Genetic variability and structure of *Mnemiopsis leidyi* Populations in the Caspian and Black Seas based on mitochondrial DNA sequencing

Laloei F. [1*]; Taghavi M.L.[1]; Roohi M.L.[2]

1-Department of Biotechnology, Ecology research center of the Caspian Sea, Sari, Iran.
2- Department of Biology, Ecology research center of the Caspian Sea, Sari, Iran.
* Corresponding author's email: Laloei@yahoo.com

Abstract:

The genomes of three groups of *Mnemiopsis leidyi* (Black sea, north and south of the Caspian Sea) were comparatively analyzed with mitochondrial DNA sequencing. Genetic distances were computed based on the allele frequency. The Hardy-Weinberg Equilibrium was checked according to the test of χ^2. Genetic differentiation and hierarchical partition of genetic diversity were evaluated by F_{ST}. A clustering dendrogram was made based on the results of N.J. methods using the MEGA4 software package. The sequence fragment was 520- 560 base pairs (bp). Ten alleles resulted in 15 genotypes across in all three populations. The level of genetic variability was moderate in the three populations. Number of alleles in Black sea, north and south of the Caspian Sea were 5, 7, 6 and the average expected heterozygosity values were 0.69, 0.74, and 0.71, respectively. On the other hand, F_{ST} values ranged between 0.125 to 0.211 in the populations. Two populations of south and north of the Caspian Sea were from most distinct (F_{ST}=0.211). Significant deviations from Hardy–Weinberg equilibrium at the variable sites were in each population. The AMOVA analysis is consistent with the previous analysis. Genetic variation within population is very high (89%), while among populations within regions and among regions is low (8.0% and 3.0% respectively).The Neighbour-joining dendrogram constructed on the basis of the D_A distances showed only two major cluster consisting of the Black sea (3 individuals) population and the other populations.

Keywords: *Mnemiopsis leidyi*; Sequencing; Mitochondrial DNA; Population genetic