## The Influence of Soybean Frequency in Rotation on Disease Pressure

The diverse wheat–canola–corn–soy and corn–soy crop sequences resulted in lower root rot severity compared to canola–soy and continuous soybeans.

SOYBEANS HAVE BECOME the third most popular crop grown in Manitoba but are still considered relatively new to the province. On many farms, soybeans are grown frequently throughout a crop rotation. This raises questions about what impact the frequency of soybeans in rotation might have on the risk of disease development.

Root and stem pathogens are the most concerning disease pests of soybeans due to their potential impact on yield and quality. Foliar diseases are commonly found but are generally of less concern. According to annual disease surveys, Fusarium root rots have been found in nearly all soybean crops across Manitoba, but often at low incidence. Despite the low incidence of many soybean pathogens to date, disease pressure is expected to rise as soybean production continues.

The goal of this research was to assess the incidence and severity of soybean diseases associated with different crop sequences, building on a project conducted by Dr. Yvonne Lawley examining soybean frequency in rotation.

Lawley's four-year study had four different crop sequences established at Carman, St. Adolphe and Melita from 2014 to 2017: 1) soy-soy-soy-soy, 2) canolasoy-canola-soy, 3) corn-soy-corn-soy and 4) wheat-canola-corn-soy. For the current project, disease pressure was assessed in 2017 when all crop sequences were in the soybean phase (year 4). Ten soybean plants were randomly selected from each plot and brought back to the lab for analysis.

Soybean roots, stems and leaves were visually assessed and given a severity rating. Next, any suspected pathogens were isolated from infected plant parts using conventional laboratory methods (i.e., plated on petri dishes). Finally, diseases were confirmed in the greenhouse following Koch's postulates. This means healthy soybean plants were inoculated with pure cultures of isolated pathogens to confirm the ability of the disease to infect soybeans (i.e., pathogenicity).

Figure 1. Root rot severity (%) in continuous soybean, canola–soy, corn–soy and wheat–canola–corn–soy sequences at Melita, Carman and St. Adolphe in 2017.



## Koch's Postulates

In 1890, the German physician and bacteriologist Robert Koch established four criteria for assessing whether a given pathogen is the cause of a disease:

- 1 the pathogen must be present in all cases of the disease,
- 2 it can be isolated from the host and grown in pure culture,
- 3 it is reproduced when inoculated into a healthy host and
- 4 it is the same as its original form when recovered from the infected host.

This research identified several soybean diseases, including root rot, anthracnose (*Colletotrichum truncatum*), white mould (*Sclerotinia sclerotiorum*), pod and stem blight/Phomopsis seed decay (*Diaporth/ Phomopsis* complex) and frogeye leaf spot (*Cercospora sojina*). Fusarium root rot was the most prevalent and damaging disease (Figure 1). Of the seven total *Fusarium* species identified, *F. oxysporum* was most common, making up 50% of the isolates.

Additional organisms were found, including *Colletotricum spaethianum* which is not known to infect soybeans and *Plectosphaerella cucumerina*, a potential latent infection that may live its life in the plant without expressing visual symptoms.

The diverse wheat-canola-corn-soy and corn-soy crop sequences resulted in the lowest root rot severity. However, alternating canola-soy had greater root rot severity, following a similar trend as continuous soybeans. These results suggest that root rot pressure is more variable and generally riskier when alternating soybeans with another crop, compared to growing soybeans in a more diverse rotation.

Root rot severity also varied by location. Continuous soybeans resulted in greater root rot severity at Melita (80%) compared to Carman (53%) and St. Adolphe (42%) (Figure 1). This highlights the need to assess disease risk on a field by field basis, rather than by crop sequence alone. **•** 

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