

Phylogenetic Analysis of the Thunnus Tuna Fish Using Cytochrome C Oxidase Subunit I Gene Sequence

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Abstract : Species in Thunnus are organized due to the similarity between them. The closeness between *T. maccoyii*, *T. thynnus*, *T. tonggol*, *T. atlanticus*, *T. albacares*, *T. obsesus*, *T. alalunga*, and *T. orientalis* are in different degrees. However, the genetic pattern of differentiation has not been presented based on individuals yet, to the author's best knowledge. Hence, we aimed to analyze the difference in individuals level of tuna species to identify the factors that contribute to the maternal lineage variety using Cytochrome c oxidase subunit I (COXI) gene sequences. Our analyses provided evidence of sharing lineages in the Thunnus. A phylogenetic analysis revealed that these lineages are basal to the other sequences. We also showed a close connection between the *T. tonggol*, *T. thynnus*, and *T. albacares* populations. Also, the majority of the *T. orientalis* samples were clustered with the *T. alalunga* and, then, *T. atlanticus* populations. Phylogenetic trees and migration modeling revealed high proximity of *T. thynnus* sequences to a few *T. orientalis* and suggested possible gene flow with *T. tonggol* and *T. albacares* lineages, while all *T. obsesus* samples indicated unique clustering with each other. Our results support the presence of old maternal lineages in Thunnus, as a legacy of an ancient wave of colonization or migration.

Keywords : Thunnus Tuna, phylogeny, maternal lineage, COXI gene

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