Canada

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.

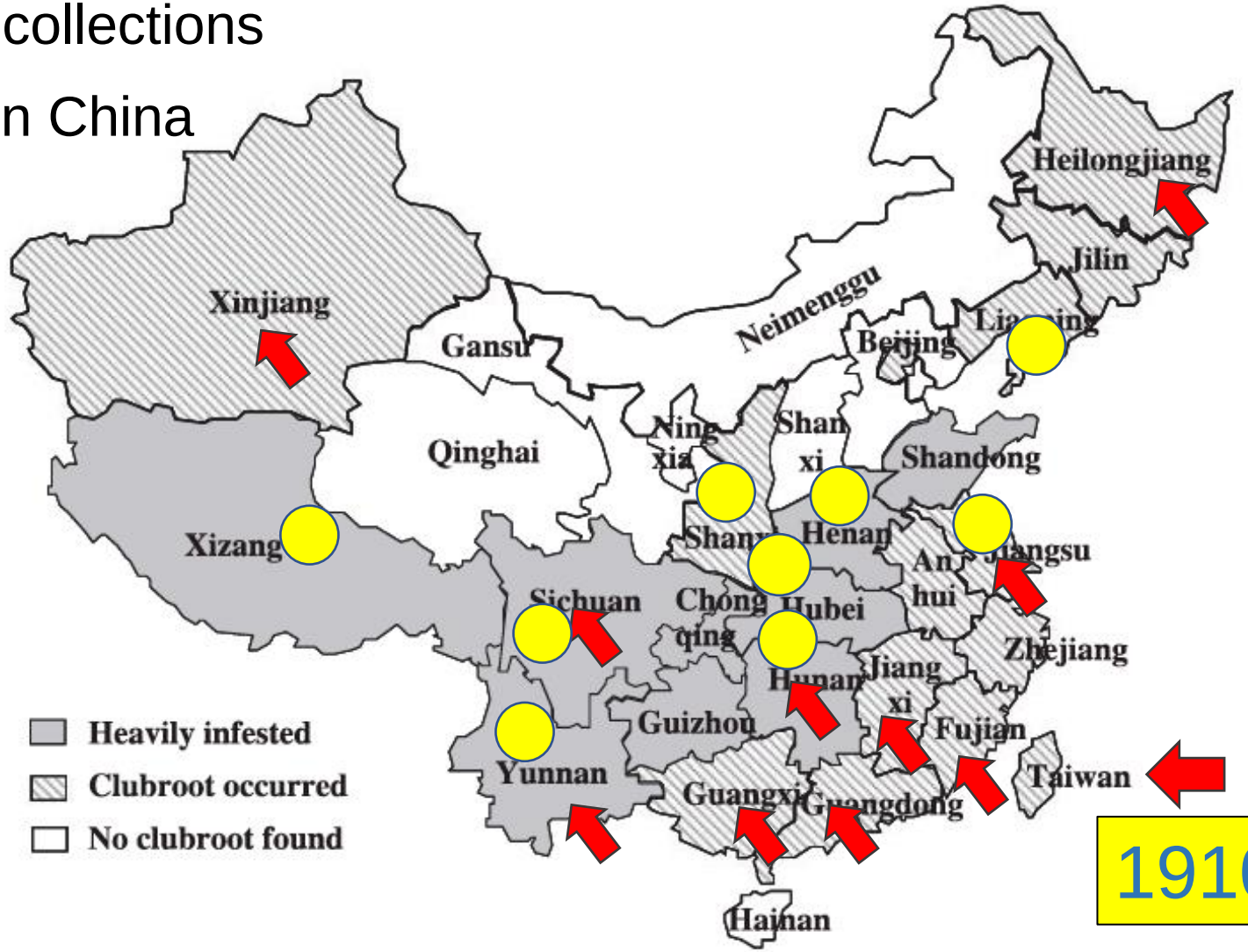
Objective

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.

