# Impact of diversified crop rotations on soil fungal communities

# Yining Niu<sup>1,4</sup>, Luke D. Bainard<sup>1</sup>, William E. May<sup>2</sup>, Chantal Hamel<sup>3</sup>, Yantai Gan<sup>1\*</sup>

<sup>1</sup>Agriculture and Agri-Food Canada (AAFC), Swift Current Research and Development Centre, SK, S9H 3X2;

<sup>2</sup>Indian Head Research Farm, AAFC, Indian Head, SK, SOG 2KO;

<sup>3</sup>Quebec Research and Development Centre, AAFC, Québec, QC G1V 2J3, Canada

<sup>4</sup>Gansu Provincial Key Laboratory for Aridland Crop Science, Gansu Agricultural University, Lanzhou, 730070, China \*Presenter: yantai.gan@agr.gc.ca



### Introduction

Diversifying crop rotations with pulse crops have been reported to improve soil water and nutrient conditions. With those benefits, there is a tendency to increase the frequency of pulses in crop rotation. However, little is known about the rotational effect on soil microbial communities. The objective of this study was to determine the effect of rotation sequence or previous crop on the composition of soil fungal communities in the pea rhizosphere.

#### **Materials and Methods**



Six diverse crop rotation systems were evaluated at the Agriculture and Agri-Food Canada Research Farm in Indian Head (50°32'N, 103°40'W), Saskatchewan. Pea (P, Pisum sativum L.), lentil (L, Lens culinaris Medik.), and hybrid canola (C, Brassica napus L.) were rotated in different intensities with wheat (W, *Triticum aestivum* L.) or oats (O, Avena sativa L.),. The 4-yr rotation cycle was completed in 2015. All phases of each rotation were present every year with 4 replications. Rhizosphere soil in pea plots were sampled at flowering stage both in 2015 and 2016.

Total DNA was extracted from approximately 0.25 g of rhizosphere soil using the *PowerSoil* DNA Isolation Kit following the manufacturer's instructions. The universal fungi primer pair ITS1F and 58A2R were used to amplify ITS1 region of the rhizosphere fungal community by polymerase chain reaction (PCR). Purified amplicons were pooled in equimolar and paired-end sequenced (2×250) on Illumina Miseq PE250.

Illumina paired sequences were merged and trimmed to remove primers following the procedure of UPARSE pipeline. The RDP classifier was used to assign taxonomy to the OTUs using the UNITE fungal ITS database. Data were analyzed using the *Imer* function of *Ime4* package in R. Permutational multivariate analysis of variance (PERMANOVA) was used to test the factors on soil fungal communities using the *adonis* function in vegan package. The mantel test in *vegan* package was used to examine the correlation between soil fungal community composition and soil properties based on the distant matrix.

#### **Results and Discussion**

 $\succ$  There was a significant difference in the richness of rhizosphere fungal communities between years, with those in 2015 significantly higher than in 2016. The rotation sequence or previous crop had a significant effect on fungal evenness (Pielou's index) in 2015. However, no significant effect on the richness (Chao1 index) of pea rhizosphere fungal communities in 2015 or 2016. The lowest level of rhizosphere fungal evenness were observed in the pea preceded by lentil in 2015.

Fig. 1. Nonmetric multidimensional scaling (NMDS) ordination of rotation on soil fungal communities in 2015 (a) and 2016 (b). Symbols indicate the mean axis coordinates ( $\pm$ se) for each rotation. A significant (P<0.05) year effect was observed for soil fungal community composition and thus the year 2015 and 2016 are present separately. Rotation sequence of WCOP = wheat-canola-oat-pea; CWCP= canola-wheat-canola-*pea*; WLOP=wheat-lentil-oat-pea; WPCP= wheat-pea-canola-pea; WPLP=wheat-pea-lentil-pea; WPOP=wheat-pea-oat-pea. Boldface word of pea in the rotation indicates pea sequence in each rotation.



- > Both rotation sequence and previous crop had a significant impact on the rhizosphere fungal composition (Fig. 1, 2). The effect of rotation sequence was greater than the effect of previous crop.
- $\succ$  Percent pathotroph reads in the rhizosphere fungal community differed significantly among the rotations in 2016 (Fig. 3). Rotation sequence with two peas and lentil as a break crop (WPLP) had significantly higher proportion of fungal pathotrophs in the rhizosphere compared to rotation with two peas and canola as a break crop (WPCP).
- > The Mantel test showed that the fungal community were significantly correlated with soil properties in 2015, but no significant relationship was observed in 2016. Variation partitioning by RDA revealed that soil pH accounted for 9.6%, Mn for 5.4%, Ca for 4.3% and Mg for 1.90% of the rhizosphere fungal community variation.



Fig. 2. Nonmetric multidimensional scaling (NMDS) ordination of previous crop on soil fungal communities in 2015 (a) and 2016 (b). Symbols indicate the mean axis coordinates (±se) for each crop. A significant (P<0.05) year effect was observed for soil fungal community composition and thus the year 2015 and 2016 are present separately.

## Conclusions

- $\succ$  Crop rotation sequences promoted the diversification of soil fungal communities after four years of cropping. The rotation sequences contributed to the changes in soil physiochemical properties which serves as the mechanisms that influence pea rhizosphere fungal communities.
- $\succ$  Increasing the frequency of pea in rotation decreased fungal evenness, lead to a higher build-up of pathogens in the soil, but this had not cause a yield decline after the first 4-yr



 $\succ$  The impacts of rotation frequency and intensity on soil microbiomes were altered by environmental conditions, which interacted with soil properties.

Acknowledgement **Fig. 3.** Effect of rotation sequence (a) and previous crop (b) on the proportion of relative abundance of fungal reads (mean±se) that assigned to trophic mode of pathotroph (>0.25% of total reads) in 2015 and 2016. Error We acknowledge Lee Poppy and the technical support crew for field operation and plot management, and the financial support from Agriculture and Agri-Food Canada and Saskatchewan Pulse Growers. bars with different letters indicates a significant difference of pathotroph reads (P<0.05) among rotation sequences or previous crop in rhizosphere fungal communities in 2016. anada