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DIVERSITY OF THE LAURENCIA COMPLEX (CERAMIALES, RHODOPHYTA) IN LUSITANIAN MACARONESIA

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1. INTRODUCTION

Current knowledge on the systematics of the *Laurencia* complex (Rhodophyta, Ceramiales) is based on molecular studies combined with traditional morphological characters. Previous phylogenetic analyses based on *rbc*L sequences have established six genera within this complex: *Laurencia* Lamouroux, *Osmundea* Stackhouse, *Chondrophycus* (Tokyda *et* Saito) Garbary *et* Harper, *Palisada* Nam, *Yuzurua* (Nam) Martin-Lescanne and *Laurenciella* Cassano, Gil-Rodríguez, Sentíes, Díaz-Larrea, M.C. Oliveira & M.T. Fujii. However, generic assignment and specific identification of the members of the *Laurencia* complex is still problematic due to the high phenotypic plasticity of most species as well as the overlap between characters usually considered as taxonomically informative. In that context, DNA barcoding appears as a proficient alternative to morphological features for species assignment. In the present preliminary study, we assessed the diversity of the *Laurencia* complex based on partial COI and LSU markers in *Lusitanian* Macaronesia (Azores, Madeira and Canary Islands). In addition, preliminary phylogenetic analyses were completed using three independent markers (LSU, COI and *rbc*L) as well as the combined data set, with the aim to infer the phylogenetic relationships and biogeographic affinities of members of the complex from Macaronesia.

2. MATERIALS AND METHODS

Samples of members of the *Laurencia* complex were collected in 2011-2013 in Azores, Madeira and Canary Islands (Fig.1.) Subsamples were dried and preserved in silica gel for molecular analyses. Total DNA was extracted, using the DNeasy Plant Mini Kit (Qiagen, Hilden, Germany). LSU-5' region, COI-5' region and *rbc*L gene were amplified. Sequencing reactions were performed by *Genoscope* (www.genoscope.fr, Evry, France) and *Macrogen* (dna.macrogen.com, Amsterdam, the Netherland). Forward and reverse sequence reads were assembled with the software Codoncode (Dedham, MA) and a multiple sequence alignment was constructed in MEGA 5. A Neighbor-Joining tree based on p-distances was inferred from LSU-5' and COI-5' markers to assess the species delineation. In addition, phylogenetic relationships were inferred using the three independent markers (LSU, COI and *rbc*L) as well as the combined data set, with MrBayes v.3.0 beta 4 and PhyML 3.0.