Distribution of clubroot-infested provinces in China

The origin of our collections

Clubroot spread in China

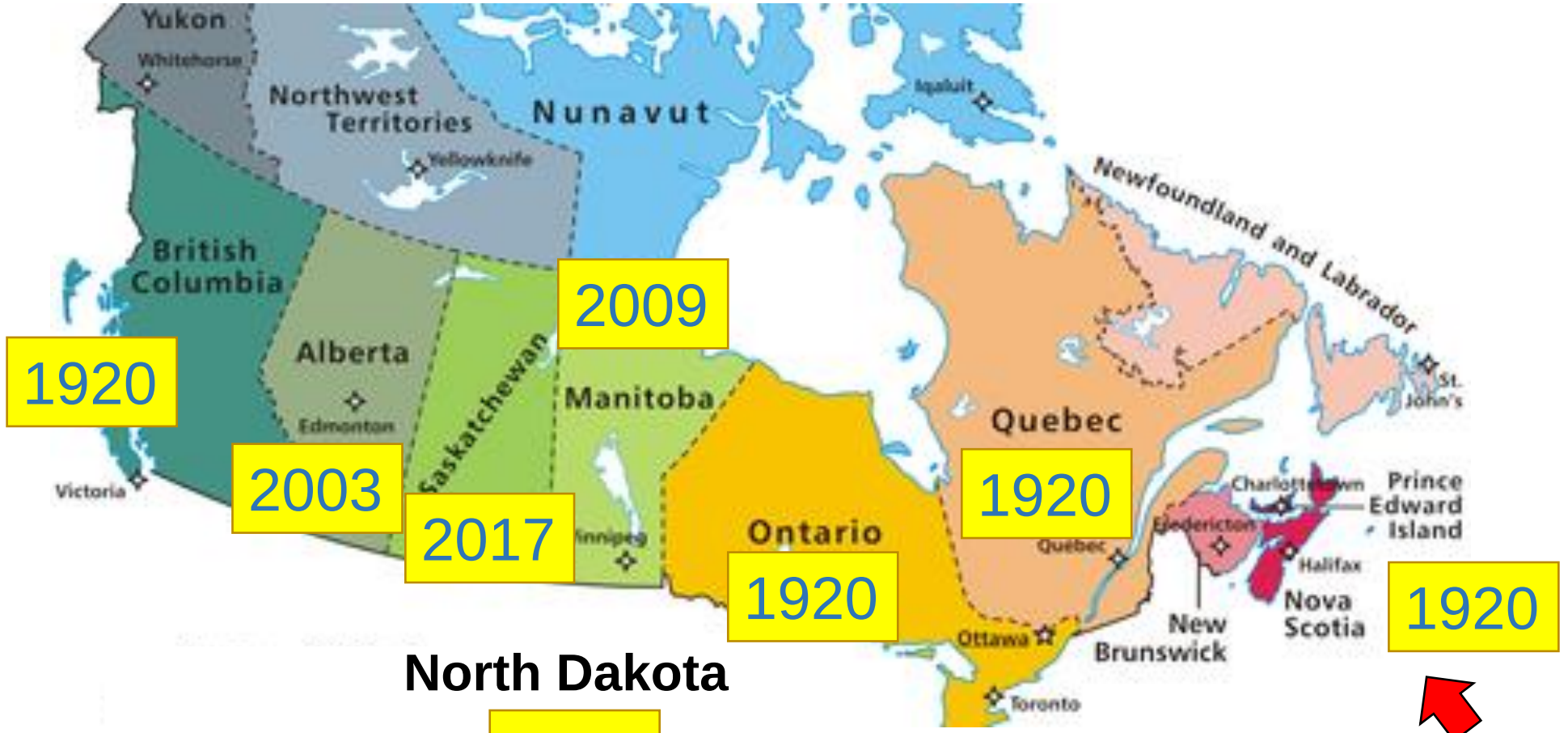


Europe

1910

A. L. Chai et al.

Distribution of clubroot in North America

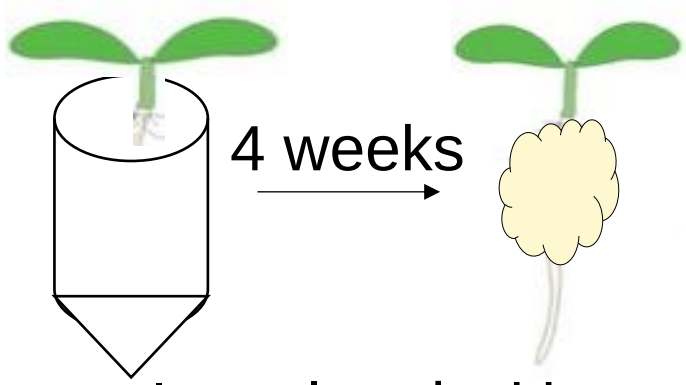


Materials & methods

Crop: Canola (*B. rapa*), Pathogen: *P. brassicae*

Inoculation- DNA extraction

52 field and single spore isolate collections



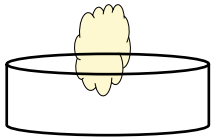
4 weeks

B. rapa Inoculated with different isolates

