A DNA BARCODE APPROACH OF THE *LAURENCIA* COMPLEX (CERAMIALES, RHODOPHYTA) IN THE TROPICAL AND SUBTROPICAL ATLANTIC OCEAN

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INTRODUCTION

The diversity of the *Laurencia* complex is being assessed in tropical and subtropical Atlantic by an international cooperation project involving Brazil, Mexico, Spain (Canary Islands), Portugal (Azores and Madeira) and USA (Florida) on the base of molecular data allied to a detailed morphological study of species. The diversity of the complex was analyzed for the first time for the Atlantic Ocean, including specimens from all five localities, using the plastid 23S rRNA gene (UPA), which has been investigated as potential DNA Barcode marker for photosynthetic eukaryotes. The COI-5P gene was also used as DNA barcode, and the *rbc*L gene was used for phylogenetic inferences.

MATERIAL AND METHODS

Samples of the *Laurencia* complex, collected in Brazil, Portugal (Azores and Madeira), Spain (Canary Islands), Mexico (Caribbean Sea) and Florida (USA), were sequenced using the markers Universal Plastid Amplicon (UPA), COI-5P and *rbc*L. For COI-5P and UPA were performed neighbor-joining (NJ) analyses using PAUP 4.0b10. For *rbc*L, the phylogenetic relationships were inferred with PAUP 4.0b10 and MrBayes v.3.0 beta 4. The range of genetic divergence for the markers used was calculated using "uncorrected 'p' distance with PAUP.

