Virulence and pathotype characterization of *Plasmodiophora brassicae* populations collected from clubroot resistant canola cultivars in Western Canada 2018

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INTRODUCTION

Clubroot, caused by *Plasmodiophora brassicae* Wor., is an important soilborne disease of canola (*Brassica napus* L.) and other crucifers. The management of clubroot in Alberta, Canada, relies heavily on the planting of clubroot resistant (CR) canola. The first CR canola cultivar was released onto the Canadian market in 2009, but by 2013, resistance breakdown had been documented in two fields. Currently, a loss or erosion of clubroot resistance had been confirmed in a cumulative total of 170 fields across Alberta, likely as a result of pathotype shifts in the *P. brassicae* population. Most field isolates capable of overcoming resistance are classified as pathotype A on the Canadian Clubroot Differential (CCD) Set. Since pathotype A is a variant of pathotype 3 on the system of Williams, it is known commonly as pathotype 3A. Knowledge of pathotype composition is important for guiding resistance breeding activities, and continued monitoring of the performance of CR canola cultivars was carried out in 2018.

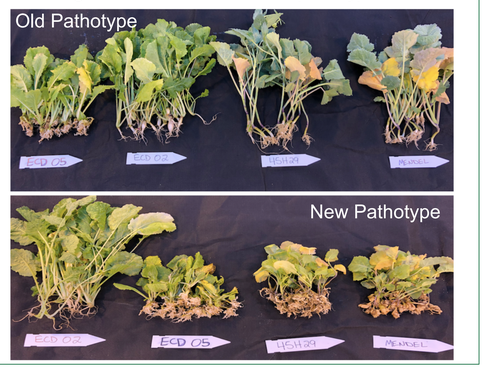
METHODS

Canola roots with typical clubroot symptoms were collected from 124 fields from Alberta, Manitoba and Saskatchewan in 2018 where CR cultivars had been planted. Resting spores of *P. brassicae were extracted* from multiple clubbed roots of each field. The concentration of *P. brassicae* resting spores in filtrates from symptomatic root tissue homogenates was measured with a hemocytometer (VWR, Mississauga, ON) and adjusted to 1 × 10^7spores mL-1 with sterile deionized water. The resulting spore suspension was used to inoculate 1-week-old seedlings of 13 host genotypes from the Williams, Somé *et al.,* and CCD set, which had been germinated on moistened filter paper in glass Petri dishes. The plants grew for 6 weeks under greenhouse conditions. They were harvested, washed and rated on a 0-3 scale. Based on the unique virulence pattern they produced on the CCD set (Table 1), a letter was assigned to distinguish a unique pathotype. The experiment was arranged in a randomized design, with 4 repetitions per host, and 12 seedlings per repetition.

Table 1: Pathotype classification scheme on the hosts of the CCD set

	Pathotype designation[a,b]																
CCD	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	X
Williams	3	2	5	3	8	2	5	3	5	8	5	5	6	8	3	8	5
Somé *et al.*	P_2	P_2	P_2	P_2	P_2	P_2	P_3	P_2	P_2	P_3	P_3	P_3	P_2	P_2	P_3	P_2	P_3
Differential Host[c]	Reaction[d]																
ECD 02	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
ECD 05	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
ECD 06	+	+	+	+	+	+	−	+	+	−	−	−	+	+	−	+	−
ECD 08	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+
ECD 09	+	+	+	+	+	+	−	+	+	−	−	−	+	+	+	+	−
ECD 10	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
ECD 11	−	+	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−
ECD 13	+	+	−	+	−	+	−	+	−	−	−	−	+	−	−	−	−
Brutor	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Laurentian	+	+	−	+	+	+	−	+	−	+	−	−	−	+	+	+	−
Mendel	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+
Westar	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
45H29	+	+	+	+	+	−	+	−	−	+	+	−	−	−	+	+	+

Figure 1: Galls from a field with an old pathotype versus galls from a field with a new pathotype



RESULTS

Of the 124 samples submitted, 1 of the 6 samples submitted from Manitoba, had overcome resistance and was a confirmed new pathotype. Of the 10 samples submitted from Saskatchewan, no samples showed evidence of resistance breakdown. Of the103 samples submitted from Alberta, 87 of the samples had overcome resistance and were confirmed new pathotypes.

