

Ohnmar Aung 2009: Genetic Diversity of Hatchery and Wild Populations of *Cirrhinus cirrhosus* (Bloch, 1795) in Myanmar. Master of Science (Aquaculture), Major Field: Aquaculture, Department of Aquaculture. Thesis Advisor: Associate Professor Supawadee Poompuang, Ph.D. 70 pages.

Six microsatellite loci from *Barbodes gonionotus*, *Cyprinus carpio* and *Labeo rohita* were used to reveal genetic difference from five wild and five domesticated stocks of mrigal, *Cirrhinus cirrhosus* in Myanmar and one hatchery stock in Vietnam. Two hundred and eleven wild samples were collected from the Ayeyarwaddy and Thanlwin River systems and 216 samples were collected from five hatcheries stations under the Department of Fisheries. Forty three samples from a hatchery in Vietnam were used for comparative purposes.

All microsatellite loci examined displayed high levels of polymorphism in all populations. A total of 112 alleles were detected at six loci, ranging from 10 alleles at locus *Bgon22* to 29 alleles at locus *MFW17*. For Myanmar populations, mean number of allelic richness ( $A_r$ ) in the hatchery samples ranged from 5.24 to 8.41, and in the wild samples ranged from 5.34 to 8.52. Vietnam hatchery stock, however, exhibited lower value of allelic richness at 2.31. Expected heterozygosities ranged from 0.56 to 0.79 in the wild samples and from 0.69 to 0.79 in the hatchery populations. Six populations showed significant deviations from H-W equilibrium for all loci after sequential Bonferroni adjustment.

The estimate of  $F_{ST}$  value (0.134) indicated high levels of differentiation among populations. The MDS plot based on pairwise  $F_{ST}$  values displayed four groups of Myanmar samples and a distinct group of VN samples which separated from the rest. Results of clustering analysis were in agreement with the MDS analysis. AMOVA analysis revealed no genetic differentiation between wild and hatchery samples from Myanmar ( $F_{CT} = 0.000$ ;  $P > 0.05$ ), and 97.15% of genetic variation could be attributed to within populations variation ( $F_{ST} = 0.028$ ;  $P < 0.05$ ). In conclusion, Myanmar populations exhibited relative high genetic diversity and cryptic population genetic structure was found in the hatchery populations. The population genetic information obtained in this study should prove useful for aquaculture management, breeding programs and enhancement programs of mrigal populations in Myanmar.

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