

AGR1622: Moving Forward to Sustainable Development of Saskatchewan Pulse Industry - long-term research collaboration between Agriculture and Agri-Food Canada (AAFC) and Saskatchewan Pulse Growers (SPG)

It is known that host plants influence root-associated fungal communities that, in return, affect the performance of the host. However, little is known about how the root-associated microbial community would affect performance of crops under different rotation systems. In this project, we assessed the effects of crop rotation comprising of canola (C), lentil (L), oat (O), pea (P), and wheat (W) and the crops prior to these rotation crops on the performance and rhizosphere fungal communities. A total of 24 alternative crop rotation systems were conducted at the Indian Head Research Farm, Saskatchewan, in a split block trial with four replicates. The trial started in 2012. Each year, crop yield and growth-related characters were recorded from each plot. Soil was sampled at flowering. Rhizosphere DNA was isolated using standard methods. The internal transcribed spacer (ITS) was amplified using ITS1F/ITS2 primers set through 454 pyrosequencing and Illumina Miseq PE250 for analyzing rhizosphere fungal communities. DNA sequence data were analyzed using standard bioinformatics programs.

Both crop rotations and previous crops had significant impacts on crop performance. Pea yield was the highest in WLOP rotation (3494 kg ha^{-1}) followed by WCOP rotation (2943 kg ha^{-1}), while WPCP rotation had the lowest pea yield (2045 kg ha^{-1}). Peas preceded by oats had significantly higher yield ($P < 0.0098$) compared to peas preceded by canola, lentils, or wheat. Wheat yield was significantly higher ($P < 0.012$) when rotated with pulse or canola (PCPW and PLPW) in compare to oats (COPW, LOPW and POPW). The wheat yield was about 20% higher in plots preceded by canola (3593 kg ha^{-1}) and lentils (3533 kg ha^{-1}) than by oats (2948 kg ha^{-1}).

Both rotation sequence and previous crop significantly affected rhizosphere fungal community composition, and the effect of rotation sequence was greater than the effect of the previous crop. The lowest level of fungal evenness was observed in peas of the rotation WPLP, and in peas preceded by lentils. The fungal community was the most diverse in peas preceded by wheat and least diverse in peas preceded by canola. The proportion of pathotrophs increased in intensive pulse rotations such as WPLP. *Fusarium* genus was the predominant pathogens among the rotations. *Olipidium brassicae* was highly abundant, while *Botrytis cinerea* was more abundant in WPLP in 2016 only. Rotations with oats increased the relative abundance of *F. solani* and *F. graminearum*, but inclusion of lentils in the rotation decreased *F. solani* abundance. Pathotrophs such as *O. brassicae*, *Mortierella elongata*, and *B. cinerea* increased in peas preceded by lentils.

Redundancy analysis showed that soil micronutrients such as Magnesium, Calcium, Copper, and available Potassium affected the fungal community but the effects were generally small. This study emphasized the importance of crop diversification for improved soil properties and increased systems productivity. It also highlighted the role of individual crops in rotations to manage rhizosphere fungal communities, and ensure the productivity and profitability of cropping systems.