RESULTS

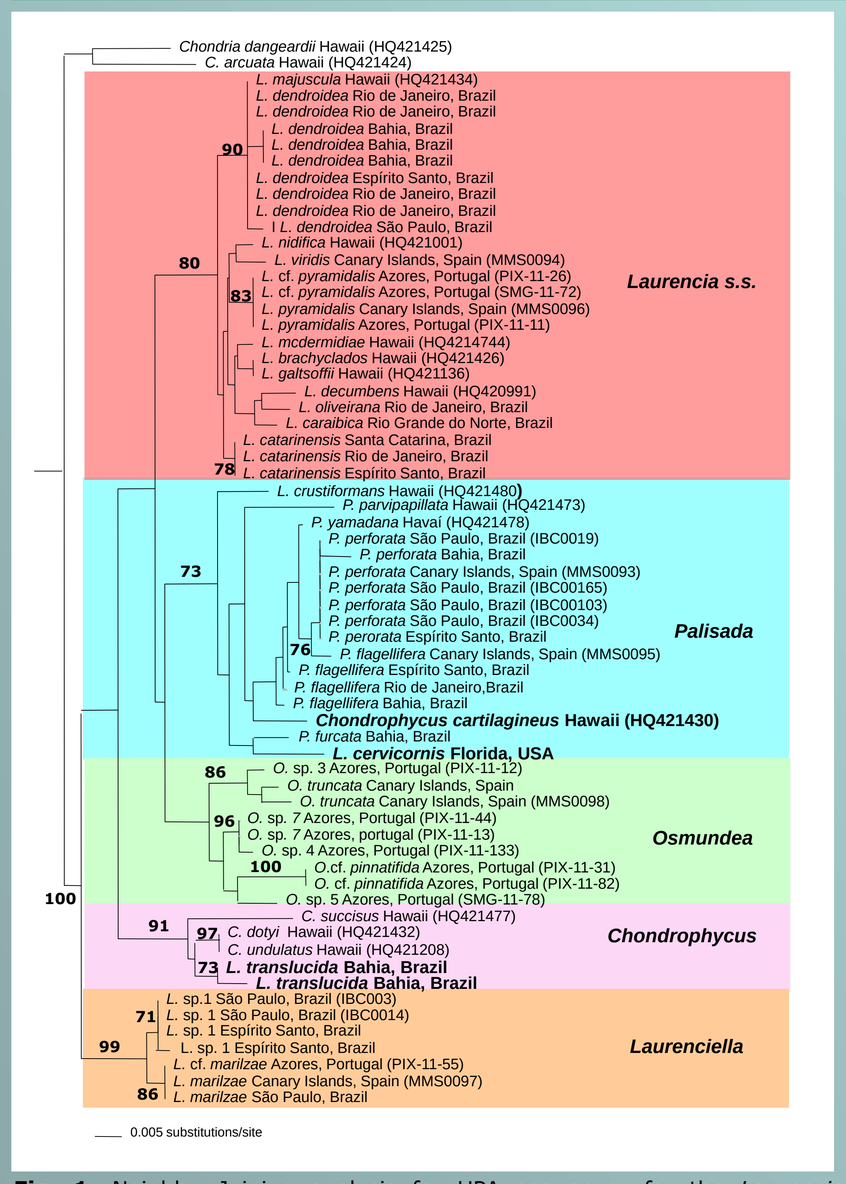


Fig. 1. Neighbor-Joining analysis for UPA sequences for the *Laurencia* complex. The bootstrap values for 2000 