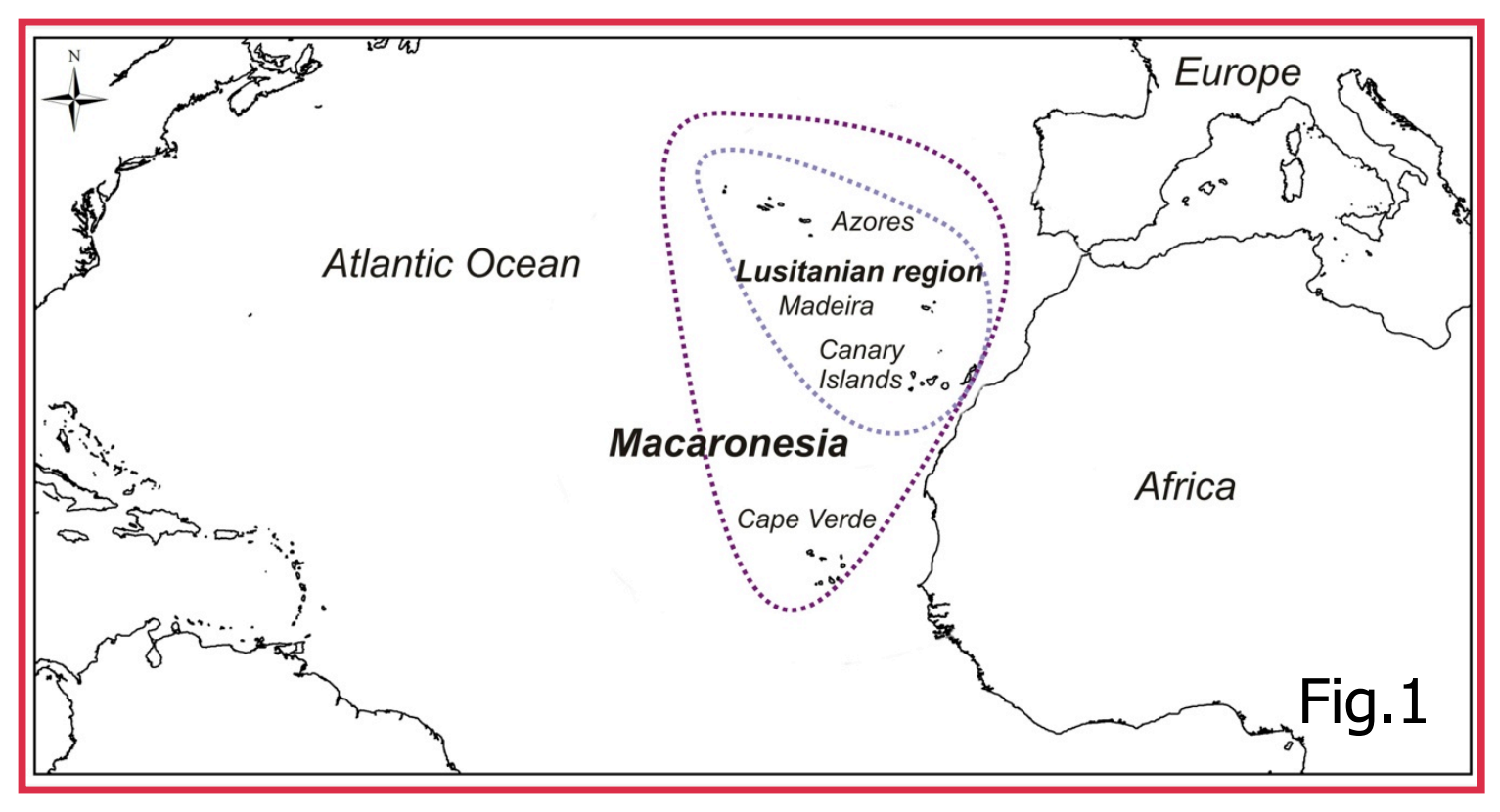

Fig.1

3. PRELIMINARY RESULTS

Fig.2

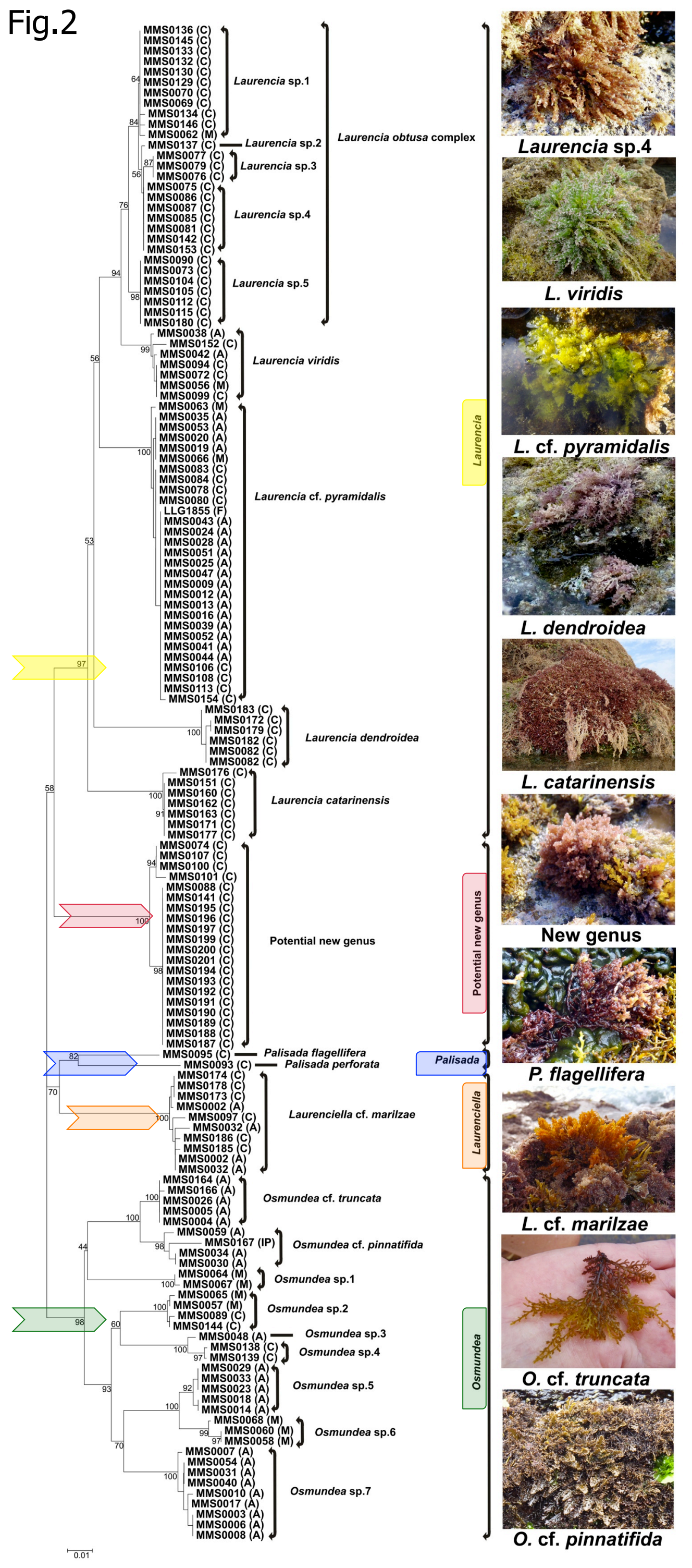

Fig.3

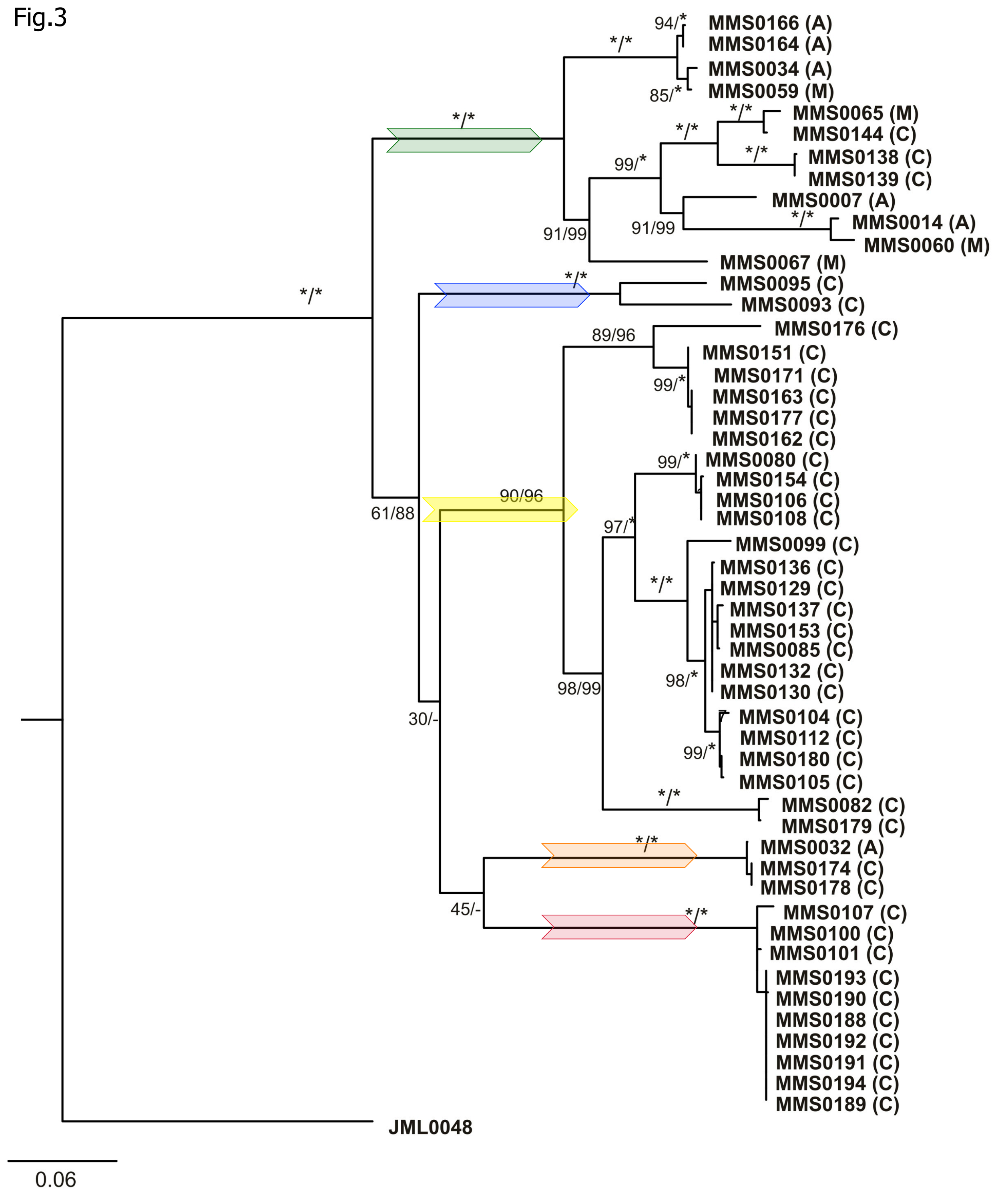

Fig.4

Fig.2. Neighbor-joining tree inferred from COI-5'. Bootstrap values are indicated at the nodes. Morphological diversity of *Laurencia* complex taxa from *Lusitanian* Macaronesia. (A) Azores; (C) Canary Islands; (M) Madeira. Fig.3. Phylogenetic hypothesis obtained by Maximum Likelihood inference of a data set containing three genes (partial LSU, COI and *rbc*L). Numbers at the nodes indicate Maximum Likelihood bootstrap values followed by Bayesian posterior probability; * bootstrap=100 and posterior probability=1. Fig.4. Maximum Likelihood phylogram inferred from analyses of *rbc*L DNA sequences. Numbers above branches correspond to support values for Maximum Likelihood bootstrap/ and Bayesian inference posterior probability; * bootstrap=100 and posterior probability=1.

5. CONCLUSIONS

1. The information obtained from the analysis of the LSU and COI sequences are consistent. Both markers are shown as powerful tools for the delineation of species. Macaronesian specimens cluster in 22 clades, which we consider correspond to *Laurencia catarinensis*, *L. dendroidea*, *L.* cf. *pyramidalis*, *L. viridis*, *Palisada flagellifera*, *P. perforata*, *Laurenciella* cf. *marilzae*, *Osmundea* cf. *truncata*, *O.* cf. *pinnatifida* and 13 potential new taxa.

2. The phylogenetics reconstructions achieved from concatenated alignment of genes LSU, COI and *rbc*L and from *rbc*L sequence analysis of specimens from Macaronesia and sequences from GenBank show the presence of 9 known species included the genera *Laurencia*, *Osmundea* and *Palisada* and 5 potential new taxa included in the *Laurencia* genus, 7 in the *Osmundea* genus and one potential new genus.

