2024 Oilseed Disease Situation Report

for the

Western Committee on Plant Diseases

of the

Western Forum on Pest Management

Compiled by

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CHAPTERS:

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PROVINCIAL DISEASE SURVEYS

Flax Disease Situation Report: Alberta and Saskatchewan in 2024

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In year 2024, flax disease survey was conducted in 25 flax crops in Saskatchewan and seven flax crops in Alberta for a total of 32 flax crops. All surveys were conducted between August 12th and September 23rd. Maturity and stand establishment were measured on a scale of 1 to 5, where 1 is very poor stand (<30% stand)/green boll and 5 is excellent (91-100% stand)/brown boll (100% stand = 350 plants/m^2). Disease prevalence was measured as the percentage of crops affected by each disease out of all crops surveyed. For pasmo incidence assessment, a hundred flax plants in each field were examined to calculate the percentage of flax plants affected by pasmo in a field, and pasmo severity as the percentage of stem area covered by pasmo symptoms averaged over diseased plants. The other diseases were recorded either absent or present in each field.

Of all crops surveyed in Saskatchewan, more than half of crops (60%) was at the yellow to brown boll stage, and 32% of crops were at the brown boll stage. Only 8% of crops were at the green to yellow boll stage and at the yellow boll stage combined. In Saskatchewan, 28% of crops had a decent plant stand (51-75%), and 24% of crops had the excellent plant stand of 91 – 100%. Twenty percent of the flax crops had a good stand (76 – 90% stand) and only 8% had a lower stand (31 – 50% stand). Lodging at low level (1 – 10% of field) was found in 16% of crops surveyed in Saskatchewan. No crop stage, stand or lodging data was available from the survey in Alberta and stand data was missing from 20% of crops in Saskatchewan. Most crops appeared to have experienced good growing season with less drought pressure compared to last year. A few crops reported aphid or cricket infestations.

Pasmo was the most prevalent disease found during this survey and the disease prevalence was 53% of all crops (86% in AB, 44% in SK). The incidence level of pasmo tended to be low and ranged from 3 to 70% in all crops. The low incidence level (1 – 10%) was the most common at 22% (29% in AB, 20% in SK) and 11 – 30% incidence level was the next common at 19% (29% in AB, 16% in SK). The 31 – 60% incidence level was observed only in two crops in Alberta (29% in AB, 6% in all crops). One crop in Saskatchewan (4% in SK, 3% in all crops) had incidence higher than 60%. Pasmo severity was not high and ranged from 0.6 to 45% in all crops. The severity level of 6 – 25% was the most common and found in 22% of all crops (29% in AB, 16% in SK). A severity level of 1 – 5% was more common in Alberta and found in 16% of all crops (57% in AB, 4% in SK). The severity level of 26 – 50% was observed in 16% of crops in Saskatchewan but not in Alberta, and it was 6% of all crops. Pasmo data was missing from one crop in Saskatchewan (3% of all crops). One crop in Saskatchewan reported a minor incidence of lodging at low area potentially due to pasmo days after the survey was done. The report was noted but not

included in the data presented here because the direct diagnosis was not made. Both pasmo incidence and severity levels were low in Saskatchewan in 2024 compared to 2022 (Islam et al. 2023). This potentially was because of relatively dry conditions in July and August when pasmo typically develops. Less and less land has been seeded with flax in last few years and this could also contribute to the lower disease pressure due to the less pathogen inoculum in the environment.

The prevalence of other diseases was also often low in 2024. Alternaria blight was observed in 16% of in Saskatchewan but not in Alberta. In Alberta, other undiagnosed symptoms were observed in 71% of crops. Aster yellows was observed in 16% of crops in Saskatchewan and 29% of crops in Alberta. No Fusarium wilt or powdery mildew was found in Saskatchewan or Alberta. Powdery mildew was observed on some entries in the pasmo nursery that was seeded with a wide range of germplasms and registered varieties on September 24th at Aberdeen, Saskatchewan. Several flax seedlings in experimental plots at Aberdeen and Swift Current, Saskatchewan showed seedling blight/wilt symptoms in early July and root samples were collected. After plating the root samples, *Rhizoctonia* spp. was recovered from nine of 15 samples and no other potential pathogens were recovered. Stem samples were taken from some of surveyed fields where pasmo-like symptoms were observed and plated to confirm the disease. *Septoria linicola* (cause of pasmo) was not detected in any samples submitted so far.

Islam T, Nabetani K, Kutcher HR, Peru C, Akhavan A, Jacob C, Roberts S, Brown M, Noble A, et al. 2023. Flax disease situation report: Manitoba and Saskatchewan in 2022. Can Plant Dis Surv.103:130–131. In Can J Plant Pathol.

Manitoba Survey of Canola Diseases in 2024

Submitted by Yong Min Kim and Sonia Wilson

METHODS

A total of 138 canola crops were surveyed between August 5 and October 2 in the major canola production regions of Manitoba. Regions included Southwest (57), Central (34), Northwest (35), Eastern/Interlake (12). The majority of the crops were surveyed before swathing while plants were between growth stages 5.1 and 5.5 (Harper and Berkenkamp 1975). Disease assessments were made in each field by collecting 20 plants from each of five sites at least 20 m from the edge of the field and separated from each other by at least 20 m. Fields were assessed for the prevalence (percent fields infested) and incidence (percent plants infected per field) of sclerotinia stem rot (*Sclerotinia sclerotiorum*), blackleg (*Leptosphaeria maculans*), aster yellows (AY phytoplasma), foot rot (*Rhizoctonia* spp., *Fusarium* spp.), verticillium stripe (*Verticillium longisporum*) and clubroot (*Plasmodiophora brassicae*). For sclerotinia stem rot, each plant was rated for severity according to a rating scale of 0 to 5 (Kutcher and Wolf, 2006). For blackleg, plants were scored for either basal stem cankers or lesions that occurred on the upper portions of the stem. Blackleg basal stem cankers were rated for severity based on a rating scale of 0 to 5 that estimates the amount of disease in the basal stem cross-section. If present, clubroot symptoms were rated using a scale of 0 to 3 (Kuginuki et al. 1999). The prevalence and percent severity (Conn et al. 1990) of Alternaria black spot (*Alternaria brassicae*, *A. raphani*) were also determined. When diseases were observed in the crop, but not in the sample of 100 plants, they were recorded as “trace” and counted as 0.1%. Results are presented in two formats: 1) based on values from diseased crops only and 2) based on values from all crops surveyed (provincial basis).

RESULTS AND COMMENTS

Sclerotinia stem rot was observed in 57% of the crops surveyed. The average incidence in crops with the disease was 8% with an average severity of 2.9. The average incidence was highest in the Central region (11%) and lowest in the Eastern/Interlake region (3%). The average severity of sclerotinia was highest in the Central region (3.5) and lowest in the Eastern/Interlake region (1.6). The mean incidence of sclerotinia stem rot based on all crops surveyed (provincial basis) was 5% with a mean severity of 1.7.

Canola samples were confirmed positive for blackleg through basal stem cross-section analysis. This disease was present in 76% of Manitoba canola crops surveyed with an average disease incidence of 15% in diseased fields. The average incidence was highest in the Eastern/Interlake region (27%) and lowest in Northwest region (7%). The average severity of blackleg basal cankers in diseased fields was 1.6 with the highest severity in the Southwest region (1.7) and the lowest in the Eastern/Interlake region (1.2). The mean incidence of blackleg basal canker for the province (all crops surveyed) was 12% with a mean severity of 1.2.

