Development of a disease risk assessment tool for *Fusarium* species

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Abstract:

Fusarium species are important soilborne pathogens with wide host range. Diseases caused by pathogenic *Fusarium* species are known to be prevalent here in Canada. The development of a disease risk assessment tool for the identification and quantification of *Fusarium* species would aid in determining the mitigation of threats caused by pathogenic *Fusarium* species. In 2020, thirty-two soil samples were collected from two crop rotation study locations (Carman and Kelburn) in Manitoba, Canada. Fifty-one fungal isolates collected from soil were morphologically characterized as *Fusarium* species. Sequences of the *TEF1α* gene identified the species as *Fusarium acuminatum, F. commune*, *F. oxysporum, F. redolens*, *F. merismoides*, and *F. solani*. In 2021, diseased soybean plants were collected from the same two locations and were utilized for *Fusarium* isolation. Eighty fungal samples were characterized as *Fusarium* isolates. Preliminary results of the *TEF1α* gene sequences from diseased soybean plants revealed collections of *F. acuminatum, F. clavum, F. equiseti, F. graminearum, F. redolens, F. oxysporum, F. sporotrichioides,* and other putative *Fusarium* species. These collections of *Fusarium* species are currently being used for the development of a disease risk assessment tool for soil samples.

Background:

- ✓ Most members of the *Fusarium* species complexes are pathogenic.
- ✓ Pathogenic *Fusarium* species cause wide range of plant diseases.
- ✓ Pathogenic *Fusarium* species produce mycotoxins that reduce crop yield and quality of crop products, especially cereals.
- ✓ Studies have shown that *Fusarium* species that cause Fusarium Head Blight (FHB) on wheat can cause and Fusarium root rot on soybean (Hafez et al., 2021).
- ✓ *Fusarium commune*, a newly identified species (Skoovgard et al., 2003), has been continuously reported to cause diseases on soybean (Ellis et al., 2013), rice (Husna et al., 2020), lotus (Deng et al., 2022), forest nurseries (Kim et al., 2011), potato (Osawa et al., 2021), strawberry (He et al., 2022), grapes (Zhang et al., 2022), and on many other plants.

Methods:

1. This project is part of a crop rotation study (Table 1) where soil samples were collected in Year 7 and diseased soybean samples were collected in Year 8.

Table 1. Crop rotation study operation at Carman and Kelburn, Manitoba.

