

Dear Dr. Dr. Qaraman M. Koyee

I am writing to invite you to review the following manuscript, which has been submitted to Basrah Journal of Agricultural Sciences:

Manuscript Number: **BJAS-D-050-021**

Genetic variation among fish species in terms of evolution and lineages

For your convenience, the Abstract is provided below.

Abstract: Three tests of phylogenetic including likelihood-joining tree, neighbour-joining tree, and minimum evolution tree have been used using *sox3* gene. Here, phylogenetic analysis was used to detect the genetic affinity and common ancestors for selected species that belong to the same or different families. This study showed the most appropriate methods for testing the genetic affinity among species and the methodology of each test according to the requirement of molecular applications. RNA predicted structure and minimum free energy were also included in this study because of their contribution to the detection of the orthologous gene and variance in RNA folding among species related to the different families. The genetic distance in the studied populations was calculated to know the most appropriate way to find out the genetic similarity among the studied species. The low distance-variance value of each group indicated significant genetic affinity among the species of the same family, this result is more consistent with the test of maximum-likelihood tree indicating the validity of this test to measure the genetic affinity among species that have common ancestors.

We hope you are willing to review of the manuscript. If so, would you be so kind as to return your review to us during 15 days.

Thank you



**Editor Prof. Dr. Atheer H. Ali
10th May 2021**