Blackleg stem lesions were present in 58% of canola crops in Manitoba with an average incidence of 13% in diseased fields. Stem lesions were most prevalent in the Central region and observed in 82% of fields surveyed. The average disease incidence was highest in the Central region (16%) and lowest in the Eastern/Interlake region (3%) in diseased fields. Stem lesions were rated as present or absent, so there are no severity ratings. On a provincial basis (all crops surveyed), the mean incidence of blackleg stem lesions was 7%.

Aster yellows was observed in 28% of canola crops surveyed in Manitoba, and in all regions, with an average incidence of 2% in diseased fields. Verticillium stripe was found in 60% of canola crops with an average incidence of 32% in diseased fields. On a provincial basis, the mean incidence of verticillium stripe was 19%. Foot rot was not observed.

Alternaria pod spot was observed in 38% of canola crops surveyed in the province in 2024, with an average incidence of 23% in infected crops. The prevalence of pod spot was highest in the Eastern/Interlake region (67%) and lowest in the Southwest region (28%). The average severity of Alternaria pod spot across the province (all crops surveyed) was <1%.

In 2024, there were two new symptomatic cases of clubroot in the RMs of Lorne and North Cypress-Langford, outside of the 138 canola fields surveyed. Additionally, one positive case was documented outside of the survey in the RM of Roblin, detected through soil samples submitted to the Manitoba Canola Growers Testing Program. Soil samples from 40 fields in the Southwest region have been collected and are currently being processed for clubroot DNA analysis.

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Saskatchewan Canola Disease Situation Report 2024

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General comments:
According to the Saskatchewan Agriculture's weekly crop report (ending on October 14, 2024), harvest is virtually complete across Saskatchewan. As of October 14th, 98% of canola has been combined.

Canola Disease Survey – ***conducted by the Saskatchewan Ministry of Agriculture, Saskatchewan Association of Rural Municipalities and industry agronomists.***

This report includes the preliminary results of the 2024 Saskatchewan canola disease survey and includes the survey results from 208 surveyed fields located across the major canola growing regions of Saskatchewan (Table 1). This is a progressing work, and all the information presented here may change or evolve and ultimately, the results will be published in the Canadian Phytopathological Society Canadian Plant Disease Survey. Crops were surveyed before swathing while crops were between growth stages 5.2 and 5.5 (Harper and Berkenkamp, 1975). Survey dates ranged between August 5 and September 26. Disease assessments were made in each field by collecting 20 plants from each of five sites (100 plants per field) located at least 30 metres from the field edge and separated from each other by at least 20 metres. Fields were assessed for both prevalence (per cent of fields with symptoms of the disease) and incidence (per cent of plants surveyed with symptoms of the disease per field). The diseases assessed include: sclerotinia stem rot (*Sclerotinia sclerotiorum*), blackleg (*Leptosphaeria maculans*), aster yellows (*Candidatus Phytoplasma* asteris), foot rot (*Rhizoctonia* sp., *Fusarium* sp.), alternaria black spot (*Alternaria brassicae*, *A. raphani*), fusarium wilt (*F. oxysporum* f.sp. *conglutinans*), verticillium stripe (*Verticillium longisporum*), powdery mildew (*Erysiphe cruciferarum*), downy mildew (*Peronospora parasitica*), white rust (*Albugo candida*), grey stem (*Pseudocercosporella capsellae*), bacterial pod spot (*Pseudomonas syringae* pv. *maculicola*) and clubroot (*Plasmodiophora brassicae*). Severity ratings were also conducted for both sclerotinia stem rot and blackleg. For sclerotinia stem rot, each plant (100 per field) was rated for severity according to a rating scale of 0 to 5 described by Kutcher and Wolf (2006). For blackleg, plant stems were cut and then scored for basal stem cankers severity using a rating scale ranging from 0 to 5. Average severity values for blackleg and sclerotinia stem rot in each field were calculated as the sum of the severity ratings divided by the total number of plants examined. Stem lesions were recorded when observed on the upper stem. The prevalence of alternaria black spot (*Alternaria brassicae, A. raphani*) in the field was recorded. For all the diseases assessed, prevalence and average disease incidence or severity values were calculated across the entire province and separately for each of six regions within Saskatchewan.

Sclerotinia stem rot was reported in 56% of canola crops surveyed. The average incidence in the province was 9%. Incidence was highest in the Northeast region (18%) and lowest in the Southeast regions (1%). The provincial average sclerotinia stem rot severity was 0.24. Severity varied across the province ranging from 0.03 to 0.51 in different regions (Table 1).

Blackleg basal symptoms were present in 92% of canola crops surveyed in Saskatchewan (Table 1). The average incidence in the province was 23%. The average blackleg basal canker incidence was highest in

the Northwest regions (36 %) and lowest in the Southwest region (8%). The average severity of basal cankers across the province was 0.4. The highest severity was in the Northwest region (0.8); while the severity was lowest (0.1) in the Southwest region.

Blackleg stem lesions was assessed separately from blackleg basal canker and were present in 50% of canola crops surveyed with an average incidence of 5%. The highest average incidence was in the West central region (15 %) and the lowest incidence was in the Southeast region (1 %).

Aster yellows was present in 71 % of canola crops surveyed. This prevalence estimate includes fields where aster yellows symptoms were observed within the 100-plant sample or at trace levels in the field outside of the sample sites. It is possible to have a region with a relatively high prevalence but a low or even 0% average incidence. This occurred where aster yellows symptoms were observed in the surveyed field, but symptoms were not present in the 100-plant sample assessed in any of the fields. The average incidence in the province was 0.6 %. The incidence of aster yellows ranged from 0.4 to 1% across the regions. Aster yellows had a prevalence of 25%, based on the observations in the five surveying sites within each surveyed field looking only at the total of 100 plants.

Alternaria black spot prevalence is calculated as the per cent of fields surveyed where the disease was observed within the field. Alternaria black spot was observed in 69 % of fields in 2024. The highest prevalence was in the Northeast (94%) and the lowest prevalence was in the West-central (32%).

Symptoms of powdery mildew were seen in two of the surveyed fields, while suspect symptoms potentially suggesting verticillium stripe were seen in 19 % of canola crops surveyed. Verticillium stripe suspect samples were sent to the lab for further confirmation and results are pending.

Symptoms suggesting foot rot, downy mildew, white rust, and bacterial pod spot were not found in any of the surveyed fields assessed.

Like in 2023, the Saskatchewan Ministry of Agriculture conducted a verticillium-specific survey in 2024, targeting 100 fields across Saskatchewan to assess the prevalence and incidence of the disease and help evaluate the risk this disease poses to canola production in Saskatchewan. This survey is an “after-harvest” specific survey in addition to the general canola disease survey. The verticillium specific survey is still a work in progress with samples being analyzed in the lab for further confirmation and results are pending

In 2024, the Saskatchewan Ministry of Agriculture, with support from SaskCanola, Saskatchewan Crop Insurance Corporation (SCIC) and the Saskatchewan Association of Rural Municipalities (SARM) Plant Health Technical Advisors, worked to better understand the distribution of clubroot in Saskatchewan through the 2024 clubroot monitoring program. This involved in-field surveillance in high clubroot risk areas and throughout the province, encouraging the on-farm monitoring for the clubroot pathogen through the clubroot soil testing program and offering support to manage the disease in fields identified as positives through previous years and continued extension. The purpose of this program was to increase our understanding of the distribution and severity of clubroot in regions where the disease and/or pathogen are known or more likely to occur due to relatively tighter rotations and in areas not surveyed in previous surveys, also to contribute to managing the spread of clubroot in province. The in-field surveillance has been completed, and data entry and soil sample testing are currently underway. This information will be used to raise awareness of the clubroot situation in Saskatchewan to promote

proactive clubroot management prevention and update the clubroot distribution map to be released in early 2024.

Table 1. Prevalence, mean incidence and severity of sclerotinia stem rot and blackleg of canola in Saskatchewan in 2024.

