**Methods**

Tomato genetic resources

We obtained seeds for selected tomato genotypes in consultation with Dr. Roger Chetelat at the UC Davis TGRC. These include a diverse sample of domesticated tomato’s closest wild relative (S. pimpinellifolium) from throughout its range (Peru, Ecuador …) as well as heritage and modern varieties of *S. lycopersicum*. We bulked all genotypes in long-day (16h) greenhouse conditions at UC Davis in fall 2014. Plants were grown under metal-halide lamps (temp, RH?) in (XX pot diameter) filled with potting soil (Sunshine mix #1, Sun Gro Horticulture) (XX fertilizer). Plants were pruned and staked upright, and fruits were collected as they matured.

Fruits were stored at 4C in dry paper bags until seed cleaning. Seeds and locule contents were incubated at XX temp in XX% protease solution, then rinsed in dI H2O and air-dried. Seeds were then stored in a cool, dry, dark location until further plantings.

We bleach-sterilized all seeds prior to germinating on germination paper in growth chambers. At XX days we transferred seedlings to soil (SunGro) and grew all plants in growth chambers in 24C, short-day (10h) conditions with 180-190 uM light intensity and 60% RH. The flat was covered with a humidity dome during germination. We bottom-watered with DI H2O every two days for two weeks, and at week 3 watered every two days with added nutrient solution XX.

Selection of Botrytis population

Botrytis genetic resources

Selection of genotypes

Botrytis isolates were maintained as conidial suspensions in 30% glycerol for long term storage at -80C.

For regrowth, spore solutions were diluted to 10% in 50% filter-sterilized grape juice, then plated onto 39g/L potato dextrose agar (PDA) media. Isolates were grown at 25C in 12h light, and replated every 2 weeks.

Detached leaf assay

Detached leaf assay as useful approximation of whole-plant: Sharma 2005, Mulema and Denby 2012, Cowley 2014, Boydom 2015

To study the effect of genetic variation in host and pathogen on lesion formation, we infected 12 diverse tomato varieties with the above 96 Botrytis isolates. We used a randomized block design with three replicates in each of two experiemnts. We randomly sampled 5 leaves per plant, and 2 leaflet pairs per leaf. We tracked apical vs. basal leaflet pairs. Leaflets were placed on 1% phytoagar in seed flats, with humidity domes on top.

Spores were collected from mature (1-2 week old) Botrytis cultures, and diluted to 10 spores/ uL in 50% filter-sterilized grape juice. 4ul droplets of spore suspensions were inoculated onto detached leaves at room temperature with 24h light. Control leaves were mock-inoculated with 4uL of grape juice without spores.

We photographed all leaflets at 72 hours post inoculation for downstream image analysis.

*Automated Image Analysis*

We measured lesion areas using the EBImage and CRImage packages (Pau et al., 2010; Failmezger et al., 2010) in the R statistical environment (R Development Core Team and Team, 2009). Leaflets were identified as objects with green hue, and lesions were identified as low-saturation objects within leaves. Images masks were generated for both the leaf and lesion, then manually refined by a technician to ensure proper object calling. The area of these leaves and lesions were then automatically measured as pixels per lesion and converted to area using a 1 cm reference within each image.

Statistical analysis

Words

population structure can drive false positive associations. To address this concern we conducted additional GLMs for both camalexin and lesion area for each isolate separately to determine how much phenotypic variance is attributable to the residual population structure within our population. The F‐tests revealed that the

211 residual population structure accounted for a significant amount of variation for camalexin in response

212 to all four isolates, but was not significant for lesion area (Table S2). Importantly, however, the

213 proportion of variance attributable to the phylogenetic group was on average only 7 % of the level

214 of phenotypic variation attributable to differences among the accessions (Table S2, Fig. 2). Model

215 corrected means for genetic mapping were derived from this model using this population to remove

216 potential effects derived from residual population structure. Importantly, the distribution of these

217 model corrected means were largely unimodal with only slight skewing that did not require

218 transformation given the large sample size (Figs. S3 and S4). Thus, this approach should also help

219 reduce false positive associations attributable to the general population structure.

Spearman’s rank correlations among phenotypes to see if there is a significant correlation of lesion size across plant hosts?

For GWA we used model-corrected means (lsmeans) from the full experimental model in a separate ridge-regression GWA model per plant genotype. Ridge regression approach as used by (Cite Corwin). It provides heteroscedastic SNP effect estimates but not direct p-values per SNP.

“To identify significant SNPs in the model, we calculated an significance effects threshold by randomly permuting the phenotypes among the genotypes 1,000 times and pulling the 99th percentile from the distribution of effects derived from the permutations. Because this permutation maintains relationship of genotypes within the matrix, it maintains any population structure across the permutations and should help to control for spurious effects caused by population structure.