Figure 1: 2018 pathotype designation based on Somé *et al.,*

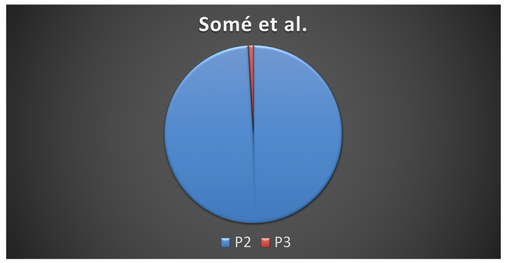


Figure 2: 2018 pathotype designation based on Williams

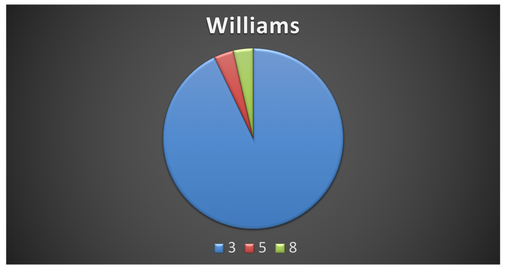


Figure 3: 2018 pathotype designation based on the CCD set

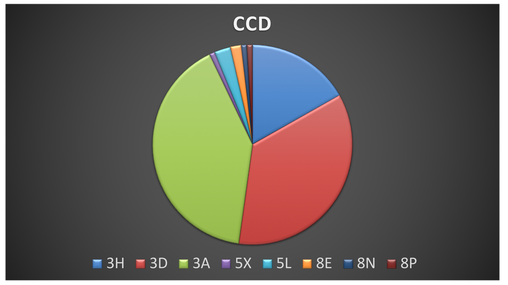
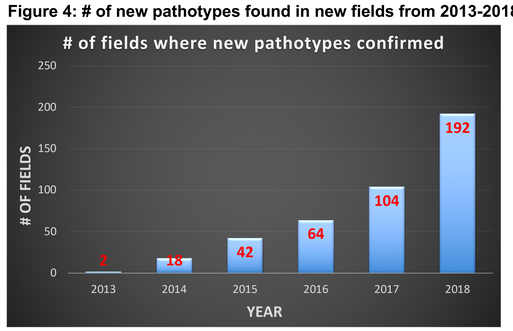


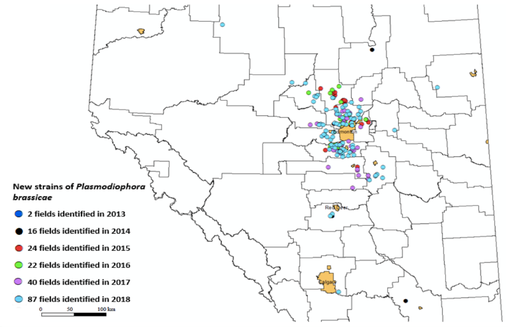
Figure 4: # of new pathotypes found in new fields from 2013-2018



DISCUSSION

A total of 88 fields with confirmed resistance breakdown in 2018 is the most new virulent pathotypes confirmed in a single year (Fig 4, Fig 5). Most new pathotypes in 2018 can be characterized as pathotype 3A on the CCD set (Fig 3). The results suggest that the loss or erosion of resistance continues to become more widespread in Alberta, and that pathotype 3A should be included in resistance screening activities.

Figure 5: Distribution of new pathotypes found from 2013-2018



CONCLUSION

The widespread emergence of new pathotypes brings a serious threat to Canadian oilseed farmers. Continued pathotyping efforts are crucial in understanding distribution, and identifying most common new pathotypes, for example pathotype 3A, as a focus for breeding efforts. CR canola is the most effective defense tool for farmers against clubroot, however with the continued spread of new pathotypes in which no commercially available resistant cultivars exist, management strategies must be tailored to prevent further spread and infection.

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