



# Genetic differentiation of *Octopus minor* (Mollusca, Cephalopoda) off the northern coast of China as revealed by amplified fragment length polymorphisms

J.M. Yang<sup>1</sup>, G.H. Sun<sup>1</sup>, X.D. Zheng<sup>2,3</sup>, L.H. Ren<sup>1</sup>, W.J. Wang<sup>1</sup>, G.R. Li<sup>1,4</sup> and B.C. Sun<sup>5</sup>

<sup>1</sup>Shandong Marine Resource and Environment Research Institute, Yantai, China

<sup>2</sup>Fisheries College, Ocean University of China, Qingdao, China

<sup>3</sup>Institute of Evolution and Marine Biodiversity, Ocean University of China, Qingdao, China

<sup>4</sup>Fisheries and Life Science College, Shanghai Ocean University, Shanghai, China

<sup>5</sup>Freshwater Fisheries Research Institute of Linyi, Linyi, China

Corresponding author: X.D. Zheng

E-mail: [xdzheng@ouc.edu.cn](mailto:xdzheng@ouc.edu.cn)

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**ABSTRACT.** *Octopus minor* (Sasaki, 1920) is an economically important cephalopod that is found in the northern coastal waters of China. In this study, we investigated genetic differentiation in fishery populations using amplified fragment length polymorphisms (AFLPs). A total of 150 individuals were collected from five locations: Dalian (DL), Yantai (YT), Qingdao (QD), Lianyungang (LY), and Zhoushan (ZS), and 243 reproducible bands were amplified using five AFLP primer combinations. The percentage of polymorphic bands ranged from 53.33 to 76.08%. Nei's genetic identity ranged from 0.9139 to 0.9713, and the genetic distance ranged from 0.0291 to 0.0900. A phylogenetic tree was

constructed using the unweighted pair group method with arithmetic mean, based on the genetic distance. The DL and YT populations originated from one clade, while the QD, LY, and ZS populations originated from another. The results indicate that the *O. minor* stock consisted of two genetic populations with an overall significantly analogous  $F_{ST}$  value (0.1088,  $P < 0.05$ ). Most of the variance was within populations. These findings will be important for more sustainable octopus fisheries, so that this marine resource can be conserved for its long-term utilization.

**Key words:** *Octopus minor*; Population structure; North China coast; AFLP