

Association of a Soybean Raffinose Synthase Gene with Low Raffinose and Stachyose Seed Phenotype

The *Plant Genome* 1:135–145.

A calculation error was committed in preparing the data for Figure 2 in this manuscript. The following text in the Expression Analysis by Quantitative RT-PCR section should be:

Replace

“Expression of the three putative raffinose synthases was determined using quantitative RT-PCR. The results indicated that the putative raffinose synthase genes have similar transcript levels in all tissues examined as compared to the housekeeping gene elongation factor 1 α (Czechowski et al., 2005).”

with

“Expression of the three putative raffinose synthases was determined using quantitative RT-PCR and compared to the housekeeping gene elongation factor 1 α (Czechowski et al., 2005). The results indicated that the putative raffinose synthase genes RS2 and RS3 have similar transcript levels in developing seeds, with a trend towards increased expression as the seeds expanded for RS2; the RS3 transcript level decreased during the 9 to 11 mm seed stages. RS1 expression levels were highest for leaf and seedling tissues.”

The final sentence of the section remains unchanged:

“In addition, there was no significant decrease in expression of the raffinose synthase genes in developing seed tissues from PI 200508.”

The revised figure follows. ■

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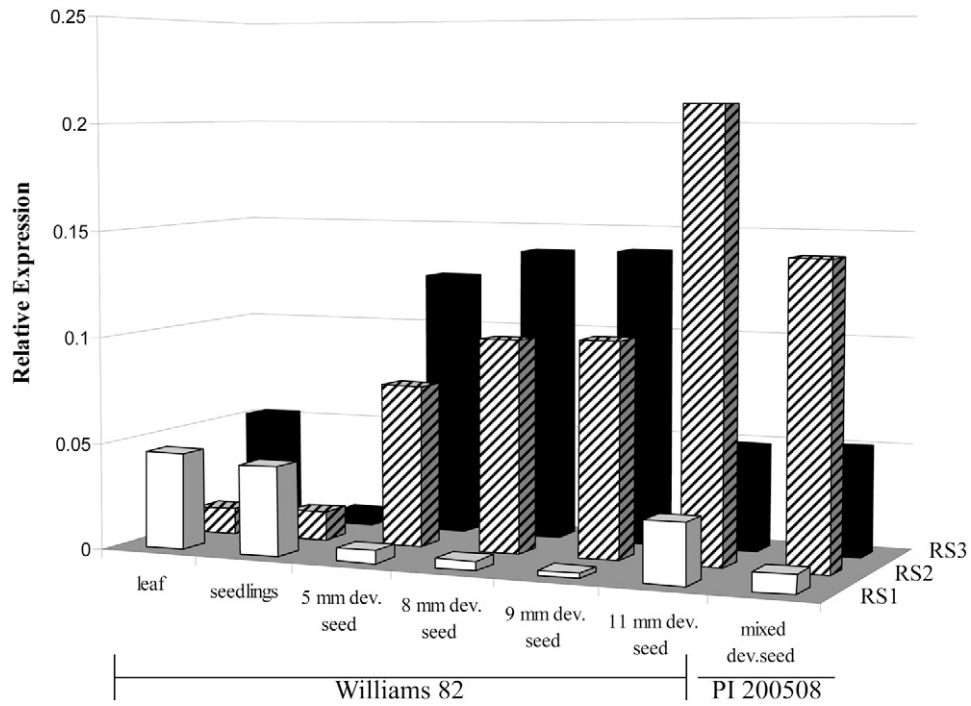


Figure 2. Relative expression of putative raffinose synthases for multiple soybean [*glycine max* (L.) Merr.] Tissues determined by quantitative rt-pcr. Left to right: the first six sets of bars represent expression of the candidate genes in williams 82 tissue. The last set of bars represent expression in mixed developing seed tissues from pi 200508. The three putative raffinose synthases are along the z-axis. Bar heights represent the average values from three replicates expressed relative to the housekeeping gene (elongation factor 1 α) control.