

RNA-seq analysis of the Asiatic *Vigna* to examine differential gene expression during germination and early plant development

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Seed germination strategies varies between plant that place cotyledons above ground in epigeal germination or reserve them belowground in hypogeal germination. The type of cotyledon emergence is usually fixed for many plant families; however, for Fabaceae species (also known as the legumes), such as those in the genus *Vigna*, both epigeal and hypogeal germination are observed. In this study, we examined phenotypic variation of these germination traits, as well as differentially expressed genes (DEGs) during early seedling development among *Vigna* species in the subgenus *Ceratotropis* (“Asiatic *Vigna*”) using RNA sequencing. Thousands of DEGs were detected among multi-species comparisons, reflecting numerous genetic factors influencing timing of gene expression during early development of *Vigna* species. Gene ontology enrichment analyses further revealed functional variation associated with the germination strategies. Possible key functions and select genes further differentiating the Asiatic *Vigna* species, were also identified. These functions included, but were not limited to, stress and defense responses, signal transduction, and photosynthesis, reflecting trade-offs associated with differing germination types. Such trade-offs during seedling development have important agroecological implications in terms of crop productivity, crop diversity, and a plant’s response to environmental conditions. While there remains a need for a more in depth genetic analysis of seedling morphological traits among the Asiatic *Vigna*, results of this study do provide preliminary research into functions influencing gene expression during early plant development in this genus. The results further highlight the need for increased plant genomic resources, particularly a genus-wide pan-genome.