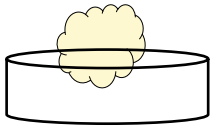
Disinfection

Antibiotic treatment

Tissue culture

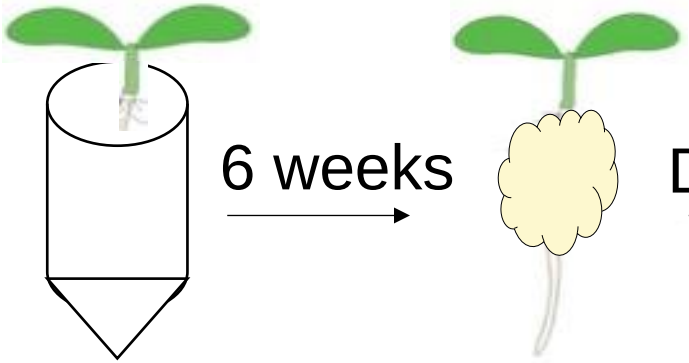


In darkness at 25c



Subculture

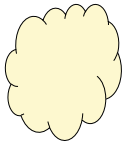
DNA EXTRACTION



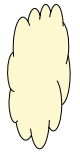
6 weeks

B. rapa Inoculated with different isolates

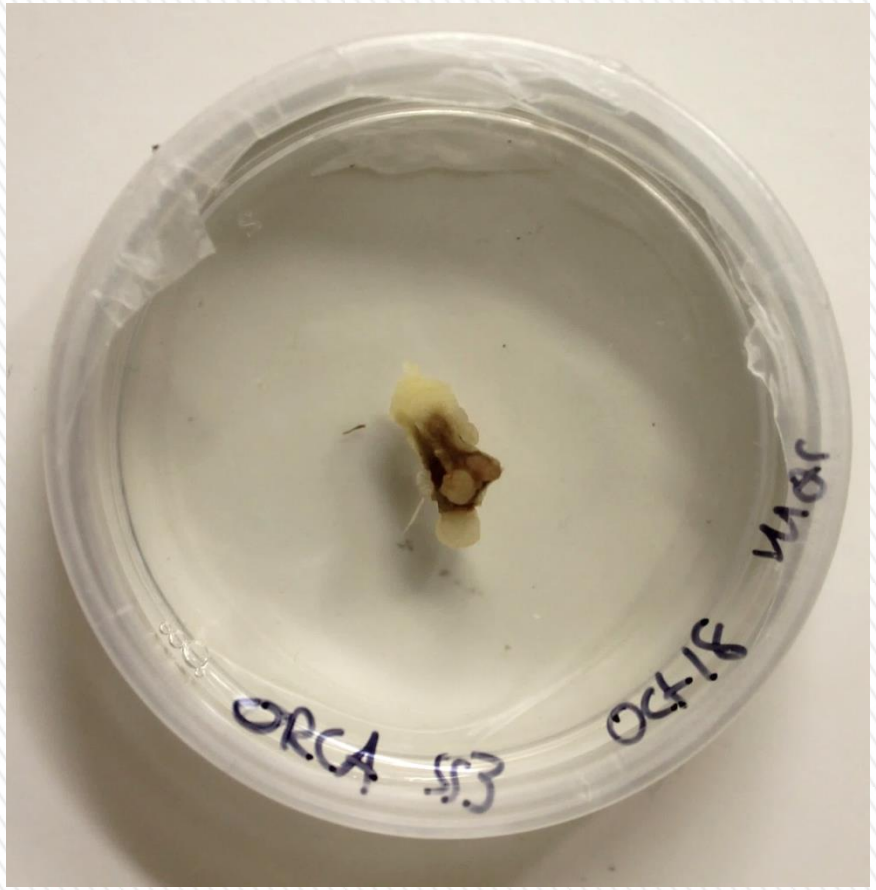
Disinfection



Freeze dry



Tissue culture



Two-week-old dual callus culture of *Brassica rapa* var. *Chinensis* and *plasmodiophora brassicae*

