

# Identification of Molecular Markers Linked to Apomixis in *Panicum Maximum*

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The inheritance of apomixis in *Panicum maximum* Jacq. was previously ascertained on the basis of a 1:1 segregation (apomitic:sexual) with apomixis under control of a single locus of dominant inheritance. A bulked segregant analysis using RAPD technique was carried out to identify molecular markers linked to apomixis in an F1 population of *P. maximum*. Four markers linked to the apomixis locus (apo-locus) were found. Segregation data, together with this marker were used to generate a map of the region. Their location ranged from 8.63 cM to 24.39 cM of the apo-locus. These markers were then tested in another F1 population of this species and only two markers co-segregated with apomixis, located at 7.66 cM and 18.49 cM from the apo-locus. The markers' selection efficiency was high for both populations demonstrating the potential of these markers for assisted selection. The large amount of time and labor required by the current method for determination of the reproductive mode makes the identification of molecular markers linked to apomixis extremely important. Our results will allow for a rapid and efficient identification of hybrid progenies still in the seedling phase. The use of these markers will be a great contribution for the *P. maximum* breeding program.

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