

Stability of DNA content and molecular cytogenetic markers in the genus *Stylosanthes* (Fabaceae)

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Abstract/Resumo

Stylosanthes (Leguminosae) comprises about 50 species, and some with great economic importance. Species are widely used as forages, and also as green fertilizer, useful to recover degraded areas due to its adaptability to low fertility soils and nitrogen fixing capacity. The genus is distributed in tropical and subtropical areas. Brazil is considered the larger diversity center, with great inter and intraspecific variation. Although breeding studies have been increased, the taxonomic situation of the group remains unsettled and controversial. The occurrence of polyploidy and hybrids, as well as many additional synonyms reinforce the importance to add new information on the genus. Cytogenetic data are scarce, even considering as an important tool to give relevant information about the genome. Here we describe, for the first time, karyotypic aspects and the DNA content of diploid species (*S. grandifolia*, *S. gracilis*, *S. hippocampoides*, *S. acuminata* and four varieties of *S. guianensis*) by using molecular cytogenetic techniques (CMA/DAPI banding and *in situ* hybridization) and flow cytometry. Seeds germination was induced by temperature variation (18 °C to 40 °C) and growth hormones (CEPA 0.1 mM) in a germination chamber. Meristems of roots were used to slides preparation. Chromosomes were stained with CMA/DAPI for banding patterns analysis, and ribosomal 5S and 45S rDNA sites were mapped using *in situ* hybridization technique. To estimate the DNA content, *Pisum sativum* was used as a reference standard. The chromosomal morphometry showed a symmetrical karyotype with few variations among the species. The number of CG rich regions ranged from 2 to 4. Two 5S and 45S sites were observed in most species, excepting in *S. acuminata*, in which four 45S markers were identified. DNA content estimation was ~2.50 pg in all species. These new data constitutes an important contribution for evolutionary history studies of this group, opening new possibilities for future comparisons among genomes of different *Stylosanthes*, and with great value for breeding programs of species with economic importance.

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