE*; MORROW, CC; THACKER, RW; DIAZ, MC; BOURY-ESNUALT, N; CÁRDENAS, P; HAJDU, E; LÔBO-HAJDU, G; PICTON, BE; COLLINS, AG; NMNH, Smithsonian Institution, Queen's University, Belfast, Northern Ireland, University of Alabama at Birmingham, Museo Marino de Margarita, Venezuela, Université d'Aix-Marseille, France, Uppsala University, Sweden, Museu Nacional/Universidade Federal do Rio de Janeiro, Brazil, Universidade do Estado do Rio de Janeiro, Brazil, National Museums Northern Ireland, UK; redmondn@si.edu
New 18S rDNA Sequence Data Suggest Exciting New Hypotheses for Internal Relationships of Demospongiae (Phylum Porifera).

The systematics of sponges (Porifera) is extremely difficult to decipher and constantly evolving. Here we present some exciting results on the phylogenetic relationships within Demospongiae based on 18S rRNA data. We add over 420 new nearly complete demosponge 18S sequences to approximately 180 existing sequences from GenBank. Our dataset includes over 35 genera that had not been included in molecular phylogenies to date, shedding new light on their familial affinities. We present several new hypotheses suggesting further revision and refinement of the emerging, more consensus-based, systematics of demosponges. Among numerous results are the following hypotheses: 1) within Myxospongia Chondrosia is sister to a monophyletic Verongida making the order Chondrosida paraphyletic; 2) within Keratosa, Dendroceratida is weakly supported as monophyletic, while Dictyoceratida has high support and is split into two highly supported clades, Spongiidae + Irciniidae + most Thorectidae and Dysideidae + remaining Thorectidae; 3) numerous lineages within Haploscleromorpha have undergone simplification of skeletal structure; 4) within Democlavia (=Heteroscleromorpha), nearly all of the independently derived clades of Morrow et al. 2012 are valid; and 5) freshwater Spongillida and lithistid Vetulinidae are sister groups with a close relationship to Scopalinidae.