



Expression analysis of programmed cell death related genes in soybean seeds

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Soybean is a globally relevant crop which represents an important source of protein for worldwide populations. During seed development, its dry mass builds up due to deposition of reserves, achieving its maximum at the reproductive R7 stage. At the transition from R7 to R8 stage, the mechanisms of desiccation tolerance are intensified. Programmed cell death (PCD) is a vital process triggered by abiotic and biotic stresses. In plants, it is activated by excess of salicylic acid and influx of calcium ions, as well as by reactive oxygen species (ROS) and by DNA fragmentation. In soybean, BiP proteins (molecular chaperone binding proteins) attenuate the propagation of cell death signals induced by stress. This study aims to analyze the expression of genes involved in pathways which trigger PCD during seed development. Soybean transcriptome libraries for certain developmental stages such as 4, 12-14, 22-24 days after fertilization (DAF), 5-6, 100-200mg (fresh and quiescent) and 400-500mg (fresh) have been used. The expression data for each selected gene were evaluated through RPKM values (reads per kilobase per million of mapped readings). We have selected 173, 538 and 5 genes related to water and oxidative stress and genes with annotations for BiP, respectively. Of the 173 genes related to water stress, eight genes annotated as RD22 (desiccation responsive) were seen as expressed throughout seed development, until quiescence. Of the 538 oxidative stress-associated genes, eight were seen as expressed in quiescent phase, and are annotated as CAT2 (Catalase 2); eight were annotated as SOD (superoxide dismutase 1). The 5 BiP-annotated genes, all have high expression in both early and middle stages of seed development, which drastically decreases in quiescent seeds. RD22, Cat2, SOD and BiP genes are possibly related to PCD-induced events in developing soybean seeds.

Palavras-chave: Gene expression, Programmed cell death, Soybean seeds

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