3. Our results reveal that it is necessary to conduct further analysis in order to obtain robust phylogenetic reconstructions which reflect relationships between different genus, since these are not sufficiently consistent.

4. Morphological and chemical studies of the samples in combination with the study of molecular characters will help us in the delimitation of species.

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P66 – Diversity of the *Laurencia* Complex (Ceramiales, Rhodophyta) in Lusitanian Macaronesia

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P67 – Comparison of Nutrient Requirements of Common Diatoms from Four Ecoregions in Georgia

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P68 – Evolution of Euglenoid Chloroplasts

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P69 – Will the Real Picobiliphyte Please Stand up?

L. K. Medlin[1], R. Seenivasan[2] and M. Melkonian[2]

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P70 – Diversity of Planktonic Algae in a Coastal Wetland "La Encantada", Peru

L. Mendoza, **V. Rimarachín-Ching** and I. Samanez,

Museo de Historia Natural San Marcos - UNMSM, Peru

P71 – A New Pathogenic Fungus *Alernaria* sp. Caused Red Rot Disease of *Pyropia/Porphyra yezoensis* Cultured in Northern China

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P72 – Morphological Diversity of Cyanobacteria and Microalgae in the Coastal Lomas Formations in the Peruvian Desert

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P73 – Contribution of Calcium to the Cell Wall Structure in the Brown Alga, *Ectocarpus siliculosus*

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Hokkaido University, Japan

P74 – Investigation of the *Gracilaria gracilis* Proteome Response to Nitrogen Limitation

