

# CRYPTIC SPONGE SPECIES, MUCH MORE THAN WRONG TAXONOMICAL IDENTIFICATION

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## Abstract

Sponges represent the earliest branching metazoans in Earth, with an estimated number of ca. 12,000 species at the end of the XXI century. Many of those species are morphologically cryptic and remain to be revealed by molecular markers. By analyzing three gene partitions in individuals of the so far know *H. columella* across the Mediterranean, we concluded that it consisted of at less two morphologically cryptic species. The deep Mediterranean populations of *Hemimycale* corresponded to the Atlantic *H. columella*, while the shallow Mediterranean populations belonged in a new species. Biological traits differentiate both species more than morphological traits.

*Keywords: Rocky shores, Biodiversity, North-Western Mediterranean, South Adriatic Sea, North-Central Mediterranean*

## Introduction

Sponges are sessile, aquatic filter-feeders that represent the earliest branching metazoans in Earth, with a total of more than 8,000 accepted species and ca. 12,000 predicted to the end of the 21 century [1]. Many of those potential species remain hidden within supposed widespread morph-species [1]. Molecular markers are the tools of choice to reveal morphologically cryptic species. However, discovered new species should be also recognizable by phenotypic traits if their incorporation into taxonomy and biodiversity censuses is wanted [2]. Species that remain cryptic represent not only a drawback for sponge biodiversity assessment but to ecological and applied research projects as often they deeply differ in biological traits and thus interact in contrasting ways with other sharing habitat species.

*Hemimycale columella* (Demospongiae:Poecilosclerida) is a well known sponge, widely distributed across the Northeastern Atlantic and Mediterranean basins (<http://www.marinespecies.org/porifera>). [3] recorded that some shallow populations disappeared yearly after reproduction. However deep populations remain stable for years (authors obs.). Searching for the potential causes of these contrasting behaviors, we analyzed the species genetic differences across the Mediterranean by using three gene partitions (nuclear and mitochondrial).

## Methods

Sampling of what was known as *H. columella* was performed by Scuba diving at six locations across the North, Central and East Mediterranean basins. COI, 18S and 28S gene partitions were amplified and sequenced in at least three randomly selected individuals per population. Phylogenetic trees were constructed under the Neighbor Joining (NJ), Bayesian Inference (BI) and Maximum likelihood (ML) clustering methods. Morphological traits of the sequenced individuals were carefully examined searching for between species, phenotypic differences. Spicules were observed and measured through Scanning Electron Microscope.

## Results and discussion

The resulting phylogenies with the three gene partitions consistently separated two monophyletic groups of individuals. Those from deeper Mediterranean populations clustered with the Atlantic *H. columella* sequence downloaded from the Genbank, while sequences from shallower populations across the Mediterranean were identical and formed a well-supported distinct clade.

The spicules (anisostrongyles, exclusively) were similar in shape and size across populations. Only slight differences in external color tinges, sponge thickness and height of the ring that surrounds inhaling areas could be discerned.

The up to now known as *H. columella* is a complex of at least two morphologically cryptic species. Biological features differentiate both species more than morphological traits, as the Mediterranean clade has an annual life span while *H. columella* is multiannual. Moreover both clades harbor contrasting microbiomes (Garate et al., this symposium).

## References

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