

DIVERSITY OF RED MACROALGAE (RHODOPHYTA) OF SÃO PAULO STATE, BRAZIL, BASED ON BARCODING, MORPHOLOGY AND GEOGRAPHIC DISTRIBUTION (RHODO-SP)

Mariana Cabral de Oliveira

Institute of Biosciences / University of São Paulo (USP)

Main researchers: Mutue T. Fujii, Orlando Necchi Jr.

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Praia do Costa, Ubatuba, SP, illustrating one of the collection sites in the marine environment (Photos M.C. Oliveira)

In this project we propose the screening of the red macro algae (Rhodophyta) biodiversity for the State of São Paulo (Brazil), which includes more than 50% of the diversity known for this group in the country. For that, the DNA bar-coding technique will be used supplemented with morphological and geographical distribution. These data will be integrated to the Biota database. Studies on the biodiversity of marine algae from the State of São Paulo have been carried out since 1950; however, this knowledge is based on morphological data being sporadically supplemented with molecular data. The

taxonomic identification of red algae is notoriously difficult due to: (i) a relatively simple morphology and anatomy, which are convergent in many species, (ii) phenotypic plasticity and (iii) complex life-cycles with heteromorphic stages. The comparisons of DNA sequences have been fundamental for biodiversity studies and for the inference of the relationships among the different groups of organisms. The DNA bar-coding technique generates a great amount of data in relatively short time. These data, organized and available in databanks, can be used for many different types of research, including biodiversity screenings, conservation, the detection of cryptic and exotic species, development of DNA probes for various applications, taxonomy and phylogenetic studies, ecophysiology, forensics and others.

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

So far over 1,000 specimens were collected, and 906 sequences have been generated for five different molecular markers: 324 *cox1*, 160 *rbcL*, 34 SSU rDNA, 150 UPA and 238 *cox2*. Our analyses indicate that *cox1* barcode region is a suitable marker for the delineation of Rhodophyta species, supporting its use as a DNA barcode and also in identifying cryptic species and phenotypic plasticity. Moreover, once there is a reliable database of sequences available for comparison, the sequencing of *cox1* is an easy and relatively rapid tool for species identification of red algae. With the same purpose, we are also sequencing another UPA barcode marker. This second marker has shown to be a little more conserved than the *cox1*, however, it is easily amplified and sequenced. Other markers for phylogenetic analysis have also been obtained (*rbcL* and SSU) for selected species. These sequences and the morphological analyses are being deposited in the Bold database. With the obtained data, new records and species are being detected, as well as the potential introduction of exotic ones. The project also aims to list the species and their distribution in the state, as well as the production of a photographic guide.



Botryocladia bahamensis (scale 0-0.3-cm), material collected in Laje de Santos, SP (Photo R. Rocha, Jorge)

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Mariana Cabral de Oliveira

Instituto de Biociências
Universidade de São Paulo (USP)
Departamento de Botânica
Rua do Matão, travessa 14, 321, Butantã
CEP 05508-900 – São Paulo, SP – Brasil

+55-11-3091-7630
mcdolive@usp.br
<http://www.ib.usp.br/rhodosp>