R. K. Naidoo[1], M. S. Rafudeen[2] and V. E. Coyne[2]

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P75 – A Specific Antifouling Strategy of *Sargassum siliquastrum* (Phaeophyceae) against Epiphytism of *Neosiphonia harveyi* (Rhodophyta)

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P76 – Systematics of Section *Turfosa* of the Genus *Batrachospermum* (Batrachospermales, Rhodophyta)

O. Necchi[1], D. W. Lam[2], D. C. Agostinho[1], J. Kwandrans[3], P. Eloranta[4], J. Kostkeviciene[5], I. S. Chapuis[6] and M. L. Vis[2]

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DNA Barcoding and Geographic Range of Macroalgae from Central-Southern Chile

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Field trips carried out in rocky intertidal and shallow subtidal along the Chilean coast from 33°1' S to 43°54' S between 2011-2013 allowed us to evaluate the distribution range of several macroalgal species (Rhodophyta and Phaeophyceae). Sampling also provided material to carry out DNA barcoding analysis (mitochondrial Cytochrome Oxidase I gene - COI) in order to test the effectiveness of this method. With the data already obtained, we provided information of algal biodiversity from locations with restricted access and scarce information (e.g. southern Chiloé Island, Melinka Island). Six red algal species extended their distribution range and from those, four corresponded to non-indigenous species. Some species increased their range up to 1000 km. Mitochondrial COI gene sequences data provided rapid and accurate approach for species-level identification in several red and brown macroalgae specimens collected and will be valuable information for taxonomical and phylogeographical studies along the Southeastern Pacific. This study was funded by CONICYT-Chile through the FONDECYT 11110437 project.

