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Short Communication

***In silico* analysis of SSRs in mitochondrial genomes of fishes**

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Abstract

The availability of fish mitochondrial (mt) genomes provides an opportunity to explore the simple sequence repeats. In the present study, mt genomes of 85 fish species reported from Indian subcontinent were downloaded from NCBI and computationally analysed for finding SSRs types, frequency of occurrence, mutation and evolutionary adaptation across species. A total of 92 microsatellites in different nucleotide combinations were detected in 59 species. 26 interspersed SSRs, mostly poly (AT)_n were found in the D-loop regions in the species of Cyprinidae. Fifty-six SSRs of 12 bp fixed length were observed in eight genes only. Further, identical repeat motifs were found on the same location in ATP6 and ND4 genes, which were biased towards particular habitat. The comparison of ATP6 and ND4 gene sets to other homologous sequences showed point mutations. This study explores the SSRs discovery and their utility as marker for species and population identification.

Keywords

Fish, microsatellites, mitochondrial genome, point mutation, population genetics

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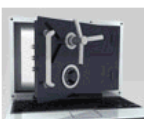
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