replicates are shown on the branches (only values above 70 were considered).

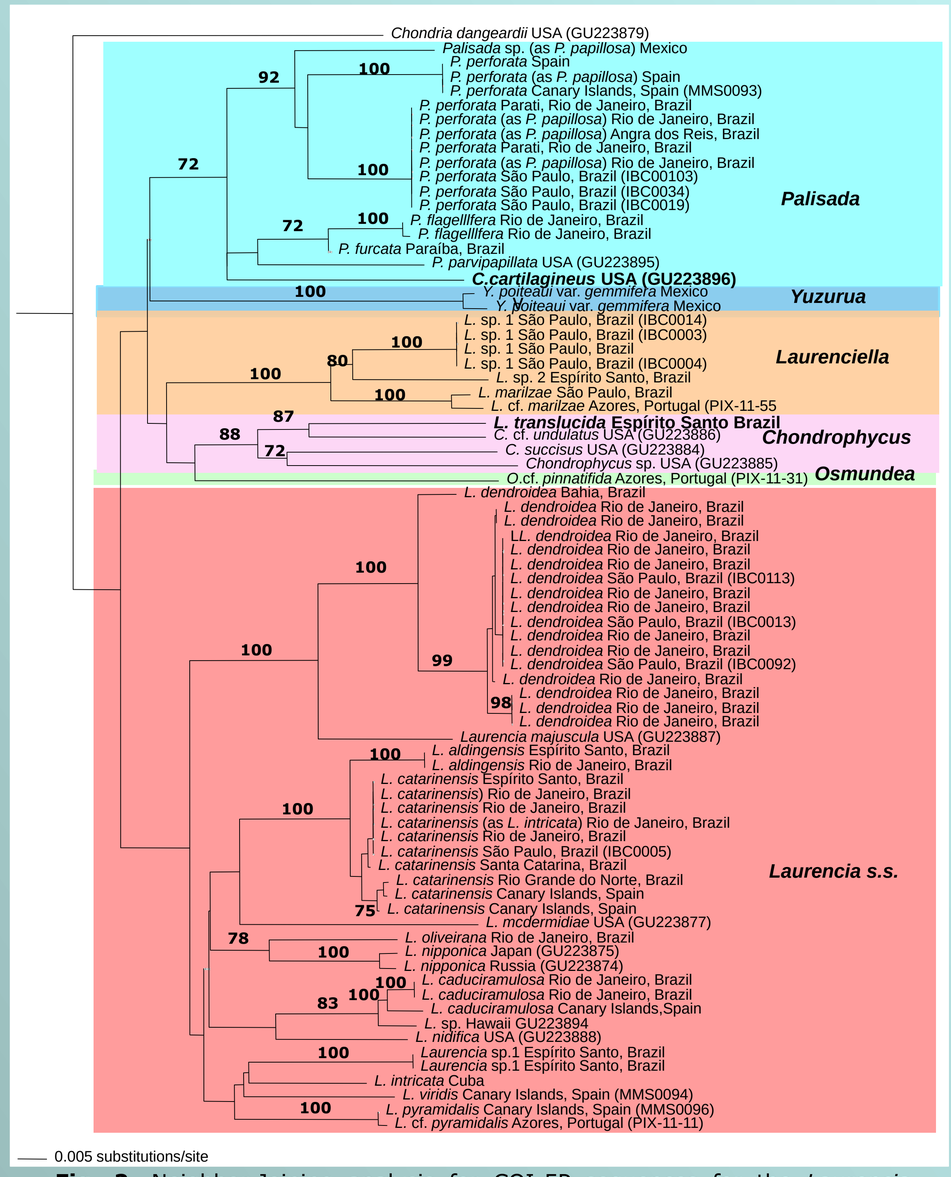
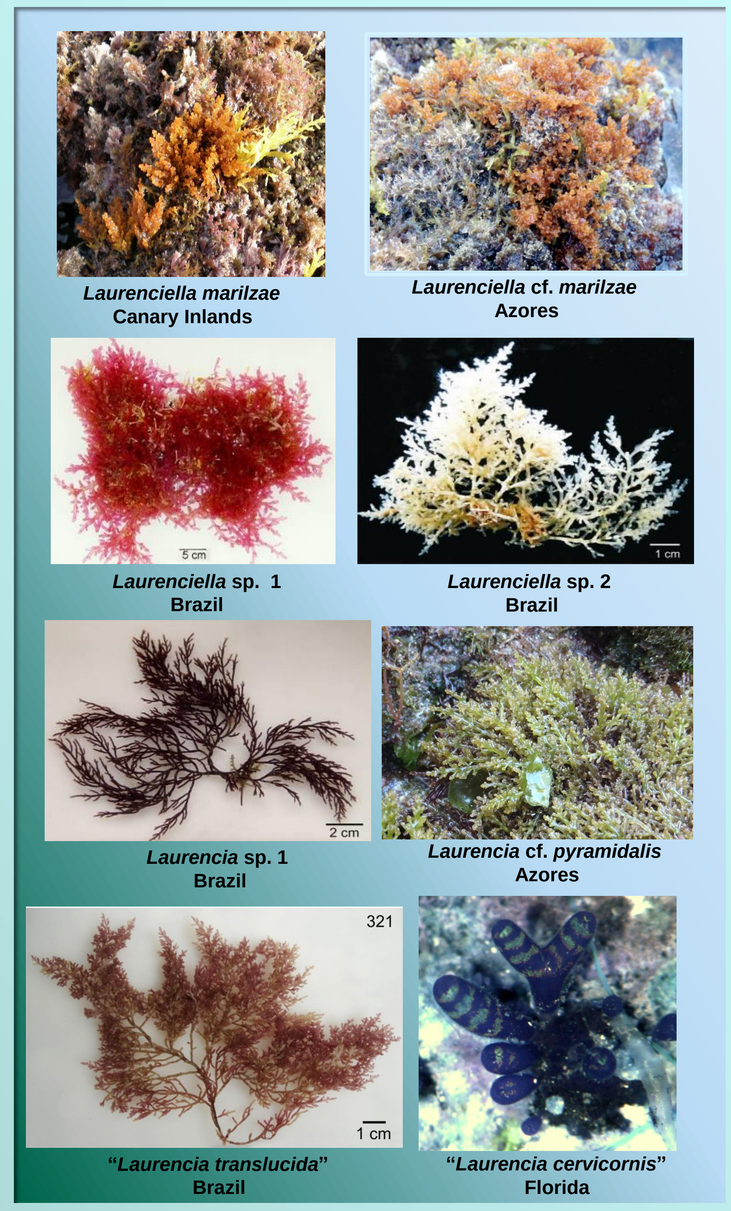


