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DNA BARCODES UNLOCKING THE PHENOTYPIC PLASTICITY IN ADULT AND LARVAE: A CASE STUDY IN CERIANTHARIA (CNIDARIA, ANTHOZOA)

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Abstract

The life cycle of Cnidaria is the focus of few studies, especially in Anthozoa. This entails in a scenario of little knowledge of the different larval stages of most species. In the present work we verified by DNA barcoding techniques the phenotypic variation of larvae of "morphological species" that for a long time were identified in different genera, but that by the molecular data could be correctly identified as a single species. This study demonstrates that many assumptions made for various stages of life cycle in Cnidaria may be totally wrong and approaches with DNA Barcoding should be prioritized for this verification.

Background

Studies on the behavior and life cycle of cnidarian species in the laboratory and *in situ* are still rare for many groups of cnidarians, especially Ceriantharia (Tiffon, 1987), although such studies are essential to identifying the species and populations (e.g., Jarms et al., 2002). The subclass Ceriantharia (tube anemones; members of Anthozoa), known for the beauty of their polyps, suffer from confusing taxonomy (Stampar et al., 2014). The life cycle of Ceriantharia (e.g. Fig. 1) is little known, being described in only half a dozen species. Even so, some ancient studies (between 50-100 years ago) already indicate a considerable variation of forms as a consequence of the environment (Nyholm, 1943). One of the main taxonomic problems within the group is the existence of larval forms that have been named and accepted as valid species. A possible approach to solving this problem is the use of DNA barcoding.

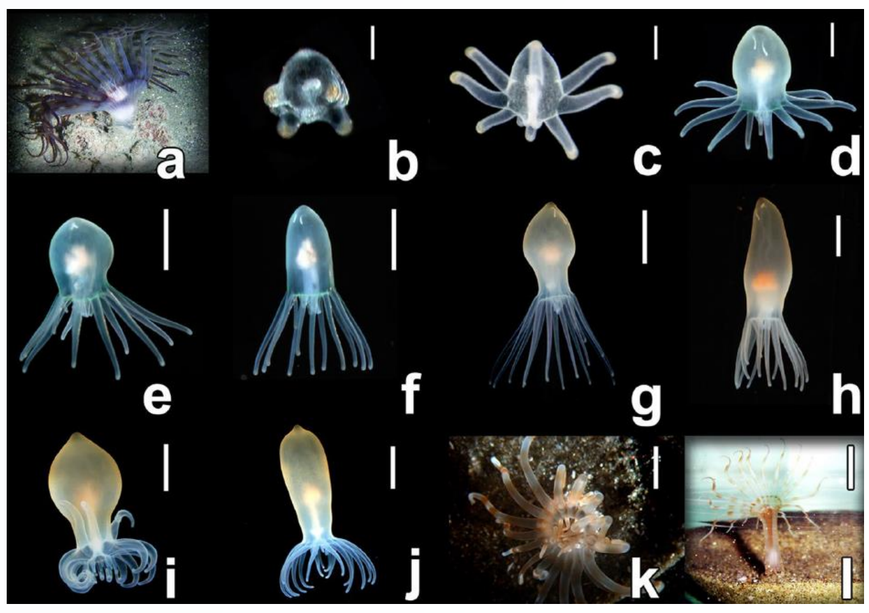

Figure 1: Images of different stages of the life cycle of *Isarachnanthus nocturnus*, from São Sebastiao Channel, southeastern Brazil (after Stampar et al., 2015).

Results

This study compared DNA barcoding, morphological, and developmental data of larval and adult stages of two morphologically defined species from related genera, *Arachnanthus* sp. (Fig. 2-3) and *Isarachnanthus nocturnus* (Fig. 1-2), from the same region (São Sebastião, São Paulo, Brazil). As expected, morphological data showed the classical specific division from these two genera. Development data also indicated a clear divergence between them in larval morphology and growth. However, molecular DNA barcoding and other DNA markers (16S, ITS1 and ITS2) data showed a total absence of variation in sequences in all samples.

