

CLASSIFICATION OF SPINY LOBSTERS IN VIET NAM USING DNA BARCODING

Nguyen Anh Hieu, Nguyen Nguyen Thanh Nhon,
Đang Thuy Binh, Duong Van Sang, Pham Thi Hanh

Summary

Lobster is a nutritious food with high commercial value and is the main aquaculture species in Vietnam. Despite its ecological and economic importance, the taxonomic status of lobster species (especially spiny lobsters) has not been fully resolved. The present study collects 4 common lobster species (*Panulirus ornatus*, *P. homarus*, *P. polyphagus* and *P. longipes*) in Central Vietnam, *P. ornatus* (Australia), *P. ornatus* and *P. homarus* (Sri Lanka). DNA barcoding techniques were applied to molecular identification, to investigate the evolutionary relationships and haplotype diversity of lobster species. The results showed that the genetic difference of *P. polyphagus* is lowest (0-1,3%), while the genetic difference of *P. longipes* is highest (0-5.3%) due to the existence of two subspecies. The phylogenetic tree and haplotype networks showed a wide geographical connection of lobster species. *P. homarus*, *P. polyphagus* and *P. longipes* showed a highly geographic variation across individual haplotypes. Using DNA barcodes to the classification of 4 species of lobster in Vietnam, the similarity of each species compared to the sequence on Genbank is very high: *P. ornatus* is 99.84 – 99.98%, *P. homarus* is 99.94-99.98%, *P. polyphagus* is 99.68 – 99.98%, *P. longipes* is 99.07 - 100%. This study contributes to show the genetic of lobster in Vietnam, providing a scientific basis for resource management and sustainable aquaculture.

Keywords: Classification, DNA barcode, lobster