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Phenotype and genotype variation of different population of striped red mullet (Mullus surmuletus, Linnaeus 1758)

Samy Yehya El-Zaeem Alexandria University, Egypt

Tariation in phenotype and genotype based on morphometric, landmark based on morphometric character indices, meristic counts and ISSR fingerprint of different population of striped red mullet (Mullus surmuletus), from different environments; Alexandria, Red sea, Senegal and China were analyzed phylogenetically to study and compare the amount of differences in phenotypes and genotype. The results revealed that there were significant differences (P≤0.05) in most of morphometric and landmark based on morphometric character indices, while insignificant differences were detected meristic counts among different population tested. The hierarchical cluster analysis based on quantitative phenotype (morphometric landmark-morphometric and meristic character indices), grouped the four population into three major category groups; the first: Alexandria and Senegal group; the second: Alexandria, Senegal and Red sea population; and the third: China population group. A dendrogram also showed that Alexandria and Senegal group appears to be more phenotypically similar compared to Red sea population. Moreover, China population group appears to be more phenotypically different compared to the others. The results of genetic similarity coefficients among the different population of striped red mullet based on ISSR showed the highest interpopulation genetic similarity (83%) between Alexandria and Red sea population. While, the lowest genetic similarity (65%) was recorded between Red sea and Senegal populations. Therefore, it was observed in this study that either the phenotype analysis or the genotype analysis based on ISSR fingerprinting can be used to discriminate fish populations up to the intraspecific level, or both the phenotype and genotype analyses can be used to assess the degree of phenotypic plasticity shown by different phenotypes.

selzaeem@yahoo.com