Region (No. of Crops)	Sclerotinia			Blackleg Basal Canker			Blackleg Stem Lesions	
	Prev[1]	Inc[2](Inc[3])	Sev[4] (Sev[5])	Prev[1]	Inc[2](Inc[3])	Sev[4] (Sev[5])	Prev[1]	Inc[2](Inc[3])
Northeast (31)	97	18 (18)	0.51 (0.53)	97	25 (26)	0.42 (0.44)	35	4 (10)
Northwest (26)	35	3 (7)	0.10 (0.29)	92	36 (39)	0.78 (0.84)	42	4 (10)
East-Central (60)	82	16 (20)	0.41 (0.51)	98	24 (24)	0.34 (0.34)	50	4 (9)
West-Central (29)	45	6 (13)	0.17 (0.39)	90	20 (23)	0.30 (0.30)	83	15 (19)
Southeast (37)	30	1 (5)	0.04 (0.15)	95	25 (27)	0.40 (0.43)	49	1 (3)
Southwest (25)	20	2 (10)	0.03 (0.16)	68	8 (11)	0.14 (0.21)	44	2 (4)
Overall mean Crops (208)	56	9 (16)	0.24 (0.43)	92	23 (25)	0.39 (0.42)	50	5 (10)

[1]Average per cent prevalence of disease in all canola crops in 2024 Saskatchewan Canola Disease Survey
[2]Average per cent incidence of disease in all canola crops in 2024 Saskatchewan Canola Disease Survey both with and without the given disease
[3] Average per cent incidence of disease in canola crops in 2024 Saskatchewan Canola Disease Survey infected with given disease
[4] Average severity of disease in all canola crops in 2024 Saskatchewan Canola Disease Survey
[5]Average severity of disease in canola crops in 2024 Saskatchewan Canola Disease Survey infected with given disease

Table 2. Total prevalence and mean incidence of aster yellows and prevalence of foot rot and alternaria black spot in canola crops surveyed in Saskatchewan in 2024.

Region (No. of Crops)	**Aster Yellows**		**Foot Rot**	**Alternaria black spot**
	Total Prev[1]	Inc[1,2](Inc[1, 3])	Prev[4]	Prev[5]
Northeast (31)	77	1 (3)	0	94
Northwest (26)	73	1 (3)	0	61
East-Central (60)	82	0.5 (2)	0	81
West-Central (29)	72	0.6 (2)	0	32
Southeast (37)	73	0.4 (3)	0	76
Southwest (25)	32	0. 4(3)	0	48
Overall mean Crops (208)	71	0.6 (3)	0	69

[1]For aster yellows, total prevalence includes fields where symptoms were present in the 100 plant sample or at trace levels in the field outside of the sample sites but the incidence is calculated on the 100 plant sample only.
[2]Average per cent incidence of disease in all canola crops in 2024 Saskatchewan Canola Disease Survey both with and without the given disease.
[3]Average per cent incidence of disease in canola crops in 2024 Saskatchewan Canola Disease Survey infected with the disease
[4]Average per cent prevalence of disease in all canola crops in 2024 Saskatchewan Canola Disease Survey.
[5]Average per cent prevalence of disease in canola fields that were assessed for alternaria black spot

Alberta Canola Disease Survey Results 2024

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Four hundred and eight canola fields in Alberta were surveyed between July 26 and October 18, 2024. Clubroot (372 fields) and blackleg (401 fields) were rated for prevalence, incidence and severity. The presence/absence of sclerotinia main stem infections (408 fields) and verticillium stripe (408 fields) symptoms were noted. Canola plants were rated at ten sample points in each field along a W-shaped transect with each location >20 m apart and from the field margin. Roots of 190 plants were rated in the field for clubroot using 0-3 scale for clubroot as described by Horiuchi and Hori (1980) and modified by Strelkov et al. (2006). One hundred plants were rated for clubroot at the field entrance and then 10 plants at each of the other nine locations. The lower six to twelve inches of ten stems were collected at each of the ten sample points (100 stems/field) and rated for blackleg, sclerotinia stem rot and verticillium stripe. Blackleg severity was rated using a 0-5 blackleg (WCC/RCC 2009).

Survey results are shown in Table 1. Blackleg was again the most prevalent disease, reported in 96.5% of fields, followed by, sclerotinia stem rot (14.2%) and clubroot (6.8%). Symptoms suspicious for verticillium stripe will undergo testing to confirm the presence of *Verticillium longisporum*, however multiple suspicious samples have already tested positive for the presence of *V. longisporum,* and an additional ~10 fields (not part of this survey) have been reported positive for verticillium stripe. Prevalence of all measured canola diseases was slightly higher in 2024 compared to the previous year, except for stem rot (Fig 1.)

These results are not a complete summary of all survey data collected and should be considered an interim report. A final report including all information from the Alberta canola survey will be published in v105 of the Canadian Plant Disease Survey (https://phytopath.ca/publication/cpds/).

ACKNOWLEDGEMENTS
Field visits for clubroot rating and canola stem collections performed by Agricultural Fieldmen, or other county/municipal staff, are very gratefully acknowledged.

Table 1. Canola disease survey results for Alberta in 2024.

	Number of fields visited	Number of fields rated	Prevalence (%)	Incidence Ave. (%)	Severity Ave. (0-3)
Clubroot	408	336	6.8	0.7	0.01
Blackleg	408	401	96.5	32.5	0.62
Sclerotinia	408	408	14.2	0.9	n.d.[1]
Verticillium	408	408	t.b.d.[2]	t.b.d	n.d.

[1]n.d. = no data collected
[2]t.b.d. = to be determined

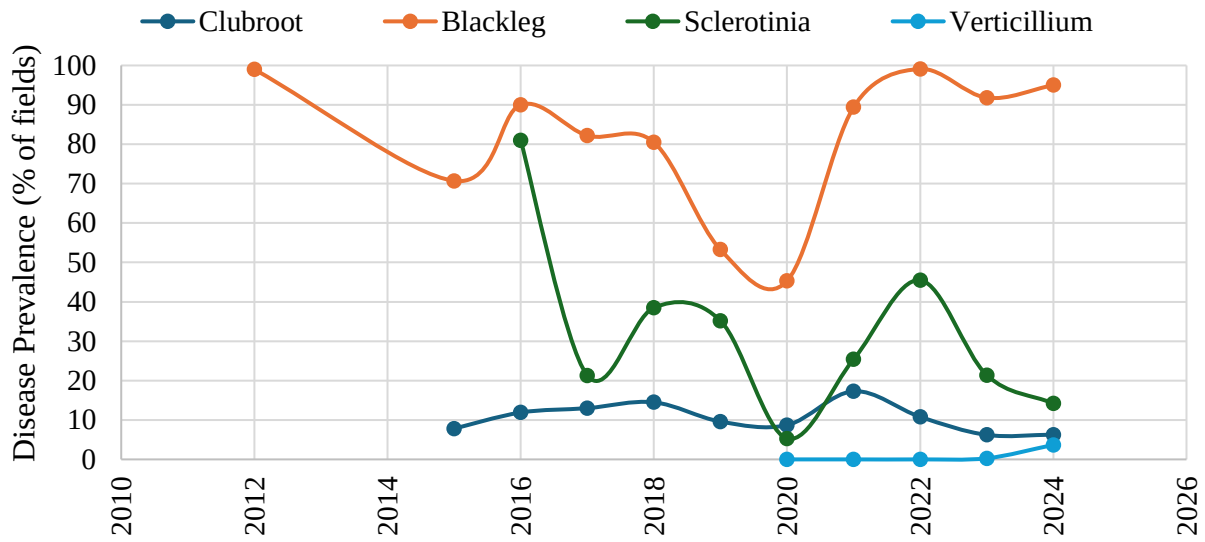

Figure 1. Prevalence of canola diseases in Alberta, 2012 – 2024.

