Genome similarity of *Plasmodiophora brassicae* collections from Canada, China, and the USA

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Introduction

New virulent pathotypes of *Plasmodiophora brassicae* are increasing rapidly on canola (*Brassica napus* L.).

Need for information on genetic similarity among pathogen populations.

**Limitations:**

- Mixture of pathotypes
- Biotrophic nature
- Can not be cultured
- Soil microbes

USDA National Institute of Food and Agriculture.
Objective

To develop whole-genome sequences of pathogen collections from across Canada, assess their genetic similarity, and compare with collections from the USA, China and Europe.
The origin of our collections

Clubroot spread in China

Distribution of clubroot-infested provinces in China

A. L. Chai et al.
Distribution of clubroot in North America

North Dakota

USA

Europe

1853

1920

2003

2009

2017

2013
Materials & methods

Crop: Canola (*B. rapa*), Pathogen: *P. brassicae*
Inoculation- DNA extraction

B. rapa Inoculated with different isolates

4 weeks

Disinfection
Antibiotic treatment

In darkness at 25c

Subculture

DNA EXTRACTION

B. rapa Inoculated with different isolates

6 weeks

Disinfection

Freeze dry

52 field and single spore isolate collections
Tissue culture

Two-week-old dual callus culture of *Brassica rapa* var. *Chinensis* and *plasmodiophora brassicae*
Materials & methods: WGS and analyses

HiSeq PE run by National Research Council of Canada

Assembly: DNA-seq libraries were aligned on the published e3 reference genome and assembled using the SeqMan Ngen software (DNASTAR Inc.)

Analysis of variants: ArrayStar software

Phylogenetic tree: Hierarchical clustering by R packages
Old collections from eastern and western Canada

Chinese collections

Prairies (AB, SK, and MB)

USA and new collations from eastern Canada
Similarity between single spore isolates and their original source
Old collections from eastern and western Canada

Chinese collections

Prairies (AB, SK, and MB)

USA and new collations from eastern Canada

Genome similarity before and after the change of pathotype from a field
Old collections from eastern and western Canada

Chinese collections

Prairies (AB, SK, and MB)

USA and new collations from eastern Canada

Pathotype is not a primary factor in gene similarity
Host is not a primary factor in gene similarity
**Conclusion**

- Factors affecting genome similarity: Geographic location and virulence
- Each clade consists of different pathotypes: The pathotype is not the primary factor in genome similarity
- Low similarity between samples collected from a site before and after a change of pathotype.
- The new pathotypes are possibly resulted from selection of existing genetic variation and not a recent mutation.
- Collections across much of North America differed from the collections in Alberta, which in turn differed from the new pathotypes.
- Tissue culture provides high quality *P. brassicae* DNA for downstream application
Thank you