



Pôster – Evolução e biogeografia

A genetic framework for Rhopaliophora evolution

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Any culture-related laboratory would be considered the optimal starting point for a genetic project, mainly if they are considered as desired main objectives genomics and evolution. Cnidaria is a well known animal group (~11,000 extant species) but besides a few species, they lack genetic information in classical and new fronts like genome sizes, cytogenetics and genome sequencing. From these premises/context we developed an evolutionary genomics approach to take advantage of Rhopaliophora species in culture, starting with genome sizes. We defined the genome size of 97 cnidarian species using Flow Cytometry technique, including the new smallest and biggest genome size for the group; from these, 40 are related to Scyphozoa and 8 to Cubozoa. From this first outcome and taking account their phylogenetic context, we targeted a selected group of species as priorities to genome sequencing. They included Coronatae (*Nausithoe aurea*, *Thecoscyphus zibrowii* and *Linuche anguila*), Semaestomeae (*Sanderia malayensis*) and Rhizostomeae species (*Rhopilema esculentum*, *Lichnorhiza lucerna* and *Stomolophus meleagris*); as outgroups, we sequenced a cerianthid and a zoanthid species (*Palythoa mizigama* and *Ceriantheomorphe Braziliensis*, respectively). All these datasets are being explored in several hypotheses, mainly in terms of macroevolution and evolutionary dynamics (ex, genome sizes, life cycles and non coding regions). As an additional outcome, new collaborations were established with international groups and we are proposing a new international network of cnidarian culture experts to enhance cnidarian research from culture and living specimens.

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