Nut Munpholsri 2014: Development of Microsatellite Markers and Their Application in Population Genetics Studies of Short Mackerel *Rastrelliger brachysoma* (Bleeker, 1851) and Indian Mackerel *R. kanagurta* (Cuvier, 1816). Master of Science (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Associate Professor Supawadee Poompuang, Ph.D. 90 pages

The aim of this study was to develop microsatellite markers for population genetics of *R. brachysoma* and its congener *R. kanagurta* from the Andaman Sea of Thailand. Because the two species share very similar morphology, Truss system analysis was used to confirm their identification. A total of 413 fish were measured. Mean values (± SD) were 15.51±1.14 cm and 18.77±1.19 cm for folk length, 4.31±0.38 cm and 4.64±0.31 cm for body depth, and 3.60±0.16 and 4.04±0.18 for ratio between fork length and body depth of *R. brachysoma* and *R. kanagurta*, respectively. Two principal components clearly separated fish samples into two groups.

Microsatellites were isolated from an enriched library, of which 64 positive clones from 331 contained 18 microsatellite loci. Primers were designed for 11 loci and six loci with dinucleotide repeats amplified DNA samples of *R. brachysoma*. Characterization of these six loci in *R. brachysoma* from the Gulf of Thailand (N = 52) revealed that the average number of alleles per locus ranged from four to ten alleles. Cross-amplification of six microsatellites was observed in *R. kanagurta*. However, two loci were in linkage disequilibrium ($P< 0.05$). Population genetics studies of short mackerel and Indian mackerel were based on data from four loci, including *Rbr-7*, *Rbr-8*, *Rbr-13* and *Rbr-14*. All four populations of R. brachysoma, two from the Gulf of Thailand (Samutsongkram and Petchaburee) and two from the Andaman Sea (Ranong and Satul), displayed similar and moderate genetic variation with an average of 5.7 to 7 alleles per locus and average observed heterozygosity at all loci of 0.44 to 0.5. There was no genetic differentiation among populations (F_{ST}= -0.0043). Two groups of *R. brachysoma* were displayed by the UPGMA dendogram, with bootstrap values of 68.9 and 71.2 respectively for the Gulf of Thailand and the Andaman Sea. Populations of Indian mackerel exhibited similar and relatively high levels of genetic variation an average of 7.50 to 9.75 alleles per locus and average observed heterozygosity at all loci of 0.64 to 0.72. There was no evidence to support genetic differentiation between the Andaman Sea populations of Indian mackerel (F_{ST}-0.0073).

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