

Abstract

Arachnids are a highly speciose group of arthropods with about 130 000 extant species from 12 orders. Some arachnid species are of economic and medical interest. They also offer various opportunities to study the link between genome and karyotype variability and morphological and ecological diversification, evolution and adaptation. The knowledge about arachnid karyotypes and genomes is, however, still limited. The available data show wide range of diploid chromosome numbers ($2n$), monocentric or holocentric chromosomal structure, variability in sex chromosome systems (especially in spiders) and modifications of meiosis. The main objective of this doctoral thesis was to study by conventional and molecular cytogenetic methods the mechanisms of karyotype evolution in haplogyne spiders (with monocentric and holocentric chromosomes), and further in two families (Charinidae and Phryniidae) from the closely related order Amblypygi. The selected groups offer unique insights into fundamental karyotype traits of the arachnid clade Tetrapulmonata, and they also enable to analyse the role of polyploidy in arachnid karyotype evolution and the evolutionary mechanisms behind the emergence of holocentric chromosomes. Our data suggest that holocentric chromosomes are an autoapomorphy for the haplogyne superfamily Dysderoidea. A sister lineage Caponiidae display high numbers of monocentric chromosomes and considerably larger genomes, implying the polyploidization event at the base of this clade. Our findings support the notion that holocentric chromosomes in spiders might have evolved via multiple chromosome fusions. Intriguingly, the presence of sex chromosomes did not pose a constraint for polyploidy to emerge. We further showed high rate of karyotype repatterning among studied amblypygids, with probably high ancestral $2n$ and its subsequent recurrent decrease by fusions and/or translocations, and with important contribution of pericentric inversions. The striking differences in karyotype traits provided suitable cytotaxonomic markers for species identification, especially when integrated with phylogenetic and morphometric data. Our findings open the door for new directions in arachnid cytogenetic and genomic research, mainly towards deciphering the roles of rearrangements and sex chromosomes in (cryptic) diversification of this speciose arthropod clade.