

## WHAT MOLECULAR TOOLS TELL US ABOUT OCTOPODS SYSTEMATICS ?

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Octopods systematics is still controversial and in spite of important efforts, numerous problems remain. There are nomenclatural confusions in all the geographical areas and a lot of « species complexes » are unresolved. The many inadequately described taxa and the largely single character based classification are serious handicaps for improving the current Octopods classification. To reform the systematics and to give it well-built foundations, it is necessary to begin a complete review of the group by redefining the lowest classification taxa. The genus *Octopus* which represents at least 60% of the Octopoda species must be first examined. But taking into account that the separation of the family Octopodidae into three subfamilies may not be correct, the sample studied have to be enlarged to all the Octopodidae genera.

The aim of the present work is to use molecular phylogeny as a complementary approach to bring more information about the Octopods relationships. The phylogenetic analyses are based on the 3' end of the 16S rRNA gene (500 bp) and the third sub-unit of the cytochrome oxidase gene (700 bp) at the level of both DNA and protein sequences. Phylogenetic trees were calculated under three algorithms : Neighbor-Joining, Maximum of Parsimony and Maximum Likelihood. The data were also submitted to Bootstrap tests. The usefulness and the resolution scale of the two mitochondrial markers used will be discussed. The sample studied covers a broad spectrum of the Octopoda classification including : several individuals of the cosmopolitan *Octopus vulgaris* from various geographical areas, several *Octopus* species complexes (Macropus complex, Aegina complex, etc...) and other genera of the Octopodinae, a large sample of Eledoninae species, the two more important genera of the subfamily Bathypolypodinae (*Bathypolypus* and *Benthooctopus*) and members of other families. The results obtained confirm the paraphyly of the Octopodidae. Different research directions for finding discriminant characters are proposed. The *Octopus* genus is shown to be a catch-all genus and must be recentered to fewer species. The Octopodinae genera have to be reexamined all together and it seems necessary to redefine them. A large portion of the current *Octopus* species will be included in these restored taxa. The same conclusions can be drawn for the two other subfamilies examined : Bathypolipodinae and Eledoninae.

The analyses presented highlight that the Octopod classification will view major changes over the next ten years and probably might be completely reshaped. And molecular phylogeny will actively participate to these large modifications. Molecular tools help morphologists to determine discriminant characters by confirming or not their hypotheses and by bounding monophyletic groups. So it is necessary to develop active collaborations between molecular biologists and morphologists.

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