

Abstract

Xenopus frogs are interesting models for different kinds of studies, due to their particular characteristics. The different levels of polyploidy in different frogs make them also valuable models for cytogenetic and evolutionary analysis. This project investigates the evolutionary dynamics of chromosomal rearrangements within the family Pipidae, focusing on members from the genera *Xenopus*, *Silurana*, and *Hymenochirus*. We examined the chromosome morphology and rearrangements in the allotetraploid frog, *Xenopus calcaratus*, revealing distinct characteristics between its subgenomes. The a-subgenome is more conserved, while the b-subgenome has evolved more rapidly. A specific chromosomal translocation observed in *X. mello tropicalis* but not in *X. calcaratus* highlights differences in chromosomal rearrangements between these species. We suggested that a single allotetraploidization event led to the emergence of *X. mello tropicalis*, *X. epitropicalis*, and *X. calcaratus*, with the translocation occurring post-divergence of *X. calcaratus* but pre-speciation of *X. mello tropicalis* and *X. epitropicalis*. Another scenario involves two independent allotetraploidization events.

We also explored the roles of polyploidization and divergence in the evolution of repetitive elements in six species of African clawed frogs. Combining cytogenetic and genomic data analysis, we mapped U1 and U2 small nuclear RNAs and histone H3 in both diploid and allotetraploid species. The results showed conservation of these elements in diploid and tetraploid species from the subgenus *Silurana*, while variation was observed among allotetraploid species from the subgenus *Xenopus*. These findings suggest that polyploidization initially duplicates tandem repeats, but their copy number can vary over time due to reduction and expansion.

Preliminary analysis of the genome of *X. borealis* revealed around 4-6% differences between its two subgenomes, providing initial insights for future research. Additionally, we discovered that the *Hymenochirus boettgeri* from the Congo is tetraploid, with significant differences from captive diploid populations. This suggests the need for further research to clarify the taxonomy and evolutionary history of *Hymenochirus*. We propose distinguishing the captive population as *Hymenochirus* sp. from the wild population, which retains the name *H. boettgeri*.