

Population genetics of Indian giant river-catfish,



The giant river-catfish *Sperata seenghala* is one of the commercially important freshwater catfishes of India with wide distribution in all major rivers and reservoirs. This fish has huge demand in domestic market due to high nutritional value and low number of intramuscular bones. Conversely, the culture practices for this fish have not yet been standardized and capture fisheries is the only source to meet the demand. This may lead to over exploitation of resources and subsequent population reduction. Knowledge on genetic structure of populations is prerequisite to formulate sustainable management and conservation measures. In the present study, 15 microsatellites were used to characterize population genetics of *S. seenghala* collected from river Brahmaputra, Ganga, Godavari, Mahanadi and Narmada. Locus-wise, the number of alleles varied from 8 to 19 with an average of 12 alleles per locus. The mean observed and expected heterozygosity values varied from 0.622 to 0.699 and 0.733 to 0.774, respectively. Several loci have shown deviation from Hardy–Weinberg equilibrium and no significant linkage disequilibrium between pairs of loci

was detected. Pair-wise F_{ST} values between populations ranged from 0.135 (Brahmaputra–Ganga) to 0.173 (Brahmaputra–Narmada) and confirmed the moderate to high genetic differentiation among the populations. AMOVA, Structure and Principal Co-ordinate analyses showed significant genetic differentiation among the sampled populations of *S. seenghala*. A total of 65 private alleles were recorded across populations. This study confirmed the distinctiveness of each population of *S. seenghala* from five major rivers of India. These populations could be treated as distinct management units (MUs) for assessment and management purpose.

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