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Transcriptomic changes associated with fruit quality and crop productivity in common bean

Abstract: Fruit quality and crop productivity in legume species are critically influenced by maturation and dehiscence developmental processes (Tang et al., 2013). These stages of fruit development are well characterized in the Arabidopsis plant model but not in legumes, as is the case of common bean *Phaseolus vulgaris* (Li and Olsen, 2016). Here, we used RNA-seq to compare immature and mature stages of pod development in two accessions (PMB0225 and PHA1037) of this species, which also differ in other important agronomical traits such as dehiscence and fiber content. The most recent update of the *Phaseolus vulgaris* reference genome was used for the alignment of RNA-seq short reads, then computing fold changes among the different developmental stages. In this way, we were able to derive a list of differentially expressed genes (DEG) that are associated with pod maturation in both accessions, mainly involved in transmembrane transporter activity, carbohydrate metabolism and photosynthesis. Furthermore, among DEGs between dehiscent and indehiscent fruits we found genes related to oxidation-reduction and lipid metabolic processes.

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References

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