

PREreview of bioRxiv article “A generalist pathogen view of diverse host evolutionary histories through polygenic virulence”

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Abstract

This is a review of Caseys et al. bioRxiv doi: <https://doi.org/10.1101/507491> posted on June 25, 2019. This study aims at addressing whether coevolutionary models of host-pathogen interactions apply to a generalist pathogen that exhibits quantitative virulence across a broad range of plants. They generated an exhaustive virulence matrix for the necrotrophic fungus *Botrytis cinerea* on 90 genotypes of 8 plant species. They conclude that this pathosystem doesn't fit traditional arms-race coevolution models with quantitative variation in susceptibility distinct from the phylogenetic relationships between the examined plants.

Main Comments

This study aims at addressing the important question of whether coevolutionary models of host-pathogen interactions apply to a generalist pathogen that exhibits quantitative virulence across a broad range of plants. They generated an exhaustive virulence matrix for the necrotrophic fungus *Botrytis cinerea* on 90 genotypes of 8 plant species. They conclude that this pathosystem doesn't fit traditional arms-race coevolution models with quantitative variation in susceptibility distinct from the phylogenetic relationships between the examined plants.

The paper reports interesting data and is framed around an evolutionary message. They draw strong conclusions about how the *Botrytis* pathosystem drastically differs from classic arms-race evolutionary models of plant-pathogen interactions. Although, I wouldn't be surprised that this fascinating and still poorly understood generalist fungus would display unique features, I'm not convinced that the evolutionary conclusions are justified based on the described experiments.

One issue is sampling. The majority of the isolates are from grapes, yet grapes are not tested as a host and the assays involve a mix of plant species and genotypes that may have never been exposed to the California grape population of the fungus. This is a serious experimental issue as the paper centers on coevolutionary arguments yet the dominant coevolutionary system in the sample collection (*B. cinerea* vs grape) is never tested.

A related point is that coevolutionary models of host-pathogen interactions imply coevolution at the level of local host/pathogen populations whereas the sampled fungus strains and host plants tested here are not supported by an ecological/biological rationale. In fact, besides the California grape isolates, the pathogen samples are from a global population and there is no evidence as far as I know that for example Arabidopsis is naturally infected by *B. cinerea*. Thus I do question whether evolutionary statements can be drawn from the studied pathogen/host collection in the absence of ecological or biological evidence of coevolution.

In addition, the inclusion of crop species is an issue as far as generating coevolutionary hypotheses. Does variation in genetic resistance in these crops reflect coevolutionary dynamics or is it an indirect consequence of crop domestication and breeding for other traits.

I'm also concerned about drawing general conclusions about strain host specificity as the coefficient of variation of mean lesion area across the plant species. First, this is based on single measurements and doesn't take into account other aspects of the infection cycle which may be more relevant to the coevolutionary dynamics. Second, averaging can be misleading given that specialization by definition means decreased virulence on alternative hosts. Thus the statement "strains with increased host specificity had on average lower virulence across all Eudicots" is neither surprising nor contradictory to theoretical expectations as stated. This is exactly what one would expect for typical specialist strains.

Another issue is the impact of these interactions on pathogen and plant fitness, which are important to appreciate before drawing evolutionary models. Although *B. cinerea* can indeed be a destructive pathogen in agricultural systems it is unclear to this reviewer how it impacts the fitness of its native host plants; and vice versa the extent to which this pathogen relies on plant infection for its reproduction (unlike say an obligate biotroph). To me this is a critical part of the comparison between *B. cinerea* and other pathogens/parasites that have unequivocal negative impact on their hosts and/or are dependent on their hosts leading to strong selection dynamics for resistance/virulence. In other words, strong selection pressures are an important aspect of the equation when weighing theoretical expectations for an arms race.

It is also important to point out that there are notable examples of pathogens that exhibit clear arms race dynamics and quantitative variation in virulence, but somehow infect phylogenetically unrelated plant species. These include *Phytophthora capsici* (pepper and cucurbits), *Phytophthora palmivora* (monocots and dicots), the multihost rust fungi and others. Even though these pathogens infect a phylogenetically discontinuous range of host plants, individual genotypes of their host species can exhibit classic strong genetic resistance. This context is important for the discussing the observation that variation in plant susceptibility does not track plant phylogeny.

Other comments

Figure 3 clearly shows that *C. endivia* has a distinct pattern of susceptibility compared to the other taxa. In fact, there is even a cluster of *B. cinerea* strains that seem more aggressive on *C. endivia* than on any of the other plants tested. Not sure how these observation fit with the conclusion about absence of connections between susceptibility vs plant phylogeny and the lack of specialization.

Reviewers

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