

P2.28 - DREB gene family in drought tolerant maize lines

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The evolutionary and the economic performances of the plant are affected directly by reducing its survival in the natural environment and its productivity in agriculture. Plants respond to water stress by biochemical and physiological modifications that may be involved in tolerance or adaptation mechanisms. The molecular bases of water stress tolerance remains unknown. Candidate genes induced by water-deficit stress in plants relatively sensitive to cellular dehydration have been identified and characterized, mainly in the model plant *Arabidopsis thaliana* (Vinocur and Altman, 2005; Verslues et al., 2006) such as the DREB gene family. DRE (*Dehydration Responsive Element*) is present in one or multiple copies and has been reported to promoter expression of many genes related to drought stress (Yamaguchi-Shinozaki and Shinozaki, 1994; Kasuga et al., 2004). Many of these genes seem to be related to the maintenance of structure and basic cellular function during water deficit, low temperatures and high salinity (Shinozaki and Yamaguchi-Shinozaki, 1994). Considering that, studies of DREB gene family in the tolerant and sensitive maize genotypes at different time course and in different maize genotypes have been performed. These results will help associate the effect of the DREB gene in drought tolerant maize lines. Parallel to this study experiments with a specific DREB gene from JIRCAS has also initiated recently to demonstrate its effect in transgenic plants.

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P2.29 - Expression Quantitative Trait Loci analysis of two genes encoding rubisco activase in soybean (*Glycine max* (L.) Merr.)

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Ribulose-1,5-bisphosphate carboxylase/oxygenase activase (RCA) catalyzes the activation of Rubisco *in vivo*, and plays a crucial role in photosynthesis. However, until now, little is known about the molecular genetics of RCA in soybean (*Glycine max* (L.) Merr.). Here, we cloned and characterized two genes encoding the longer isoform and the shorter isoform of soybean RCA (*GmRCA α* and *GmRCA β* , respectively). The two corresponding cDNAs are divergent in both the translated and 3'-untranslated regions. Analysis of genomic DNA sequences suggested that the corresponding mRNAs are transcripts of two different genes, and not the products of one single alternatively splicing pre-mRNA. Two additional possible -form RCA encoding genes, *GmRCA03* and *GmRCA14*, and one additional -form RCA encoding gene, *GmRCA11*, were also isolated. To examine the function and modulation of RCA genes in soybean, we determined the expression level of *GmRCA α* and *GmRCA β* , Rubisco initial activity, photosynthetic rate (P_N) and seed yield in 184 soybean recombinant inbred lines. Correlation of gene expression levels with three other traits indicates that RCA genes could play an important role in regulating soybean photosynthetic capacity and seed yield. Expression quantitative trait loci (eQTL) mapping revealed four *trans* eQTLs for *GmRCA α* and *GmRCA β* . These results could provide a new approach for the modulation of RCA genes to improve P_N and plant growth in soybean and other plants.