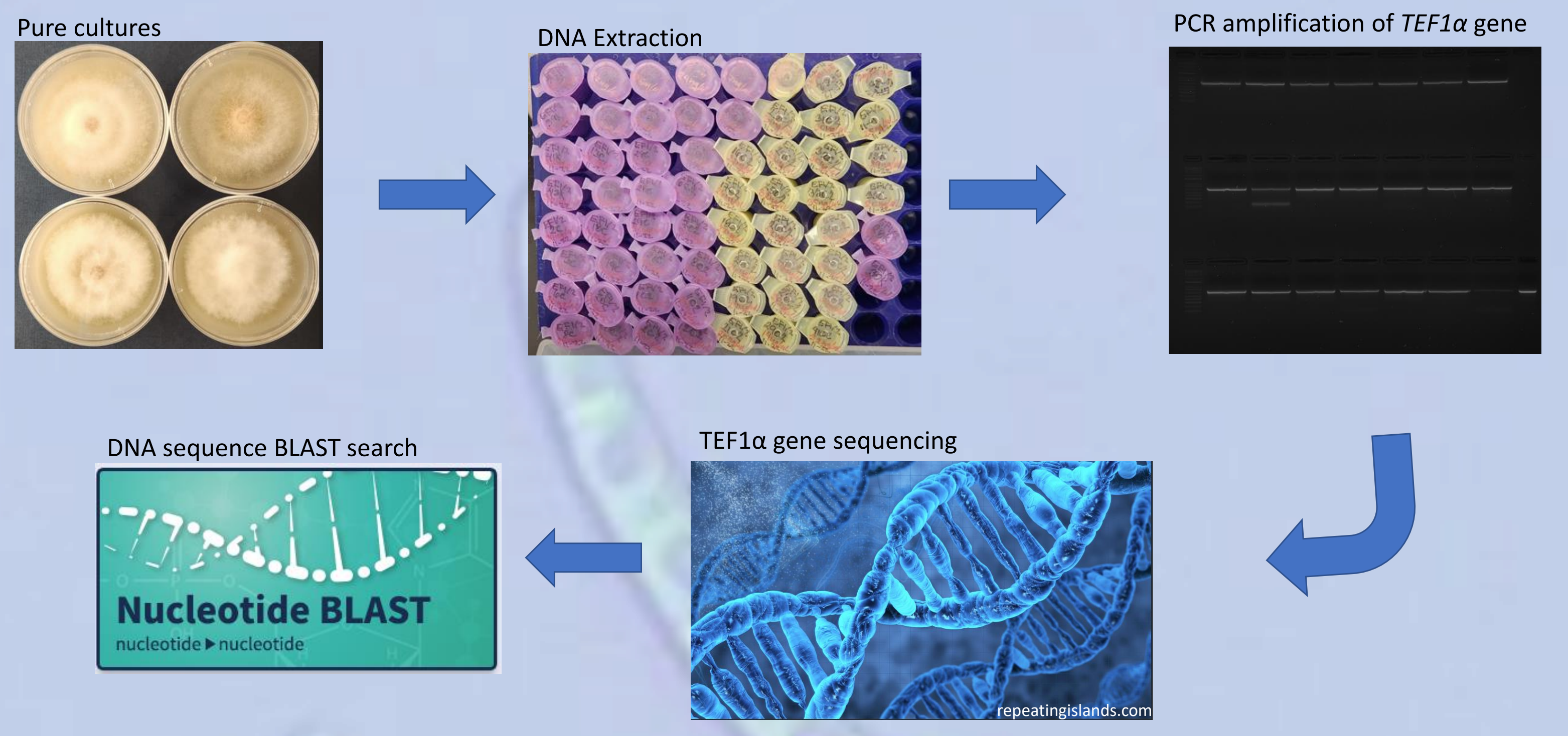
Treatments		2014	2015	2016	2017	2018	2019	2020	2021
		Year 1	Year 2	Year 3	Year 4	Year 5	Year 6	Year 7*	Year 8*
1	Continuous soybean	Soybean	Soybean	Soybean	Soybean	Soybean	Soybean	Soybean	Soybean
2	Soybean every second year (low carbon rotation crop)	Canola	Soybean	Canola	Soybean	Canola	Soybean	Canola	Soybean
3	Soybean every second year (high carbon rotation crop)	Corn	Soybean	Corn	Soybean	Corn	Soybean	Corn	Soybean
4	Soybean every fourth year	Wheat	Canola	Corn	Soybean	Wheat	Canola	Corn	Soybean

*Highlighted years are the source of this study.

2. *Fusarium* collections were isolated from soil samples and diseased soybean roots:

3. Pure cultures of *Fusarium* isolates were morphologically characterized:

4. *TEF1α* gene sequencing of *Fusarium* species candidates:



