XXII International Symposium in Genetics and Plant Breeding
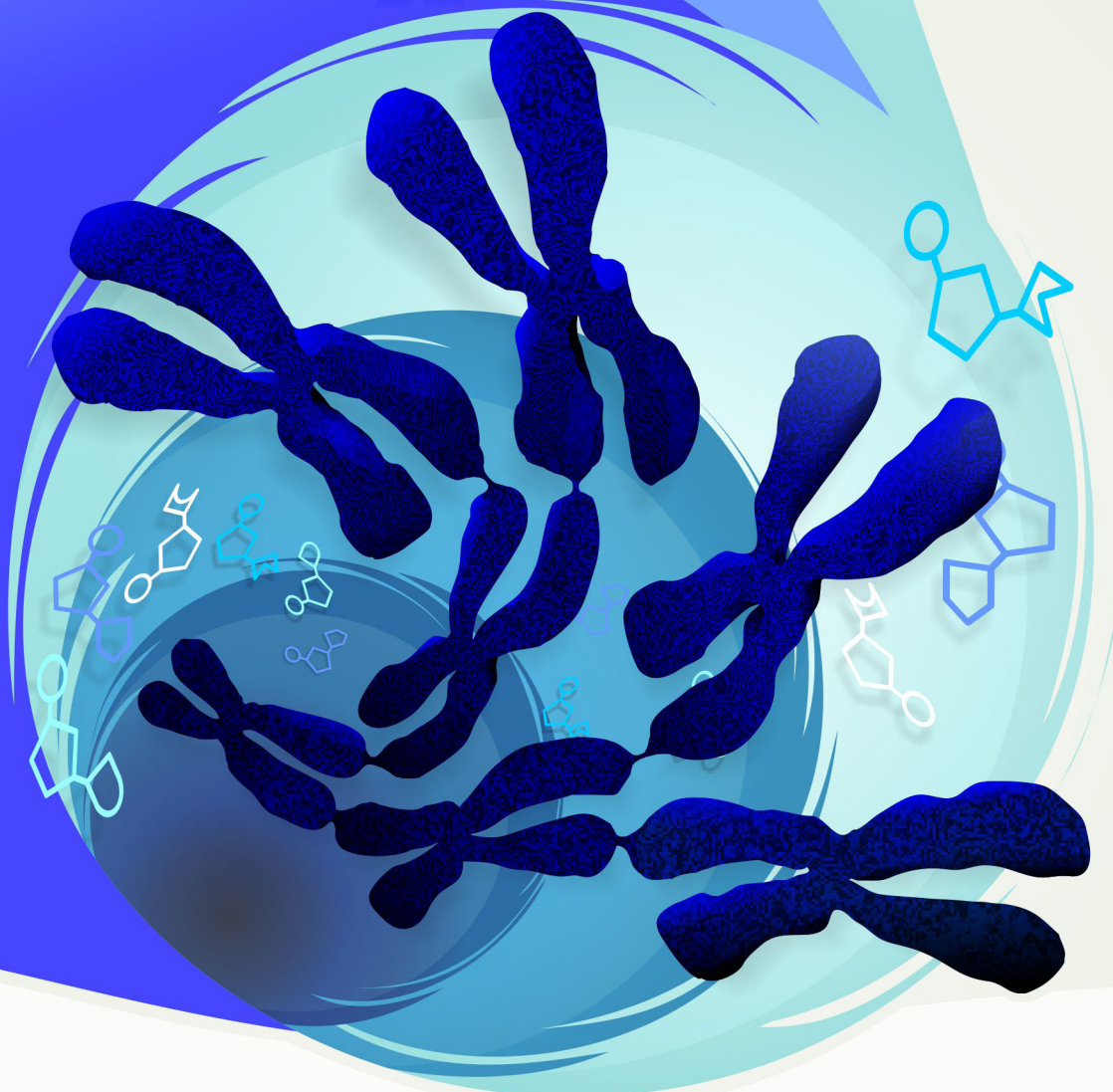
Polyploidy challenges and implications in Genetics and Plant Breeding

Part of the Plant Science Symposia Series

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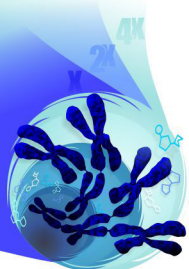Agriculture Division of DowDuPont™

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GENETIC DIVERSITY OF Paspalum L. ACCESSIONS FROM VIRGATA GROUP BASED ON MOLECULAR MARKERS

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Paspalum genus is known for containing species of good forage and turf value. The genus is widespread throughout the American continent, with more than 210 species occurring in Brazil, of which species from the informal botanic group Virgata present good forage potential, such as *P. conspersum*, *P. regnellii* and *P. virgatum*. The cited species are tetraploid and sexual. Some germplasm banks (GB) are held all over the world so as to conserve the genetic diversity of *Paspalum* spp., including one maintained *ex situ* at Embrapa Pecuária Sudeste (EPS), São Carlos, SP, Brazil. One of the recurrent issues in GB is the occurrence of redundant accessions, which demand more resources, and the identification of duplicates increases the efficiency in GB management. This study aims the estimation of genetic diversity and population structure of group Virgata accessions from the EPS GB and the verification of duplicates using molecular characterization. With these purposes, 33 accessions of Virgata from this GB were evaluated with 15 novel specific SSRs markers and 7 ISSRs ((CT)8-G, (AC)8-T, (GT)8-C, (AG)8-C, (ATG)5GA, (GA)8-C e (AGAC)4GC). Total DNA were extracted according to CTAB method and PCR performed according to the literature. The SSRs fragments were separated on a 6.5% polyacrylamide gel and the ISSRs on a 2% agarose gel. Fragments were visually scored for the presence (1) or absence (0) of homologous DNA bands and transformed in a binary matrix, which was used to estimate the Jaccard dissimilarity coefficients (D) of each pair of accessions and to obtain an UPGMA (Unweighted Pair Group Method with Arithmetic mean) grouping. Population structure was estimated using a Bayesian analysis using the software STRUCTURE. The most likely number of clusters was obtained through ΔK values. D values among the genotypes ranged from 0.10 to 0.97, with a mean value of 0.69. The dissimilarity of 10% is not significant enough to consider two accessions as duplicates, so it was considered that there are no redundant accessions. The UPGMA dendrogram separated the accessions in four groups, being group I and group II composed by accessions of *P. conspersum* and *P. virgatum*, respectively, and groups III and IV of *P. regnellii*. This grouping corroborates the closer phylogenetic relationship previously reported between *P. conspersum* and *P. virgatum* than with *P. regnellii*. STRUCTURE analysis showed the best K is 2, which separates the accessions of *P. conspersum* from the other species´ accessions. However, when analyzing K=4, the same UPGMA grouping pattern is observed. These results are of high importance for the breeding program in progress at Embrapa and (1) indicate that there is a great genetic variability among the accessions and (2) help to drive intra and interspecific crosses according to the genetic dissimilarity.