

# PROGRESS AND PROSPECTS FOR MOLECULAR BREEDING IN THE SOUTH AFRICAN SUGARCANE VARIETY IMPROVEMENT PROGRAMME

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Commercial sugarcane varieties are polyploid hybrids with unequal chromosome contributions from the original *S. officinarum* and *S. spontaneum* ancestors, and are likely to have more than ten copies of most chromosomes (Butterfield *et al.*, 2001). The complexity of the genotype means that sugarcane is not amenable to directed genetic manipulation through conventional breeding (e.g. by the formation of inbred lines), which influences the efficiency of variety improvement. Sugarcane breeding programmes worldwide generally follow extensive recurrent selection schemes, in which tens to hundreds of thousands of genotypes are tested each year in the hope of recovering superior individuals. The potential for molecular tools to improve breeding efficiency has long been recognised, and the South African sugar industry has been supporting research in this area since the early 1990s. This investment is beginning to have a direct impact in the SASEX breeding programme.

Progress over the past few years includes the following:

- Gene sequences involved in the response of varieties to infection by smut (*Ustilago scitaminea*) have been identified (Heinze *et al.*, 2001, Thokoane and Rutherford, 2001).
- Gene sequences involved in the response to mosaic (Sugarcane mosaic *potyvirus*) have been identified (Richards *et al.*, 2004).
- These sequences have been used to generate a database of 275 DNA polymorphisms, from which a number of molecular markers associated with resistance to smut, mosaic and eldana (*Eldana saccharina*) have been discovered.
- In 2002, eleven parents used in the breeding programme had information on molecular markers, and this was used to design specific crosses to improve the likelihood of obtaining eldana resistant offspring. This was the first time markers have been used as tools in breeding decisions in any sugarcane breeding programme.
- In 2003, marker information was extended to 65 parent genotypes. This enabled a much wider range of cross combinations to be specifically designed in order to improve resistance to eldana.
- A new method to map the position of molecular markers on the sugarcane chromosomes has been developed. This involves exploiting the linkage disequilibrium (i.e. detecting the absence of recombination) that exists in the sugarcane genome due to its breeding history (Butterfield *et al.*, 2003).
- Applying the linkage disequilibrium map to individual genotypes has greatly increased the information content of the marker data, as it allows the visualisation of allelic genetic variation across the co-segregating chromosome groups. This enables marker information to be used more precisely in breeding, compared to the simple *presence* versus *absence* of individual markers.

- In order to capitalise more fully on these new methods, the marker database has been extended by a further 1056 anonymous DNA polymorphisms. This has facilitated the discovery of a larger number of significant markers for resistance to eldana, smut and mosaic. In addition, the linkage disequilibrium map has been extended from 82 markers in 35 linkage groups, to 622 markers in 157 linkage groups. This information will be available for making breeding decisions in the 2004 crossing season.

Work to date has concentrated on using molecular markers in breeding for eldana resistance, and to a lesser extent, smut resistance. The power of map-based molecular breeding will increase further when yield and quality traits are added to the map, and breeding can be done for multiple traits simultaneously. A new mapping project is planned, in which 90 genotypes from the SASEX breeding programme will be used to map and identify markers for important traits contributing to cane yield and quality. In addition, new technology that offers the potential to increase the throughput of marker screening at reduced cost is being pursued through collaboration at the International Consortium for Sugarcane Biotechnology (ICSB). High-throughput, low-cost technology will be the key to exploit the benefits offered by molecular breeding in the future.

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