

Abstract

Ray-finned fishes (Actinopterygii) exhibit the greatest biodiversity among vertebrates. The vast majority of extant actinopterygian fish species belong to clade Teleostei - a lineage whose significant evolutionary success might have resulted from a teleost specific whole-genome duplication (TSGD) that occurred at the onset of this group, subsequent to its divergence from the rest of actinopterygian lineages. Despite the growing body of sequenced fish genomes and analyses of their transcriptomes, the largest contribution to understanding fish genomes comes from analyses of DNA content and from cytogenetics. Genomes of ray-finned fishes and especially those of Teleostei exhibit vast diversity and rapid dynamics of repetitive DNA sequences whose variability is reflected in a wide range of fish genome sizes and in the dynamics behind karyotype differentiation. Therefore, ray-finned fishes offer a unique opportunity to study genome variability as a driving force underlying morphological and ecological diversification, evolution and adaptation. Particularly, the mapping of repetitive DNA sequences by means of fluorescence *in situ* hybridization (FISH) has proven to be a very useful and informative approach during the last two decades and contributed greatly to our understanding of the fish genome architecture together with new insights into a large amount of evolutionary, ecological and taxonomic matters and questions. The present study is focused on karyotype differentiation, specifically on the distribution of repetitive sequences and polyploidy events in selected species of Teleostei and Chondrostei with the aim to integrate cytogenetic and taxonomic approaches in order to provide a more complex view of particular evolutionary and ecological features of the respective fish groups. Together with conventional cytogenetic analysis, we employed FISH with probes complementary to tandem repetitive sequences such as ribosomal rRNA genes (rDNA), retrotransposable elements and telomeric (TTAGGG)_n sequences. Additionally, we performed comparative genome hybridization (CGH) and genomic *in situ* hybridization (GISH) in order to compare the genomes of hybrid specimens or closely-related species. Our data clearly show that the dynamics and variability of repetitive sequences may play a significant role in ecological adaptation and speciation, as well as in polyploid genome evolution and that this can be traced even in species groups with generally conserved karyotype macrostructure (particularly for the level of diploid chromosome number, 2n). Our results have demonstrated the importance of integrating cytogenetic/cytogenomic approaches with other biological disciplines and that molecular cytogenetics has an enormous potential in the post-genomic era, hence offering new insights towards extending the knowledge on different kinds of unsolved evolutionary-ecological questions related to the evolution of the fish genome.