

Abstract

Spiders are diverse group of arthropods with a worldwide distribution. They are important predators and colonized successfully most terrestrial ecosystems. Despite importance of this group, the information about the spider karyotypes is still limited, especially in mesotheles, mygalomorphs, and haplogyne araneomorphs. The presented Ph.D. thesis is focused on the karyotype evolution of selected clades of haplogynes and mygalomorphs, specifically on the families Pholcidae and Atypidae. Techniques of standard and molecular cytogenetics were used to determine the karyotypes and the pattern of nucleolus organizer regions (NORs). Obtained results allow to revise the diploid number and sex chromosome system of mygalomorph *Atypus karschi* (Atypidae) and determine probable ancestral karyotype of the genus *Atypus*. *A. karschi* exhibits one NOR, which is adjacent to the large heterochromatin block composed of inactivated rDNA.

Concerning the family Pholcidae, obtained results increase substantially the number of analysed species belonging to this family. Obtained data allowed to study for the first time karyotype evolution of haplogynes on a family level, for the first time also the evolution of NORs. Pholcids show a low diploid number, $2n♂$ ranges from 9 to 33. Pholcid karyotypes are predominated by biarmed chromosomes. In the course of evolution, diploid numbers have often been reduced by fusions. The morphology of the chromosomes entering the fusion was first changed by inversions to acrocentric or subtelocentric. The sex chromosome systems and patterns of NORs are very diversified. My studies discovered seven sex chromosome systems, namely X0, XY, X₁X₂0, X₁X₂X₃0, X₁X₂Y, X₁X₂X₃Y, and X₁X₂X₃X₄Y. Phylogenetically original is the X₁X₂Y system, which is probably ancestral to araneomorph spiders. My study revealed the evolutionary plasticity of the X₁X₂Y system. Its evolution included translocations between X₁ and X₂ chromosomes, inversions of X chromosomes, and increase of Y chromosome size. The X₁X₂Y system has been transformed to other systems in some groups. The X₁X₂0 system arose from the loss of the Y chromosome, the XY system from the fusion of X chromosomes. From these systems, the X0 system arose in some evolutionary branches, either by fusion of X chromosomes (from the X₁X₂0 system) or by loss of the Y chromosome (from the X0 system). The X₁X₂X₃0 system of *Smeringopus pallidus* arose from the X₁X₂0 system, either by X chromosome fission or nondisjunction. The most complicated systems were found in the subfamily Ninetinae (X₁X₂X₃Y and X₁X₂X₃X₄Y). These systems arose from the X₁X₂Y system like the system found in *S.*

pallidus. Number of NOR loci varies from one to nine, they are located on the autosomes and frequently expanded on the sex chromosomes, possibly by ectopic recombination. Sex-chromosome linked NORs are probably involved in the achiasmatic pairing of sex chromosomes. The number of NORs has increased over the course of evolution. In some groups, the number of NORs, including sex-chromosome linked NORs, has been subsequently reduced. Similar to other haplogynes, male meiosis of pholcids includes a diffuse stage, and these spiders usually have a very low number of chiasmata in male meiosis.

Keywords: chromosome rearrangement, diffuse stage, FISH, Haplogynae, karyotype evolution, Mygalomorphae, nucleolus organizer region, rDNA, sex chromosome.