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Survey for Verticillium Stripe of Canola in Alberta in 2024

CROP: Canola
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ABSTRACT: Thirty-six canola fields were surveyed for the presence of Verticillium stripe across central and southern Alberta in 2024, with 100 plants examined in each field. An additional 22 symptomatic samples were provided by agronomists for disease rating and further testing. Disease symptoms were observed in approximately 10% of the fields visited. In laboratory analyses, 74% of survey samples and 44% of samples submitted by agronomists were identified as blackleg, while only 1% and 8% were confirmed as Sclerotinia stem rot and Verticillium stripe, respectively. The simultaneous occurrence of blackleg and Verticillium stripe was noted in some fields. Isolation of *V. longisporum* is ongoing, with the Verticillium fungus recovered in 85% of samples collected in the most severely infested field. These findings suggest that canola production in Alberta is at risk from *Verticillium* stripe, although its prevalence is lower compared to that in Manitoba.

INTRODUCTION: Verticillium stripe, caused by *Verticillium longisporum*, was first detected in Manitoba in 2014 and has since been observed with increasing frequency across the Prairies. Currently, management strategies are limited, and fully resistant canola cultivars are not available. This survey aimed to document the occurrence of Verticillium stripe in central and southern Alberta in 2024, regions where the disease was previously not well known.

METHODS: Thirty-six canola fields were surveyed between October 1 and October 10, 2024. In each field, one hundred canola plants were examined from five sites following a W-shaped pattern, with distances between sites exceeding 50 m. Plants exhibiting stem striping, shredding or black specks (microsclerotia) on or beneath the epidermis were collected and rated for Verticillium severity using a 0-5 modified disease scale (Cui et al., 2023). The scale is defined as follows: 0 = healthy plant; 1 = stem discoloration; 2 = microsclerotia on 1–25% of the plant; 3 = microsclerotia on 26–50% of the plant; 4 = microsclerotia on 51–75% of the plant; and 5 = microsclerotia on 76–100% of the plant, with complete necrosis. In addition to the plant samples collected during the survey, 22 symptomatic samples provided by agronomists from August 21 to September 26, 2024, were also received for disease rating and further testing.

In the laboratory, stem samples were cut both vertically and horizontally. Shredded stems without black specks but containing sclerotia were identified as infected by *Sclerotinia sclerotiorum*. Stems with black specks were examined under a dissecting microscope. Those with pycnidia and a pink coloration around the pycnidia were identified as *Leptosphaeria maculans* (blackleg), while the microsclerotia produced by *V. longisporum* were approximately six times smaller.

RESULTS AND DISCUSSION: Survey results indicated visual symptoms in about 10% of fields, with disease severity ranging from 1.0 to 2.8. In the laboratory evaluation, 74% of samples collected during the survey

and 44% of the samples submitted by agronomists were identified as blackleg. Only 1% and 8% of samples were confirmed as Sclerotinia stem rot and Verticillium stripe, respectively. Blackleg and Verticillium stripe occurred simultaneously in some fields and plant samples. Additionally, clubroot and Fusarium root rot and wilt were identified in some fields.

Isolation of *V. longisporum* is in progress. A field infested by verticillium stripe was detected among those evaluated, where the fungus was recovered from 85% of the plant samples collected. Together, these results suggest that canola production in Alberta is at risk from Verticillium stripe, although the disease is not as prevalent in Alberta as in Manitoba. The full results of this survey will be presented in the *Canadian Plant Disease Survey.*

ACKNOWLEDGEMENTS: This survey was supported financially by Canola Agronomic Research Program (CARP) and Western Grain Research Foundation (WGRF), with in-kind support from the University of Alberta.

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Survey for early detection of clubroot in the Peace Region, British Columbia

Submitted by Katie Goldenhar

The British Columbia Ministry of Agriculture and Food (BCMAF), in collaboration with BC Grain Producers Association, conducted a 2-year survey (2023/2024) for early detection of clubroot in the Peace Region, British Columbia. All soil samples (N=145) were negative, collected from harvested canola fields.

PROVINCIAL PEST LAB REPORTS

Crop Diagnostic Centre, Manitoba Agriculture.

Submitted by Manika Pradhan, Manitoba Agriculture

Table: showing summary of diseases diagnosed on **oilseed** crop samples submitted to the Manitoba Agriculture Crop Diagnostic Centre in 2024.

Crop	Disease/symptom	Causal/associated agent(s)	Number of samples
Canola	Alternaria black spot	*Alternaria* sp.	7
	Anthracnose	*Colletotrichum* sp.	9
	Aster yellows	*Phytoplasma*	1
	Blackleg	*Leptosphaeria maculans*	10
	Cladosporium leaf spot	*Cladosporium* sp.	1
	Grey stem	*Pseudocercosporella capsellae*	1
	Root rot	*Fusarium* sp., *Pythium* sp.,	
		Rhizoctonia solani	7
	Sclerotinia stem rot	*Sclerotinia sclerotiorum*	1
	Stem stripe	*Verticillium* sp.	5

Saskatchewan Ministry of Agriculture Crop Protection Laboratory

James Bush, Haylee Hachkewich, Cerese Bawolin, Brett Rumpel, Alexis Warren, Cory Jacob, Alireza Akhavan, and Clark Brenzil (Saskatchewan Ministry of Agriculture)

Table: Oilseed Sample Diagnoses Completed at the Saskatchewan Ministry of Agriculture Crop Protection Laboratory During 2024

Crop Sample Diagnoses	Details / Scientific Name	Number
Canola		**10**
Blackleg	*Leptosphaeria biglobosa* and *Leptosphaeria maculans*	4
Common Root Rot	*Fusarium* sp. and *Cochliobolus sativus*	1
Herbicide Damage	n/a	4
Stem Rot	*Sclerotinia sclerotiorum*	1
Mustard		**2**
Herbicide Damage	n/a	2
Camelina		**1**
Environmental	n/a	1

Alberta Agriculture & Irrigation, Plant Health Lab, Edmonton, AB.

Submitted by Jie Feng

Table: Diseases diagnosed on canola and mustard samples submitted to the Alberta Plant Health Lab in 2024.

Crop	Disease/symptom	Causal/associated agent(s)	No. of samples
Canola	Clubroot	*Plasmodiophora brassicae*	60
	Wilting, girdling	*Leptosphaeria maculans or L. biglobosa, Fusarium* spp.*, Sclerotinia* sp.*, Rhizoctonia solani*	9
	Root rot, swelling	*Fusarium torulosum, Lelliottia amnigena and Pseudomonas marginalis*	2
	Damping off	*Leptosphaeria maculans, L. biglobosa, Fusarium* spp.*, Rhizoctonia solani*	1
Mustard	Wilting	*Pythium* spp*. (P. dissotocum, P. oopapillum, P. acanthicum, P. inflatum, Globisporangium irregulare, G. hypogynum or G. schmitthenneri or G. acrogynum*)*, Rhizoctonia solani, Fusarium solani*	4
Total			**76**

British Columbia Ministry of Agriculture and Food (BCMAF) Plant Health Lab

Submitted by Pragyan Burlakoti, Plant Diagnostic Pathologist, BC Ministry of Agriculture and Food (BCMAF)*, Abbotsford, B.C.*

Diseases diagnosed on oilseed samples submitted to the Plant Health Lab – BCMAF:

Crop	Disease/symptom	Causal/associated organism	Number of positive samples
Canola	**Clubroot survey[a]**	***Plasmodiophora brassicae***	**0**

[a] A total of 60 soil samples (collected from Northern BC) were tested for *Plasmodiophora brassicae* a.k.a clubroot pathogen during September to October, 2024.

