A multilocus sequence analysis of Xanthomonas campestris reveals a complex structure within crucifer-attacking pathovars of this species

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Résumé en anglais	Previous classification of Xanthomonas campestris has defined six pathovars (aberrans, armoraciae, barbareae, campestris, incanae, and raphani) that cause diseases on cruciferous plants. However, pathogenicity assays with a range of strains and different hosts identifies only three types of symptom: black rot, leaf spot and bacterial blight. These findings raise the question of the genetic relatedness between strains assigned to different pathovars or symptom phenotypes. Here we have addressed this issue by multilocus sequence analysis of 42 strains. The X. campestris species was polymorphic at the 8 loci analysed and had a high genetic diversity; 23 sequence types were identified of which 16 were unique. All strains that induce black rot (pathovars aberrans and campestris) were genetically close but split in two groups. Only three clonal complexes were found, all within pathovar campestris. The assignment of the genome-sequenced strain 756C to pathovar raphani suggested from disease symptoms was confirmed, although this group of strains was particularly polymorphic. Strains belonging to pathovars barbareae and incanae were closely related, but distinct from pathovar campestris. There is evidence of genetic exchanges of housekeeping genes within this species as deduced from a clear incongruence between individual gene phylogenies and from network structures from SplitsTree analysis. Overall this study showed that the high genetic diversity derived equally from recombination and point mutation accumulation. However, X. campestris remains a species with a clonal evolution driven by a differential adaptation to cruciferous hosts.

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