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Identification and characterization of genes controlling soybean seed setting

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To understand the gene expression networks controlling soybean seed set and size, transcriptome analyses were performed in three early seed developmental stages using two genotypes with contrasting seed size (V1 and V2). We found many candidate genes by weighted gene co-expression network analysis, like BR-signaling kinase (BSK), which was identified as hub genes operating in the seed coat network in middle seed growth stage. Overexpression of a candidate seed size regulator, *GmCYP78A5*, in transgenic soybean, resulted in enlarged seed size and increased seed weight.

Heat map analysis of each development stage in both of V1 and V2 showed that genes encoding proteins for starch and sucrose metabolism were significantly enriched in early seed development. Further study found two novel sugar transporters, *GmST1* and *GmST5*, were highly and specifically expressed in early seed developmental stage. Histochemical expression of *GUS* gene in p*GmST1*::*GUS* and p*GmST5*::*GUS* transgenic plants exhibited that these two genes were both specifically expressed in seed coat. Functional characterization by generation of transgenic soybean that overexpressing or knockout the *GmST1/5* is undergoing.

Together, the analyses discovered a large number of potential key regulators controlling soybean seed set, seed size, and consequently its yield potential, thereby providing new insights into the molecular networks underlying soybean seed development.