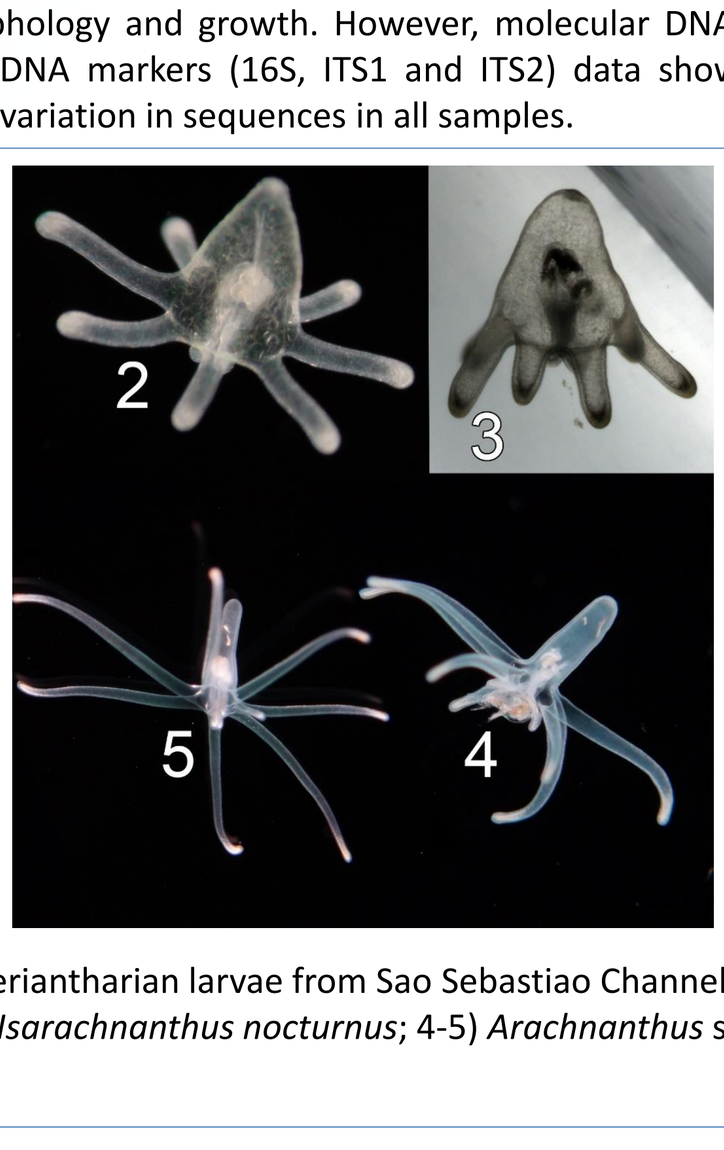

Figure 2: Ceriantharian larvae from Sao Sebastiao Channel, Sao Paulo, Brazil. 2-3) *Isarachnanthus nocturnus*; 4-5) *Arachnanthus* sp. (?)

These results indicate two alternative scenarios: i) if they are true different species, a drastic morphological differentiation should happen in a very short period of time from speciation; ii) if they are the same species, there is considerable phenotypic plasticity in the studied species. We defend the last one, occurrence of different reproductive periods with different morphological results of larvae and adults.

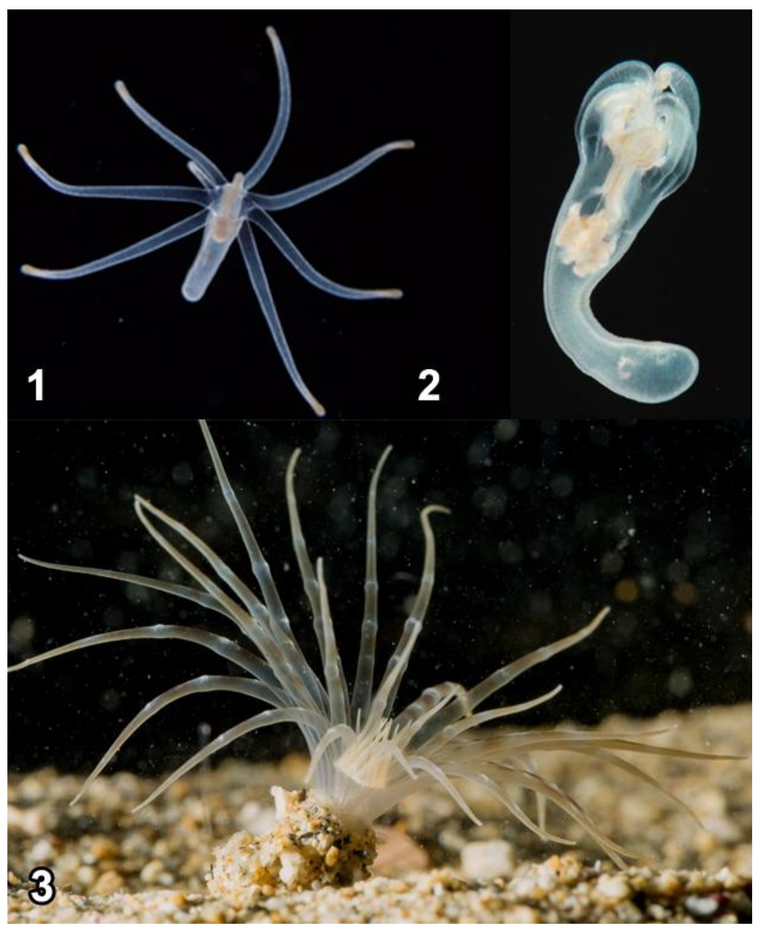

Figure 3: Images of different stages of the life cycle of *Arachnanthus* sp. (?).

These results become more important when molecular data of other *Arachnanthus* and *Isarachnanthus* species are included, as results from Pacific Ocean specimens indicate that there may be no division between these two genera.

Discussion

In fact, we have a very interesting scenario. There are two different morphospecies, but in this case only phenotypic expressions related to the environment. Exactly in this case, we have two types of reproductive forms that are influenced by the seasons. In winter, we have shorter larval cycle (focused on population maintenance) and in the summer, we have a longer life cycle (focused on dispersion). The problem on the taxonomy side is that each type of reproduction results in a differentiated adult form. In this case, the variation is so extreme that it indicates the mixing of more than one genus within the same biological lineage. As discussed in Stampar et al., 2015, this type of scenario is apparently not restricted to the case reported above. Other species/genera also present this on some level. For example, our studies indicate that the life cycle of *Ceriantheomorphe* may provide something similar, at a lower level, which may be the explanation for existing taxonomic misconceptions. In this way, we argue that the group needs a strong review and not focused only on punctual data with the observation of preserved animals. We believe that much of the data may be misleading because of this type of high phenotypic plasticity. This is already well known in Medusozoa, but in Anthozoa it has never been deeply studied.

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