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Poster paper

Marker-assisted selection for smut resistance

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Conventional breeding has made progress in improving the agronomic performance of sugarcane in the last few decades. One way to further increase genetic gain is to increase the selection intensity or effective population size by removing plants with undesirable traits using molecular markers. The first step in marker-assisted selection (MAS) is to identify markers linked with the target trait, followed by validation of this association between selected markers and the trait; and then use in routine selection.

Here, we demonstrate the potential application of MAS in sugarcane breeding for resistance to sugarcane smut. Markers associated with smut resistance were identified by association mapping where 480 clones, including popular parents, were genotyped using the 48K SNP chip developed by CSIRO. PCR-based KASP primers were designed for selected SNPs and then used for genotypic screening of 384 clones from the clonal assessment trial (CAT) stage. These clones were grown at Sugar Research Australia (SRA) Woodford for conventional evaluation of smut resistance.

Statistical analysis revelaed that five of the SNP markers showed highly significant association with smut resistance. Selection using the markers identified all highly susceptible clones and most of the intermediate clones in SRA's Northern germplasm pool but was significantly less effective in SRA's Southern breeding program.

These markers will be applied at the seedling stage of the Northern program to identify smut susceptible clones that can be eliminated prior to field evaluation. Further genetic analysis and validation work will be conducted to establish the selection platform in the other breeding programs.

Key words Sugarcane, smut, association mapping, marker-assisted selection (MAS)