Population genetic structure of *Octopus mimus* in the East Pacific

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The East Pacific can be divided into biogeographic provinces, which potentially impact the population genetic structure of marine species. *Octopus mimus* Gould, 1852 is a shallow-water species with significant fishery value. Therefore, identification and understanding of the genetic population structure of this species is essential for effective fishery management. A total of 240 *Octopus* COI gene sequences from Mexico (n = 10), Nicaragua (n = 96), and Peru (n = 134) across three biogeographic provinces (Cortez, Panamanian, and Peru-Chilean) and the Equatorial front region were analysed. A BLAST analysis at GenBank identified all sequences as *O. mimus* with a high similarity value (99.70-100 %). The Maximum likelihood phylogenetic tree grouped *O. mimus* and *O. hubbsorum* Berry, 1953 together (bootstrap value

= 96), suggesting these two species are the same. The Equatorial front population showed the highest haplotype and nucleotide diversity (h = 0.77, π = 0.48). Population expansion was observed in Panamanian and Peru-Chilean provinces. The haplotype network revealed two distinct haplogroups differing by four mutational steps. Significant population genetic structure (Φ_{ct} = 0.67, p < 0.001) was detected. The first group included populations from Cortez and Panamanian provinces, while the second group encompassed populations from the Peru-Chilean province. A similar result was obtained when populations within the Equatorial front range were grouped separately.

Additionally, 176 samples from the Panamanian province (n = 129), the Equatorial front (n = 17), and the Peru-Chilean province (n = 33) were further investigated using six nuclear microsatellite markers. In contrast to the COI sequences result, the microsatellites result shows the highest allelic richness and effective alleles (Na = 18.50, Ne = 7.90) in the Panamanian province, while the Equatorial front shows the lowest allelic diversity (Na = 11.83, Ne = 7.29). The initial AMOVA analysis from the microsatellite markers revealed a finer population structure with four groups of populations (F_{ct} = 0.037, p < 0.01), including two groups within the Panamanian province and the other two groups from the Equatorial front and Peru-Chilean provinces, respectively. This is in concordance with the four clusters of populations (Evanno's ΔK = 4) obtained from the STRUCTURE clustering analysis. These outcomes show a slight difference from COI genes AMOVA results.

The next step in this study is to delve deeper into the microsatellite results and examine the population genetic structure based on all the COI sequences from both *O. mimus* and *O. hubbsorum* available on the GenBank database. Through the analysis of a more extensive dataset and comparing results from two different genetic marker approaches, we expect to gain better insight into the population genetic structure of *O. mimus* and present more informed ideas for fishery management and conservation in this area.

Keywords
Cephalopod; Marine Fisheries; El Niño; Ocean Currents