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Contribution to the taxonomy of *Sargassum* with specimens from French West Indies and south of the Madagascar coasts

Rousseau F.¹, Marani G.¹, Blanfuné A.², Pena-Martin C.³, Robledo D.⁴, Le Gall L.¹ & Thibaut T.²

¹Institut de Systématique, Evolution, Biodiversité (ISYEB), France / ²Institut Méditerranéen d'Océanologie (MIO), France / ³Universidad de Alicante / ⁴Department of Marine Resources, CINVESTAV-IPN

The genus *Sargassum*, is the most diverse genus among brown algae with 360 species currently accepted¹. Although, the news highlight the abundant stranding events of two species on the coasts of the West Indies and Florida with dramatic economic consequences, the other species are all benthic. While the genus is well defined, species delineation based on morphological characters remains controversial with many species complexes for which phenotypic plasticity hampers the identification of diagnostic traits. To better evaluate species boundaries and their actual distributions, more studies coupling an integrative taxonomic approach including molecular characters and a comprehensive sampling strategy are needed.

In this study, we focused on 237 specimens mainly collected during the expeditions "Our Planet Reviewed" along the coasts of Martinique, Guadeloupe (French Antilles) and southern Madagascar.

Preliminary results on their molecular diversity are presented here as NJ trees for the two markers ITS2 and RuBisCO spacer for which we obtained the largest number of sequences. The newly produced sequences (130 for ITS2 and 58 for rbcL) were gathered with GenBank sequences used in recent studies^{2,3,4,5,6,7} to provide a first molecular identification. The best partition of species hypotheses proposed by ASAP is given at right of the trees.

