

Natural Variation of Pennycress Metabolome and Transcriptome, an Emerging Crop for Aviation Biofuel

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Project Goals: Investigating pennycress natural variation to identify candidate genes and biomarkers associated with oil accumulation.

Pennycress (*Thlaspi arvense*) is a member of family Brassicaceae which produces seed oil ideally suited for use as a renewable source of biodiesel and aviation fuel¹. However, for this plant to become an economically viable and sustainable bioenergy crop, molecular and genetic resources must be developed to guide strategies for increasing oil production through breeding and/or genetic manipulation. In this work, we investigated the natural variation of central carbon metabolism in pennycress among twenty-one accessions sourced from distinct geographic regions to identify candidate genes and biomarkers associated with oil accumulation. The biomass components, targeted metabolome, and transcriptome of each line were analyzed at two different stages of embryo development, and positive and negative correlations between the levels of intracellular metabolites and transcripts with oil accumulation were identified. Additionally, two accessions with diverse oil content (30% vs 40%), were analyzed in greater detail under more controlled conditions at five developmental time points. One of the pathways that illustrated the largest metabolic variation between the two lines was the tricarboxylic acid cycle, in which intermediaries displayed significant differences. Also, the content of several compounds involved in sucrose biosynthesis and/or degradation suggest contrasting regulation of sugar metabolism. Altogether, this work has identified oil biomarkers that may prove useful in the breeding and rational bioengineering of pennycress.

References

1. Fan, J.Q., Shonnard, D.R., Kalnes, T.N., Johnsen, P.B. & Rao, S. A life cycle assessment of pennycress (*Thlaspi arvense* L.) -derived jet fuel and diesel. *Biomass & Bioenergy* **55**, 87-100 (2013).

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