

Comparative approach sex chromosomes in *Belostoma* species by genomic in situ hybridization (GISH) regarding to the evolutionary process

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Abstract/Resumo

All *Belostoma* species studied possess holokinetic chromosomes and an inverse relationship between chromosome number and chromosome size because autosomal and/or sex chromosome fusions and sex chromosome fragmentations have seemingly played the most important role in their karyotype evolution. The modal diploid chromosome number $2n=26+X1X2Y/X1X1X2X2$ (male/female) observed in ten species and reduced chromosome numbers (16, 14, and 8) with a simple sex chromosome system XY/XX (male/female) detected in other six species could be indicating two paths of karyotype evolution. In species with a multiple sex chromosome system (X1X2Y), the NOR is located on an autosomal bivalent, whereas in species with a simple sex chromosome system (XY) it is placed on both sex chromosomes. Genomic in situ hybridization (GISH) assay could be a useful tool to compare the genome of *Belostoma* species, which have different karyotype numbers and sex chromosome systems, providing information on the genome organization and distinctive location of DNA fractions on sex chromosomes. We examined the composition of sex chromosomes from *B. elegans* ($2n=26+X1X2Y/X1X1X2X2$), *B. micantulum* ($2n=14+XY/XX$), and *B. oxyurum* ($2n=6+XY/XX$) by means GISH due to they can be considered as model species to ascertain the possible trends of karyotype evolution. We hybridized labelled male genomic probe of each species to each corresponding male chromosome preparations with an excess of unlabelled female genomic DNA of the same species. *Belostoma micantulum* and *B. oxyurum* presented larger Y chromosomes than *B. elegans*, and the genomic probes displayed strong binding in 40-60% of the total length of Ys. However, the male probe of *B. elegans* highlighted to its whole Y chromosome. Based on these results and our previous data, we may conclude that the Y sex chromosome constitution in *B. micantulum* and *B. oxyurum* was originated by fusion between the ancestral NOR-autosomal bivalent and the original sex chromosomes. The advantage of this approach allowed us to study chromosome rearrangements as well as to identify homeologous chromosomes of related species. Therefore, application of molecular cytogenetic techniques constitutes for elucidating chromosome evolution in this group.

Keyword/Palavras-chave: Karyotype evolution; Sex chromosomes; GISH; Holokinetic chromosomes

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