Using of Sequence Characterized Amplified Regions –SCAR- N14 for marker-assisted selection in *Brachiaria* breeding to select for apomixis

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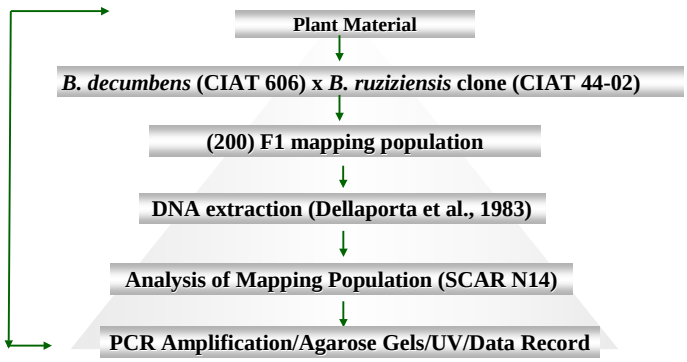
INTRODUCTION

Species of *Brachiaria* are the most widely planted commercial forage grasses in tropical America, with approx. 40-50 million hectares of *Brachiaria* pastures sown in Brazil alone (Valle & Miles 1992). The commercial species *B. decumbens* is an apomitic tetraploid, and *B. ruziziensis* was generated as a tetraploid from its sexual diploid species (Swenne, et. al., 1981; Ndikumana, 1985). *B. ruziziensis* is cross compatible with the commercial *B. decumbens*. It is now possible to combine desirable agronomic traits from different *Brachiaria* species in true breeding apomitic cultivars.

In *Brachiaria*, Palacios et al., (CIAT annual report 1994), identified the molecular marker SCAR N14 that is linked to a putative single apomixis gene. We describe the procedure to genotype multiple individuals (3700) with SCAR N14 to evaluate cosegregation of this marker with apomixis, in progenies generated from crossing the two *Brachiaria* species.

MATERIALS AND METHODS



Methodology. Used in the evaluation for apomixis in *Brachiaria*

1. Gel Electrophoresis Tanks

2. Casting base, Gel tray and combs compatible with multi-channels pipettes

Figure 1. Agarose Gel Electrophoresis System

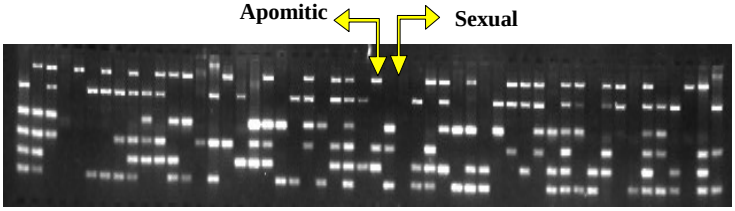


Figure 2. Agarose electrophoresis gel of 312 samples loads every 7 minutes and run at 280 volts in 1.5% agarose, stained with ethidium bromide and visualized with UV.

The yellow arrow identified the band for presence or ausence of apomixis that co-segregate with SCAR N14.

RESULTS AND DISCUSSION

We had used SCAR N14 to identify the individuals that co-segregate with it in a *Brachiaria* F1 mapping population, maintained vegetatively in the greenhouse. We used a cross with 200 individuals between a sexual induced tetraploid, *B. ruziziensis* clone (CIAT 44-02) as female parent, with a natural apomictic and tetraploid apomitic *B. decumbens* (CIAT 606).

As show in the figure 1 and 2, we can evaluate 3744 individuals per gel in two hours or less, using 12 combs of 52 teeht/1.0 mm and 3ul PCR product on short lengths.

With SCAR N14 we can screening large populations to identifify at level of plantless, the individuals that co-segregate with the marker.

If we compare this methodology and the use of test of progenie, the methodogy of MAS reduce costs and time.

CONCLUSIONS

For the specific case of *Brachiaria*-breeding program at CIAT, a PCR-based specific sequence characterized amplified region (SCAR N14) could be used to facilitate the use of marker-assisted selection (MAS) as a new tool for the screening of large populations to identify, at level of plantlets, the individuals that co-segregate with the marker, in order to improve selection efficiency and the capture of the desirable character in new *Brachiaria* varieties. Moreover, the use of MAS in *Brachiaria* reduces the costs and time, which would be an advantage of using the molecular marker (SCAR N14) and phenotypes in selection strategies.

PERSPECTIVES

- Use of the molecular marker (SCAR N14) in a MAS in *Brachiaria* program at CIAT

REFERENCES

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Palacios et al., (CIAT annual report 1994)

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Valle & Miles 1992