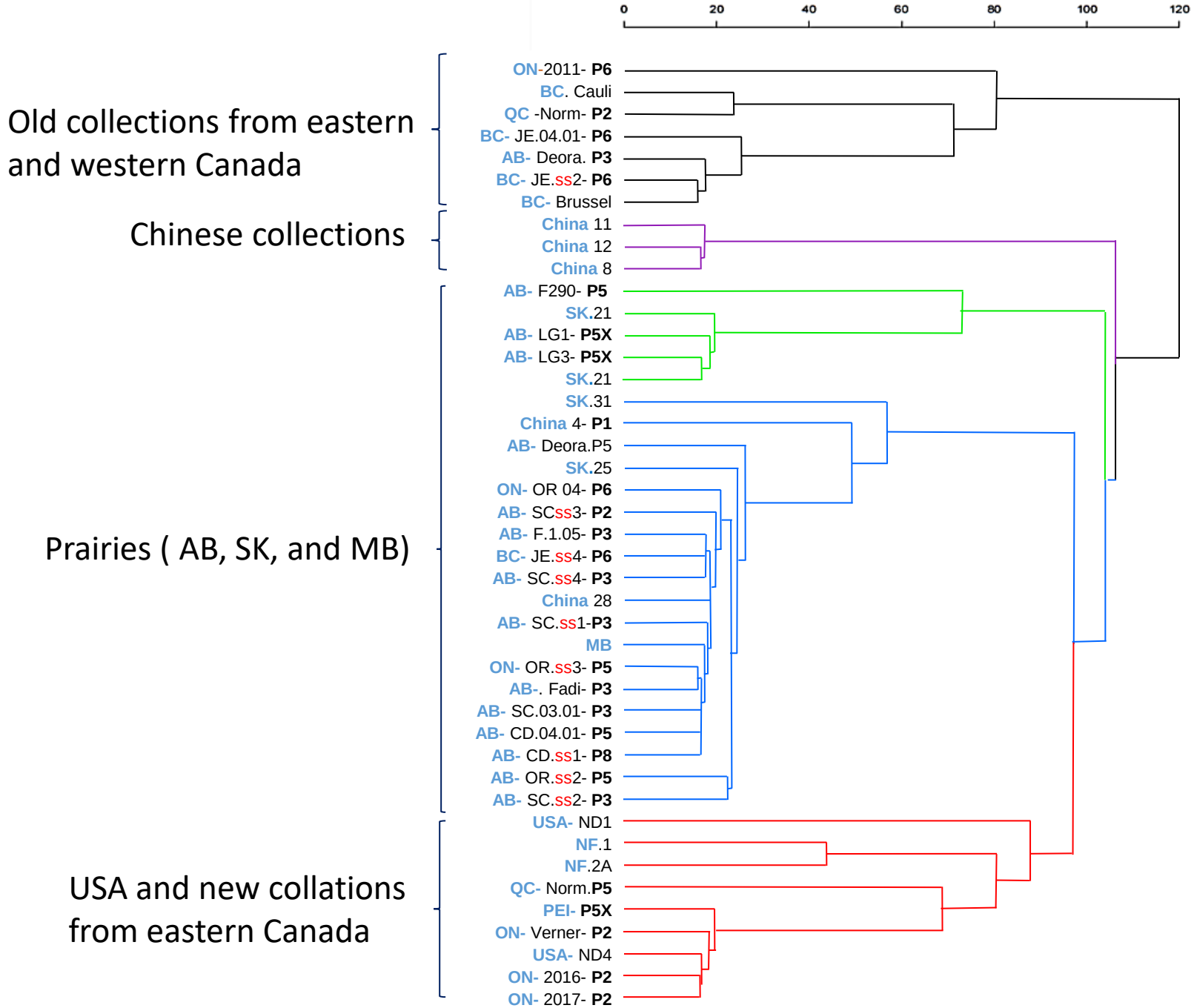
Materials & methods: WGS and analyses

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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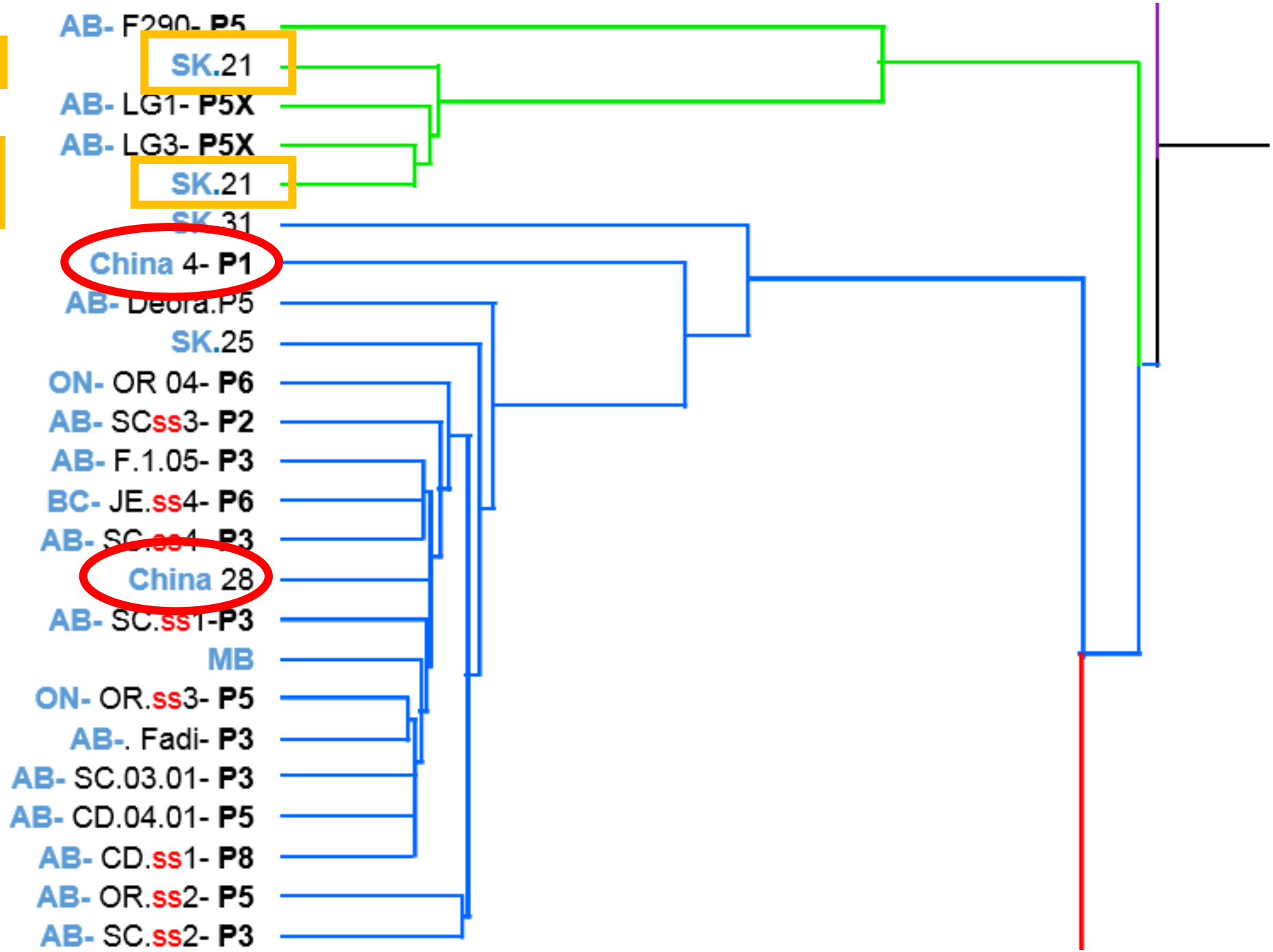
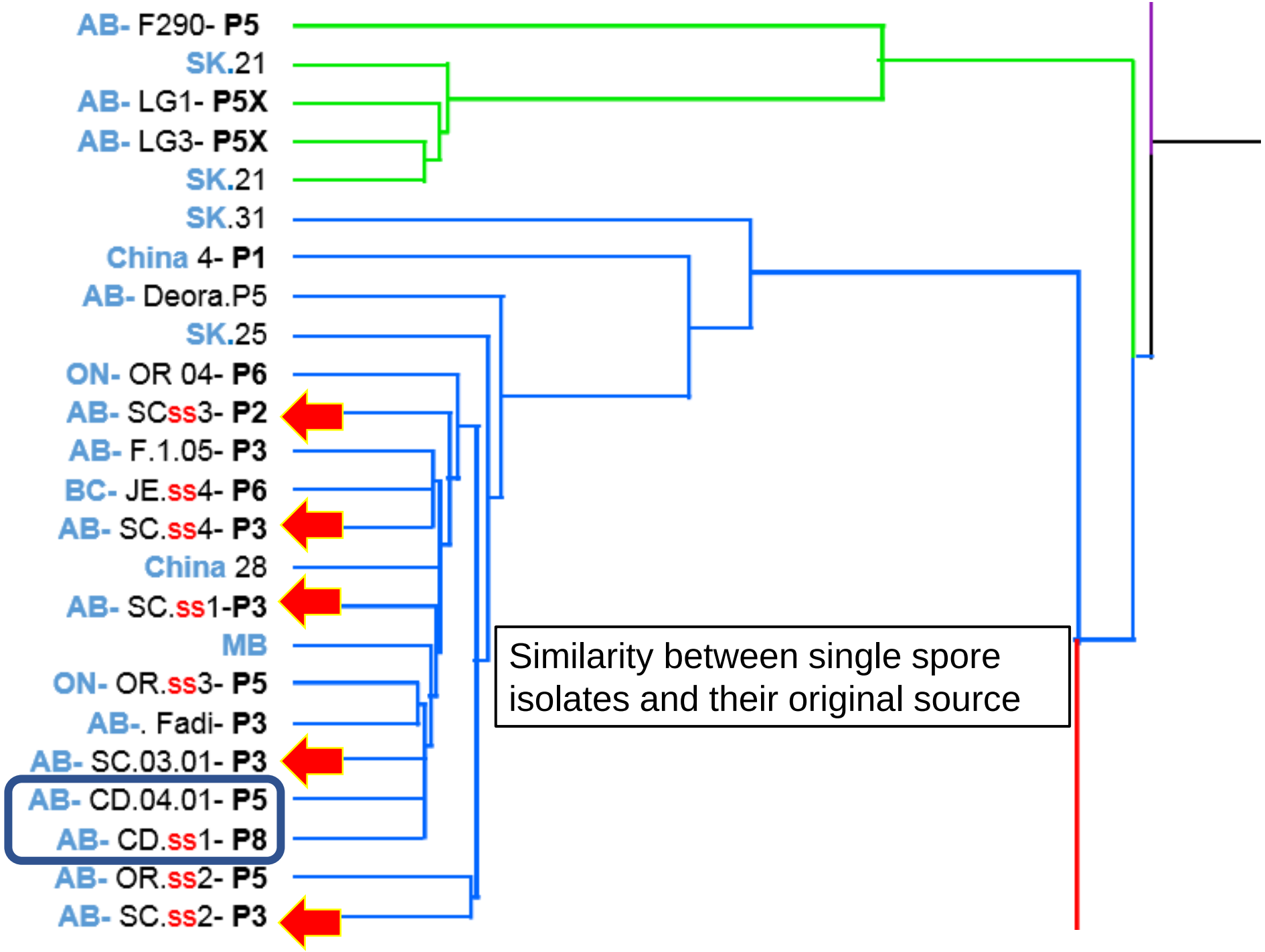
120
ON-2011- P6
BC. Cauli
QC -Norm- P2
BC- JE.04.01- P6
AB- Deora. P3
BC- JE.ss2- P6
BC- Brussel
China 11
China 12
China 8
AB- F290- P5
SK.21
AB- LG1- P5X
AB- LG3- P5X
SK.21
SK.31
China 4- P1
AB- Deora.P5
SK.25
ON- OR 04- P6
AB- SCss3- P2
AB- F.1.05- P3
BC- JE.ss4- P6
AB- SC.ss4- P3
China 28
AB- SC.ss1-P3
MB
ON- OR.ss3- P5
AB-. Fadi- P3
AB- SC.03.01- P3
AB- CD.04.01- P5
AB- CD.ss1- P8
AB- OR.ss2- P5
AB- SC.ss2- P3
USA- ND1
NF.1
NF.2A
QC- Norm.P5
PEI- P5X
ON- Verner- P2
USA- ND4
ON- 2016- P2
ON- 2017- P2
Old collections from eastern and western Canada
Chinese collections
Prairies (AB, SK, and MB)
USA and new collations from eastern Canada

