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ISSR genetic variability of *Cenchrus ciliaris* L. half-siblings obtained by open pollination

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INTRODUCTION

Cenchrus ciliaris L. (Buffel grass), a widely used forage C4 grass, reproduces mainly by aposporic apomixis. Half-sib families were obtained by open pollination of a facultative apomictic plant (Sx) with high cross fertility.

The objective was to assess genetic variability among individuals from the obtained half-sib families by ISSR molecular markers.

MATERIALS AND METHODS

Ten individuals, randomly selected at field (31, 47°S, 64, 15°W, Córdoba, Argentina), from three half-sib families (2, 9 and 16), obtained by open pollination, and the parental genotype (Sx) were used.

Genomic DNA was isolated using the PlantZol (TransGen Biotech Co., Ltd., China) commercial kit. Fifteen ISSR universal primers were assayed.

A binary data matrix for presence (1) or absence (0) of bands was constructed, and a distance matrix was obtained by the Dice similarity index (sqrt (1-S)) transformation.

A descriptive analysis, a principal coordinate analysis (PCoA), with a minimum spanning tree (MST), an unweighted pair group method with arithmetic mean (UPGMA) hierarchical clustering and an analysis of molecular variance (AMOVA) were performed using Info-Gen statistical software.

RESULTS

All ISSR primers generated amplification products in all individuals. From the 252 generated bands, 72.2% were monomorphic and 27.8%, polymorphic.

Twelve polymorphic primers were detected with a proportion of polymorphic bands that ranged from 5% to 87% and PIC values that went up to 0.32.

UPGMA hierarchical clustering (Fig. 1A) and PCoA with MST (Fig. 1B) confirmed the existence of five groups formed by individuals from different half-sib families.

AMOVA revealed significant differences ($p \leq 0.001$) among half-siblings.

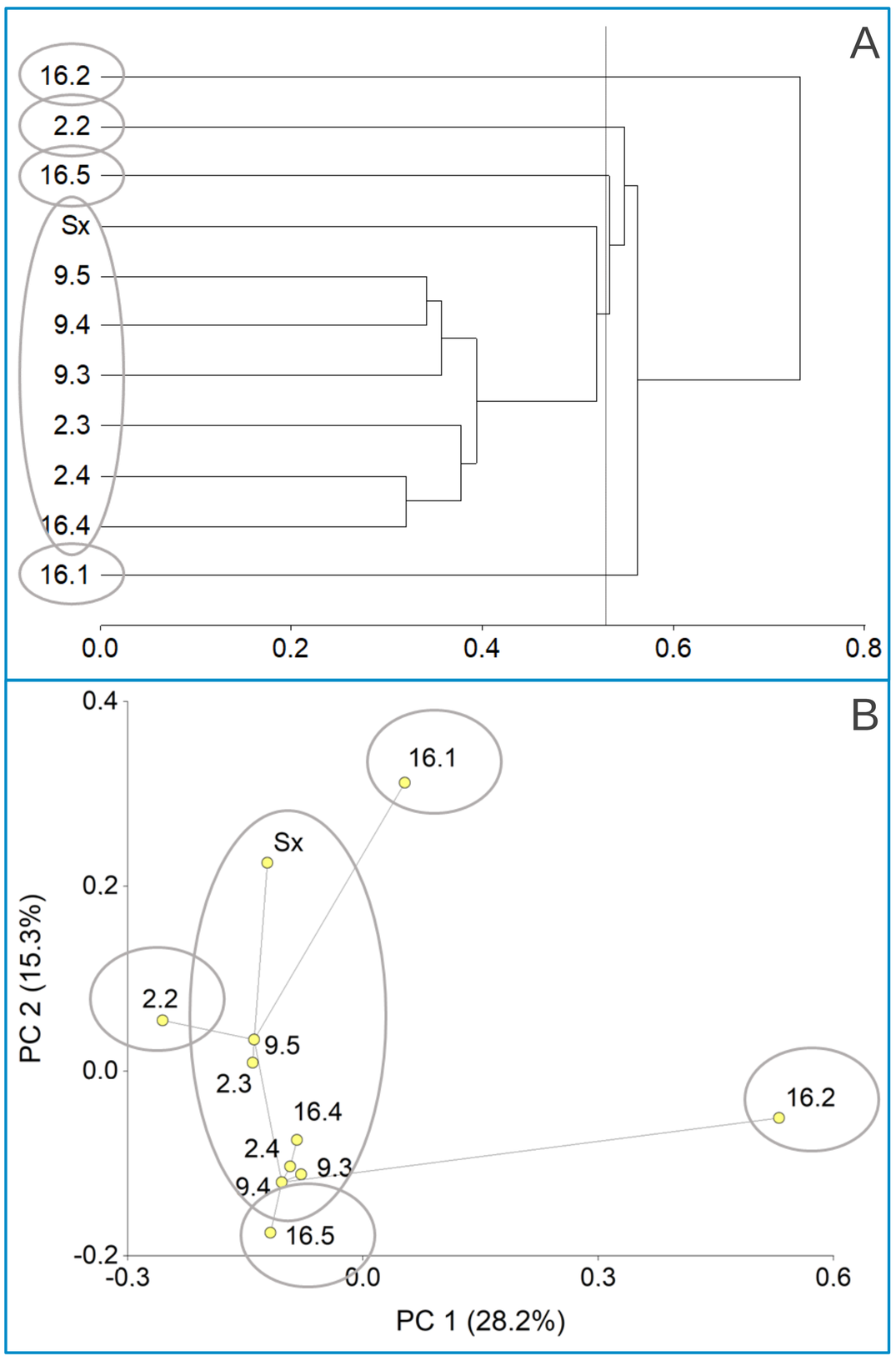

Fig. 1. ISSR genetic variability among individuals from three half-sib families (2, 9 and 16) and parental genotype (Sx) in Buffel grass. (A) Dendrogram from UPGMA hierarchical clustering and (B) biplot from principal coordinate analysis overlapped with minimum spanning tree, both obtained by (sqrt(1-S)) Dice similarity index transformation.

CONCLUSIONS

ISSR markers allowed detection of genetic variability among closely related individuals. Genetically distinct individuals could be useful for breeding purposes in Buffel grass.

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