HSP70 DNA SEQUENCE VARIATION IN GENETICALLY ENHANCED TILAPIA STRAINS OF FARMED TILAPIA (*Oreochromis niloticus*)

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ABSTRACT

GER, LAUREN CHRISTINE E., Department of Biological Sciences, College of Arts and Sciences, Central Luzon State University, Science City of Munoz, Nueva Ecija, Philippines, **JUNE 2019, HSP70 DNA SEQUENCE VARIATION IN GENETICALLY ENHANCED TILAPIA STRAINS OF FARMED TILAPIA (*Oreochromis niloticus*)**

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The HSP70 is considered as most conserved member of Heat Shock Proteins that is regulated during thermal stress. It is an ATP- dependent molecular chaperone that participates in wide range of cellular processes especially in protein folding and remodeling. HSP70 has been verified to govern in fish during stress and in the occurrence of damaged protein. In this study six genetically enhanced tilapia strains (GIFT, GET EXCEL, iBEST, Red tilapia- BFAR, Red tilapia –FAC CLSU and FaST) have been used. Using maximum parsimony, maximum likelihood and neighbor –joining showed the hyperdiversity of FaST strain on other tilapia strains that may assume that it will perform differently from other strains. The other five strains (GIFT, iBEST, Red tilapia –BFAR, Red Tilapia –FAC CLSU and GET EXCEL) showed no variation from each other. Also the separation of clades between genetically enhanced tilapia strains and their founder stocks. The branch length of genetically enhanced strains was always extended. This also revealed that there is no significant difference in terms of HSP70 DNA sequences from each other and indicates that they have an equal potential to completely adapt to climate change especially in intense heat.

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