Title: Germination and Seed Size Variability in Camelina

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Project Goals: Camelina is a Brassica oilseed crop that has great potential to become a sustainable source of bioenergy in the US. However, the low nitrogen use efficiency and the low seed and oil yield compared to other major oilseed crops hinder this potential. The goal of this project is to decipher the genetic and physiological mechanisms that determine the nitrogen use efficiency and oilseed yield during the most critical processes of the camelina life cycle: 1) how camelina, in partnership with soil microbes, maximizes its ability to absorb and assimilate nitrogen into vegetative biomass; and 2) upon the transition to reproductive growth, how nitrogen is efficiently remobilized from senescing tissues (leaves and silicles) into sinks (seeds) to optimize yield potential by increasing seed size and enhancing oil synthesis.

Abstract Text:

Predictable germination is critical to the life cycle of productive crop growth. Within an optimal environment, isogenic seed can demonstrate considerable germination variability. We examined sources and causes of variable germination in camelina, with a focus on seed size. The oilseed camelina generally reproduces through self-pollination, with outcrossing rates of 0.09-0.28%, resulting in largely homozygous lines; however, the seed batch produced by a single plant still varies in size. Indeed, across accessions and seed size mutants, we observed differences in not only the mean seed size—as measured by length, width, and area—but also the variance. For example, the accession Suneson produced seed batches more variable in seed size compared to other accessions grown in the same conditions. Seed size (Huang et al 2021) is positively correlated to time to 50% germination. We therefore hypothesize that variable seed size across batches result in more variable germination. Seed size batch variability was also impacted in TILLING mutant lines produced in the Licalla background, with a subset of mutant families having highly variable seed batches relative to others. Furthermore, non-Mendelian patterns of inheritance of seed size in the mutant lines suggest epigenetic factors influencing seed size. Epigenetic factors also may play an important role in seed germination in camelina given our observation that some accessions were sensitive to nitrogen fertility of the previous generation. Low nitrogen conditions also resulted in delayed and varied germination, which may represent an environmentally induced dormancy effect enabling camelina seed to overwinter. An important candidate regulator of seed size is miR167a (Na et al, 2019), which, when overexpressed specifically in camelina seeds, results in larger seed size. The larger seed size may arise through a delay in development, wherein the expression pattern of transgenic seed 10 and 12 days after fertilization are similar to wild-type seed at 8 days after fertilization. Examining the genetic

network tied to miR167a overexpression points to several candidate regulators, with one of the most highly connected genes, *DELAY OF GERMINATION1* (*DOG1*) found in the module of genes with delayed expression in the overexpression line. Further work will tie these observations, examining the role of *DOG1* in camelina seed size variation and impacts on germination variability in light of epigenetic factors.

References/Publications

1. Na, G., Mu, X., Grabowski, P., Schmutz, J. and Lu, C., 2019. Enhancing microRNA 167A expression in seed decreases the α-linolenic acid content and increases seed size in Camelina sativa. *The Plant Journal*, *98*(2), pp.346-358.
2. Li, H., Hu, X., Lovell, J. T., Grabowski, P. P., Mamidi, S., Chen, C., Amirebrahimi, M., Kahanda, I., Mumey, B., Barry, K., Kudrna, D., Schmutz, J., Lachowiec, J., & Lu, C. 2021. Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. *The Plant Genome, 14* (2), e20110.

Funding Statement: This research is supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science Program grant no. DE-SC0021369.