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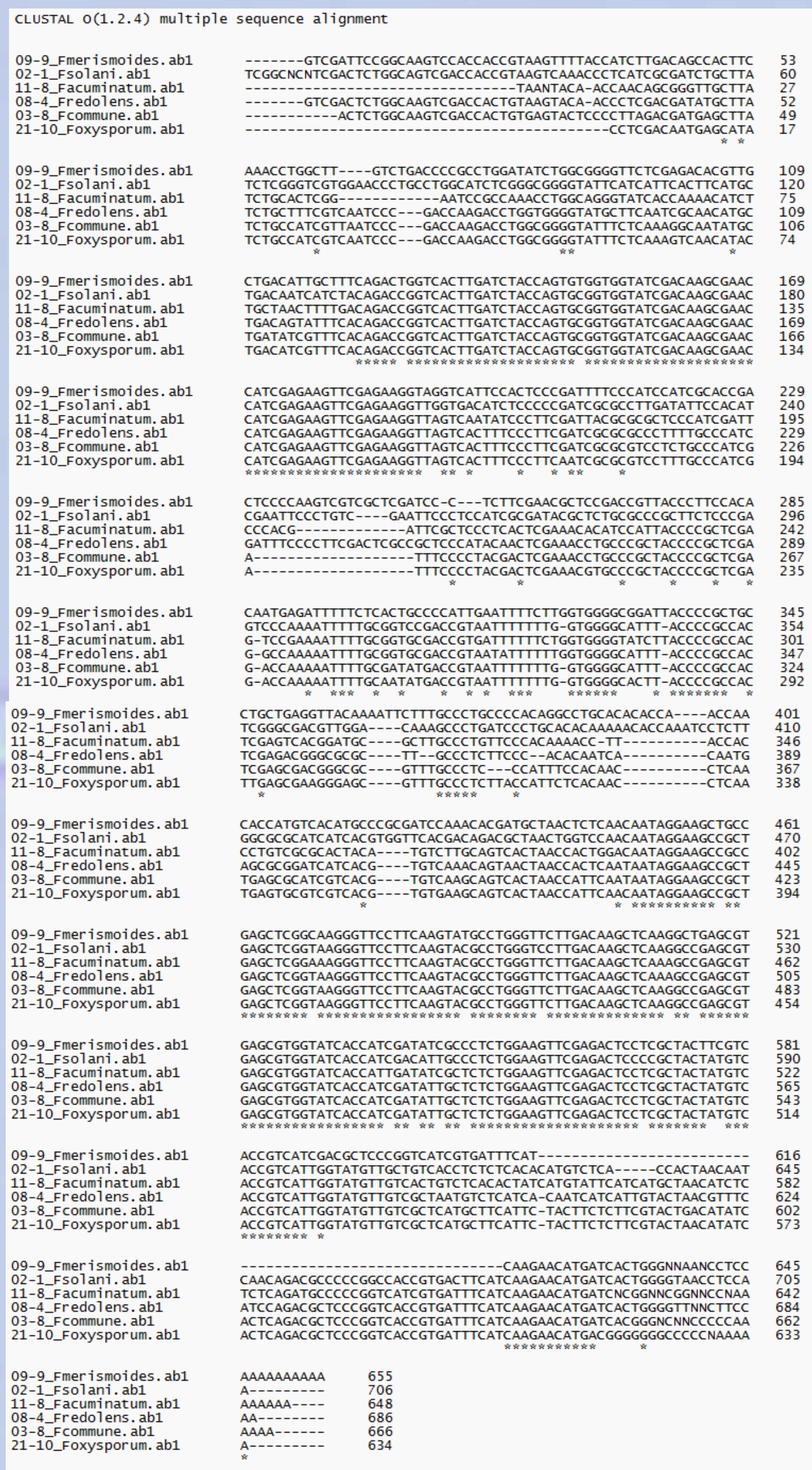
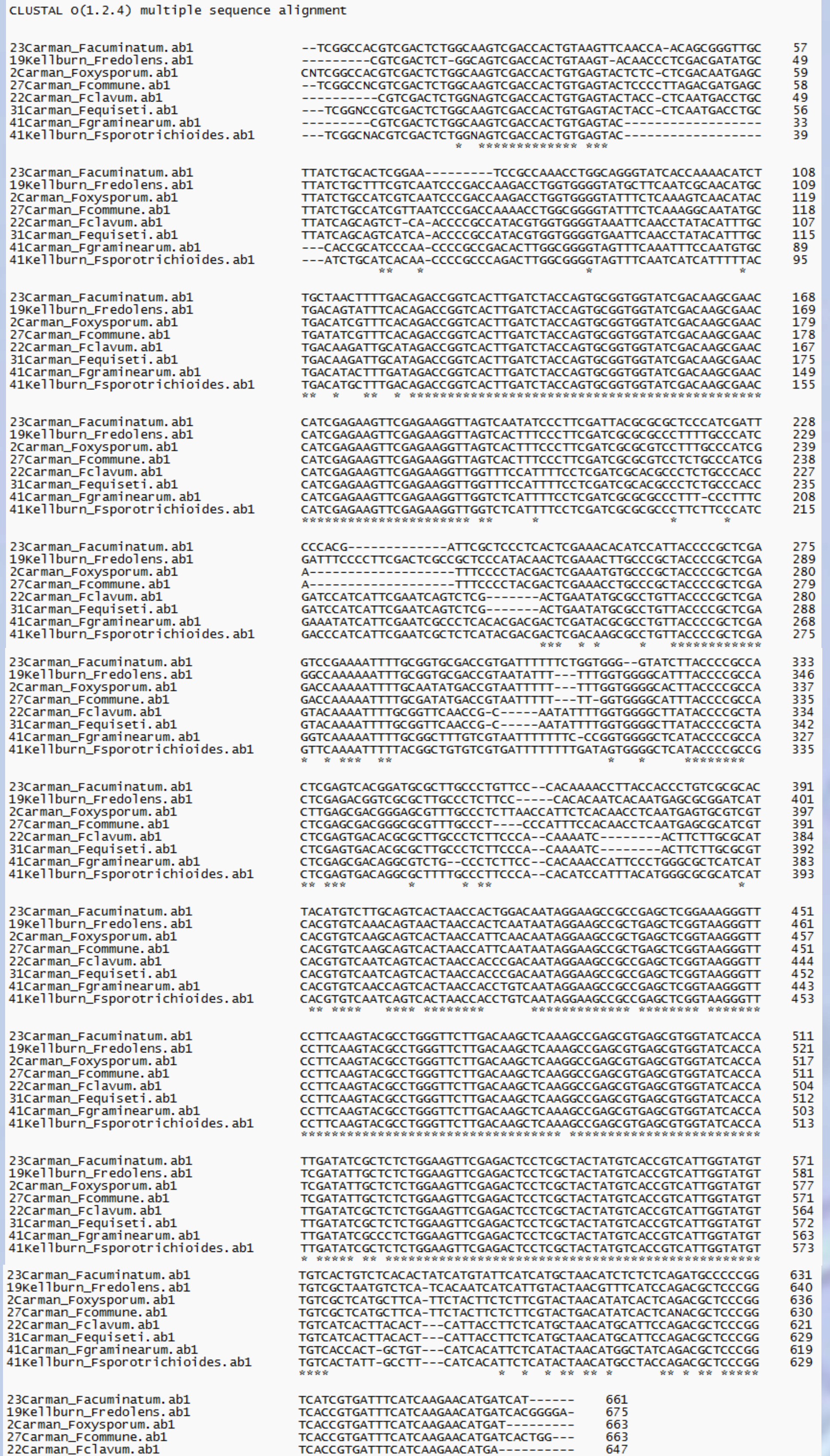
Results:

- ✓ *TEF1α* gene sequence alignment of *Fusarium* species representatives identified from soil (left) and soybean root rot (right):

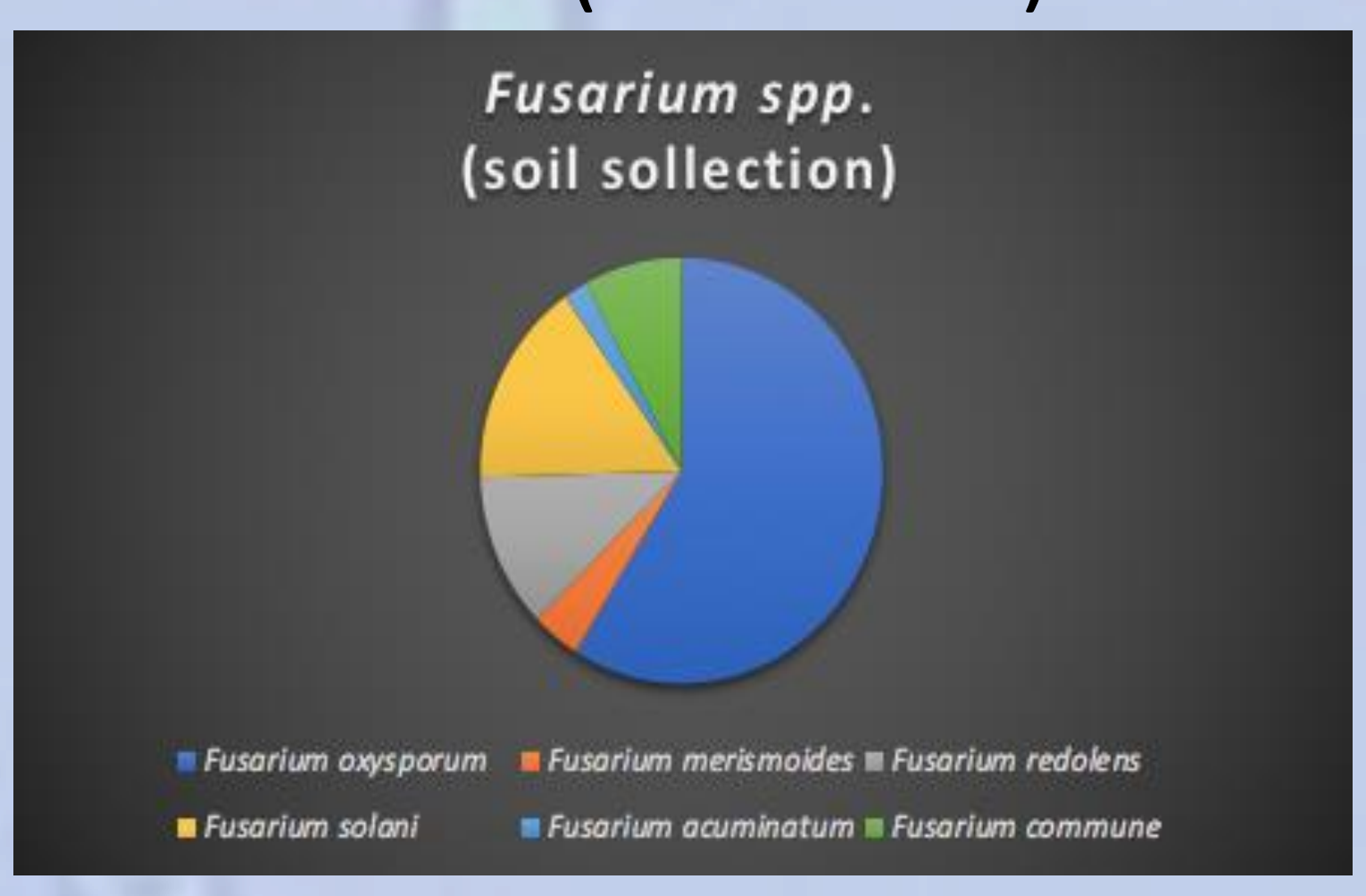


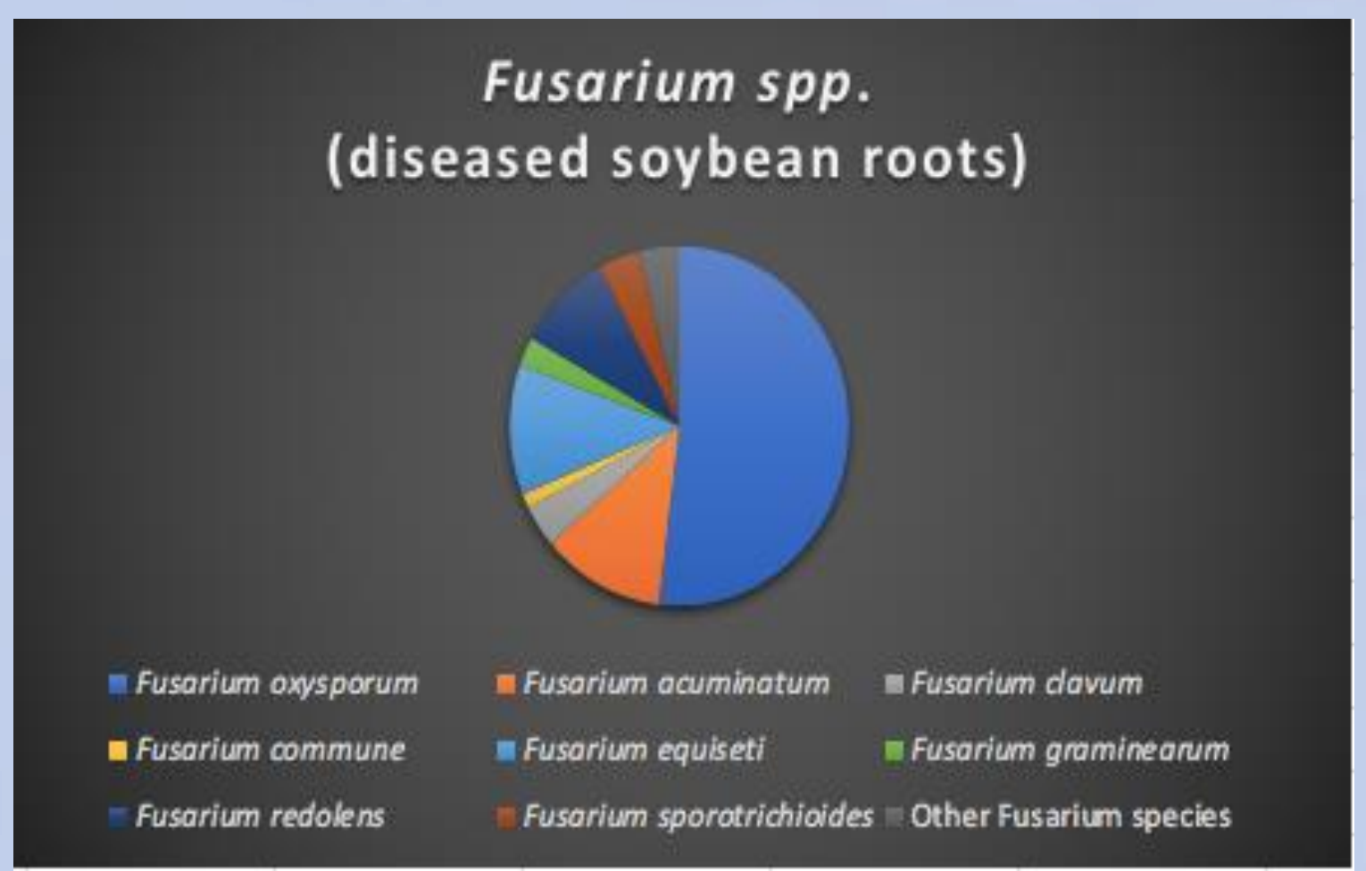
CLUSTAL O(1.2.4) multiple sequence alignment



