

First insight of genetic diversity, phylogeographic relationships and population structure of marine sponge *Chondrosia reniformis* from the eastern and western Mediterranean coasts of Tunisia

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November 19, 2021

Abstract

The cytochrome oxidase subunit I (COI) gene was amplified and analyzed for 70 Mediterranean *Chondrosia reniformis*, collected from eight localities in Tunisia. Polymorphism results revealed high values of haplotype diversity (Hd) and very low nucleotide diversity (π). Thus, these results suggest that our sponge populations of *C. reniformis* may have undergone a bottleneck followed by rapid demographic expansion. This suggestion is strongly confirmed by the results of neutrality tests and “mismatch distribution”. The important number of haplotypes between localities and the high genetic differentiation (F_{st} ranged from 0.590 to 0.788) of the current *C. reniformis* populations could be maintained by the limited gene flow N_m (0.10 - 0.18). Both haplotype Network and the biogeographic analysis showed a structured distribution according to the geographic origin. *C. reniformis* populations are subdivided into two major clades: Western and Eastern Mediterranean. This pattern seems to be associated with the well-known discontinuous biogeographic area: the Siculo-Tunisian Strait, which separates two water bodies circulating with different hydrological, physical, and chemical characteristics. The short dispersal of pelagic larvae of *C. reniformis* and the marine bio-geographic barrier created high differentiation among populations. Additionally, it is noteworthy to mention that the “Mahres / Kerkennah” group diverged from Eastern groups in a single sub-clade. This result was expected, the region Mahres / Kerkennah, presented a particular marine environment.

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