Project Title:

Investigating Fusarium oxysporum Races and Root Rot in Ontario Processing Peas: Implications for Disease Management

Research Location:

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Project Duration: ~2.5 years

Funded by:

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Ontario Processing Vegetable Growers (OPVG)

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Introduction:

Fusarium wilt, caused by *Fusarium oxysporum f. sp. pisi* (Fop), poses a major threat to global green pea production, with yield losses reaching up to 75%. Developing resistant pea cultivars remains the most sustainable long-term solution; however, Fop exhibits considerable pathogenic variability, with races 1, 2, 5, and 6 reported worldwide. Although these races have been detected in western Canada, their prevalence in Ontario is unknown. Additionally, growers face significant yield and profit losses from the pea root rot complex (PRRC), a disease involving multiple pathogens, including *Aphanomyces euteiches*. This project aims to (1) identify Fop races present in Ontario, assess the resistance of commercial pea cultivars to these races, and (2) survey pea fields for PRRC damage and pathogen composition. Findings will support economic growth by improving yield and profitability, guide future breeding programs, and provide tools and knowledge to better manage pea diseases in Ontario.

Objectives:

1: Determine the races of *Fusarium oxysporum f. sp. pisi* present in Ontario and assess resistance among selected pea cultivars.
2: Survey pea fields for root rot damage and identify causal organisms through plant and soil analyses.

Methods:

Objective 1: To investigate Fop races, we required *Fusarium oxysporum* (Fop) isolates and the appropriate pea differential lines.

Fop Isolates:

Pea samples were collected from six Ontario pea fields in 2025 (A: Granton; B: Kerwood; C: Dereham Centre; D: Kirkton; E: Dresden; F: Mt. Elgin). One pre-plant soil sample per field was collected in May, followed by symptomatic plant samples from June–July at various growth stages. Field surveys and sample collection were conducted by collaborator Elaine Roddy. Samples were washed, rated using a 1–7 scale (Esmaeili Taheri et al., 2017), and photographed. Rhizosphere soil was collected from soil adhering to plant roots.
Plant tissues (≤0.5 cm segments of crown, stem, and roots) were surface-sterilized and plated on Rose Bengal, V8, and PDA media, all supplemented with ampicillin and streptomycin. Soil samples were plated on modified MVB medium and half-strength PDA with antibiotics. Cultures were incubated at 22°C with a 12 h light/dark cycle for 7 days. Emerging colonies were subcultured on PDA. Fungal isolates were identified morphologically based on colony characteristics and macroconidial morphology.

Pea Differential Lines:

Pathogenicity and race determination require reactions on a set of pea differential lines (Little Marvel, Darkskin Perfection, WSU 23, WSU 28, WSU 31, New Season, New Era). Although race testing is scheduled for project Years 2 and 3, seed acquisition efforts began proactively. Requests for seed were submitted to the USDA Germplasm Resources

Information Network (GRIN) on July 11 and September 16, with our UPS account provided for shipping.

Objective 2: Root Rot Survey and Casual Organisms:
Field sites, samples, sample collection procedures, and fungal isolation methods were the same as those used for Objective 1.

Results:

Objective 1: Fop Isolates:
Approximately 68 plant samples were collected across the six fields. Sample distribution was: field A (10), field B (5), field C (15), field D (17), field E (6), field F (15). Isolation frequencies of *F. oxysporum* were as follows (Figs. 1-3):
Field A: 100% of crown pieces; 20% of stem pieces; 10% of root pieces
Fields B and C: 80% of crown pieces; 80% and 40% of stems; 47% and 27% of roots
Fields D and F: 47% of crown pieces; 24% and 47% of stems; 18% and 13% of roots
Field E: 100% of crown pieces; 50% of stems
Overall, F. oxysporum was most frequently isolated from crown tissues. The pathogen was also detected in most soil and rhizosphere samples.
Approximately 50 F. oxysporum isolates were selected and maintained for future molecular and pathogenicity studies.

Pea Differential Lines:
Two seed requests have been submitted to GRIN. We understand delays are occurring due to backlog, and we expect to receive the differential lines by late this year or early next year to maintain progress toward project milestones.

Objective 2: Root Rot Survey and Casual Organisms:
Six pea fields were surveyed at pre-plant and multiple growth stages. Above-ground symptoms were minimal, and overall disease incidence was low.
Root health ratings among 68 plants were as follows: 6% healthy rating 1, 37% rating 2 (< 1cm black discoloration on tap root), 28% rating 3 (about 1 cm dark brown discoloration), 13% rating 4 (< 2 cm discolorations surrounding the tap root), 10% rating 5 (> 2 cm discoloration) 3% ratings each for 6 and 7 (6: tap root like 5, but lateral roots are either lesioned or detached; and 7, complete root discoloration). Multiple *Fusarium* species were isolated, including *F. oxysporum*, *F. solani*, and an unidentified *Fusarium* species pending confirmation (Figs. 1-3). *Aphanomyces euteiches* was not isolated, even after repeated attempts. Root rot in Ontario may therefore be driven primarily by a complex of *Fusarium* species.
This represents Year 1 findings; continued sampling is planned to improve reliability.