DNA from club

DNA from Callus culture

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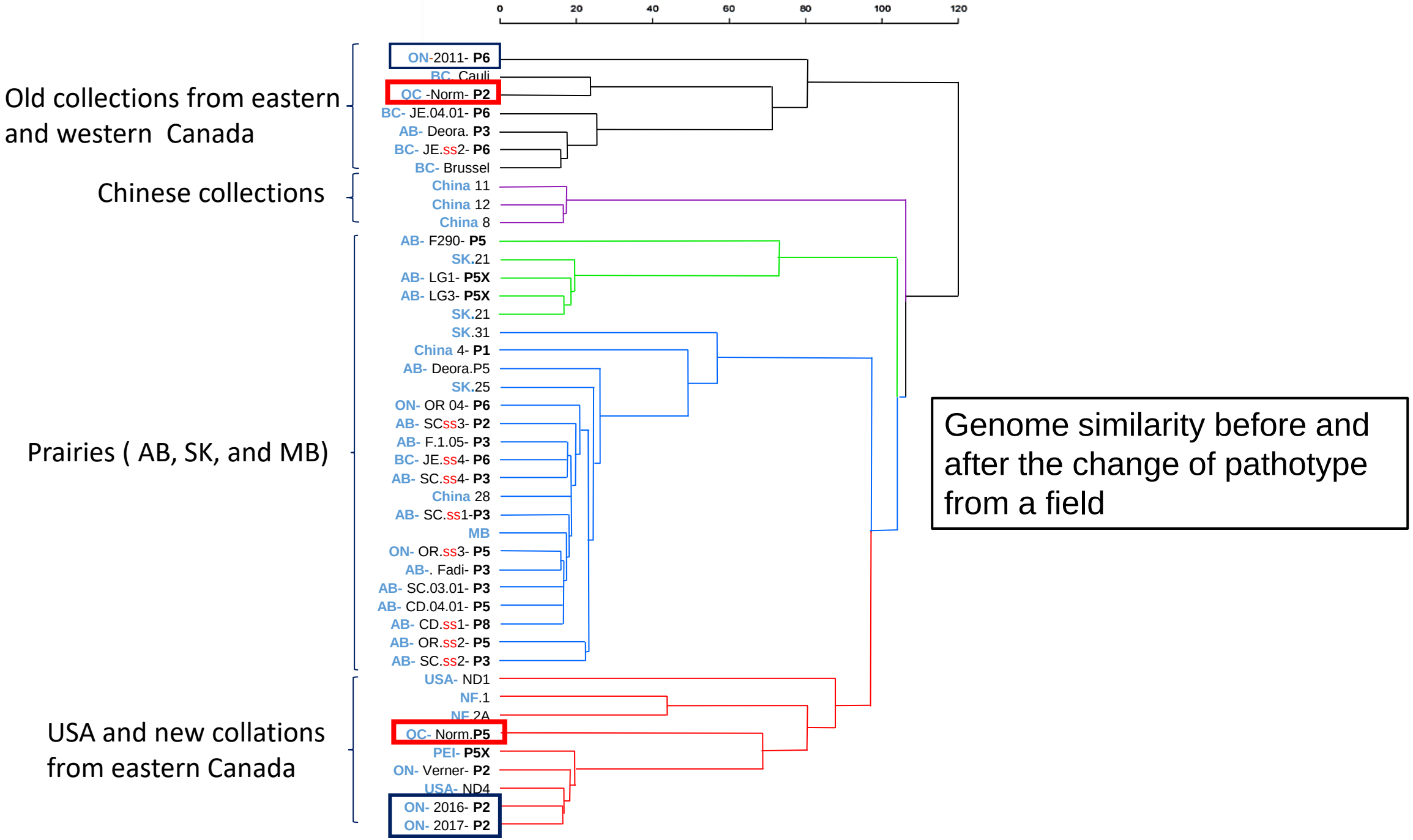
Similarity between single spore isolates and their original source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Old collections from eastern and western Canada
Chinese collections
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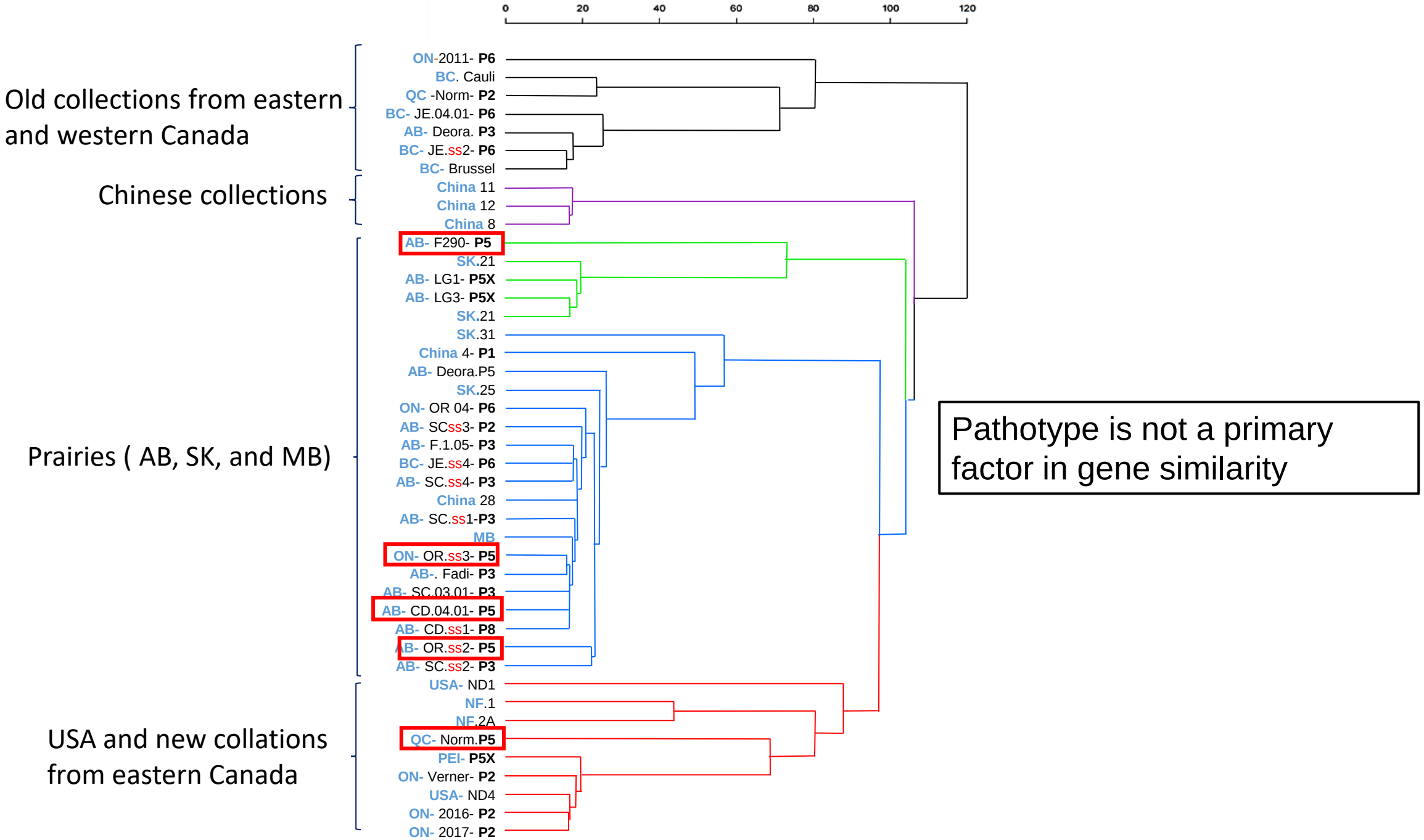
USA and new collations from eastern Canada
