
Microbiome of Canola Root: Structure and Variations

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Abstract

The fungi in the rhizosphere have a large influence on plant development and growth. Some of these **micro-organisms** protect plants against pathogens, mitigate the impact of abiotic stress, or facilitate plant nutrition. These organisms influence each other and form complex webs of interactions. Deciphering the structure and function of the fungal **microbiome** of crop plant rhizosphere is a necessary step toward optimizing the efficiency of plant production. We tested the hypotheses that (1) the diversification of cropping systems influences the fungal microbiome of canola **rhizosphere**, (2) canola has a fungal **core-microbiome**, i.e. a set of fungi that are always associated with canola, and (3) that some taxa have a determining influence on the structure of the communities (hub-taxa) within the core-microbiome. In 2013 and 2016 we used the canola phase of five cropping system, from the less to the most diversified, that included one of two types of canola (Roundup Ready® and Liberty Link®), in an existing long-term (6 years) field experiment. The experiment has a randomized complete block design with four blocks, and is replicated at three locations: Lacombe (Alberta), Lethbridge (Alberta) and Scott (Saskatchewan). Our results show that **crop diversification** has significant impact on the structure of rhizosphere fungal communities ($p = 0.0337$) for all sites. We also discover and described a canola core-microbiome made of **47 OTUs** in 2013 and identified *Exophiala sp.*, *Mortierella sp.*, *Fusarium solani*, *Ulocladium daucii* and *Humicola grisea* as the **hub-taxa** among this core. However this core microbiome was variable and could identify only one member in 2016 : *Olpidium brassicae*. Our results are presented as a basis for the development of ecological engineering strategies for the improvement of canola production.

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