

Borworn Tontiworachai 2007: Population Genetic Structure of Asian Catfish (*Clarias batrachus* Linn.) in Moon River Basin of Ubon Ratchathani and Si Sa Ket Province.
Master of Science (Genetics), Major Field: Genetics, Department of Genetics.
Thesis Advisor: Associate Professor Amnuay Jondeung, Dr.phil. 98 pages.

Two hundred Asian catfishes were collected from ten different locations in Moon River Basin of Si Sa Ket Province (Pho Si Suwan, Rasi Salai, Yang Chum Noi, Mueang Si Sa Ket and Kanthararom) and Ubon Ratchathani Province (Warin Chamrap, Mueang Ubon Ratchathani, Trakan Phuet Phon, Tan Sum and Phibun Mangsahan). The total genomic DNA was extracted from muscle tissue of fish samples and used as templates for the amplification of the control region and *16S rRNA* in mitochondrial DNA. The PCR product of control region of was digested with 4 restriction enzymes *Tas* I, *Tru* I, *Rsa* I and *Hin*1 II and of *16S rRNA* with *Dpn* II, *Hae* III, *Tas* I, *Msp* I and *Rsa* I. The RFLP analyses of control region revealed 4 haplotypes which composed AAAA, AAAB, BAAA and BAAB. Haplotype AAAA, AAAB and BAAA were main haplotypes in all samples. Haplotype AAAA and AAAB were found in 10 locations and haplotype BAAA were found only in 8 locations. There were only 2 haplotypes; AAAAA and ABABA, found in *16S rRNA* analyses. Haplotype AAAAA was found in 10 locations and haplotype ABABA was found only in Phibun Mangsahan. All haplotypes of two segments implied that these haplotypes disperse in all locations of study area. Nucleotide diversity of control region ranged from 0.046 to 0.106 and of *16S rRNA* among 0.000 to 0.044 and nucleotide divergence mean ranged from 0.014 to 0.493. The results of RFLP analyses in Asian catfish have similar haplotypes and low nucleotide diversity value but high nucleotide divergence. Analysis of AMOVA test revealed that the variation between population and within population were 17.46 and 76.71 percent in control region and 10.53 and 89.47 percent in *16S rRNA*, respectively. Statistical test showed no significant result at 0.05 level. Phylogenetic tree showed three distinct population groups; (I) Warin Chamrap location; (II) Mueang Ubon Ratchathani and Phibun Mangsahan locations; and (III) a group of mixed seven locations.

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