

## A core AFLP map of aposporic tetraploid *Paspalum notatum* (Bahia grass)

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**Keywords:** *Paspalum notatum*, apospory, genetic map, AFLP, molecular markers

**Introduction** *Paspalum notatum* (Bahia grass) is a perennial rhizomatous species that reproduces by aposporous apomixis. Tetraploid races ( $2n=4x=40$ ) are widely distributed from Central to South America and constitute one of the most valuable natural forage grasses for the subtropical areas of Paraguay, southern Brazil and north-eastern Argentina. Apospory in the species is controlled by a single locus, which exhibits a distorted segregation ratio. The objectives of this work were to develop a core genetic linkage map of the species by using AFLP markers and characterize the genomic region related to apospory.

**Materials and methods** A mapping population of 113 individuals was generated by crossing a tetraploid sexual plant (Q4188) with an aposporous individual from accession Q4117. Progenies were classified for their mode of reproduction (asposporous vs. non-aposporous) by molecular and cytoembryological analyses according to Martínez *et al.* (2003). AFLP markers were generated employing *EcoRI* and *MseI* primers with 1 and 3 selective bases (Stein *et al.*, 2004). A  $\chi^2$  test was used to determine the goodness of fit between the observed and expected genotypes for each class of segregation ratio. Data from the aposporous genotype were analyzed independently using the mapping program JoinMap1.4 with LOD values between 3.0 and 5.0. Male linkage groups were constructed considering single dose (SDA) and distorted alleles. Map units in cM were derived employing the Kosambi mapping function.

**Results** As a result of using a tetraploid F<sub>1</sub> mapping population derived from non-inbred parents, different allelic configurations per locus were observed (Table 1). Classification of F<sub>1</sub> plants for their mode of reproduction showed 98 non-aposporous and 15 aposporous individuals.

**Table 1** Segregation of AFLP markers in the mapping population

Type of marker	Number of markers in each class of segregation ratio						Total
	1:1 <sup>a</sup>	3:1 <sup>b</sup>	5:1 <sup>b</sup>	3:1/5:1 <sup>b</sup>	11:1 <sup>c</sup>	Distorted <sup>d</sup>	
Paternal	166	23	14	24	-	33	260
Maternal	245	20	11	20	-	16	308
Both	-	60 <sup>c</sup>	-	-	38	5	103

<sup>a</sup> single dose alleles (SDAF), <sup>b</sup> double dose alleles, <sup>c</sup> allelic bridges, <sup>d</sup> at  $p < 0.01$

A total of 199 markers segregating from the male parent were used for the linkage analysis. A core AFLP map was built with 146 markers distributed in 22 linkage groups.

The total genetic map distance covered was about 1,430 cM, with an average of approximately 10 cM between markers. The linkage group carrying the locus for apospory (apo-locus) was defined by 28 loci over a distance of 32 cM. Twelve markers were completely linked to the apo-locus, while the rest showed recombination values between 0.6 and 18 cM, either side of it. The complete co-segregation of several markers and apospory confirmed the suppression of recombination in this genomic region reported by Martínez *et al.* (2003). The average distance between markers in the apo-group was about 1 cM.

**Conclusions** A core genetic linkage map of aposporous tetraploid *P. notatum* was built with AFLP markers. It can be employed for fundamental research as well as for localising genes of agronomic interest. The structure of the linkage group carrying apospory suggests that it could be a large chromosome segment containing several genes. A detailed molecular analysis of this segment, based on the utilisation of the molecular markers linked to apospory, could allow the identification of the gene/s controlling the trait in the species.

### References

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