**IN BRIEF**

**97 Shades of Grey: Genetic interactions of the grey mold, *Botrytis cinerea*, with wild and domesticated tomato**

Although a vineyard full of decaying grapes infected with noble rot is a blessing for sweet wine producers, the causal agent, *Botrytis cinerea* (grey mold), is responsible for huge crop losses globally, both pre- and post-harvest. Individual isolates of the necrotrophic fungus can infect an extremely broad host range, which includes cereals, fruits, vegetables and ornamentals (Elad et al., 2015). This host promiscuity is due, in part, to the relatively high amount of allelic variation observed among *B. cinerea* isolates present, crucially, in multiple proteins involved in its *modus operandi* of infection. Such standing genetic variation effectively provides the pathogen with beneficial alleles that have been ‘tried and tested’ by selection, thus enabling it to rapidly adapt to new environments and/or infect new host species. Host resistance to generalist pathogens also involves multiple defense mechanisms and pathways. Taken together, this results in a quantitative *B. cinerea* virulence phenotype (Rowe and Kliebenstein, 2008).

A new study by Soltis and colleagues utilises the tomato-*B. cinerea* pathosystem to measure how genetic diversity in both the host plant and a generalist pathogen interact to impact resistance/susceptibility, but on a previously unimaginable scale! By infecting 6 domesticated (*Solanum lycopersicum*) and 6 wild (*S. pimpinellifolium*) tomato accessions each with 97 genetically-distinct *B. cinerea* isolates, they obtained 3276 independent measurements for 1164 unique genotype x genotype interactions, in the form of necrotic lesion areas.

Analysis of the variation captured by this high-power dataset showed predictably that lesion size was significantly and equally affected by tomato genotype and pathogen isolate. Surprisingly, however, the tomato domestication status was only associated with a small, albeit significant, increase in susceptibility to the pathogen. Crop domestication is widely regarded as decreasing resistance to (specialist) pathogens and reducing genetic diversity, in comparison to wild relatives. This is exemplified by lower phenotypic variation. In this study, however, such phenotypic bottlenecks were not observed. Although these unexpected findings may be peculiar to tomato-*B. cinerea*, it does raise questions about the contribution of human domestication *per se* to the virulence of generalist pathogens, and the applicability of the classic model of an evolutionally arms-race between plant and pathogen to a generalist species.

So, what then is the genetic basis for the observed variation in *B. cinerea* virulence on different tomato accessions? Specialist pathogens that infect a very narrow host range (often limited to a single species) frequently have only a handful of large-effect qualitative loci controlling virulence. In contrast, genome-wide association (GWA) mapping across the 97 isolates revealed that *B. cinerea* virulence on tomato is highly polygenic, with numerous small-effect single nucleotide polymorphisms (SNPs) associated with lesion area. This is directly akin to the polygenic basis of resistance in the host plant, as previously described by this group (Zhang et al., 2017). Crucially, few of these SNPs were found to be significantly linked to *B. cinerea* virulence on all of the tomato accessions, supporting the existence of host x pathogen genotypic interactions.

The GWA mapping enabled the identification of several hundred *B. cinerea* genes linked to differential resistance in tomato, including novel virulence candidates. Interestingly, detailed positional examination of the multiple SNPs within one of these genes (encoding a pectinesterase), revealed that most were located in upstream regulatory regions. This suggests that different *B. cinerea* isolates may deploy differential transcriptional regulation of downstream virulence-related mechanisms.

Although overall the contribution played by domestication was minor, two of the *B. cinerea* isolates exhibited significantly increased virulence on the domesticated tomato cultivars versus wild relatives. Utilising the available data for these isolates alone identified a subset of pathogen genes (mainly involved in enzymatic and transport functions), that are specifically linked to tomato domestication, and potentially to domestication of other plant host species too.

Taken together, the findings of Soltis and coworkers truly highlight the tenacity of *B. cinerea* as a plant pathogen! Different isolates of the generalist pathogen are capable of intermating meaning that the fungus has at its disposal a huge repertoire of polymorphic virulence loci allowing it to not only customise its virulence according to host genotype but also enabling it to rapidly adapt to any newly evolved plant defense mechanisms. And if this weren’t enough, *B. cinerea* additionally possesses the ability to shift to a new host niche. Thus, breeding durable resistance to *B. cinerea* in the field is extremely challenging and will likely require a genome-wide appreciation of virulence/resistance at the level of both the pathogen and the host.

**Emily Breeze**

**School of Life Sciences,**

**University of Warwick, Coventry, UK**

[**emily.breeze@warwick.ac.uk**](mailto:emily.breeze@warwick.ac.uk)

**ORCID ID: 0000-0001-5383-5448**

**REFERENCES**

**Elad, Y., Pertot, I., Cotes Prado, A.M., and Stewart, A.** (2015). Plant Hosts of *Botrytis* spp. In *Botrytis* – the Fungus, the Pathogen and its Management in Agricultural Systems (Springer International Publishing: Cham), pp. 413–486.

**Rowe, H.C. and Kliebenstein, D.J.** (2008). Complex Genetics Control Natural Variation in Arabidopsis thaliana Resistance to *Botrytis cinerea*. Genetics **180**: 2237–2250.

**Soltis, N.E., Atwell, S., Shi, G., Fordyce, R., Gwinner, R., Gao, D., Shafi, A., and Kliebenstein, D.J.** (2019). Interactions of tomato and *Botrytis* genetic diversity: Parsing the contributions of host differentiation, domestication and pathogen variation. The Plant Cell xxx

**Zhang, W., Corwin, J.A., Copeland, D., Feusier, J., Eshbaugh, R., Chen, F., Atwell, S., and Kliebenstein, D.J.** (2017). Plastic Transcriptomes Stabilize Immunity to Pathogen Diversity: The Jasmonic Acid and Salicylic Acid Networks within the Arabidopsis/ *Botrytis* Pathosystem. THE PLANT CELL ONLINE **29**: 2727–2752.

**Figure legend:**

***Botrytis cinerea* x tomato diversity.** Individual leaflets from 6 domesticated (*Solanum lycopersicum*) and 6 wild (*S. pimpinellifolium*) tomato accessions were inoculated with 97 *B. cinerea* isolates and lesion areas quantified. Domesticated tomato accessions exhibited decreased resistance over their wild relatives with 80% of the pathogen isolates being more virulent on domesticated tomato leaves.

*[Adapted from Soltis et al., (2019), Figures 1 and 3.]*

