The Microbiome of Camelina Grown Across Eastern Washington

Elle Barnes[1], Chuntao Yin[2], Daniel Schlatter[3], Hao Peng[4], Cody Willmore[5], Susannah Tringe[1,6], and Timothy Paulitz[5]

[1]US DOE Joint Genome Institute, Berkeley, CA; [2]USDA-ARS, Brookings, SD; [3]USDA-ARS, St. Paul, MN; [4]Washington State University, Pullman, WA; [5]USDA-ARS, Pullman, WA; [6]Lawrence Berkeley National Laboratory Berkeley, CA

Camelina (*Camelina sativa* L.) is a biofuel, oilseed and rotation crop grown in dryland farming systems. The agronomic characteristics of camelina have been extensively investigated in the inland Pacific Northwest. Camelina is fairly disease resistant, has good tolerance to frost and drought, and can be grown under low input conditions. Although the acreage in WA is small, it still has potential as a rotation crop. In 2020, the Department of Energy funded a large grant with collaborators in WA, MT and CA to investigate the nitrogen use efficiency, genetics and microbiology of camelina. We are screening over 200 lines in the field for nitrogen use efficiency. We hypothesized that the rhizosphere microbiota (the community of microbes associated with plant roots) may play a role in nutrient uptake. We sampled 33 locations across eastern Washington covering different precipitation zones, from wheat fallow to annual cropping. After planting camelina in soil collected from 33 locations, we isolated over 3000 bacterial isolates from camelina roots, the largest collection of root-associated bacteria on this crop. The rhizosphere culture collection was dominated by a small number of bacterial genera (Fig. 1). We are currently testing these for their ability to increase camelina growth, and have identified isolates of *Pseudomonas* that stimulate growth with urea as the N source. We also used high-throughput DNA sequencing to characterize fungal and bacterial communities. Location was a significant driver of camelina microbiome composition. Rhizosphere bacteria communities were dominated by *Sphingomonas*, which we did not isolate very frequently in culture. Further, *Rhizobium* was the dominant genus inside the root, again not represented in our collection. Future work is focused on identifying isolates that will promote growth, increase N uptake, protect against disease and confer drought resistance to camelina.

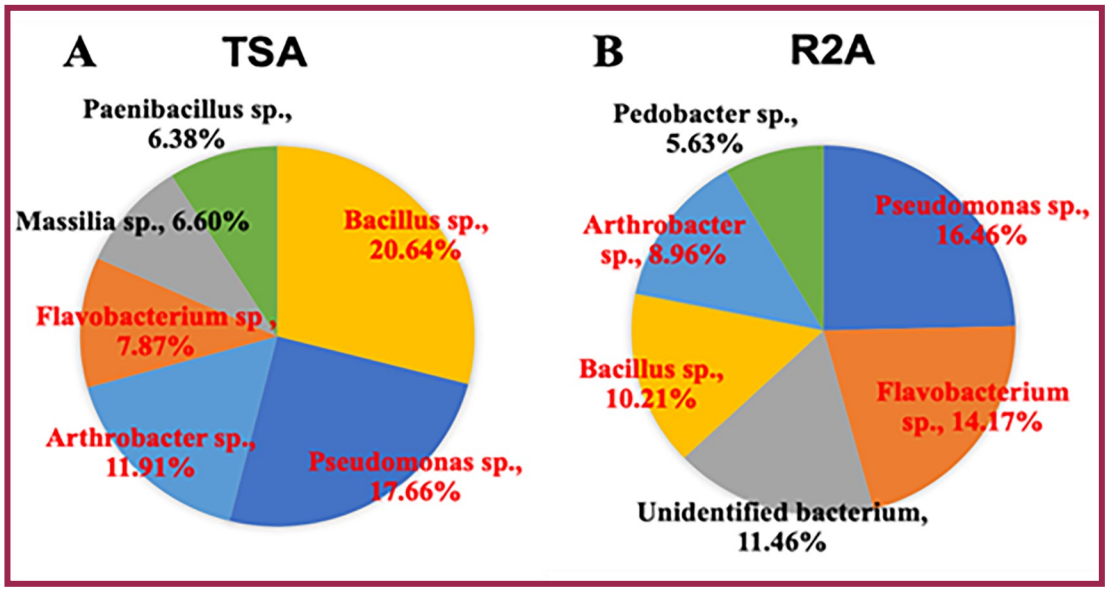

Figure 1. Most abundant bacteria isolated from roots of camelina. TSA= tryptic soy agar. R2A is another type of medium for slower growers.