

# Barcoding needs morphology and vice versa: the case of a new East African Sesarmid crab species

S. Fratini<sup>1</sup>, C.D. Schubart<sup>2</sup>, F. Dahdouh-Guebas<sup>3,4</sup> & S. Cannicci<sup>1</sup>

<sup>1</sup>Department of Evolutionary Biology, University of Florence, via Romana 17, Florence, Italy.

<sup>2</sup>Biologie 1, Universität Regensburg, 93040 Regensburg, Germany.

<sup>3</sup>Laboratory of Systems Ecology and Resource Management, Université Libre de Bruxelles - ULB, Av. F.D. Roosevelt 50, CPI 169, B-1050 Brussels, Belgium.

<sup>4</sup>Laboratory of Plant Biology and Nature Management, Mangrove Management Group, Vrije Universiteit Brussel -VUB, Pleinlaan 2, B-1050 Brussels, Belgium. E-mail: [sarafatini@unifi.it](mailto:sarafatini@unifi.it) / [stefano.cannicci@unifi.it](mailto:stefano.cannicci@unifi.it)

## Abstract

In 2003 a DNA-based identification system, founded on the mitochondrial gene, cytochrome c oxidase subunit 1 (mtDNA COxI), was proposed by Hebert and co-workers (2003) as a method for diagnosing species identification. Numerous studies validated this method demonstrating that congeneric species of animals/plants regularly possess substantial sequence divergence in their COI genes, generally higher than 2%. Notwithstanding, the method is bound to fail in some specific circumstances, indicating as, in our opinion, a DNA-based system must be firmly anchored within the knowledge and techniques of traditional taxonomy. Moreover, in the specific case of identifying hybrid species, due to the exclusively maternal inheritance of mtDNA, a system that also takes the nuclear genome into account needs to be adopted.

In accordance with this hypothesis, in this study we show the case of a new species of sesarmid found in Tanzanian and Kenyan mangroves of Ras Dege and Gazi Bay, respectively. The species, at a first sight, was morphologically identified as *Parasesarma lenzii*, described by Crosnier in 1965 for Madagascar. However, its genetic COxI-based comparison to *P. lenzii* specimen from Singapore revealed that our specimens did not belong to this species. In addition, based on the barcoding the collected specimens were genetically identified as *P. leptosoma*, although they looked morphologically very different from this species. Which were the reasons of these conflicting results? For resolving this question, we enlarged genetic comparisons to a total of twenty specimens of sesarmid crabs, mainly from East Africa. On the whole, three mitochondrial genes (COxI, and the large and the small rRNA subunit, 16S and 12S) and one nuclear gene (the rRNA 28S) were sequenced. The highest divergence values between species pair are generally associated to the COxI, while, conversely, the 28S is the most conservative: however, the opposite trend was recorded for the comparison between the new species and *P. leptosoma*. Results are also discussed in terms of phylogenetic relationships and speciation modality.

## Keywords

Sesarmidae, systematic, mitochondrial DNA, nuclear marker, taxonomy

## References

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