Electronic Supplementary Material

The following information accompanies the article:

GENETIC DIVERSITY AND BIOGEOGRAPHICAL PATTERNS OF *CAULERPA PROLIFERA* ACROSS THE MEDITERRANEAN AND MEDITERRANEAN/ATLANTIC TRANSITION ZONE

Elena Varela-Álvarez[1(*)], Ana C. Balau[1], Núria Marbà[2], Julio Afonso-Carrillo[3], Carlos M. Duarte[2, 4] and Ester A. Serrão[1]

[1]Centro de Ciências do Mar, CCMAR-CIMAR, Universidade do Algarve, Campus de Gambelas, 8005-139 Faro, Portugal.

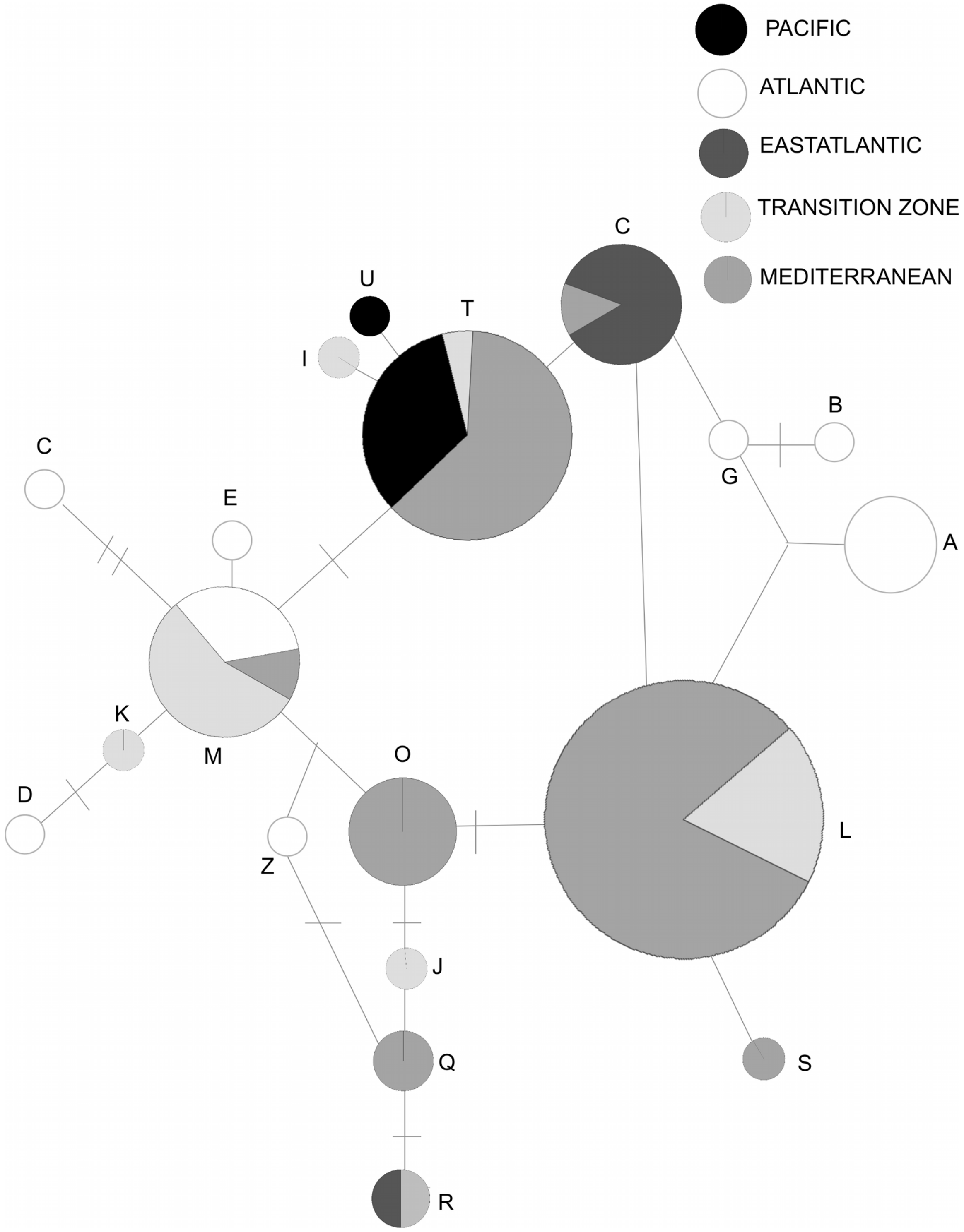
[2]Department of Global Change Research, IMEDEA, CSIC-UIB, Instituto Mediterráneo de Estudios Avanzados, 07190 Esporles, Mallorca, Spain.

[3]Departamento de Biología Vegetal (Botánica), Universidad de La Laguna, 38071 La Laguna, Canary Islands, Spain.

[4] Red Sea Research Center, King Abdullah University of Science and Technology, Thuwal, 23955-6900 Kingdom of Saudi Arabia.

(*) Corresponding author: evarela@ualg.pt and/or elena_varela@yahoo.co.uk

Figure S1: Median-joining network of 87 Nuclear ITS2 region haplotypes of *C. prolifera*. The area of each circle is proportional to the number of individuals sharing a particular haplotype. Colors refer to geographical areas, and the size of each slice is proportional to the number of sequences with that haplotype. Each haplotype is defined by its corresponding letter. A line between ITS types represents one mutational step. Pairwise distance values for all haplotypes were estimated defining the limits of parsimony above the 95% level where gaps are eliminated. The network considering gaps as events (data not shown) gave the same lack of the phylogeographical signal. Haplotypes with more than 9 mutational (H and F) steps could not be connected to the network with 95% confidence. TCS considerer in this analyses 21 profiles among the 87 sequences.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