



Genotypic and phenotypic analysis shows *Ralstonia solanacearum* cool virulence is a quantitative trait not restricted to “Race 3 biovar 2”

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Abstract

Ralstonia spp. cause bacterial wilts of many tropical crops but some strains, known as Race 3 biovar 2 (R3bv2), cause potato brown rot in cool tropical highlands. R3bv2 strains are highly regulated because of their supposedly unique cool virulence. Strains sub-classified in sequevars 1 or 2 based on the *egl* sequence are considered R3bv2 by USDA-APHIS. However, some non-sequevar 1/2 strains are also cool-virulent and it is not known if all sequevar 1/2 strains are cool virulent. Therefore, we sequenced genomes of 76 potentially cool virulent *R. solanacearum* strains and compared them to 30 available genomes using an evolutionary genomics framework. These analyses demonstrated that a single clonal lineage within sequevar 1 is responsible for nearly all brown rot outbreaks worldwide. In parallel, we measured virulence of ten representative strains on tomato and potato at 22°C and 28°C, as well as their ability to cause latent infections and colonize potato tubers. This revealed that cool virulence and host preference are interacting quantitative traits. The highest cool virulence was restricted to the sequevar 1 pandemic clonal lineage. Tested sequevar 2 strains were only moderately cool virulent on potato, while some sequevar 4 and 28 strains were highly cool virulent and aggressively colonized tubers. Cool virulence on potato is thus not strictly correlated with the currently regulated R3bv2 group. Moreover, traits beyond cool virulence likely explain the alarming success of the pandemic lineage. Genomic data are publicly available in LINbase to facilitate genome-based identification of potentially threatening strains.