AGROBACTERIUM-MEDIATED TRANSFORMATION OF SUGARCANE

By

PRIYA A. JOYCE, NICOLE J. TURNER
and PRAKASH LAKSHMANAN

David North Plant Research Centre, BSES Limited, Indooroopilly, Qld
CRC Sugar Industry Innovation through Biotechnology,
John Hines Building, The University of Queensland, Qld

GENETIC engineering of crops is moving from the experimental to the commercial stage. Based on the gain in productivity achieved in genetically modified (GM) plants in other major world crops, GM sugarcane is likely to make a significant impact in increasing the profitability and sustainability of the Australian sugar industry.

There are two ways to engineer sugarcane: via biolistic and Agrobacterium-mediated transformation. The latter method is preferred, as generally only one or two copies of the new gene are inserted into the plant genome, which ensures stability of transgene expression.

However, reports of transforming sugarcane by Agrobacterium are few and are not easily reproducible.

This study was undertaken to develop a reliable and repeatable system for routine transformation of sugarcane.

Four strains of Agrobacterium were screened for transformation of sugarcane callus. Using neomycin phosphotransferase gene (NPTII) as the selectable marker and β-glucuronidase (GUS) as the reporter gene, the role of different gene regulatory elements, culture conditions and other parameters in sugarcane transformation were studied.

All four strains were able to infect and transfer genes in sugarcane. The parameter that most influenced transformation efficiency was the condition during co-cultivation of the bacterium. Sugarcane plants have been produced with all four strains.

Polymerase chain reaction (PCR) analysis and/or GUS staining have confirmed that these plants contain both genes. Results of molecular analysis of these transgenic plants will be presented. We now have an Agrobacterium-mediated sugarcane transformation system that can be adopted for routine transformation.