CURRENT OILSEED DISEASE RESEARCH SUMMARIES

Drs. Stephen Strelkov & Sheau-Fang Hwang (University of Alberta) – Ongoing Research Projects

1. **Study**: Investigating the conditions favoring Verticillium stripe development and yield losses
   Principal investigators: Sheau-Fang Hwang, Stephen E. Strelkov, & Rudolph Fredua-Agyeman, University of Alberta; Fouad Daayf, University of Manitoba
   Funding: Canola Agronomic Research Program (CARP), Western Grains Research Foundation (WGRF) (2024-2028)
   Objectives:

- Examine the effects of interactions between *V. longisporum* and *L. maculans* in canola, combined with in *in-vitro* studies and in in-soil studies; established the relationship between yield and disease severity, and the effect of inoculum timing on disease development under field conditions.
- Evaluate the effect of soil pH on growth of *V. longisporum* and disease development and severity
- Screen canola lines and accessions for resistance to *V. longisporum* and use genome-wide association mapping to identify single nucleotide polymorphism (SNP) markers for resistance to this pathogen.
- Investigate the impact of canola defenses on pathogen responses and adaptive mechanisms by: (i) Investigate how canola defenses to each pathogen affect the other pathogen, and how the latter reacts; (ii) Attempt to explain how potential pathogen adaptation mechanisms lead to the host-pathogen outcomes observed in the field.
- Determine the pathogenicity and lineage of the collected *V. longisporum* isolates and the host specificity/range of this pathogen
- Assess the effects of VL seed infection rate on disease severity and direct examination of the impact of seed-to-seedling transmission

2. **Study**: A comprehensive survey of Verticillium stripe and establishment of a disease nursery in Morden MB
   Principal investigators: Ahmed Abdelmagid**,** Agriculture and Agri-Food Canada, Morden Research Centre, Manitoba; Sheau-Fang Hwang & Stephen E. Strelkov, University of Alberta
   Funding: Canola Agronomic Research Program (CARP) (2024-2027)
   Objectives:

- To conduct a comprehensive survey to measure the impact of V. longisporum on canola. This proposed survey will also allow us to build a collection of V. longisporum isolates for use in any breeding program and help in the establishment of a disease nursery population with local strains of the pathogen.
- To establish a permanent Verticillium stripe nursery in Morden for use in all future research on this emerging disease under field conditions for the benefit of growers and the canola industry.

3. **Study**: Methods to isolate and maintain clubroot for improved resistance screening and labeling
   Principal investigators: Stephen E. Strelkov, Sheau-Fang Hwang & Rudolph Fredua-Agyeman, University of Alberta
   Funding: CARP & WGRF (2024-2027)
   Objectives:

- To develop best practices to maintain clubroot isolates in planta to avoid virulence shifts
- To optimize microlaser technology as a fast and efficient way to obtain single-spore isolates for characterization and distribution

4. **Study**: Clubroot Pathotype Evaluation and Monitoring
   Principal investigators: Stephen E. Strelkov, Sheau-Fang Hwang, University of Alberta; Michael Harding, Alberta Agriculture and irrigation
   Funding: CARP & WGRF (2024-2027)
   Objectives:

- Tracking clubroot occurrence, severity and spread
- Generation of P. brassicae field isolates from infected roots
- Monitoring pathotype composition and virulence shifts, including identification of resistance-breaking pathotypes and their prevalence
- Providing recommendations to the Clubroot Steering Committee and other stakeholders regarding pathotypes of particular concern and emerging issues

5. **Study**: Clubroot resistance gene function based on whole genome sequences, gene editing and resistance phenotypes
   Principal investigators: Stephen E. Strelkov, Rudolph Fredua-Agyeman & Sheau-Fang Hwang, University of Alberta
   Funding: Alberta Canola, SaskCanola, RDAR (2023-2028)
   Objectives: To characterize CR genes based on genome-wide association analyses between clubroot disease data and the whole genome sequence (WGS) data from UA clubroot resistance donors and 28 *Brassica* hosts available from the National Center for Biotechnology Information (NCBI) and *Brassica* database (BRAD) websites.
6. **Study**: Efficient identification of *Plasmodiophora brassicae* pathotypes by metabarcoding
   Principal investigators: Stephen E. Strelkov, Sheau-Fang Hwang & Rudolph Fredua-Agyeman, University of Alberta
   Funding: Alberta Canola, RDAR (2022-2025)
   Objectives: To generate a DNA metabarcoding assay that can aid in the efficient, accurate, replicable and high-resolution identification of clubroot pathotypes.
7. **Study**: Microbiome-driven clubroot management in canola
   Principal investigators: Stephen E. Strelkov, Sheau-Fang Hwang, & Rudolph Fredua-Agyeman, University of Alberta; & Leonardo Miguel Galindo González (CFIA)
   Funding: RDAR, CAP (2021-2024)
   Objectives:

- The proposed research will provide an alternative solution that can be integrated into a sustainable clubroot management plan.
- Study the changes in the microbiome composition of canola genotypes with contrasting responses to clubroot pathotype 3A.
- Determine if resistant cultivars with diverse genotypes recruit similar communities, and if the same happens with susceptible cultivars.
- Identify differences in diversity and relative abundance of endophytic and rhizospheric microorganisms between canola genotypes with contrasting responses to clubroot pathotype 3A.
- To generate and evaluate balanced microbiome communities that can be used to complement integrated management of clubroot disease.

8. **Study**: New clubroot pathotypes and second-generation resistance
   Principal investigators: Stephen E. Strelkov, Sheau-Fang Hwang & Rudolph Fredua-Agyeman, University of Alberta
   Funding: CARP, WGRF (2021-2024)

Purpose: Three main objectives are to (1) evaluate the infectivity of the most important P. brassicae pathotypes on a suite of canola cultivars with 2nd generation resistance, (2) determine the pathotype composition on 2nd generation CR canola recovered from commercial fields; and (3) assess the cross-infectivity of these pathotypes across 2nd generation CR canola cultivars.

9. **Study**: Understanding Fusarium wilt and root rot of hybrid canola: occurrence, host range, disease development, resistance and yield losses
Principal investigators: Sheau-Fang Hwang & Stephen E. Strelkov, University of Alberta
Funding: ACPC & RDAR (2021-2025)
Purpose: The overall aim of this project is to improve seedling establishment, reduce root rot and wilt severity and maximize seed yield of canola by optimizing cultural methods to control the Fusarium pathogens causing seedling blight and root rot and wilt of canola.

