

Genomic organization of 5S rDNAs in *Triportheus* (Triporthidae, Characiformes): U1 snRNAs linkage and evolutionary divergence among species

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Abstract/Resumo

The 5S rDNA array is composed of multiple copies of a conserved transcriptional unit and a variable non-transcribed spacer (NTS). The NTS may include other multigene families, such as small nuclear RNAs (snRNAs) and transposable elements (TEs). Here, we integrated genetic and cytogenetic analyses to better understand the evolutionary patterns of 5S rDNAs in *Triportheus*. A total of 66 clones containing 5S rDNAs of eight *Triportheus* species were sequenced. The evolutionary divergence between species and the phylogenetic analyzes of 5S rDNAs were achieved by DnaSP and SplitsTree, respectively. We performed the fluorescence in situ hybridization (FISH) method using 5S rRNA and U1 snRNA genes as probes. The 5S rRNA gene in *Triportheus* has a coding region of 120 pb and a NTS of ~1500 pb. Inside the NTS, a high homology with the U1 snRNAs was revealed by BLASTn, evidencing that 5S rRNA and U1 snRNA sequences are linked in the same array. Different types of retrotransposons and DNA transposon fragments were also identified in the NTS. The coding region presented a low evolutionary divergence among species, thus contrasting with the much higher one of the NTS, especially for *Triportheus auritus* in which high values were found. In addition, the neighbor-network showed a clear clustering for most species. The 5S rDNA signals were localized in one or two chromosome pairs in all species, again with the exception of *T. auritus* which carried ten sites. Besides, the U1 snDNA was mapped in co-localization with one 5S rDNA site, confirming the sequence analyzes. Finally, the genetic and cytogenetic data evidenced the linkage between U1 and 5S rDNA, as well as the differential evolutionary trends of *T. auritus* in relation to other *Triportheus* species. In fact, according to previous phylogenetic studies, *T. auritus* is representative of the first lineage that differentiated in the genus, corresponding to the sister group of all *Triportheus* species. The high NTS evolutionary divergence among species highlights its variability, probably due to TEs insertion in this genomic region. A mix of the concerted and birth-and-death models is probably related to the 5S rDNA evolutionary process in *Triportheus*.

Keyword/Palavras-chave: Multigene Family; snRNAs linkage; NTS variability

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