

ASSESSMENT OF THE PHYLOGENETIC RELATIONSHIP BETWEEN *OCTOPUS VULGARIS* CUVIER, 1797 AND *O. MIMUS* GOULD 1852, USING MITOCHONDRIAL 16S rRNA

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The aim of this work was to extend our earlier work about the phylogenetic relationship between *Octopus vulgaris* and *O. mimus* using an additional gene, because the previous results were based on only one single gene, the mitochondrial cytochrome oxidase III (COIII). An additional objective was to elucidate the phylogenetic relationship between *O. vulgaris* s.s. from the Mediterranean and the so-called *O. vulgaris* from the western Atlantic. This question had to be approached since the supposed cosmopolitan distribution of *O. vulgaris* was recently called in question.

For this investigation, the diversity of 16 mitochondrial (mt) DNA sequences belonging to the inferred *Octopus vulgaris/mimus* complex and six additional octopods (*O. bimaculoides*, *O. californicus*, *O. salutii*, *Scaevurgus unicirrhus*, *Eledone moschata* and *Bathypolypus* sp.) were measured using the mt ribosomal 16S rRNA-sequences as target. Tissue samples were used from widely separated locations: coastal areas of the Mediterranean (France), Atlantic Ocean (Lanzarote, Senegal, South Africa, Tristan da Cunha, Venezuela and Brazil), the Caribbean Sea (Costa Rica) and the Pacific Ocean (Taiwan, Costa Rica and North Chile). From each sample, up to 500 base pairs of 16S rRNA were amplified by PCR, sequenced and arranged in a multiple sequences alignment. The putative phylogenetic relationships were calculated applying both distance- and character-based analyses of the data, using the PAUP*-program for the construction of phylogenetic trees.

The results obtained confirm the conclusion drawn from the earlier investigation based on COIII, and from recent morphological studies on the taxonomic position of *O. mimus* as a species distinct from *O. vulgaris*. Additional considerations deal with the distribution of *O. vulgaris* in the eastern and western Atlantic.

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Artikel/Article: [Assessment of the phylogenetic relationship between *Octopus vulgaris* Cuvier, 1797 and *O. mimus* Gould 1852, using mitochondrial 16S rRNA 117](#)