

## Abstract

The present thesis deals with the phenomenon of additional sex chromosomes in *Cimex lectularius* (Hemiptera: Heteroptera: Cimicidae) using genome size analysis combined with the classical cytogenetic approach. Also, five other cimicid species and 12 species from the family Nabidae were analysed identically for comparative purposes. The thesis also pursues a description of methodical approaches of cytogenetics and flow cytometry in the study of *C. lectularius*.

Recently analysed European specimens of *C. lectularius* from human host exhibited 12 distinct cytotypes, with a variable number of chromosomes X from two to 20 ( $2n♂ = 26+X_1X_2Y$  to  $26+X_{1-20}+Y$ ). The fragmentation hypothesis of *C. lectularius* additional chromosomes X origin was established in the second half of the 20<sup>th</sup> century. However, the present genome size measurements suggest that various chromosomal rearrangements as duplication or deletion besides the fragmentation could occur. Males with basic cytotype  $2n = 26+X_1X_2Y$  had average genome size of  $2C = 1.94$  pg, in contrast male with  $2n = 26+X_{1-7}+Y$  yielded  $2C = 2.26$  pg and also specimens with genome size decrease  $2C = 1.69$  pg appeared. The most informative turned up to be the relative genome size of sperm cells  $n = 13+X_1X_2$  and  $n = 13+Y$ , where specimens with higher chromosome number showed relative genome size increase in sperm cells with chromosomes X.

The similar cytogenetic and genome size analysis of the other five cimicid species brought the new record of variability in sex chromosome number of *C. lectularius* from bat hosts and *C. pipistrelli*,  $2n = 26+X_1X_2(X_3)Y$  and  $2n = 28+X_1X_2(X_3)Y$  respectively. However, in comparison with *C. lectularius* from human, these additional chromosomes X originated mostly by fragmentation and both cytotypes possessed specimens with very similar genome size. Moreover, genome size of all five species analysed was measured for the first time: *C. hemipterus*  $2C = 1.47$  pg, *C. hirundinis*  $2C = 1.61$  pg, *C. lectularius* from bats  $2C = 1.80$  pg, *C. pipistrelli*  $2C = 1.68$  pg and *Paracimex* cf. *chaeturus*  $2C = 1.22$  pg.

Genome size analysis in family Nabidae supported the autosomal polyploidization theory, currently sidelined. *Himacerus* species with  $2n = 32+XY$  reached twice as much nuclear DNA content ( $2C = 9-10$  pg) than *Nabis* species with  $2n = 16+XY$  ( $2C = 4-6$  pg). Besides genome size data for all nabid species studied, also the karyotype of *N. bififormis*, *N. maoricus*  $2n = 16+XY$  and  $2n = 26+XY$  for *Prostemma aeneicolle* was recorded for the first time.