**Abstract Submission Info**

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

All abstracts must be reviewed by two colleagues knowledgeable in the area. The two 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](mailto:PlantPathologySocietyAlberta@gmail.com) by October 6, 2025 with the two reviewers’ names indicated at the bottom.

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For details regarding abstract formatting, please see the instructions for authors at: <http://www.tandfonline.com/action/authorSubmission?journalCode=tcjp20&page=instructions>

**Word processor** - Microsoft Word preferred and save the document as the 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 italicised

- 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 measurements, etc. are

to conform to the requirements for manuscripts submitted to CJPP

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**EXAMPLE FROM 2024 MEETING**

**Helitrons and unequal crossing over implicated in the replication of necrotrophic effector *ToxB* in *Pyrenophora tritici-repentis***

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**Abstract**

Copy-number variation is a major driver of genome evolution and has been correlated with increased virulence and effector development in fungal plant pathogens. In the wheat tan spot pathogen *Pyrenophora tritici-repentis* (Died.) Drechs. (Ptr), the *ToxB* gene encodes a chlorosis-inducing effector that exhibits copy-number variation across isolates (reportedly ranging from 0 to 10 copies). We have utilized >20 long-read assemblies to understand the replication mechanism of *ToxB* within the Ptr genome. Our results revealed that in multi-copy isolates, *ToxB*, along with variable segments of surrounding sequences, exists as tandem unidirectional copies. Distinctive features, such as left and right terminal sequences, the presence of hairpin loops, and the lack of other conventional transposon features (i.e., LTRs, TIRs, TSDs, transposases, etc.) support the hypothesis that a Helitron-like-element is responsible for *ToxB* replication. Unequal crossing-over is also a potential driver of duplication. Additionally, our analysis showed that *ToxB* resides within a repeat-dense region rich with transposon activity, including evidence for two different Copia-like transposons disrupting and inactivating the *ToxB* reading-frame (i.e. *toxb*). The region containing *ToxB* is completely absent in isolates lacking the *ToxB* gene, indicating it is present within an accessory region. The size of the semi-conserved region may support the presence of a supernumerary chromosome arm, or perhaps an ancient, now defunct, large mobile element. Our study provides a comprehensive look at virulence gene duplication in a fungal pathogen, utilizing the Ptr genome as a case study.

Reviewed by:

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