Journal of Marine Biology I. A. U. Ahvaz – Spring 2020 –VOL.45

Population structure of sea cucumber *Holothuria parva* by 16S rRNA mitochondrial in the costs of Bushehrand Halileh from Persian Gulf

Mohammad Khalil Pazir[1]
Ashkan Ajdari[2]
Seyed Ahmad Ghasemi[3]

1. Iranian Shrimp Research Center, Iranian Fisheries Science Research Institute, Agricultural Research, Education & Extention Organization (AREEO), Bushehr, Iran.
2. Offshore fisheries Research Center, Iranian Fisheries Science Research Institute, Agricultural Research, Education & Extention Organization (AREEO), Bushehr, Iran.
3. Department of Marine Biotechnology, Persian Gulf Studies and Research Center, Bushehr Persian Gulf University, Iran.

***Corresponding author:**

Received date: 2020.03.12
Reception date: 2020.04.30

Abstract

Population structure of sea cucumber *Holothuria parva* in the coasts of Bushehr and Halileh from Persian Gulf was determined by 16S rRNA of mitochondrial genome sequencing in autumn and winter seasons of 2019. In Bushehr and Halileh populations, 2 and 4 haplotypes were identified out of 374 nucleotide sites, respectively, and haplotype 2 was the most abundant in Bushehr population and was observed as a common haplotype with Halileh population. The average haplotypes diversity on the coasts of Bushehr and Halileh was 0.5 and 1, respectively, but nucleotide diversity in the above two populations was 0.0013 and 0.0053, respectively. Due to the high gene flow in the studied populations and the low genetic distance, gene differentiation in both populations was -0.111. Therefore, based on the above and common of the haplotype, it is possible that *H. parva* collected from the cost of Bushehr and Halileh was the same population.

Keyword: *Holothuria parva*, Haplotype, 16S rRNA, Bushehr, Persian Gulf.