Fig. 2. Neighbor-Joining analysis for COI-5P sequences for the *Laurencia* complex. The bootstrap values for 2000 replicates are shown on the branches (only values above 70 were considered).



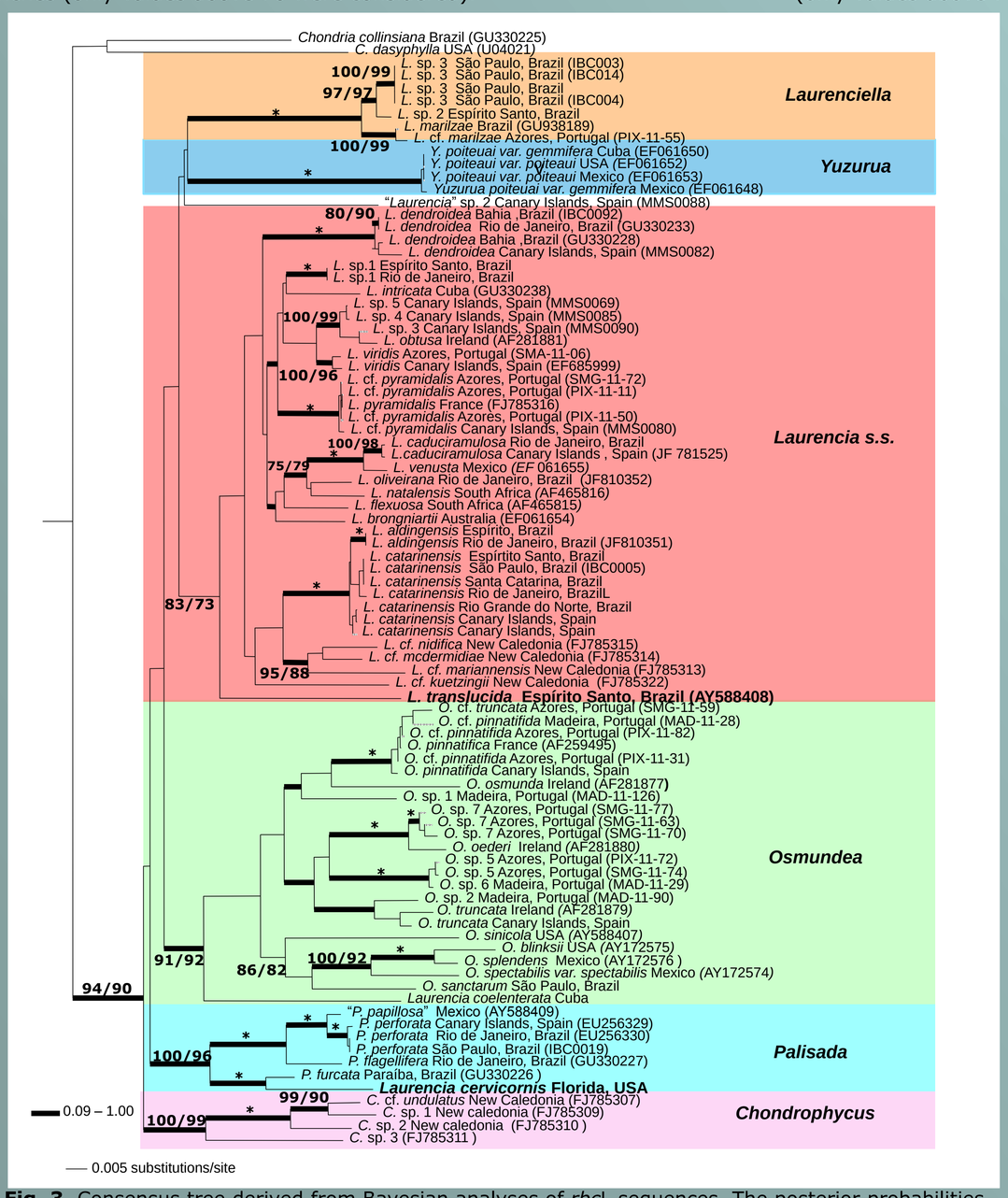


Fig. 3. Consensus tree derived from Bayesian analyses of *rbc*L sequences. The posterior probabilities are shown as thicker branches. Bootstrap supports for MP/NJ (2000 replicates) are shown at the nodes (only values above 70 were considered); *indicates bootstrap support =100%.

Tab. 1. Range of genetic divergence among DNA sequences of the *Laurencia* complex for different markers. Problematic taxa were excluded from the comparison.

Markers/ divergences (%)	*rbc*L	COI-5P	UPA
Intergeneric	5.6-11.9	6.9-13.1	3.1-7.8
Interspecific	1.9-6.2	4.0-9.3	0.8-2.9
Intraspecific	0-1	0-2.5	0-0.5

DISCUSSION

The genus *Laurenciella* established based on *rbc*L sequences was also confirmed with the use of two other markers: UPA and COI-5P, forming independent clades with high support, represented by the taxa: *L. marilzae*, *L.* sp. 1 and *L.* sp. 2. The intergeneric divergence between *Laurencia* and *Laurenciella* for UPA and COI-5P was in the range of variation obtained from other genera of the complex, 4.9-5.8% and 10.1-13.1%, respectively.

In the analyses with the UPA and COI-5P, *C. cartilagineus*, type species the genus *Chondrophycus*, joined with *Palisada*, which indicates that these two genera can be congeneric. Further analyses are necessary to clarify the position of these taxa.

