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## Next-generation sequencing analysis reveals novel insights of B chromosome evolution of the grasshopper *Abracris flavolineata*

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## Abstract/Resumo

B chromosomes are additional elements in a normal karyotype that has been considered frequently as parasitic and dispensable. These elements do not recombine with A chromosomes, could be accumulated and present nonmendelian patterns of inheritance. In most of the cases they comprise an enrichment of heterochromatic repetitive DNA, such as Satellite DNAs (satDNA). To contribute to understanding about origin, composition and evolutionary patterns of B chromosome in the grasshopper Abracris flavolineata, in this work we characterized through Illumina sequencing and graph-based clustering the most abundant tandem repeats of A. flavolineata, karyotype 2n =22,X0+B<sup>3</sup>. The analyses revealed the occurrence of ten families of satDNAs comprising about 6.279% of the male genome harboring one B chromosome. For the X chromosome and autosomes, distinct patterns of hybridization was observed between the satDNAs showing variability among them, like scattered blocks on euchromatic areas or specific ones on heterochromatic regions of the chromosomes. Five of the satDNAs recovered were distributed on centromeric and both terminal regions of the B chromosome, reinforcing the hypothesis of B chromosome origin through isochromosome formation. Two satDNA families were located only in centromere, while three families were not present in B chromosome. CL220 satDNA was the unique family shared between the B chromosome and only one A element, the chromosome 1, supporting strongly the hypothesis of its origin from this autosomal pair, also noticed previously by U2 snDNA mapping. In addition, this analysis provides new information regarding the composition and evolution of B chromosome of A. flavolineata. Furthermore, the non-spreading and specific location of satDNAs and other repetitive sequences restrict to telomeres and centromere reinforces the possible idea that this B chromosome could harbor unknown euchromatic sequences along chromosomal arms and do not present intense amplification of heterochromatic ones, as have been commonly described for other species.

Keyword/Palavras-chave: Satellite DNA; Supernumerary chromosomes; Tandem repeat

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