Publications

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- Jayasinghege, C.P.A., Ozga, J.A., Manolii, V.P., Hwang, S.F., and Strelkov, S.E. 2023. Impact of susceptibility on plant hormonal composition during clubroot disease development in canola (Brassica napus). PLANTS, 12: 2899. https://doi.org/10.3390/plants12162899
- Wang, Y., Strelkov, S.E., and Hwang, S.F. 2024. Influence of pH on the growth of Verticillium longisporum and Verticillium stripe severity in canola (Brassica napus). HORTICULTURAE, 10: 554. https://doi.org/10.3390/horticulturae10060554
- Yang, C., Fredua-Agyeman, R., Hwang, S.F., Gorim, L.Y., and Strelkov, S.E. 2024. Genome-wide association studies (GWAS) of root system architecture traits in a broad collection of Brassica genotypes. FRONT. PLANT SCI., 15:1389082. https://doi.org/10.3389/fpls.2024.1389082
- Yang, C., Fredua-Agyeman, R., Hwang, S.F., Gorim, L.Y., and Strelkov, S.E. 2024. Optimizing the evaluation of root system architectural traits in Brassica napus. CAN. J. PLANT SCI., 104: 265-269. http://dx.doi.org/10.1139/CJPS-2023-0169
- Yu, H., Chang, K.F., Hwang, S.F., and Strelkov, S.E. 2023. Characterization of the virulence and yield impact of Fusarium species on canola (Brassica napus). PLANTS, 12: 3020. https://doi.org/10.3390/plants12173020
- Yu, H., Chang, K.F., Fredua-Agyeman, R., Hwang, S.F., and Strelkov, S.E. 2024. Diversity and pathogenicity of Fusarium root rot fungi from canola (*Brassica napus*) in Alberta, Canada. INT. J. MOL. SCI., 25: 6244. https://doi.org/10.3390/ijms25116244
- Yu, H., Hwang, S.F., and Strelkov, S.E. 2024. The host range of *Fusarium proliferatum* in western Canada. PATHOGENS, 13: 407. https://doi.org/10.3390/pathogens13050407
- Yu, Z., Fredua-Agyeman, R., Strelkov, S.E., and Hwang, S.F. 2024. RNA-Seq bulked segregant analysis of an exotic B. napus ssp. napobrassica (rutabaga) F2 population reveals novel QTLs for breeding clubroot-resistant canola. INT. J. MOL. SCI., 25: 4596. https://doi.org/10.3390/ijms25094596
- Yu, Z., Strelkov, S.E., and Hwang, S.F. 2024. Evaluation of amisulbrom products for the management of clubroot of canola (Brassica napus). PLANTS, 13: 28. https://doi.org/10.3390/plants13010028
- Zhang, H., Liu, X., Zhou, J., Strelkov, S.E., Fredua-Agyeman, R., Zhang, S., Li, F., Li, G., Wu, J., Sun, R., Hwang, S.F., and Zhang, S. 2024. Identification of clubroot (*Plasmodiophora brassicae*) resistance genes causing recessive resistance in Chinese cabbage (*Brassica rapa* L). GENES, 15, 274. https://doi.org/10.3390/genes15030274

Research highlights from Gary Peng at AAFC Saskatoon

Blackleg

1. <u>Continued monitoring of *Leptosphaeria maculans* populations following the introduction of new resistant genes *on the prairies* for effective resistance deployment</u>

- Funding: CARP (2022-2027)
- Purpose: To provide industry and producers with up-to-date information on *L. maculans* populations in different regions on the prairies, which can be used to guide blackleg resistance breeding, and recommend canola cultivars with effective R genes.
- Progress: The analysis of the 2023 blackleg pathogen population across the prairie region has been completed, including a detailed breakdown by crop districts in each province. Compared to 2022, the pathogen population showed minimal change; the *AvrLm1* gene remained low across the prairie, except in a few pockets in Manitoba with moderate levels of *AvrLm1*. *AvrLm4* continued to be much lower in most parts of Alberta, relative to that in the other two provinces (**Figure 1**). The information provides a base for R-gene deployment; most specific R genes should remain effective against the current pathogen population, except for *Rlm1/LepR3*, *Rlm3* and *Rlm9*. *Rlm4* may be less effective in Alberta. Interactive maps have been developed to better visualize pathogen populations across crop districts, and a website will be pursued to host this information online to aid in R gene selection and recommendation.

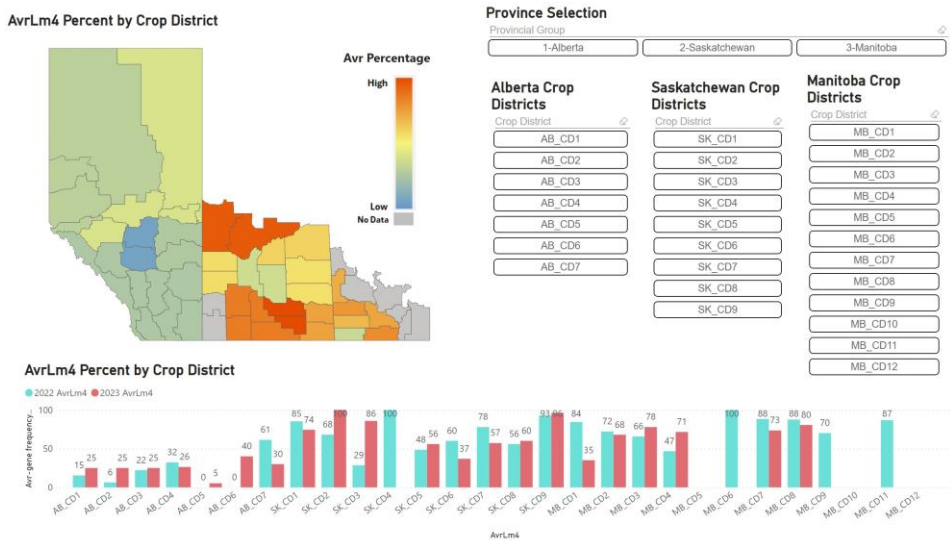

Figure 1. The presence of *AvrLm4* gene in *L. maculans* populations across different crop districts in the prairie region for 2022 and 2023 (bar chart). The heatmap shows the 2023 data.

2. <u>Exploiting susceptibility genes in canola to improve blackleg resistance</u>

- Funding: CARP (2023-2026)
- Participant: Dilantha Fernando, U of M.

- Purpose: Genetic resistance to blackleg can also be enhanced by disrupting susceptibility (S) genes, as these genes often facilitate compatibility between the pathogen and canola. This study begins with

the screening of a unique TILLING (Targeting Induced Local Lesions in Genomes) population, generated through ethyl-methane sulphonate (EMS) mutagenesis of a susceptible canola line. Additionally, canola mutants produced using CRISPR/Cas9 are included in the assessment. The findings will ultimately support genome editing efforts to reduce susceptibility to diseases in canola varieties.

- Progress: Approximately 300 TILLING lines and 130 gene-edited mutant lines have been screened, with mutants resistant to blackleg or clubroot identified. The consistency of resistance is being validated, and segregating populations are being developed for mapping and sequencing studies.

Clubroot

1. **Development and deployment of novel resistance genes to improve clubroot management on canola**

- Funding: SCAP Canola Cluster (2023-2028)
- Participants: Fengqun Yu, AAFC Saskatoon; Habibur Rahman and Nat Kav, U of A; Rob Duncan, U of M.
- Purposes: 1) Identify and characterize novel clubroot resistance (CR) genes from unique Brassica sources and genetically map them for the development of new CR genes, 2) develop SNP markers tightly linked to these new CR genes, 3) sequencing and genomic studies to better understand CR evolution, with the potential for CR gene labelling, and 4) understand the modes of action and interactions of multi-genic resistance for enhanced CR resilience and durability.
- Progress:

1. More than 1000 B. napus accessions were collected worldwide by Dr. Yu's lab, and 36 of them were found highly resistant to clubroot previously. However, genetic mapping of CR genes had only been carried out for only 3 of them. During the reporting year, 33 remaining accessions were characterized with 92 SNP markers developed by Dr. Yu to determine the presence of race-specific CR genes and race-non-specific QTLs. The results indicate that all of them carry at least one CR genes; four, three and two B. napus accessions carrying Rcr8/Rcr13, Rcr10 and the QTL identified in B. napus ECD10, respectively, but none of the B. napus accessions carries QTLs identified from the B. oleracea ECD11. Additionally, 90.9% of the B. napus accessions carry Rcr3/Rcr9/Rcr11 and 45.5% of them carry Rcr1/Rcr5. The CR B. napus accessions were also tested with two single root protoplast derived P. brassicae isolates PSI-10-SP-07 and 3A-1-SP1-5, aggressive to all single CR genes available. Only five accessions showed resistance to both strains, and lines have been developed from the five accessions and used for crossing with a canola line DH16516 to produce F1.
2. Leaf tissues were collected and DNA was extracted from five unique CR resources for DNA sequencing. They were sequenced using long reads and Hi-C sequencing platforms for DNA sequencing through service contracts. The five new canola genome sequences have been obtained and will be assembled using de novo genome assembly pipelines. Root tissues have been collected from all the lines for RNA extraction (Yu).
3. The canola inbred lines PS-FCA 15-3978 (CPS13) carrying the singe CR gene Rcr1 on A03 and RA1305.717 (CPS20) carrying the CR gene Crr1rotb on A08, as well as the hybrid carrying both CR genes, were subjected to transcriptomics, proteomics and metabolomics analysis to decipher resistance mechanisms associated with single and stacked CR genes. The data has been collected and preliminary transcriptome analysis showed good quality of sequencing data; the principal component analysis of normalized gene counts separated the data primarily by the genotype (PC1: 67% variance) and then by inoculation (PC2: 12% variance). A total of 3,024 of the 100,137 genes (3%) in the

reference genome were differentially expressed. Enrichment analysis of gene ontology showed that the pathogen induced the expression of genes involved in the regulation of systematic required resistance, as well as its associated pathways. Detailed omics data analyses, including the proteomics and metabolomics data, are ongoing. The study of resistance resilience associated with CR-gene stacking and deployment is being initiated; MTA to obtain unique commercial canola varieties is being finalized (Peng).

Publications:

1. Rouxel T, Peng G, Van de Wouw A, Larkan1 N, Borhan1 H, Fernando WGD. 2024. Strategic genetic insights and Integrated approaches for successful management of blackleg in canola/rapeseed farming. Plant Pathol. (in press).
2. Tu J, Qin L, Karunakaran C, Wei Y, Peng G*. 2024. Lignin accumulation in cell wall plays a role in clubroot resistance. Front. Plant Sci. 23: 15, 1401265.
3. Huang, SL, Zhai C, McLaren D, Lange R, Harding M, Fernando WGD, Peng G*. 2024. Reducing flea-beetle feeding wounds on canola seedlings with foliar insecticide failed to improve blackleg control. Can. J. Plant Pathol. 48: 1–14.
4. Wen R, Song T, Tonu NN, Franke C, Peng G*. 2024. Resilience of canola to Plasmodiophora brassicae (clubroot) pathotype 3H under different resistance genes and initial inoculum levels. Plants, 13: 11, 1540.
5. Wen R, Song T, Gossen BD, Peng G. 2024*. Comparative transcriptome analysis of canola carrying a single vs stacked resistance genes against clubroot. Front. Plant Sci. 15:1358605.

Research highlights from Fengqun Yu at AAFC Saskatoon

Purifying genotypes of *Plasomodiophora brassicae* and developing SNP markers linked to races of *P. brassicae* populations collected in western Canada

- Funding: WGRF, SaskCanola and Manitoba Canola Growers Association (CARP; 2021-2026)
- Objectives:

1) Develop an efficient method to produce near pure genotype isolates (NPGI)
2)Produce diverse NPGIs from clubroot galls collected in Western Canada
3)Determine race profile for each NPGI
4)Carry out genome sequencing of selected NPGIs
5)Develop SNP markers tightly linked to each Avr gene and obtain pure genotype isolates of *P. brassicae*

Progress: We have developed an innovative approach by producing single root protoplast-derived resting spore isolates (SPIs) to obtain pure genotype strains. During the reporting period, we confirmed that the field strains 3A-1, 5C and SK27 were highly mixed with >90% of heterozygous alleles. Intriguingly, all of the SPIs from the field strains had almost indetectable heterozygosity. Over 200 SPIs were produced for the project, of which 198 SPIs were selected and assessed with seven near isogenic lines (NILs) carrying single resistance genes *Rcr1, Rcr3, Rcr5, Rcr8, Rcr9, Rcr10* and *Rcr11* respectively. Based on the gene-for-gene theory, there should be seven avirulence (Avr) genes (*Avr1, Avr3, Rcr5, Avr8, Avr9, Avr10* and *Avr11*) corresponding to the respective resistance genes. In Western Canada, the presence of *Arv1, Avr3, Avr5, Avr8, Avr9, Avr10* and *Avr11* were found in 60, 58, 53, 91, 116, 74 and 90 of the 198 SPIs with the frequency of 30.3%, 28.8%, 26.8%, 35.4%, 58.1%, 36.9% and 45.5% respectively. Regional variations in the prevalence of Avr genes were observed. Manitoba exhibited the highest frequency of *Avr11* (68.0%). Saskatchewan showed the highest frequency of *Avr9* (66.0%) while Alberta had the highest frequency of *Avr8* (57.1%). The three genes (*Rcr8, Rcr9* and *Rcr11*) may not present in the clubroot resistant cultivars available on the market. Therefore, we highly recommend canola breeders to incorporate the genes into their canola cultivars. Furthermore, thirty five races were identified through combinations of Avr genes. Almost 60% of the strains belonged to one of seven races (Avr8-9, avr1-3-5-8-9-10-11, Avr3-8-9, Avr8, Avr1-3-5-9-10-11, Avr1-11, Avr9), each of which was composed of between 10-29 SPIs. Among the races, the most prevalent race was Avr8-9, accounting for 14.6% of the 198 strains. Notably, the second most prevalent race was avr1-3-5-8-9-10-11with frequence of 10.1%. This race could overcome resistance in all the NILs carrying single clubroot resistance genes and was identified in all the three provinces, which could pose a serious threat on canola production in Western Canada. To identify SNP markers associated with Avr genes, we planned to perform whole genome sequencing of *P. brassicae* SPIs. It is very difficult to obtain the pathogen tissue without non-P. brassicae contamination for DNA extraction. After analyzing the pathogen sequencing data from the public domain, we found almost 80% of DNA sequences (likely from the plant tissue and other microorganisms) could not be mapped to the pathogen genome. Through extensive efforts during the reporting period, we successfully obtained DNA with only 3.8% of unmapped DNA sequences, a significant breakthrough that has been made.

Cloning clubroot resistance genes from *B. nigra* and transferring the genes into canola through a CRISPR/Cas9 based technology

- Funding: ADF and SaskCanola (2022–2025)
- Objectives:

1) Identify the most probable candidates for the CR genes identified in *Brassica nigra*.
2) Isolate a clubroot resistance gene from *B. nigra*
3) Deliver the candidate genes into canola using a newly established CRISPR/Cas9 system

Progress: With the newly obtained SPIs of clubroot pathogen (*P. brassicae*) in our lab, we have successfully identified a differential isolate to separate BRA (resistant) from PI219576 (susceptible), although BRA and PI219576 are resistant to the vast majority of SPIs tested. This indicates a novel CR gene, namely *Rcr12*, may present in BRA while not in PI219576 (carrying *Rcr6*). A mapping-by-sequencing approach via BSR-Seq was performed for BRA because SNP markers linked to *Rcr6* identified from PI 219576 were not completely associated with *Rcr12*. Analysis of the new assembly data against a B. nigra reference genome revealed the highest PPV region is within the physical range of 3-7 Mb on chromosome B3. Further, by using a BC1 population of 1240 plants derived from CR2748 x (BRA x CR2748) and newly designed SNP markers, we have fine-mapped a 0.33 Mb region defined by two new SNP markers, i.e., HH9 (B3 location: 6337273) and HH22 (B3 location: 6667641), which shares some overlapped region with *Rcr6* on chromosome B3. However, besides the fact that the resistance phenotype is different between BRA and PI219576 with the differential SPI, comparative genomic and gene functional analysis confirmed that, although residing in a close region with multiple clustering candidate R genes, *Rcr12* is a distinct CR gene from *Rcr6*. Our cloning work on *Rcr12* has also successfully obtained a novel CR gene from the targeted region of BRA, which showed strong resistance to clubroot. By now, the newly obtained *Rcr12* gene and the other three candidate CR genes cloned from other *B. nigra* materials were ready to be delivered into canola using our CRISPR/Cas9-based vector system, which is in the process of upgrading to intragenic vectors with new promoters/terminators that are native to *Brassica napus* species.