The 'problematic' *Laurencia translucida*, an endemic species from Brazil, remains an enigmatic species. Its taxonomic position has always been controversial since it shares a combination of morphological characters to the genera *Chondrophycus* and *Laurencia.* Unlike the results with the *rbc*L gene, *L. translucida*, was positioned within the *Chondrophycus* clade by UPA and COI-5P markers. The *rbc*L sequence available of *L. translucida* seems to be chimeric. New *rbc*L sequences are necessary to confirm its taxonomic position.

Laurencia cervicornis from Florida joined with *Palisada* by the UPA and *rbc*L markers and its taxonomic position will also have to be better investigated.

The UPA gene showed to be more conserved, however, the same genetic groups were resolved with each of the three markers.

Financial support

P11 – A Taxonomic Study on *Calothrix* – Group (Cyanobacteria) Based on Morphology and Analysis of the 16s rRNA Gene Fragment
E. Berrendero[1], M. Bohunicka[2], L. Stenclova[1] and J. H. Kastovsky[1]
[1]University of South Bohemia, Czech Republic; [2]University of South Bohemia/Academy of Sciences of the Czech Republic, Czech Republic

P12 – Relative Contribution of Environmental and Spatial Processes in Structuring Stream Macroalgal Communities
C. Z. Branco[1], P. C. Bispo[1], C. K. Peres[2], A. F. Tonetto[1] and L. H. Branco[1]
[1]São Paulo State University - UNESP, Brazil; [2]Federal University of Latin American Integration – UNILA, Brazil

P13 – New Insights in the Diversity of the Genus *Lobophora* (Dictyotales, Phaeophyceae) Based on Molecular and Morphological Evidence
O. Camacho[1], T. Sauvage[1], W. Schmidt[1], D. W. Freshwater[2] and S. Fredericq[1]
[1]University of Louisiana at Lafayette, USA; [2]University of North Carolina Wilmington, USA

P14 – A DNA Barcode Approach of the *Laurencia* Complex (Ceramiales, Rhodophyta) in the Tropical and Subtropical Atlantic Ocean
V. Cassano[1], M. Machín-Sánchez[2], A. I. Neto[3], M. C. Oliveira[1], A. Sentíes[4], J. Díaz-Larrea[4], M. Gil-Rodríguez[2], L. Collado-Vides[5], A. Medeiros[1] and M. T. Fujii[6]
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P15 – Characterization of *Batrachospermum gelatinosum* (L.) De Candolle and *B. arcuatum* Kylin (Batrachospermales, Rhodophyta) from the Iberian Peninsula
I. S. Chapuis[1], **M. O. Paiano[2],** M. Aboal[3], P. M. Sánchez Castillo[1], O. J. Necchi[2], and M. M. Elmosallamy[4]
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P16 – Present Day Collections of Freshwater Red Algae (Batrachospermales, Rhodophyta) from Historically Important Sites in France
W. B. Chiasson, E. D. Salomaki, and M. L. Vis
Ohio University, USA

P17 – Morphology, Phylogenetic Relationships and DNA Barcoding of the Bangiales (Rhodophyta) from King George Island, Antarctic and its Adjacent Waters
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[1]Korea Polar Research Institute, Republic of Korea; [2]National Fisheries Research and Development Institute, Republic of Korea

P18 – Phycological Educational Endeavors: Assessing Algal Knowledge in Museums, Zoos, Aquariums, and Herbariums
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[1]Stony Brook University, USA; [2]Wenatchee Valley College, USA; [3]University of British Columbia, Canada; [4]Western Washington University, USA; [5]Maine Maritime Academy, USA; [6]University of Alabama at Birmingham, USA

P19 – Algal Turf Scrubbers: Periphyton Production and Nutrient Recovery on a South Florida Citrus Farm
P. E. D'Aiuto[1], T. J. Evens[2], J.P Albano[1] and J.M. Patt[1]
[1]United States Department of Agriculture, USA; [2]Algal Solutions, LLC, USA

western Atlantic and Red Sea specimens indicate newly found diversity representing four distinct species, with one unreported species each for Caribbean Colombia, Caribbean Panama, the NW Gulf of Mexico, and Egypt. These taxa in all likelihood correspond to new species. In addition, we propose range extensions for previously unnamed *Lobophora* spp. reported in Sun *et al.* 2012. Three recently collected species from the Red Sea are conspecific with recently characterized taxa from Japan, Palau and Malaysia, and one species from the NW Gulf of Mexico is conspecific with a sample from Curaçao in the Lesser Antilles. The morphological evidence for describing the new species of *Lobophora* will be discussed in light of the molecular-based results.

