

Jitraporn Fongissara 2007: Genetic Diversity of *Pangasius larnaudii* in Thailand.  
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The genetic diversity and genetic structure of 11 populations of Black Ear catfish (*Pangasius larnaudii*), six from the Chaopraya river basin, three from the Mekong river basin and 2 hatchery stocks, were assessed using five microsatellite primers (*Pg-2\**, *Pg-3\**, *Pg-6\**, *Pg-13\** and *Pg-20\**). The results showed that genetic variation of the wild populations was moderate and comparable to those of Mekong populations ( $A = 6.6-8.0$ ;  $A_e = 4.1-5.7$ ;  $A_r = 4.7-6.1$ ;  $H_o = 0.599-0.700$ ) and Chaophraya populations ( $A = 5.4-9.4$ ;  $A_e = 3.5-6.4$ ;  $A_r = 4.0-5.5$ ;  $H_o = 0.596-0.756$ ). The two hatchery populations showed less genetic diversity than wild populations in terms of allelic diversity, while  $H_o$  was not different. All populations were in Hardy-Weinberg Equilibrium ( $P > 0.05/55$ ) and most population pairs showed significant genetic differentiation ( $P < 0.05/40$ ). The average  $F_{ST}$  value (0.062;  $CI = 0.038-0.094$ ) indicated that genetic differentiation among populations was moderate. Among wild populations, the highest genetic distances were observed between Chiangrai and Pnom Pehn (0.111) and the smallest distances were observed between Pathumthanee-2 and Chainat (0.025); there was no correlation between genetic distance and geographical distance. A neighbor joining dendrogram placed all of the Chaophraya populations in one group while a population from Mekong River (Pnom Pehn) was clustered with the two hatchery populations and a population from Chiangrai was separated as an outgroup. The genetic information from this study is useful for conservation and fishery management of Black Ear catfish in Thailand.

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