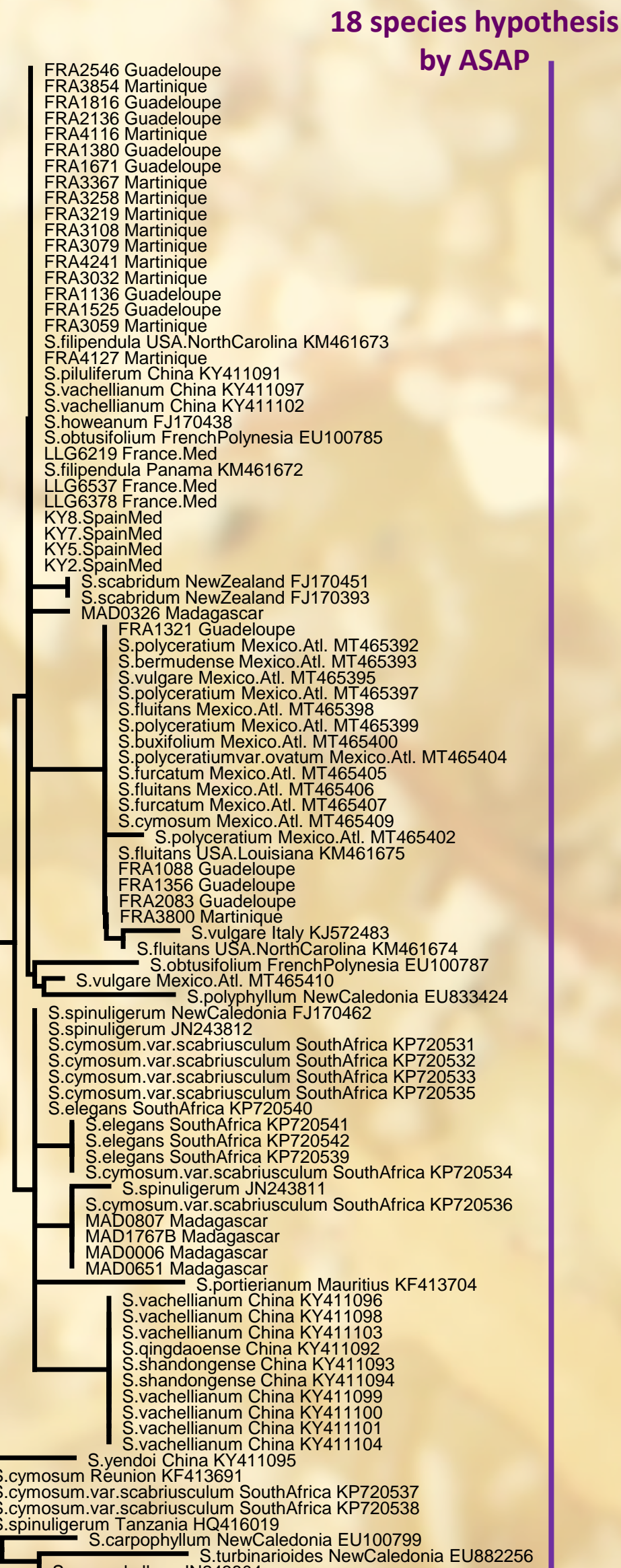
RuBisCO spacer

NJ tree (p-distance)

239 taxa

610 nt

18 species hypothesis by ASAP



Guadeloupe & Martinique only

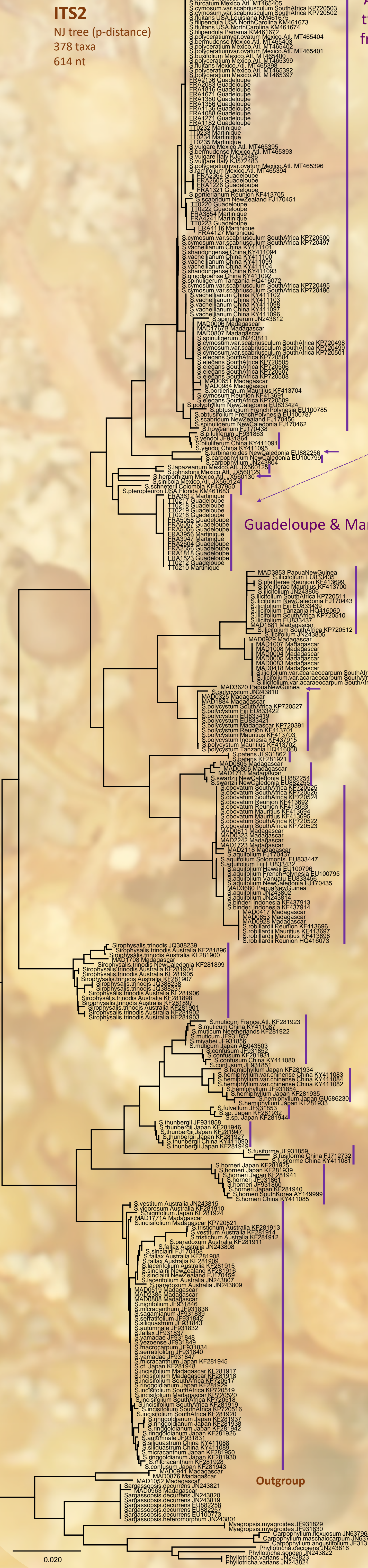
Outgroup

ITS2

NJ tree (p-distance)

378 taxa

614 nt



Guadeloupe & Martinique only

Outgroup

23 species hypothesis by ASAP



A large species complex (incl. the two pelagic ones) with specimens from Atlantic (incl. Mediterranean Sea) and Indo-Pacific coasts

Most of the sequences from specimens collected on the coasts of Guadeloupe & Martinique gathered in a group comprising at least 20 identified morphospecies. By contrast, their sequences present a very low divergence leading ASAP to propose only one species hypothesis for this group.

The other sequences of specimens from the French West Indies form an isolated lineage with no sequence match in GenBank.



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Identifying *Sargassum* species is one of taxonomists' nightmare!

It shows a strong discrepancy between the morphospecific delimitation leading to the description of 360 species and 254 infraspecific taxa and the very low sequence divergence which suggests a significant decrease of the number of species!

Both markers, ITS2 and RuBisCO spacer, used are not variable enough to allow correct delimitation at species level. Nevertheless, they remain useful for an initial identification, as they are easy to amplify and are the most represented in publicly available databases.

The aim of this preliminary study was to obtain a clearer picture of the number of species within this genus in order to select a number of specimens to sequence the genomes of the organelles.

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