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Chromosomal dynamics, molecular organization and evolutionary patterns of major ribosomal DNA in the Grasshopper *Abracris flavolineata* (Acrididae)

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Abstract/Resumo

In the grasshopper *Abracris flavolineata* it was documented huge intrapopulation variation for 18S rDNA in individuals collected in six populations, but causes for this pattern was not understand yet. In this work we aimed to elucidate the molecular structure, evolutionary patterns of the rDNA 18S distribution and its causes in the genome of *A. flavolineata*. It was used a combination of classical cytogenetic techniques, mapping of18S rDNA through Fluorescence in situ hybridization (FISH) and genomics analyses from entire sequenced genome by Illumina hiseq 2000. It was analyzed 48 individuals collected in six distantly sampling places from Brazil and Argentina. FISH analyses confirmed the variability of 18S rDNA for all six populations that presented between 6-11 chomosomes labeled. Signals were observed in chromosomes 1, 3, 6 and 9 in all individuals and also it was noticed variation of cluster sizes. It was not found a fixed pattern at intra- or interpopulation levels in population from the same geographic region or between distant ones. Silver nitrate staning revealed Nocleolar Organizer Regions (NORs) in chromosome 9 of all individuals, indicating that the expression of the rDNA cluster in this chromosome could be under selection to be expressed, and also could represent ancestral placement of this sequence. It is a pattern also shared with congeneric species. In some individuals chromosome 10 presented NORs, however for some of them FISH signals in this bivalent was not observed, indicating cryptic loci in accordance with 'dispersion-amplification-deletion' model, suggested also for rDNA dispersion for other grasshoppers. Finally the reconstruction of entire 45S rDNA presented different coverages in the conserved genes (18S, 5.8S e 25S) and in the internal transcripts (ITS 1 e ITS 2) reveling that huge part of the copies are pseudogenes. The transposons Nimb and R2 are present in 45S rDNA, although apparently they are not able to transpose sequences. All data together suggests that the high amount of rDNA in *A. flavolineata* genome is caused by occurrence of pseudogene sequences that were moved random between chromosomes caused most parsimonialy by ectopic recombination, extra-chromosomal DNA or even by transposons not localized in the 45S cluster.

Keyword/Palavras-chave: Repetitive DNA; Multigenic family; Genome; FISH; Chromosomic polimorfism

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