Article Summary. In fewer than 100 words

In this paper, we quantified virulence of a genetically diverse population of the pathogen *Botrytis cinerea*  on a collection of wild and domesticated tomato accessions to study how crop domestication impacts quantitative plant resistance to generalist pathogens. Lesion size was significantly controlled by plant domestication, plant genetic variation, and the pathogen’s genotype. Genome-wide association (GWA) mapping in *B. cinerea* identified a highly polygenic collection of genes where alleles modulated virulence on distinct tomato accessions. Critically, we identified a subset of *B. cinerea* genes where the allelic variation was linked to altered virulence against the wild versus domesticated tomato accessions.