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Title: Microsatellite Markers Reveal Genetic Differentiation of Chinese Dojo Loach *Misgurnus anguillicaudatus* in the Yangtze River Basin

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Abstract: The fish fauna in the Yangtze-based riparian ecosystem has been imperiled largely due to genetic degradation of populations. Regular genetic monitoring of the fish populations is required for an effective management and conservation. The genetic structure of Dojo loach, *Misgurnus anguillicaudatus* was investigated in twelve populations originating from the Yangtze River basin by using thirteen microsatellite loci. The number of alleles per locus varied between 2 and 8 with an average of 4.6 alleles per locus. Overall, low-to-moderate level of genetic diversity was observed in the loach populations. Significant deviations from Hardy-Wienberg equilibrium were observed in about 50% of the total locus-population combination tests. The AMOVA indicated that most of the variance existed among the individuals (90.50%) rather than among populations within groups (9.03%). Significant differentiation was found among the samples from scattered habitats with different connections to the Yangtze River ($P<0.05$). The clustering of sample populations in UPGMA dendrogram followed their geographic distribution except for Zigui and Xiaogan which clustered against their geographical origin. The factors involved in genetic differentiation and shaping the existing patterns of population structure of the loach were discussed so as to provide guidelines for conservation strategies and management programs.

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