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Extremely low genetic variability in *Etroplus suratensis* (Cichlidae) revealed by isozymes, microsatellites and mitochondrial DNA sequences

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Genetic variation in several populations of *Etroplus suratensis* in Sri Lanka was studied by isozymes, selected microsatellites, and DNA sequence of the control region (D-loop) of the mitochondrial (mt) genome. Based on seven resolvable enzymes, only a single isozyme locus, PGI-2 showed polymorphism albeit of poor degree (~1.2%), while all other nine isozyme loci were monomorphic in three populations (n=34, 20, and 30). Four PCR-amplified microsatellite loci with dinucleotide repeat motifs were not variable in the two populations studied (n=25 and 23) indicating that *E. suratensis* populations seem to be homogeneous at these microsatellite loci. Further analysis of DNA sequence of TmoM27 microsatellite locus and the flanking region (327 bp) among 48 individuals did not contain even a single SNP (single nucleotide polymorphism) site whereas the same locus of other Cichlids including *E. maculatus* is reported to be variable. DNA sequence of a 760 bp fragment of the mitochondrial control region did not contain any SNP among the 48 individuals analysed. The results suggest the possibility that extremely low genetic variability prevails in *E. suratensis* populations in Sri Lanka. A likely explanation for this may be the initial colonization of the island by a small number of genetically homogenous founders. Further loci from more geographic locations including India would be useful to investigate this hypothesis further. Potential inbreeding and associated loss of genetic variation has been linked particularly to island populations, thus, an interesting postulate to test is whether the island populations of *E. suratensis* have less genetic variation than mainland populations by using Indian counterparts of the species.

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