Canola Variety Effects on Soil Health Mediated by Nutrients and the Microbiome

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The rhizosphere is a highly active region for both biological and chemical processes and is analogous to the human gut, where microbial communities play critical roles in transforming nutrients for the health of the host. Plants interact with a host of both soil-borne diseases and soil-borne beneficial micro-organisms and extensive work across plant systems has documented that plant genotype interacts with the environment to determine these interactions. Work by our team has found that crop genotype is related to differences in siderophore activity in wheat rhizosphere and that crop genotype is also related to differences in the ability for beneficial microbes to protect against soil-borne antagonists in the Medicago rhizosphere. In canola, one of the barriers to adoption is the variability in its effects on subsequent rotational crops--in some cases canola enhances the yield of following crops but in other cases it decreases yield. Previous work by our team has documented that wheat and canola share core rhizosphere microbiome members and that these communities shift through time and under varying canola-wheat rotations. However, it is not currently known how these effects vary with canola variety or if these effects are consistent across our region. Understanding the biological and soil nutrient basis of these effects in relation to canola variety across our region will be important for both immediate recommendations for farmers seeking to incorporate canola into rotations as well as longer term efforts to improve soil health through the use of oilseed crops.

We plan to sample the microbiome of ongoing variety trials–both the loosely bound rhizosphere, which has been more closely linked to microbiome function, as well as the tightly bound rhizosphere, which has been found to vary more dramatically across plant varieties due to genetic differences. We will extract DNA and use 16S and ITS to inform us what bacteria and fungi are present, and plan to additionally use high-throughput qPCR to assess the abundance of key nutrient cycling genes. We will also conduct analysis of soil nutrients in the bulk soil to better understand connections between canola varieties, the microbiome, and soil health.