

RESEARCH ARTICLE

Octopus vulgaris (Cuvier, 1797) in the Mediterranean Sea: Genetic Diversity and Population Structure

Daniele De Luca*, Gaetano Catanese, Gabriele Procaccini, Graziano Fiorito

Stazione Zoologica Anton Dohrn, Villa Comunale, 80121, Napoli, Italy

* daniele.deluca088@gmail.com



CrossMark
click for updates

OPEN ACCESS

Citation: De Luca D, Catanese G, Procaccini G, Fiorito G (2016) *Octopus vulgaris* (Cuvier, 1797) in the Mediterranean Sea: Genetic Diversity and Population Structure. PLoS ONE 11(2): e0149496. doi:10.1371/journal.pone.0149496

Editor: Lorenzo Zane, University of Padova, ITALY

Received: July 5, 2015

Accepted: February 2, 2016

Published: February 16, 2016

Copyright: © 2016 De Luca et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: Funding provided by SP2_WP4AZ2UO03, www.ritmare.it, Ritmare Italian Flagship Project, GP GF and www.szn.it, Stazione Zoologica Anton Dohrn di Napoli, GP GF. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

Abstract

The common octopus, *Octopus vulgaris* Cuvier 1797, is a largely exploited cephalopod species in the Mediterranean Sea and the Atlantic Ocean, as well as along the coasts of Africa, Brazil and Japan, where its taxonomic identity is still debated. The assessment of its genetic structure is a pressing need to correctly manage the resource and to avoid over-fishing and collapsing of local stocks. Here we analysed genetic variation and population structure of *O. vulgaris* using thirteen microsatellite loci in seven sampling localities from the Mediterranean Sea and one from the Atlantic Ocean. We also used a DNA barcoding approach by COI gene fragment to understand the phylogenetic relationships among the specimens here investigated and the ones whose sequences are available in literature. Our results reveal high levels of allelic richness and moderate heterozygosity in all samples investigated, and a pronounced differentiation of the Atlantic and Sicilian specimens. This latter aspect seems to support the isolation of the biota within the Strait of Messina. A certain degree of differentiation was detected among the other geographic samples within the Mediterranean Sea, which is more compatible with an island model than isolation by distance. The occurrence of null alleles affected more genetic diversity indices than population structure estimations. This study provides new insights about the genetic diversity and structure of *O. vulgaris* in the area of interest, which can be used as guidelines for a fisheries management perspective.

Introduction

Marine species show contrasting patterns of population structure due to the elevated number of intervening factors. The common view of marine populations as demographically open units has been questioned over the past decades [1] and evidence is accumulating for more complex scenarios [2]. Interactions among physical and biological factors, such as marine current patterns, sea bottom topology, and dispersal capability of the species at any biological stage (gametes, larvae, juveniles, adults) can account for different levels and patterns of gene flow, requiring *ad hoc* assessments for each specific case [3–6].