Genome similarity before and after the change of pathotype from a field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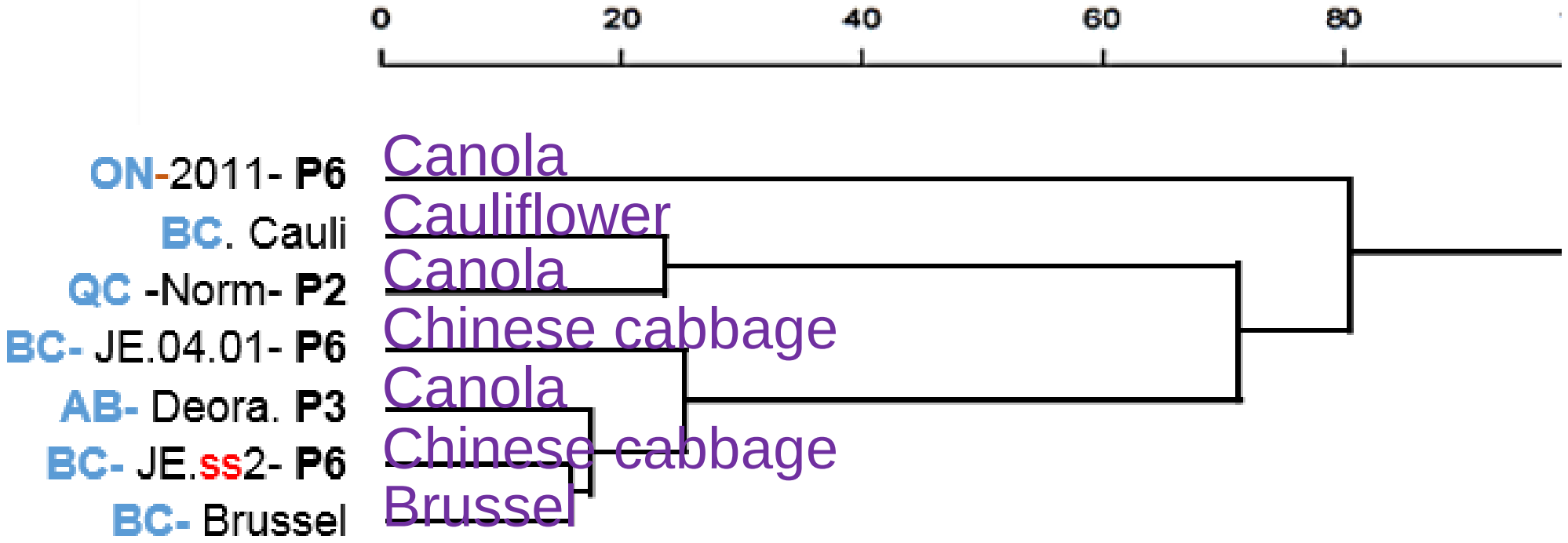
Pathotype is not a primary factor in gene similarity



Host is not a primary factor in gene similarity

Conclusion

- Factors affecting genome similarity: Geographic location and virulence
- Each clade consist 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