

## Chromosome characterization of *Melipona scutellaris* (Hymenoptera, Apidae, Meliponini) based on repetitive DNAs

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### Abstract/Resumo

Repetitive DNAs constitute a significant part of the genomes and are used as cytogenetic markers for the understanding of chromosome evolution. Bees of the genus *Melipona* presents conserved chromosome number but high variability concerning heterochromatin distribution, dividing the genus into two groups: (i) species with low quantity of heterochromatin and (ii) species with high amount of heterochromatin. Here aiming the understanding of repetitive DNAs chromosomal organization in *Melipona* we mapped through fluorescence in situ hybridization (FISH) some repetitive DNAs in *M. scutellaris*. For this, FISH were performed with the amplification products of the 18S rDNA, U2 snDNA and DOP-PCR, as well as the product of the C0t fraction and different microsatellites. The mitotic chromosomes used in FISH were obtained by squashing the brain ganglia, and in this material, being performed also the C-band and CMA/DAPI. The distribution of the C0t fraction in other species of *Melipona* was verified with membrane hybridization. Chromosome number of  $n = 9$  and  $2n = 18$  (male and female, respectively) was confirmed and a large amount of heterochromatin was observed along the chromosomes, except at the terminals that were characterized as euchromatic and only rich in different microsatellites. The heterochromatic regions were observed with richness in A + T and C + G. The FISH experiments showed signals from the 18S rDNA and U2 snDNA probes on distinct chromosomes. This demonstrates that these multigenic families followed different evolutionary paths in the chromosome evolution of the species. The DOP-PCR and C0t fraction showed signs of hybridization in the heterochromatic regions, and the C0t fraction of *M. scutellaris* was also observed in the genomes of *M. rufiventris*, *M. rufiventris rufiventris* and *M. seminigra*, evidencing the dispersion of similar repetitive elements in genomes of these three species. Thus, it was possible to characterize the karyotype of *M. scutellaris* with different cytogenetic markers. In addition, the results with membrane hybridization reinforce the hypothesis of the repetitive DNA sharing among nearby species, suggesting that there are different repetitive elements present in the genome of the genus *Melipona*.

Keyword/Palavras-chave: Heterochromatin; *Melipona*; Repetitive DNAs

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