Camelina growth impacted by bacteria and nitrogen stress

Qing Zheng[1,] * (qingzheng@lbl.gov), Chuntao Yin[2], Peter Andeer[1], Cody Willmore[3], **Chaofu Lu[4]**, Trent R. Northen[1,5], Timothy Paulitz[3], Susannah Tringe[1,5]

[1]Lawrence Berkeley National Laboratory, Berkeley, CA; [2]North Central Agricultural Research Laboratory, USDA-ARS, Brookings, SD; [3]Wheat Health, Genetics, and Quality Research Unit, USDA-ARS, Pullman, WA; [4]Montana State University, Bozeman, MT; and [5]Joint Genome Institute, Berkeley, CA.

Website URL: https://www.montana.edu/econproject/index.html

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. Specifically, we look to address: 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.

Camelina is a promising non-food oilseed crop with great potential for various applications in the US. It is normally grown as a rotation crop in the wheat-camelina systems, providing a biofuel feedstock and potentially improving cereal-based cropping systems and boosting rural economies. However, high nitrogen inputs and low oilseed yields hinder its great potential. To enhance camelina oilseed production with minimum nitrogen fertilization, it is important to understand how camelina plants interact with beneficial microbes that may enhance nitrogen use efficiency and boost oil yield.

To address how soil microbes impact camelina growth and nitrogen use efficiency, bacteria were isolated and identified from 33 locations across wheat cropping zones of eastern Washington. Soils were collected from 33 locations and camelina cv. Suneson were grown in collected soils in the greenhouse for four weeks. Bacteria from camelina rhizosphere grown in 24 of the 33 location soils were cultured in Tryptic Soy Agar and R2A media. Over 3000 bacterial colonies were isolated and 920 of them were identified by 16S rRNA sequencing. A total of 51 unique bacterial genera, belonging to 31 families, were identified. *Pseudomonas*, *Bacillus*, *Flavobacterium*, and *Arthrobacter* were the most abundant genera in our bacterial collection. Interestingly, genera *Massilia*, *Pedobacter*, *Variovorax*, and *Caulobacter*, *which are* common in wheat rhizospheres, were also found. In addition, we found that culture media had a slight but significant effect on bacterial isolation, while no significant influence of locations was observed.

To understand how camelina uses root exudates to recruit beneficial microbes under nitrogen stress, we profiled root exudate compositions during the early growth period. We first evaluated camelina growth in axenic fabricated ecosystems (EcoFABs) designed for root exudate collection. Camelina was cultivated under limited (70 ppm N) and replete nitrogen (210 ppm N) conditions in EcoFAB 2.0 with weekly collection of metabolites. We successfully cultivated camelina in EcoFABs for five weeks and the plants were harvested for root and shoot biomass measurements. The results showed that the overall camelina biomass was lower under limited nitrogen conditions, but only root biomass was significantly lower in the limited nitrogen group compared to the replete nitrogen group. We will profile exudate composition during N stress using LC-MS/MS metabolomics and conduct camelina plant-microbe co-culture experiments using isolated bacteria and synthetic communities (SynCom) to further explore how camelina uses exudates to recruit beneficial microbes that may help increase nitrogen use efficiency and oil yield.

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.