

OUTCOME SUMMARY OF PROJECT BSA 09-005

BSA 09-005: Evaluation of alterations at the transcriptome, proteome and metabolome levels of two Bt maize lines with their corresponding non-Bt counterparts, as a result of genetic modification, natural variation or environmental variation.

Project Leader: Dr Eugenia Barros

Research Institution: CSIR Biosciences

Duration: 3 years

EXECUTIVE SUMMARY

The objective of this study was to use three omics' technologies to test for unintended effects that could be derived from the modification of two maize cultivars with the same Bt gene. The four maize cultivars (two Bt and the corresponding no-Bt counterparts) were grown in the same plot in a randomized block design, in two locations and in two consecutive years. The transcriptomics technology used was RT-PCR and it tested developing embryos (25 Days After Planting) and mature kernels. It was used for the targeted analysis of 17 genes that have been reported in the literature to be expressed at different levels in some GM and non-GM maize. No differential expression was however found in this study for these genes in the cultivars tested. Three housekeeping genes were also included and the zein gene was found to be the one that was stably expressed in both embryos and kernels and not dependent on the developing stage of the maize plant.

PROJECT OUTCOMES

- The untargeted proteomics technology employed on mature kernels was 2-DE gel electrophoresis followed by sequencing of differentially expressed proteins by LC-MS/MS. No significant protein differences were observed between GM and non-GM maize.
- ¹H-NMR was used for the semi-targeted analysis of the metabolites produced by the kernels of the four maize cultivars. No significant differences were observed between GM and non-GM plants for the metabolites tested.
- Some variation was observed at the proteome level between the two maize genetic backgrounds for the two years in one of the growing sites. However the variation was not between Bt and non-Bt. Natural variation and environmental variation were the sources of any of the variation that was observed.