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Characterization of *Batrachospermum gelatinosum* (L.) De Candolle and *B. arcuatum* Kylin (Batrachospermales, Rhodophyta) from the Iberian Peninsula

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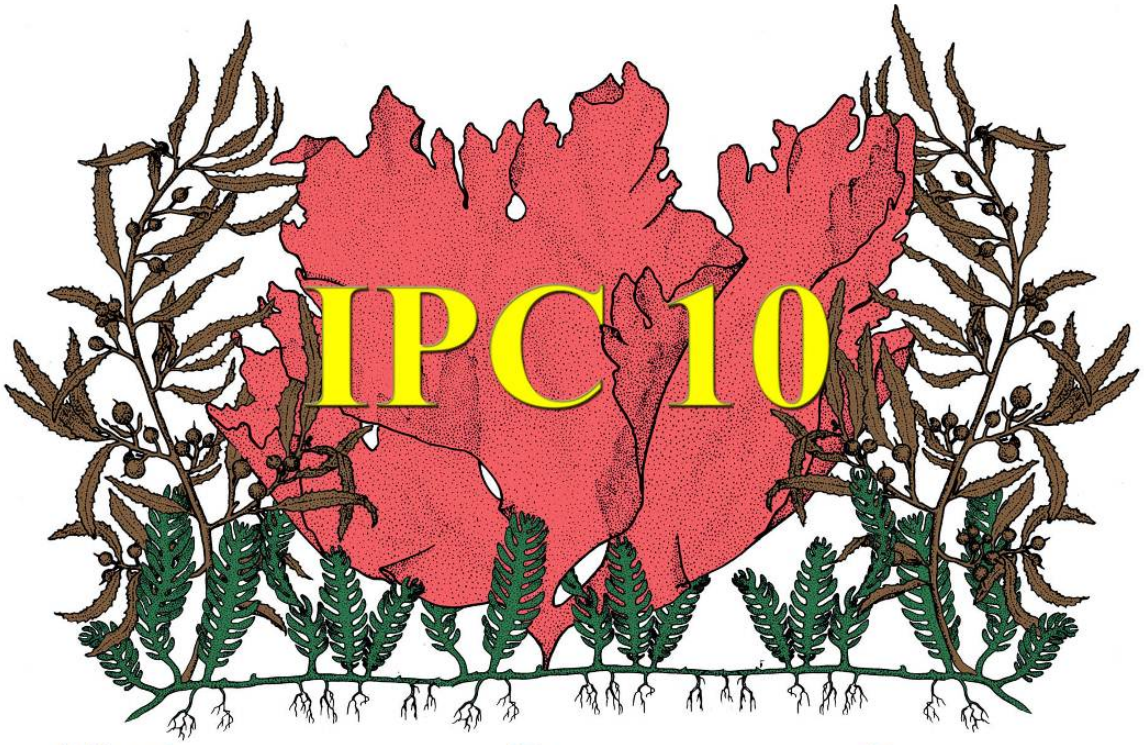
Freshwater red algae diversity in the Iberian Peninsula (Spain and Portugal) has been poorly studied. The purpose of this study is to approach the morphological and genetic variation of two most common members of the Batrachospermales in the study area, to better understand their biogeographic and phylogenetic relationships in a more global context. We compared genetically six populations each of *B. gelatinosum* and *B. arcuatum* from eight different river basins, using three molecular markers to evaluate genetic diversity: RuBisCo large subunit (rbcL) (fully sequenced at the moment), cytochrome oxidase 2-3 spacer (cox2-3) and the barcode region of cytochrome oxidase I (cox1) (preliminary data available). For the morphological comparison nine additional populations were included in the analysis. A wide morphological variation was observed for most vegetative and reproductive characters. rbcL sequences showed a relatively low genetic divergence: 98.8-100% for *B. gelatinosum* and 99.9-100% for *B. arcuatum*. We found no correlation between genetic diversity and morphological variation among the populations of both species. Some taxonomic characters are reevaluated aiming at a more reliable characterization of these species.

Program and Abstract Book



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