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Diversity of the *Laurencia* Complex (Ceramiales, Rhodophyta) in Lusitanian Macronesia

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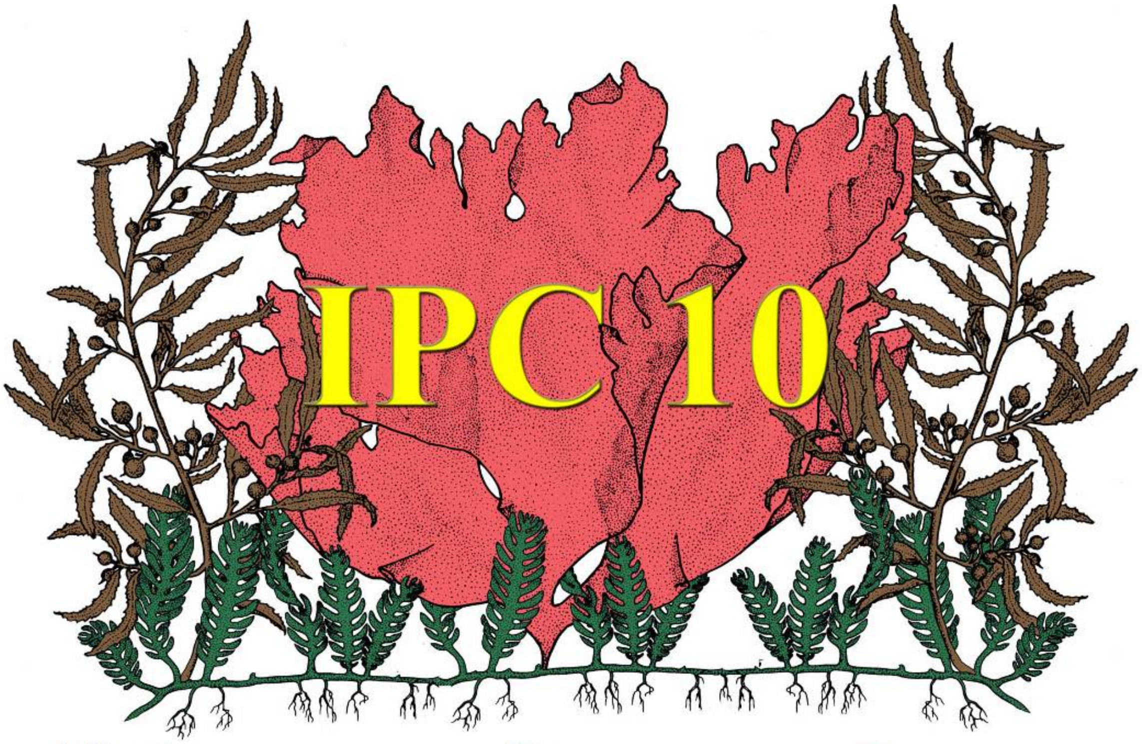
Our aim was to investigate the diversity of the *Laurencia* complex in the Azores, Madeira, Salvagens and Canary Islands, Atlantic oceanic archipelagos, which belong to the same ecoregion, Lusitanian province of the Macaronesian region. We assessed the species limits among members of the complex using DNA barcode data (partial sequences of mitochondrial COI and nuclear LSU markers). The information obtained from the analyses of COI and LSU sequences was consistent; both markers displayed adequate signal for the delineation of species. In addition, preliminary phylogenetic analyses were completed using three independent markers (rbcL, LSU, and COI) as well as the combined data set, in the aim to infer the phylogenetic relationships and biogeographic affinities of members of the complex from Macaronesia. Our results revealed the existence of several putative new species and a potential new genus included in the *Laurencia* complex. Prior the proposition of new taxa, more thorough morphological and molecular analyses of specimens of type localities, together with the results obtained in our study, are essential to assign the available taxonomic name to the different species uncovered in our studies.

Program and Abstract Book



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