

## Repetitive DNA distribution in *Agave* (Asparagaceae) bimodal karyotype

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### Abstract/Resumo

The genus *Agave* L. comprises about 300 species and is characterized by a bimodal karyotype with basic chromosome number  $x = 30$  (5L and 25S) and ploidy levels ranging from diploids to hexaploids. Species of this genus have low heterochromatin content, visualized as CMA<sup>+</sup>/DAPI bands, and one 5S and 35S ribosomal DNA sites per haploid genome. However, *in silico* analysis of the repetitive fraction of the *Agave* hybrid 11648 ( $2n = 2x = 60$ , 8.35 Mpb) revealed that ~ 67.6% of its genome is composed of different repetitive DNA families. Among the most abundant elements are Maximus, TAR and Tork (Copia), and Athila, Chromovirus and Ogre (Gypsy) LTR-retrotransposons, as well as, a single family of satellite DNA. In order to investigate the repetitive DNA distribution in this bimodal karyotype, these seven elements were labeled by nick translation and hybridized *in situ* to the hybrid 11648 metaphases. The satellite DNA was located at centromeric regions of all chromosomes, however a subset of the small chromosomes had stronger signals. All transposable elements showed a dispersed distribution, mostly non-uniform along chromosomes arms. Athila and Maximus lineages showed stronger labeling of interstitial and distal regions of the long arms of large chromosomes, while Tork and especially TAR labeled more intensely the proximal regions. Small chromosomes showed variable labeling with all repetitive elements, generally weaker than large chromosomes. Together, these data revealed that different LTR retrotransposon lineages accumulated differentially, and usually more abundantly, in the large chromosomes, whereas the centromeric satellite DNA showed a quantitative variation between chromosomes, but not related to the bimodal condition of this karyotype.

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Keyword/Palavras-chave: Bimodal karyotype; Transposable elements; Satellite DNA

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