

Molecular characterization of genetically modified soybean lines developed aiming to obtain drought tolerance.

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In the last recent decade's soybean crop showed to have a significant importance in the national economy, especially because these grains are one of the main Brazilian export commodities. However, abiotic factors, such as drought, may reflect in losses in yield productivity. Thus, the development of genotypes more tolerant drought could provide solutions to these yield losses due to water deficit. Transcription factors, like DREB1A (Dehydration Responsive Element Binding Protein) also known as CBF3 (C-repeat Binding Factors) are involved in the response of plants to dehydration stress and they possibly play a key role in vegetal ability to tolerate drought, high salinity and low temperature conditions. Super expression of such transcription factor in GM model plants has shown drought tolerance. When such strategy is coupled with the use of a stress inducible promoter, plants seem to become more drought tolerant without development reduction. The construct containing the stress inducible promoter rd29 and the coding region of AtDREB1A gene was introduced into soybean embryos via biobalistic, generating five transgenic lines named P3069, P1378, P1142, P59 and P58. Therefore, the objective was to characterize molecularly these five transgenic lines and evaluate their possibly drought tolerance in comparison their wild genotype (BR16). To perform gene expression analysis, plants were exposed to three treatments of water deficit: 0h (control), 2h and 6h. According to the results, P58 and P3069 lines strongly expressed *DREB1A* gene after 2h of water deficit, P59 slightly expressed after 6h, P1142 slightly expressed after 2h and 6h of treatments and P1378 did not express *DREB1A* gene. Results from southern hybridization showed that all obtained soybean lines were identified as independent transgenic events containing different number of gene insertions. These initial results will help to select lines showing low gene copy number and higher gene expression to develop GM elite events.

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