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Molecular study and identification of sea urchin from the Persian Gulf using 16SrDNA

Maryam Tala[1]
Saeid Tamadoni Jahromi[2*]

1- Assistant professor, Department of fisheries, Qeshm Branch, Islamic Azad University, Qeshm, Iran, Iran.
2- Associate Professor, Persian Gulf and Oman Sea Ecology Research Center, Iranian Fisheries Sciences Research Institute, Agricultural Research Education and Extension Organization (AREEO), Bandar Abbas, Iran.

***Corresponding author:**
stamadoni@gmail.com

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Abstract

Phylogeny and distribution patterns of sea urchins of the genus *Echinometra* (*Echinodermata*, *Echinoidea*) have been widely used as an outstanding model for marine speciation. In this study, the genealogy of this genus was carried out in the Persian Gulf region (Hormuz Island) in the fall 2022. After DNA extraction and sequencing using 16SrDNA gene, the genetic distance of this genus was compared and analyzed with other species reported from other parts of the world. This study showed a high degree of polymorphism and high amounts of genetic diversity between the genus *Echinometra* and other species, including in the species *Echinus esculentus* with a genetic distance of more than 32%. In this study, the genetic analysis of the sequences confirmed that Species such as H. *australiae*, H. *erythrogromma*, *bajulus Heliocidaris crassispina*, *Heliocidaris H.tubervulata*, *Pseudocentrotus depressus*, *Sterechinus neumayeri*, *Paracentrotus lividus*, *Loxechinus albus* and also *Echinus esculentus* from areas such as Canada, Australia, South Korea, Japan, New Zealand, and England were placed in the first Clyde. Also, the new sequence obtained from the genus *Echinometra* was placed in the second clade with the sequences reported from other species such as *Toxopneustes pileolus*, *Sphaerechinus granularis*, *Tripneustes gratili* from areas of the Atlantic Ocean such as Panama as well as Malaysia, South Korea and France. In the present study, the evolutionary tree shows a new haplotype of *Echinometra* genus with high genetic difference, which was distinguished from other samples registered in the World Gene Bank.

Keywords: Sea urchin, 16SrDNA, Persian Gulf.