

High genetic structure between natural populations of bighead catfish *Clarias macrocephalus* (Günther, 1864) from the Mekong Delta and Peninsular Malaysia

ABSTRACT

The tropical freshwater bighead catfish *Clarias macrocephalus* is widely distributed in Southeast Asia and is economically important in both the aquaculture and fisheries industries. In the current study, eight polymorphic microsatellite markers were employed to evaluate the genetic variation of 15 *C. macrocephalus* populations from Peninsular Malaysia, and the Mekong Delta populations of Cambodia and Vietnam. Overall, the number of alleles in *C. macrocephalus* populations ranged from 1 to 25 alleles. In general, genetic diversity was higher in the mainland populations (Cambodia, HE = 0.761 to 0.813 and Vietnam, HE = 0.759 to 0.789 with mean number of alleles of 10.13–13.88) compared to Peninsular Malaysia (HE = 0.519 to 0.699 with mean number of alleles of 4.5–10.75). High linkage disequilibrium and deviation from HWE suggest inbreeding in most Peninsular Malaysia populations which was also reflected by significant FIS values (0.217 to 0.410, $p < 0.05$). All pairwise F_{ST} ($p < 0.05$) values were significant. No evidence of bottlenecks was detected among all populations. The 15 populations formed two evolutionary units; Peninsular Malaysia versus the Mekong Delta-Cambodia and Vietnam. The findings from this study will serve as a reference for a systematic aquaculture programme and the conservation and management of wild populations of *C. macrocephalus*.