Progress Toward Objectives:

Objective 1:
Isolation and preservation of ~50 *F. oxysporum* isolates have been completed. Requests for differential line seeds have been submitted. The objective is progressing on schedule.

Objective 2:
Disease was present but generally low in severity. Multiple *Fusarium* species were isolated, and no Aphanomyces was detected. The objective remains on track.

Conclusions:

The predominant pathogen isolated from symptomatic pea roots in Ontario was *Fusarium oxysporum*, with additional isolates of *F. solani* and one unidentified *Fusarium* species. Aphanomyces euteiches was not detected. Molecular work is ongoing to further characterize Fusarium species and to determine Fop races present in Ontario.

Future Considerations:

The project is progressing as planned; however, obtaining pea differential line seeds remains a critical risk. A U.S. researcher conducting similar work (Taheri et al., 2024) was unable to share seeds. While waiting for GRIN fulfillment, we plan to use molecular assays to identify Fop races 1 and 2 as described by Jenkins et al. (2021).

Acknowledgments:

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References:

Esmaeili Taheri, A., Chatterton, S., Foroud, N. A., Gossen, B. D., McLaren, D. L., Hwang, S. F., & Gossen, B. D. (2017). *Identification and community dynamics of fungi associated with root, crown, and foot rot of field pea in western Canada*. **European Journal of Plant Pathology, 147**, 489–500. https://doi.org/10.1007/s10658-016-1017-4

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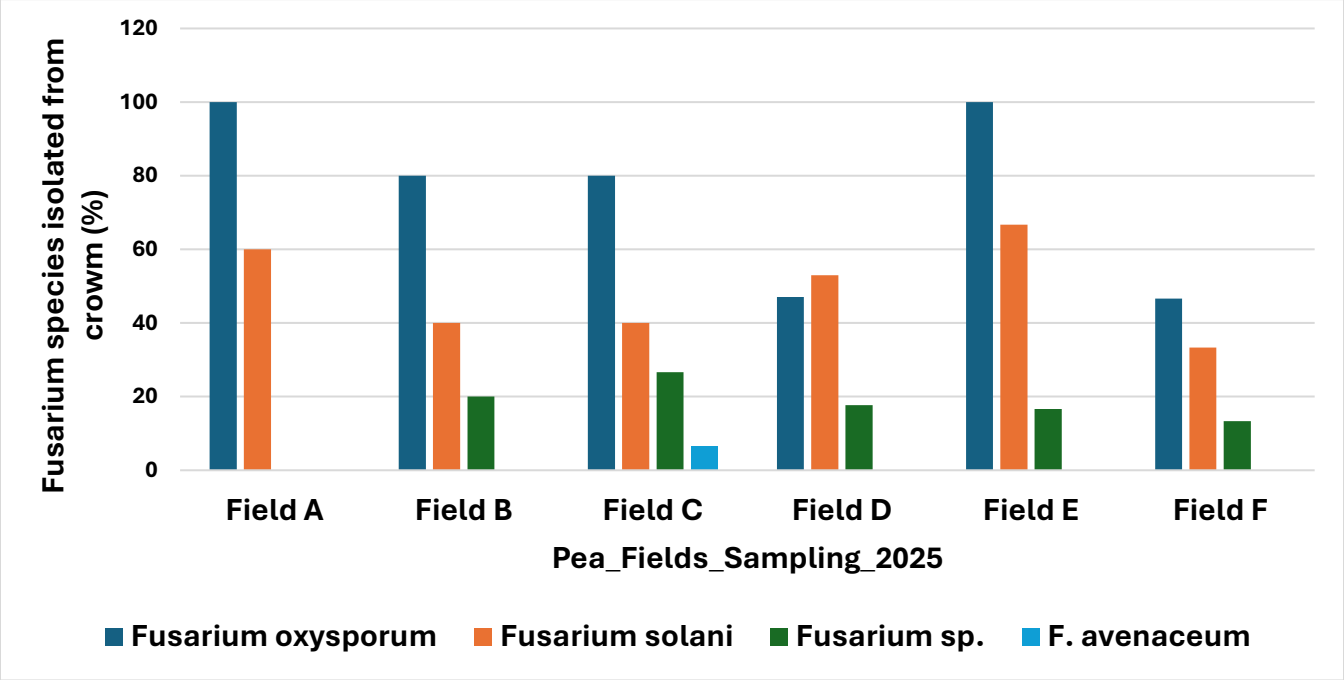

Fig. 1: Isolation of fungal organisms from crown pieces of plant samples collected from six pea fields in 2025.

