

– ABSTRACT –

Snakes (Serpentes) are a group of squamate reptiles (Squamata) that represents more than one third of the total reptile species diversity. Snake karyotype is generally conserved with the most common chromosome number of 36 (16 macro- and 20 microchromosomes) in diploid state. It is believed that this karyotype was also present in the common ancestor of all snakes. The majority of snake species belong to the group Caenophidia and share homologous ZW sex chromosomes. Snakes from the groups “Scolecophidia” and “Henophidia” have mostly poorly differentiated, homomorphic sex chromosomes, which made them impossible to distinguish from the autosomes in the past. These snakes were for many years assumed to have ZW sex chromosomes as well. However, recent studies demonstrated not only ZW but also two non-homologous XY sex chromosome systems in non-caenophidian snakes and thus the sex determination systems in snakes are much more variable than previously thought. In this thesis, eight species of henophidian snakes (representatives from the genera *Eryx*, *Cylidrophis*, *Python* and *Tropidophis*) and one caenophidian species (*Ophiophagus hannah*) were examined using conventional and molecular cytogenetic methods. However, sex chromosomes were not detected in the henophidian species, only in *Ophiophagus hannah*, the single studied caenophidian species. *Ophiophagus hannah* has highly heteromorphic ZW sex chromosomes with extensive accumulation of interstitial telomeric repeats (ITRs) and constitutive heterochromatin on its W chromosome. ITRs were also observed on one autosomal pair in *Ophiophagus hannah* and on three chromosome pairs in *Eryx muelleri*, one of the tested henophidian species, despite the shared chromosome number of $2n = 34$ with the rest of the *Eryx* species. These results correspond with the growing evidence that ITRs might be more common in snakes even with their generally conserved karyotypes. Although the total chromosome number is shared in Erycinae and may be an apomorphy of this subfamily, differences in chromosome morphology and heterochromatin locations were found between some of its species.

Key words:

boas, evolution, FISH, heterochromatin, karyotypes, pythons, rDNA, sex chromosomes, telomeres