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PII: S0168-9452(18)30007-4
DOI: https://doi.org/10.1016/j.plantsci.2018.05.024
Reference: PSL 9859

To appear in: *Plant Science*

Received date: 3-1-2018
Revised date: 22-5-2018
Accepted date: 24-5-2018

Please cite this article as: Singh J, Zhao J, Vallejos CE, Differential transcriptome patterns associated with early seedling development in a wild and a domesticated common bean (*Phaseolus vulgaris* L.) accession, *Plant Science* (2018), https://doi.org/10.1016/j.plantsci.2018.05.024

Differential transcriptome patterns associated with early seedling development in a wild and a domesticated common bean (*Phaseolus vulgaris* L.) accession

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Highlights

- Domestication of the common bean yielded larger seeds than found in wild ancestors
- Large seeds also produce early seedlings with different growth phenotypes
- Wild and domesticated early seedlings show different gene expression patterns
- Differentially expressed genes showed unique TF binding sites in promoter regions
- Some of the DE genes are known to have putative domestication signatures

ABSTRACT:

Genes that control "Domestication Syndrome" traits were direct targets of selection, like those controlling increased seed size in the common bean. However, selection for this trait brought about unintentional selection on genes controlling seedling growth. We hypothesized that wild and domesticated plants have different early seedling growth patterns as an indirect consequence of selection for a larger seed size during domestication, and those differences resulted from changes in gene expression patterns of the wild ancestor. Large seeds pose a challenge to reserve remobilization during early heterotrophic growth, particularly during a transition towards more fertile alluvial soils. To address our hypothesis, we characterized the patterns of gene expression of cotyledon, root, and leaf tissues of 7-day old seedlings of a wild and a landrace accession of the common bean. Differential expression analyses detected genes with contrasting patterns of expression between the two genotypes in all three tissues. Some of the differentially expressed genes with contrasting genotypic patterns are known to have domestication-related signatures of selection. Among these genes were some transcription factors associated with key roles in development. These genes may represent targets of indirect selection and ultimately explain the growth phenotypic differences between wild and domesticated seedlings.