AAFC Clubroot Consortium II

- Funding: Bayer, BASF, Corteva, Cargill and Nutrient (2020–2025)
- Objectives:
  1) To identify genes resistant to new pathotypes of *P. brassicae* from a *B. napus* source highly resistant to almost all the Canadian pathotypes of *P. brassicae*.
  2) To finely map resistance genes identified and develop SNP markers tightly linked to each of resistance genes
  3) To introgress resistance genes into canola

Identifying genes for resistance to the most aggressive races of *Plasmodiophora brassicae* and de novo genome sequencing of brassica lines with multiple identified resistance genes

- Funding: SCAP Canola Cluster (2023-2028), part of a joint project with Gary Peng (PI), AAFC Saskatoon; Habibur Rahman and Nat Kav, U of A; Rob Duncan, U of M.
- Project objectives:
  1) Identify novel CR genes in several unique *Brassica napus* sources and genetically map them for resistance to the races of *Plasmodiophora brassicae* aggressive on all the canola breeding lines carrying single identified genes

2) Develop robust single nucleotide markers tightly linked to these CR genes to facilitate rapid incorporation of CR genes into elite breeding lines of canola
3) Perform sequencing and develop de novo genome assemblies for clubroot resistance using *B. rapa, B. oleracea* and *B. napus* species with multiple CR loci identified to generate genomic data for a better understanding of CR evolution are meaningful labelling of CR genes in canola cultivars

Progress: Please see Dr. Gary Peng's highlights

Publications:

1. Hu H and Yu F (2024) Studies on the temporal, structural, and interacting features of the clubroot resistance gene *Rcr1* using CRISPR/Cas9-based systems. **Horticultural Plant Journal**. https://doi.org/10.1016/j.hpj.2024.04.001
2. Karim MM and **Yu F** (2024) Resynthesizing Brassica napus with race specific resistance genes and race non-specific QTLs to multiple races of *Plasmodiophora brassicae* . **Scientific Reports** https://doi.org/10.1038/s41598-024-64795-x
3. Hu H, Zhang Y and **Yu F** (2023) The fast breeding of selection-marker-free canola with *Rcr1*-rendered clubroot resistance by a CRISPR/Cas9-based vector system. **Journal of Experimental Botany** https://doi.org/10.1093/jxb/erad471
4. Karim MM and **Yu F**(2023) Identification of QTLs for resistance to 10 pathotypes of *Plasmodiophora brassicae* in Brassica oleracea cultivar ECD11 through Genotyping-by-sequencing. **Theoretical and Applied Genetics** 136:249 https://doi.org/10.1007/s00122-023-04483-y

Fernando Lab Report on Oilseeds– 2024: Unveiling New Insights in Canola Blackleg Resistance

Submitted by Dilantha Fernando, PhD.

Work on major gene resistance in Canola blackleg pathosystem – Dr. Malini Jayawardana

Funding: SaskCanola and MITACS

Host resistance plays a vital role in the management strategies to control canola blackleg in the field. The resistance in canola against blackleg is controlled by both qualitative and quantitative resistance, controlled by a single major gene (*R* gene) and minor genes, respectively.

Although *R* genes effectively control canola blackleg, several drawbacks are also reported, such as *R* gene resistance breakdown. Therefore, it is crucial to identify novel *R* genes in canola germplasm. In our lab, several *B. napus* lines having novel resistance have been identified with the aid of the greenhouse inoculations with the virulent *L. maculans* isolate umavr7 which is developed by our lab. The lines having unknown resistance were crossed with the susceptible parent Westar to obtain F1 population. The screening of the F1 population revealed that the unknown resistance gene is recessive. The disease reaction of the F2 population gave 3:1 susceptible: resistant ratio supporting that the unknown resistance is governed by a single major gene. The genetic mapping of these unknown resistance genes will be done with bulked segregant RNA sequencing.

In addition to identifying novel *R* genes, utilizing the already identified *R* genes effectively in the field is equally important. One of the common reasons for *R* gene resistance breakdown is the continuous use of same *R* gene in the field over years. Therefore, rotating *R* genes helps to delay the *R* gene resistance breakdown in the field. To study this scenario, our lab has conducted a four-year field study to study the effect of *R* gene rotation on canola blackleg disease severity. The results suggested that the *R* gene rotation reduces blackleg severity. Furthermore, the results prove that the rotation of *R* genes not only helps to control canola blackleg effectively but also provides a second chance to use the ineffective *R* genes, such as *Rlm3,* again in the field.

Canola Blackleg: Screening Canola Cultivars for Adult Plant Resistance – Dr. Shaheen Bibi

Funding: SaskCanola and MITACS

Purpose: The primary aim of this project is to investigate potential adult plant resistance (APR) in canola cultivars against *Leptosphaeria maculans*, the causal agent of Blackleg disease.

Methods: This year, over 200 lines of canola were screened in both field and greenhouse environments to assess plant resistance. Disease severity was evaluated based on visible symptoms of Blackleg infection, focusing on adult plants to determine resistance levels across different cultivars.

Next Steps: The next phase of the study involves genotyping the tested cultivars. Genome-wide association studies (GWAS) will be conducted to identify quantitative trait loci (QTLs) associated with adult plant resistance to Blackleg. These findings will contribute to understanding the genetic basis of APR in canola and potentially guide future breeding programs for disease-resistant cultivars.

Finding *Verticillium longisporum* resistance in Canola – Dr. Carol Bvindi

Funding: WGRF/MITACS/CCC

Objectives: Identification of QTLs and Single nucleotide polymorphisms (SNPs) for *V. longisporum* resistance through Genome-wide association mapping (GWAS).

Progress:

We have evaluated 250 genotypes provided by different companies and breeding programs for *V. longisporum* resistance at two locations Kelburn and Portage LaPraire in 2024 and one site in Portage LaPraire in 2024. Disease severity was scored at the end of the growing season using a scale developed in our group. For GWAS, the genotypes were genotyped using the Brassica 19K Brassica SNP array. Using the phenotype data from the field and the genotype data we will employ GWAS to identify significant QTLs and SNPs for *V. longisporum* resistance in Canola.

Verticillium detection at Ian Morrison Research Farm, Carman, MB. – Noah Van Den Driessche

We have recently identified *Verticillium longisporum* within the Carman Research station. Initial estimates earlier in the season put infection rates at 20%. Once plants had reached full maturity a disease count was preformed which revealed 70+% of plants were infected with *V. longisporum*. These counts were performed in four separate fields from different sections of the Carman farm. Revealing the presence of verticillium was not contained to a single area of Carman. No work on *V. longisporum* has been done within the Carman farm since it was first detected 10 years ago at the Kelburn farms south of Winnipeg. Anecdotal evidence from technicians at the Carman farm indicates they have seen V. longisporum symptoms in the previous years, but these were a rare occurrence. Stubble collections from 2023 were reviewed and show symptoms of *V. longisporum* but infection has not been molecularly confirmed yet.

Dr. Fernando's lab has collected stubble and soil samples from the infected fields and plans to look into how the spread has happened and how the strains found at Carman compare to other locations in Manitoba. In addition, as one of the infected fields was blackleg resistance trials, we will begin investigating the interactions between verticillium stripe and blackleg. These questions will bring about a better understanding of *V. longisporum* spread and its impacts on growers. A master's student, Narthaki Pathirana is working on this at present.