

Population Genetic Study Between Three Populations of The World Smallest Fish Species, *Paedocypris progenetica* in Peninsular Malaysia

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Structured Abstract

Background: Limitation of available information of genetic diversity within and between populations of world's smallest fish, *Paedocypris progenetica* particularly in Peninsular Malaysia is crucial for their long-term survivability, especially since they are now labelled Near Threatened. Despite its high adaptability to the surrounding environment, there's a gap in understanding the resilience and adaptability of this species, especially in conservation efforts. Thus, this study mainly aims to address this issue by analysing and comparing the genetic diversity between *Paedocypris progenetica* located at Selangor, Perak and Terengganu.

Methods: *Paedocypris progenetica* samples were collected from three population across Peninsular Malaysia using a mesh net. Samples's genomic DNA was extracted using an extraction kit, a ReliaPrep gDNA Tissue Miniprep system, and amplified using FishF1 and FishR1 primer to obtain its COI gene. PCR products were sequenced and genetic diversity between and within population were analysed. Population genetic structure was assessed through AMOVA, pairwise Fst, phylogenetic analysis and Neutrality test (Tajima's D and Fu FS test).

Results: A total of 8 haplotypes were identified among 68 samples collected. Based on the phylogenetic structure of NJ and ML, all populations showed extreme genetic isolation. Through analysis of AMOVA, Fst and Neutrality test, it was found that Selangor and Terengganu population exhibit population expansion through founder effect with low nucleotide ($\pi = 0.00035, 0.00072$) and haplotype diversity ($Hd = 0.22000, 0.42632$), whereas Perak exhibit stable population with slightly higher nucleotide diversity ($\pi = 0.00221$).and haplotype diversity ($Hd = 0.66008$).

Conclusion: In conclusion, these finding indicates that *Paedocypris progenetica* species from Terengganu, Perak, and Selangor reveals clear isolation between populations, likely driven by habitat fragmentation and the species' stenotopic nature. Terengganu and Selangor show signs of recent expansion, while Perak remains stable. The study provides comprehensive genetic information between the three population of *Paedocypris progenetica* in Peninsular Malaysia, that can be used for future conservation management of this species in this region.

Keywords: *Paedocypris progenetica*, Population Genetics, Genetic Diversity, COI Gene

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