ABSTRACT

Actinopterygian fishes exhibit the greatest taxonomical diversity of all vertebrates, making this group attractive to address numerous evolutionary questions. The role of molecular cytogenetics and cytogenomics further increase because recent advances in these fields provide more comprehensive view of fish genome organization and evolutionary dynamics, responsible for this amazing diversity. My Thesis investigates the genome organization of selected fish lineages, namely basal lineages of Actinopterygians (Lepisosteidae and Amiidae) and Teleosts (Pantodontidae), together with “modern” fishes Cobitidae and Coregonidae. I have integrated conventional and molecular cytogenetic techniques together with phylogenetic and statistical approaches. Publications included into the Thesis describe e.g. the cytogenetic variability and dynamics in closely related fish species of the genus Coregonus and the impact of repetitive sequences on the ecological speciation. In contrast to the recent cytotaxonomical diversity of Coregonids, we have detected a karyotype stability associated with asexual reproduction in spined loaches of the genus Cobitis. In the subsequent publication, we describe a surprising AT/GC genome organization in gars (Atractosteus and Lepisosteus) and summarize the knowledge of genome organization and karyotype differentiation of these basal actinopterygian lineages in the context of other major vertebrate lineages. Also we provide first reliable chromosomal data for the bowfin Amia calva, the only representative of fishes from order Amiiformes. Although bowfin represents the closest extant lineage of gars, we show its karyological and cytogenetic similarities with Teleosts. I have participated on cytogenetic analyses of the African butterfly fish Pantodon buchholzi, the only representative of the family Pantodontidae (Osteoglossiformes). The outcomes of this Thesis reveal the dynamic nature and the complexity of the fish genome, as well as the importance of cytogenetic and cytogenomic methodologies in the age of the next generation sequencing.