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The transcriptomic signature of developing soybean seeds reveals the genetic basis of seed trait adaptation during domestication

*Biao Ma**, State Key Lab of Plant Genomics, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

Jin-Song Zhang, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

Xiang Lu, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

Shou-Yi Chen, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

Cultivated soybean has undergone many transformations during domestication. We identified 2680 genes that are differentially expressed during seed maturation and established two cultivar-specific gene co-expression networks based on the analysis of 40 transcriptomes from developing soybean seeds in cultivated and wild soybean accessions. Analysis of the two networks and integration with quantitative trait locus data facilitated us to pinpoint two potential key drivers for seed trait formation, *GA20OX* and *NFYA*. *GA20OX* encodes an enzyme in a rate-limiting step of gibberellin biosynthesis, and *NFYA* encodes a transcription factor. Overexpression of *GA20OX* and *NFYA* enhanced seed size/weight and oil content, respectively, in seeds of transgenic plants. These two genes showed significantly higher expression in cultivated than in wild soybean, and the increases in expression were associated with genetic variations in the promoter region of each gene. Moreover, the expression of *GA20OX* and *NFYA* in seeds of soybean accessions correlated with seed weight and oil content, respectively. Our study reveals transcriptional adaptation during soybean domestication and may identify a mechanism of selection by expression for seed trait formation, providing strategies for future breeding practice.