

# Potential sources of sexuality in *Cenchrus ciliaris* L.: Seed fertility, environment and its implication in plant breeding

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## INTRODUCTION

*Cenchrus ciliaris* L. is an aposporic and pseudogamous apomictic species, and fully sexual plants are very rare or absent. Fertility, which seems to be influenced by environmental factors, is a character of interest for selection of putative maternal sources for hybridizations.

## OBJECTIVES

- 1) To compare seed fertility of four HSFAs.
- 2) To determine the moment of maximum cross fertility.
- 3) To determine the influence of bioclimatic variables on the expression of fertility in the HSFAs.

## MATERIALS AND METHODS

**HSFAs:** three clonal plants/genotype (named: Sx, S1, 32/9 and 191) were transplanted under a nylon cover structure, in a completely randomized design with three replications at IFRGV experimental area (31, 47°S, 64, 15°W, Córdoba, Argentina).

**Fertility:** N° caryopses/N° spikelets per panicle (panicle = experimental unit), in three panicles/HSFA.

**Treatments:** two pollination methods (OP: open and SP: self-pollination) at three flowering times: beginning (BF), flowering peak (FP) and end of flowering (EF) during three years.

**Selfed seed set:** panicles were labelled and enclosed prior to stigma exertion.

**Open pollinated seed set:** inflorescences were labelled prior to stigma exertion and exposed to foreign pollen.

At maturity, all of the panicles were individually harvested and threshed.

**Bioclimatic variables:** thermal time (°/day), photoperiod (h/day), accumulated radiation (W/m<sup>2</sup>) and precipitations (mm). These traits were recorded ten days before panicles were labelled until harvest (cycle duration).

**Statistical Analysis:** Principal Component Analysis (PCA) was carried out with all of the variables.

Mixed generalized linear model (MLGM) was fitted with binomial distribution and logit link function, taking into account the correlation among panicles from the same HSFA clonal plant and using the bioclimatic variables as covariates.

## RESULTS

The biplot resulting from the PCA (Fig.1A) explained 88.7% of the total variability.

PC1 differentiated flowering times and the first two flowering times, BF and FP, were associated with the bioclimatic variables and they were opposite to cycle duration and fertility.

PC2 allowed the differentiation of HSFAs by the pollination method applied.

High variation was observed among HSFAs under OP and three of them (Sx, 32/9 and 191) were more fertile at FP.

In contrast, all four HSFAs under SP at FP were associated with accumulated radiation.

All of the HSFAs under SP were less fertile than under OP at all flowering times, and they were less self-fertile at FP (Fig.1B).

The MLGM and DGC test results validated the PCA. The HSFAs showed different fertility expression, under different pollination methods and flowering times and were influenced by environmental conditions (p-value ≤0.05).

Highest fertility was detected in HSFAs Sx, 32/9 and 191.

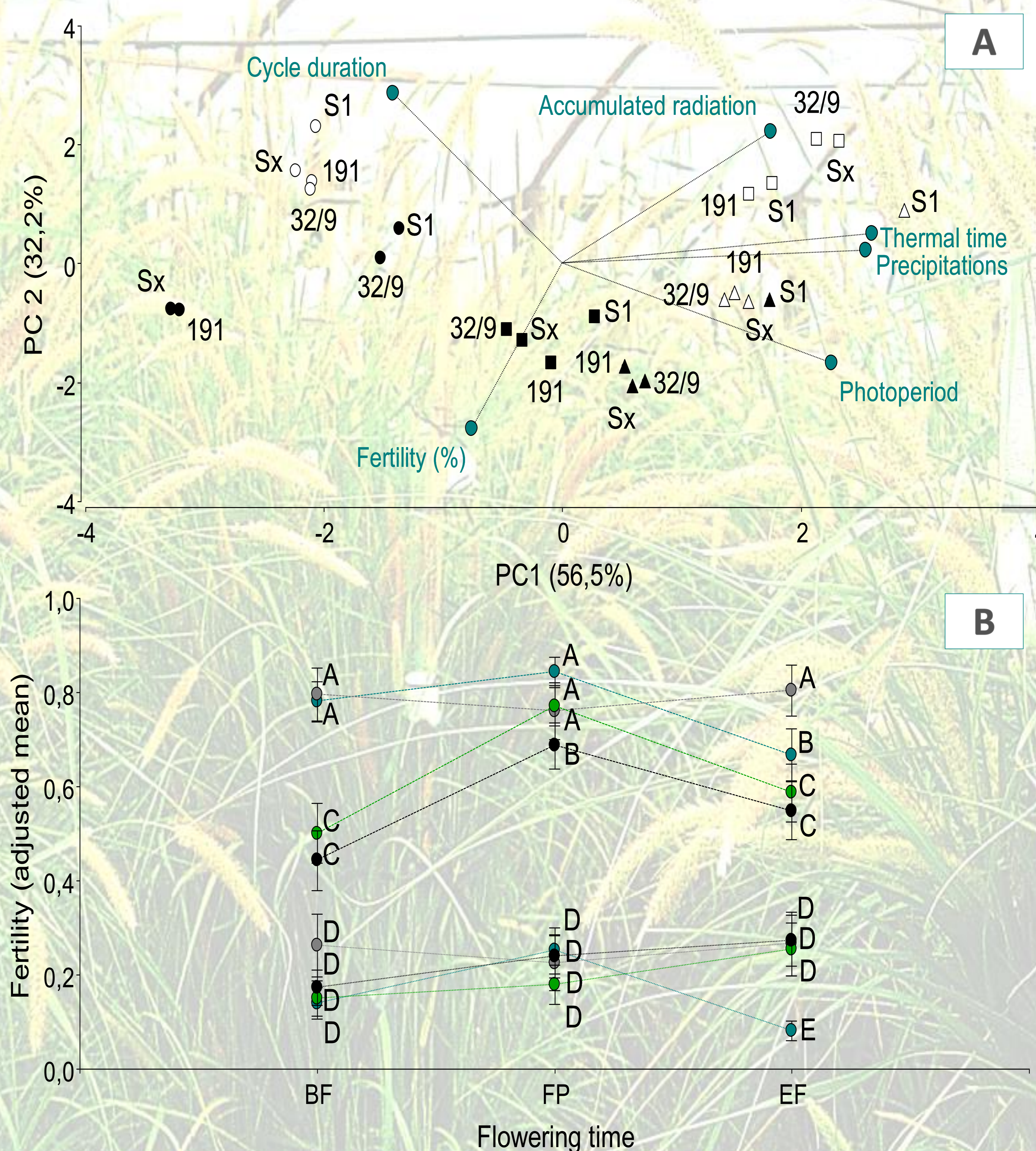


Figure 1. A. PCA's biplot carried out with all of the variables: bioclimatic, fertility, genotype, pollination method (SP: white and OP: black), flowering time (BF: triangles, FP: squares, EF: circles), and cycle duration. B. Adjusted average fertility under two pollination methods (OP: lines and SP: dots) at three flowering times (BF, FP and EF) of four HSFAs (Sx: light blue, S1: black, 32/9: grey, 191: green). Different letters indicate significant differences (p-value ≤ 0.05).

## CONCLUSION

The HSFAs Sx, 32/9 and 191 under open pollination at flowering peak would be the most promising genotypes to be pollinated to achieve the highest efficiency in hybridizations.

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