

Natural Genetic Variation of *Xanthomonas campestris* pv. *campestris* Pathogenicity on *Arabidopsis* Revealed by Association and Reverse Genetics

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The pathogenic bacterium *Xanthomonas campestris* pv. *campestris*, the causal agent of black rot of Brassicaceae, manipulates the physiology and the innate immunity of its hosts. Association genetic and reverse-genetic analyses of a world panel of 45 *X. campestris* pv. *campestris* strains were used to gain understanding of the genetic basis of the bacterium's pathogenicity to *Arabidopsis thaliana*. We found that the compositions of the minimal predicted type III secretome varied extensively, with 18 to 28 proteins per strain. There were clear differences in aggressiveness of those *X. campestris* pv. *campestris* strains on two *Arabidopsis* natural accessions. We identified 3 effector genes (*xopAC*, *xopJ5*, and *xopAL2*) and 67 amplified fragment length polymorphism (AFLP) markers that were associated with variations in disease symptoms. The nature and distribution of the AFLP markers remain to be determined, but we observed a low linkage disequilibrium level between predicted effectors and other significant markers, suggesting that additional genetic factors make a meaningful contribution to pathogenicity. Mutagenesis of type III effectors in *X. campestris* pv. *campestris* confirmed that *xopAC* functions as both a virulence and an avirulence gene in *Arabidopsis* and that *xopAM* functions as a second avirulence gene on plants of the Col-0 ecotype. However, we did not detect the effect of any other effector in the *X. campestris* pv. *campestris* 8004 strain, likely due to other genetic background effects. These results highlight the complex genetic basis of pathogenicity at the pathovar level and encourage us to challenge the agronomical relevance of some virulence determinants identified solely in model strains. **IMPORTANCE** The identification and understanding of the genetic determinants of bacterial virulence are essential to be able to design efficient protection strategies for infected plants. The recent availability of genomic resources for a limited number of pathogen isolates and host genotypes has strongly biased our research toward genotype-specific approaches. Indeed, these do not consider the natural variation in both pathogens and hosts, so their applied relevance should be challenged. In our study, we exploited the genetic diversity of *Xanthomonas campestris* pv. *campestris*, the causal agent of black rot on Brassicaceae (e.g., cabbage), to mine for pathogenicity determinants. This work evidenced the contribution of known and unknown loci to pathogenicity relevant at the pathovar level and identified these virulence determinants as prime targets for breeding resistance to *X. campestris* pv. *campestris* in Brassicaceae.

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