



Plasmid genome dynamics of sequenced strains of *Xanthomonas campestris* pv. *campestris*



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INTRODUCTION

Xanthomonas campestris pv. *campestris* (Xcc), the causal agent of black rot of crucifers, remains a threat to all Brassica crops around the world for almost 140 years.

Xcc strains have been found to contain between zero and four TALE genes found on the chromosome or on plasmids

Plasmids in *Xanthomonas* species were associated with bacteria's adaptation to antibiotics, heavy metals, and to resistant host plants via horizontal transfer of virulence genes.

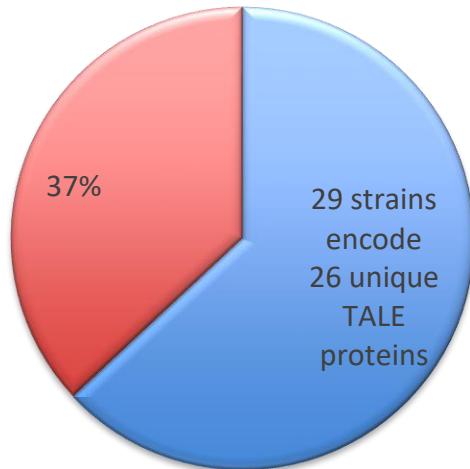
THE AIM

- improving our understanding of *Xcc* taxonomy and virulence mechanisms

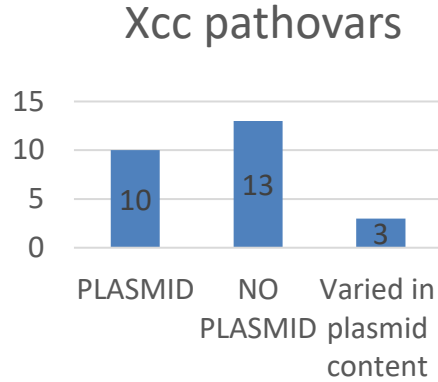
MATERIAL AND METHODS

- DNA sequencing
- RFLP of plasmid DNAs

46 Xcc isolates



RESULTS



The apparent stability of the plasmids provides a natural genetic marker that can be strain-specific and useful in epidemiological investigations

RESULTS

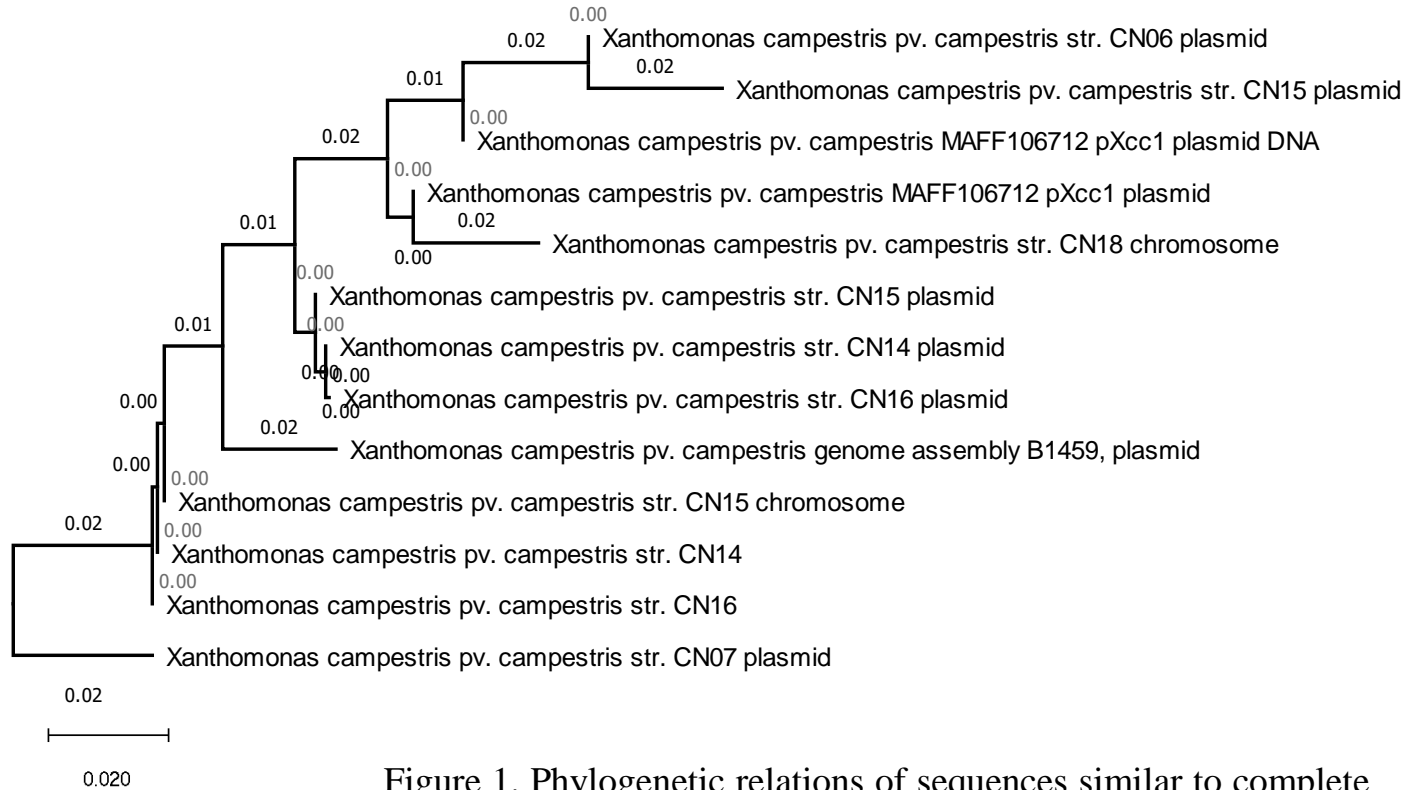


Figure 1. Phylogenetic relations of sequences similar to complete genome of MAFF106712 pXcc1 plasmid in other *Xcc* strains.

CONCLUSION

High level of inter-strain variation mediated by plasmids harboring virulence-related genes, including the T4SS and T3SS effectors highlights the importance of strain-specific genome dynamics mediated by such elements. Majority of epidemic *Xcc* strains sequenced to the date do not have plasmids but carry plasmid-homologues genes in their chromosomes. This suggests the importance of plasmid integration into bacterial chromosome via unknown so far mechanism in providing *Xcc* strains high virulence towards commercial brassicas.

THANK YOU FOR YOUR ATTENTION!