

GLOBAL ANALYSIS OF GENE EXPRESSION ASSOCIATED WITH CHLOROPHYLL RETENTION IN SOYBEAN SEEDS. **TEIXEIRA, R.N.<sup>1\*</sup>**; **SILVA, E.A.A.<sup>2</sup>**; **CAVARIANI, C.<sup>3</sup>**; **FRANÇA-NETO, J.B.<sup>4</sup>**; **LIGTERINK, W.<sup>5</sup>**; **HILHORST, H. W. M.<sup>6</sup>** (<sup>1</sup>FCA/Unesp, Botucatu - SP, Brasil, renakent@gmail.com) (<sup>2</sup>FCA/Unesp, Botucatu - SP, Brasil) (<sup>3</sup>FCA/Unesp, Botucatu - SP, Brasil) (<sup>4</sup>Embrapa Soja, Londrina - PR, Brasil) (<sup>5</sup>Wageningen University, Wageningen - Gué, Holanda) (<sup>6</sup>Wageningen University, Wageningen - Gué, Holanda)

The retention of chlorophyll in soybean seeds in Brazil has caused serious problems for producers in recent years because it is associated with a decrease of germination and vigor, and with low oil quality. The objective of this study was to evaluate the influence of the environment (high temperature and water stress) on seed performance and expression of genes related to the retention of chlorophyll during soybean seed maturation. This study was conducted with two soybean cultivars MG/BR 46 (susceptible to chlorophyll retention) and BRS 133 (tolerant to chlorophyll retention). The plants were grown in pots, in the green house, under ideal environmental conditions until the R6 stage. After this stage the following treatments were applied: control (18-26°C + full water supplement) and stressed (28-40°C + water deficiency). The seeds were harvested at three different stages of maturation (R6, R7 and R8). The experiment was performed in randomized blocks, in a factorial 2 (environmental conditions) X 3 (stages of maturation) design, constituting six treatments. Seed performance of both cultivars was analyzed, and the cultivar MG/BR 46 was subjected to microarray analysis. High temperatures and drought stress had a negative effect on the seed performance of cultivar MG/BR 46. There was a good correlation between gene expression and seed performance parameters, and also with chlorophyll content. A greater number of genes was differentially expressed at stage R6, while there were no genes significantly differentially expressed at stage R7. Of the 325 genes with a significant-fold change at stages R6 and R8, 17 were selected for further analysis of expression, confirming that they were expressed differentially in the susceptible and tolerant cultivars, showing that they are good candidate genes associated with chlorophyll retention in soybean seeds.

Palavras-chave: microarray, soybean, seed quality, chlorophyll.