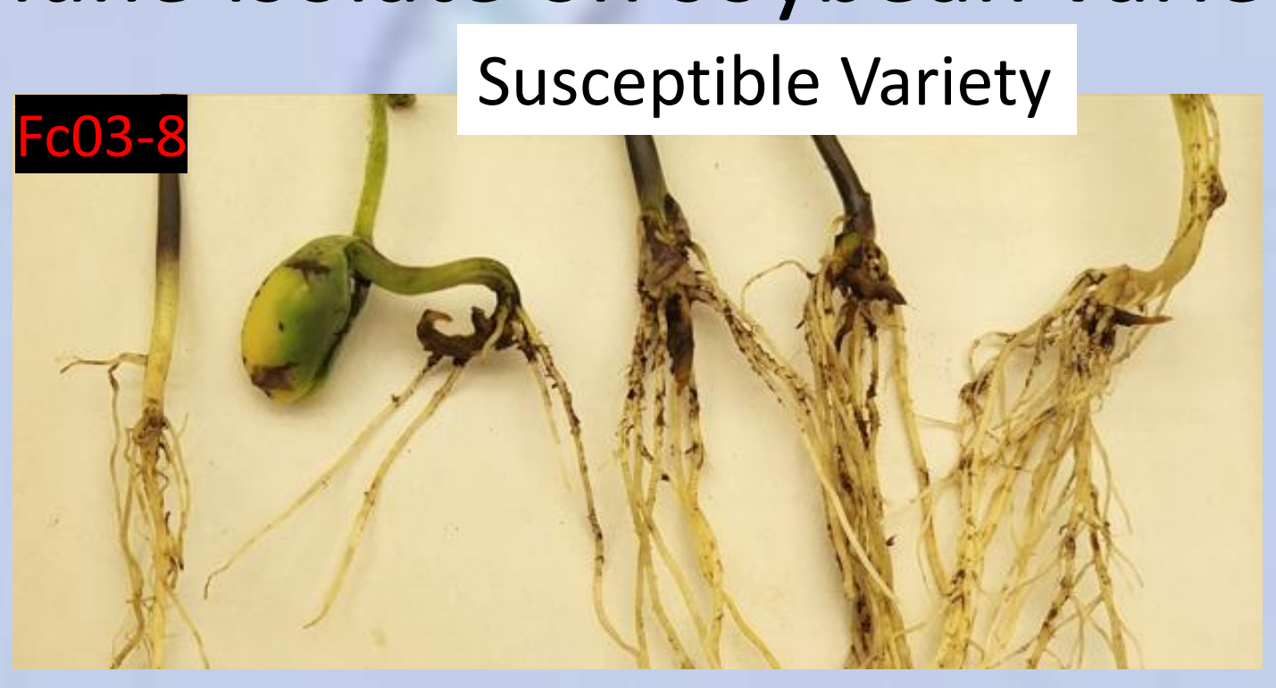
CLUSTAL O(1.2.4) multiple sequence alignment

- ✓ *Fusarium* species collected from soil and soybean root rot from Carman and Kelburn (Manitoba):





- ✓ Pathogenicity test of a *Fusarium commune* isolate on soybean varieties:



On-going experiments:

- Final optimization of designed specific primers for *F. commune* detection.
- Optimization of multiplex PCR detection of *F. solani, F. redolens, F. acuminatum*, and *F. commune* from soil samples.
- Pathogenicity test of *F. commune* isolates on rotation crops (e.g. corn).

Conclusion:

- ❖ Molecular detection of *Fusarium* species in the soil reflected the pathogens isolated from diseased soybean plants.
- ❖ *F. commune* was detected among the soybean root rot disease complex in Manitoba.