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**DEVELOPMENT AND EVALUATION OF SOME
MOLECULAR MARKERS IN EGYPTIAN
TILAPIINE**

By

HAGAR TAREK MAHMOUD ALI ELHIFNAWY

B.Sc. Agric. Sci., (Biotechnology), Fac. Agric., Ain Shams University, 2014

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Approval Sheet

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ABSTRACT

Hagar Tarek Mahmoud Ali Elhifnawy: Development and Evaluation of some Molecular Markers in Egyptian Tilapiine, Unpublished Master Thesis, Department of Genetics, Faculty of Agriculture, Ain Shams University, 2020

Tilapia are mainly freshwater fish inhabiting shallow streams, ponds, rivers and lakes and less commonly found living in brackish water. The *Tilapia zillii* was found in different water systems (Fresh and Brackish). The mtDNA D-loop sequencing of random *T. zillii* samples collected from different open and closed freshwater/brackish water bodies in Egypt was performed to define its population structure and invasive network among sampled locations to understand its effect on the Tilapia aquaculture industry in Egypt. The fresh population, Nasser lake showed the highest number of different haplotypes ($H = 5$), on the other hand, the brackish populations Ismailia farms and Idku lake recorded the highest level of haplotype diversity (1.00) but less haplotype number (3), in addition to the result of AMOVA, the water type grouping showed more variation within locations and among groups, and this reflects its importance in the distribution of fish besides. The *T. zillii* was found in different water systems (Fresh and Brackish), that concluded its ability to tolerate moderate water salinity levels. The sampled population was found to be structured; genetic differentiation was higher due to water type than water system. Nasser lake population was found to be the most diverse location in Egypt and considered to be a water gateway to the rest of the locations. Movement of the most widespread haplotypes was found to be linked through Nile water stream; however, it reaches closed systems through human factor (hatcheries and fry).

Keywords: *Tilapia zilli*, mitochondria control region, population genetics, invasive network

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