PHYLOGENY OF PHILIPPINE RED TILAPIA USING MITOCHONDRIAL GENE MARKERS

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ABSTRACT

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Red tilapia is among the enhanced strains of tilapia in the Philippines developed for attractive skin coloration, fast growth and high consumer acceptance. Despite widespread use and commercial importance, little is known about its genetic variation especially on the color variants. This study was focused on the phylogenetic relationship of red tilapia in the Philippines.

Samples of red tilapia hybrids from Laguna, Batangas, Zambales, Red hybrid at FaST facilities and FAC Red were collected at Freshwater Aquaculture Center (FAC) and Bureau of Fisheries and Aquatic Resources at Science City of Muñoz, Nueva Ecija. DNA from muscle and fin tissues were extracted. Amplification of D-Loop and 16S rRNA was done through polymerase chain reaction. Resulting sequences were subjected to BLAST. Phylogenetic trees were generated through MEGA 7.0.

All trees generated using concatenated 16s rRNA and Dloop, 16S rRNA, D-loop in Maximum Parsimony, Maximum Likelihood and Neighbor joining showed identical or similar topologies supported by high bootstrap values. The red hybrids from Laguna, Batangas, Zambales, Red hybrid at FaST facilities and FAC Red are closely related. The study highlights the hyper-divergence of the red hybrid developed by BFAR which

diverged away from the other red strains and other founder stocks. This implies high variation of this strain from the other red strains.

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