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Abstracts will be published in the conference proceedings. Participants are also encouraged to submit abstracts to the Canadian Journal of Plant Pathology (CJPP) for publication. All abstracts should be prepared according to the suggested CJPP format.

All abstracts must be reviewed by two colleagues with expertise in the area. The reviewers should not be authors of the abstract. The authors should submit the final copy of their abstract(s) in electronic format to PlantPathologySocietyAlberta@gmail.com by October 5th, 2026, and include the two reviewers' names at the bottom.

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Word processor

- Microsoft Word preferred; save the document as a doc file instead of the docx version.

Abstract font

- Times New Roman font and 12-point type preferred

Abstract title

- In bold; scientific names bold and italicized
- Only the first word of the title, proper names, and scientific names have the first letter capitalized

Author names

- In normal font, initial(s) first, followed by last name (e.g. A.B. Smith and C.B. Jones)

Affiliations

- In italics and need to include postal address and postal code (no abbreviations except for province or state names).
- First affiliation should be that of the first author. If other authors have different affiliations, those affiliations should start with the author's initials, e.g., (C.B.J.)

Abstract body

- In normal font with scientific names italicized
- [The maximum number of words for each abstract is 250, not including the title, author\(s\) and affiliation\(s\).](#)



- Scientific authorities are to be given for all scientific names the first time they are mentioned in the body of the abstract
- Abbreviations, nomenclature, symbols for units of measurement, etc. are to conform to the requirements for manuscripts submitted to CJPP

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ABSTRACT: Example from the 2025 Meeting

Mapping of a novel major gene involved in clubroot resistance from a double haploid population derived from a wild *Brassica napus* accession

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Clubroot, caused by the pathogen *Plasmodiophora brassicae*, poses a major threat to canola (*Brassica napus*) production in Canada. The use of resistant cultivars is the most effective strategy to manage this disease. Identification of novel clubroot resistance (CR) genes that confer broad-spectrum resistance to emerging pathotypes of the pathogen is therefore crucial. However, sources of clubroot resistance in *B. napus* are limited. In this study, a wild *B. napus* accession showing broad spectrum resistance to both ‘old’ and ‘new’ *P. brassicae* pathotypes was used as a donor parent in genetic crosses with the susceptible cultivar ‘Westar’. The resistant F₁ plants were used to generate 168 doubled haploid (DH) lines, which were evaluated for resistance to the ‘old’ pathotype 3H and the ‘new’ pathotype 3A. Chi-square analysis showed a 1R:1S segregation ratio for both pathotypes, indicating the presence of at least one major dominant resistance gene. Single nucleotide polymorphism (SNP) genotyping was performed using the *Brassica* 19K array. After filtering, 3,413 markers were retained for the A genome and 2,267 for the C genome for map construction and quantitative trait locus (QTL) analysis. QTL mapping identified a novel major locus on chromosome A08 conferring resistance to both pathotypes 3H and 3A, as well as minor locus on chromosome A03 conferring resistance against pathotype 3A. The markers on chromosome A08 exhibited less than 3% recombination frequency and may therefore be useful for marker-assisted selection. The novel CR gene identified in this study could represent a valuable resource for breeding clubroot-resistant canola.

Reviewed by:

- 1.
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