

3410 - Forage & Grazing Lands

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CONTENT OF NUCLEAR DNA IN BRACHIARIA SPECIES ASSESSED BY FLOW CYTOMETRY

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Brachiaria is the tropical forage grass with the greatest cultivated area in Brazil and has positively impacted animal production on pastures. Furthermore, it is responsible for the major part of the seed market both in Brazil and for export. In this study, flow cytometry was used to estimate the content of nuclear DNA of four Brachiaria species (*B. brizantha*, *B. decumbens*, *B. ruziziensis* and *B. humidicola*) from Embrapa Beef Cattle germplasm, with different ploidy levels and basic chromosome numbers. We evaluated one diploid accession each of *B. brizantha*, *B. decumbens* and *B. ruziziensis*, and the latter showed the lowest 2C-value (1.69pg) while the other two had the same value (2.00pg). The tetraploid accessions of these three species showed twice the 2C-value of diploids. Two pentaploid accessions were also analyzed: one of *B. brizantha* and one of *B. decumbens*, and the 2C-values were 4.90pg and 4.41, respectively. This pentaploid *B. decumbens* was specially selected for this study since previous cytogenetic analysis reported genome loss during meiosis, which was corroborated here. In *B. humidicola* we analyzed two accessions: one hexaploid and one heptaploid, with 2C-value equal to 4.20 and 5.22, respectively. These accessions of *B. humidicola* presented a smaller 2C-values than the hexaploid accession of *B. brizantha* (5.52pg). This probably occurred because *B. humidicola* has $x=6$ and *B. brizantha* has $x=9$, as *B. decumbens* and *B. ruziziensis*. So when the C-value (haploid genome) was considered *B. humidicola* presented the smallest genome (0.70pg), followed by *B. ruziziensis* (0.85pg), then *B. brizantha* and *B. decumbens* with the same C-value (1.00). Two interspecific hybrids from the cross between *B. brizantha* and *B. ruziziensis* were also evaluated in this work and the average 2C-value observed was intermediate to the 2C-value of the two species (3.77pg), indicating that flow cytometry technique can be used for this purpose when 2C-values are different. These results provided novel and relevant information for breeding programs, sequencing projects, and in research using molecular markers in these Brachiaria species.