DIMENSIONS OF MARINE LIFE – PATTERNS AND PROCESS OF DIVERSIFICATIONS IN PLANKTONIC AND BENTHIC CNIDARIANS

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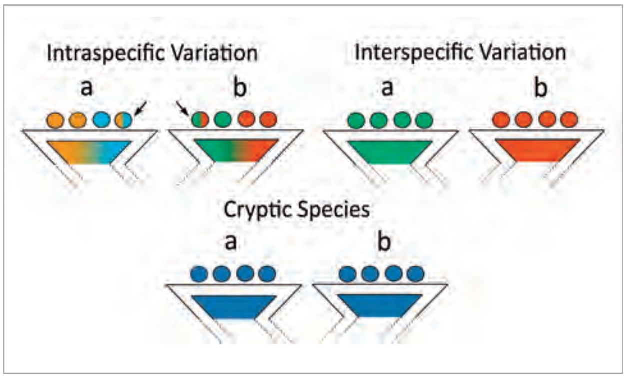

Figure 1. Levels of morphological variation, including absence of variation (cryptic species). Clades indicate different lineages, colors and shades represent the phenotype in current time, and the circles represent individuals. (From Cunha et al 2016, ODE, 16 D.O.I. 10.1007/s13127-016-0276-4).

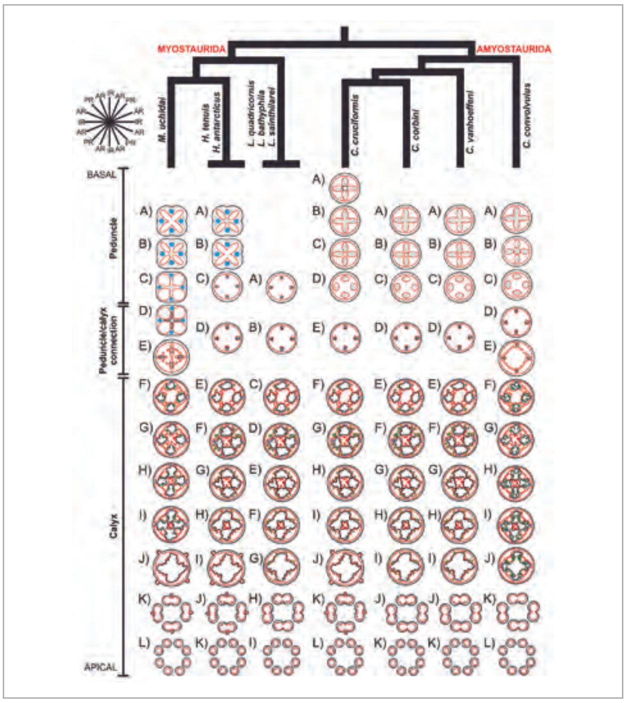

Figure 2. General body plan of different species and their phylogenetic relationship (From Miranda et al 2016, PeerJ, 4:e2594, D.O.I.: 10.7717/peerj.2594).

In order to understand marine diversification, and ultimately promote its conservation, it is clear that an integrative approach of adequate spatial, temporal, and taxonomic coverage must be developed. Marine biodiversity has been modulated by historical and recent events resulting from micro and macroevolutionary variables that act synergistically and are equally important. For instance, the assessment of historical areas of endemism and past biogeographical barriers (inferred from paleoceanographic records) provides information on the historical affinities of the biota. On the other hand, results from population genetics and phylogeographic studies, when correlated with relevant abiotic and biotic variables, provide data on the dynamics and patterns of recent communities. Consequently, both approaches may explain unique patterns of isolated communities and populations. Data on species richness is crucial since it provides estimates of phylogenetic communities that can be based on a multitude of data, obtained from sources that range from phylogenomics to population ecology to niche modeling. In the same way, assessment of introduced species and their impact on native communities, life history data, biotic interactions or experimental ecology, ecophysiological studies, and additional features, have also been investigated.

This research program correlates micro and macroevolution, integrating developmental biology, life cycles, speciation, phylogeography / population genetics, ecological niche modeling, phylogeny / taxonomy and biogeography / faunal studies. The goal is to traverse the spatial and temporal dimensions of marine life, investigating patterns and processes at nested biological levels through the study of planktonic and benthic marine invertebrates, focusing on cnidarians, a group with wide distribution and highly variable life cycles and developmental trajectories.

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

This research program is a continuation and extension of a previous thematic project, named "Biodiversity, evolution, endemism and conservation of Medusozoa from the Southwestern Atlantic Ocean". Among the project achievements, one of the most important is the significant increase in the faunal knowledge of the Atlantic and Pacific coasts of South America, culminating with an extensive monograph of the medusozoans of the subcontinent, including ~1,000 species. The study also proposed 35 new taxa, from new species to new subclasses, all based on solid phylogenetic contexts and several resulted from extensive taxonomic revisions that contributed to describe and redescribe the anatomy, morphology, morphometry and cnidome of innumerous extant and fossil taxa. We added data of natural history and ecology for over thirty taxa, many of them completely unknown hitherto, including native and introduced species. Biogeographic and phylogeographic inferences were used in theoretical and actual analysis for different methods and covering extensive areas of the southernmost regions of South America, the whole Antarctica, and Atlantic Ocean (especially deep sea data). These patterns of endemism were correlated with putative paleoceanographic barriers, which eventually allowed us to hypothesize on the ages of endemic biotas. Besides revealing several cryptic taxa, the phylogeographic approach also provided data to understand the recent population dynamics of the medusozoans and it has shown that there was remarkable convergence in the genetic structures of populations across species with different life cycles. Evolutionary results were based on several different phylogenetic inferences, including the most extensive data sets produced for medusozoan hitherto, like for the Leptothecata, Proboscoida and Staurozoa, among others. These patterns were used to infer and discuss evolutionary process relate to the life cycle and ecology of extant and fossil taxa. Some peculiar systems were also analyzed like venomics (including proteomics, transcriptomics and genomics), biomechanics and functional anatomy, all under an evolutionary perspective.

MAIN PUBLICATIONS

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