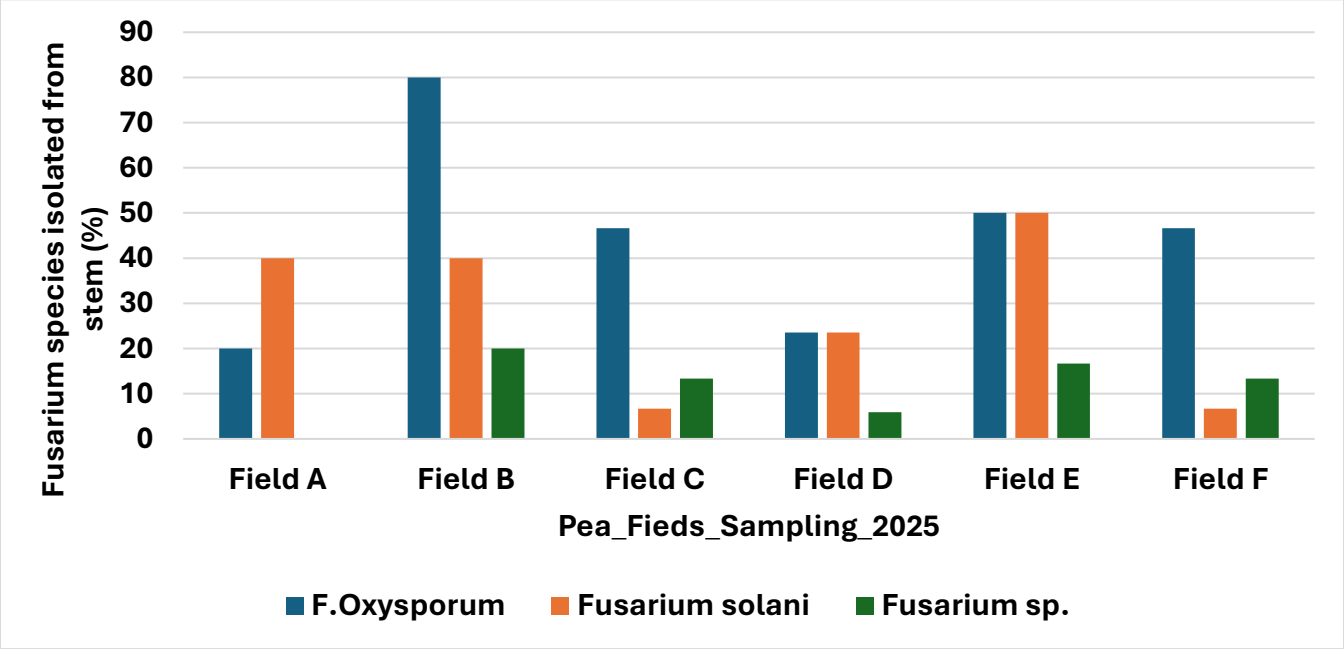

Fig. 2: Isolation of fungal organisms from stem pieces of plant samples collected from six pea fields in 2025.

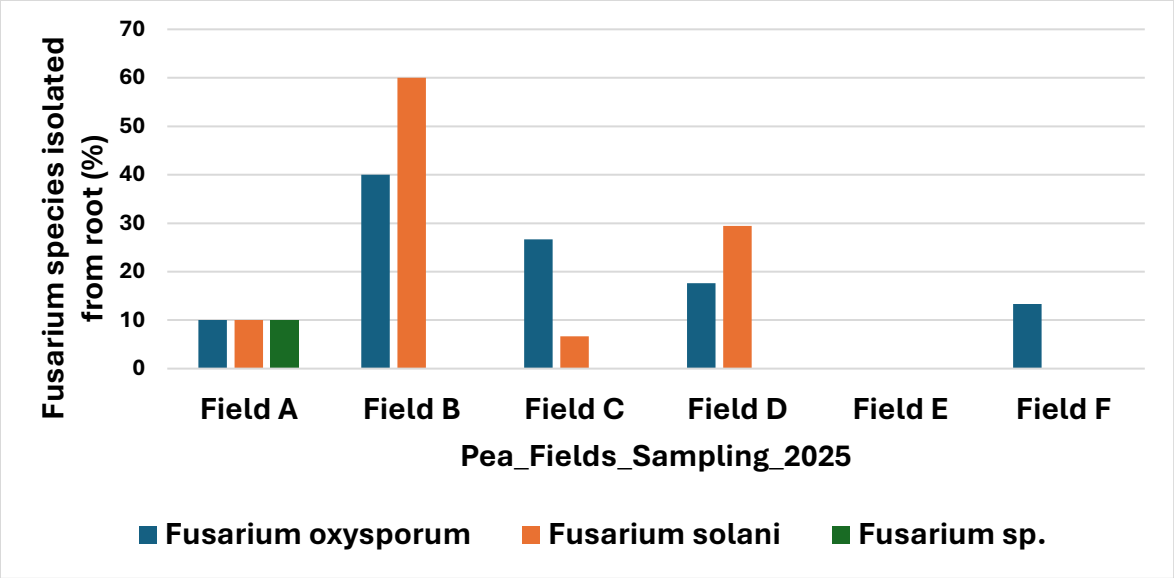

Fig. 3: Isolation of fungal organisms from root pieces of plant samples collected from six pea fields in 2025.