



## The pace of pathogens' adaptation to their host plants

Benoît Moury

UR407 Pathologie Végétale -- Montfavet, France

Correspondence to Benoît Moury ([benoit.moury@inra.fr](mailto:benoit.moury@inra.fr))

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**A recommendation – based on reviews by Benoît Moury and an anonymous reviewer – of**

Suffert F, Goyeau H, Sache I, Carpentier F, Gelisse S, Morais D, Delestre G. 2017.

**Epidemiological trade-off between intra- and interannual scales in the evolution of aggressiveness in a local plant pathogen population.** bioRxiv, 151068, ver. 3 of 12th November 2017. doi: [10.1101/151068](https://doi.org/10.1101/151068)

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Because of their shorter generation times and larger census population sizes, pathogens are usually ahead in the evolutionary race with their hosts. The risks linked to pathogen adaptation are still exacerbated in agronomy, where plant and animal populations are not freely evolving but depend on breeders and growers, and are usually highly genetically homogeneous. As a consequence, the speed of pathogen adaptation is crucial for agriculture sustainability. Unraveling the time scale required for pathogens' adaptation to their hosts would notably greatly improve our estimation of the risks of pathogen emergence, the efficiency of disease control strategies and the design of epidemiological surveillance schemes. However, the temporal scale of pathogen evolution has received much less attention than its spatial scale [1].

In their study of a wheat fungal disease, Suffert *et al.* [2] reached contrasting conclusions about the pathogen adaptation depending on the time scale (intra- or inter-annual) and on the host genotype (sympatric or allopatric) considered, questioning the experimental assessment of this important problem.

Suffert *et al.* [2] sampled two pairs of *Zymoseptoria tritici* (the causal agent of septoria leaf blotch) sub-populations in a bread wheat field plot, representing (i) isolates collected at the beginning or at the end of an epidemic in a single growing season (2009-2010 intra-annual sampling scale) and (ii) isolates collected from plant debris at the end of growing seasons in 2009 and in 2015 (inter-annual sampling scale). Then, they measured in controlled conditions two aggressiveness traits of the isolates of these four *Z. tritici* sub-populations, the latent period and the lesion size on leaves, on two wheat cultivars. One of the cultivars was considered as "sympatric" because it was at the source of the studied isolates and

was predominant in the growing area before the experiment, whereas the other cultivar was considered as "allopatric" since it replaced the previous one and became predominant in the growing area during the sampling period.

On the sympatric host, at the intra-annual scale, they observed a marginally-significant decrease in latent period and a significant decrease of the between-isolate variance for this trait, which are consistent with a selection of pathogen variants with an enhanced aggressiveness. In contrast, at the inter-annual scale, no difference in the mean or variance of aggressiveness trait values was observed on the sympatric host, suggesting a lack of pathogen adaptation. They interpreted the contrast between observations at the two time scales as the consequence of a trade-off for the pathogen between a gain of aggressiveness after several generations of asexual reproduction at the intra-annual scale and a decrease of the probability to reproduce sexually and to be transmitted from one growing season to the next. Indeed, at the end of the growing season, the most aggressive isolates are located on the upper leaves of plants, where the pathogen density and hence probably also the probability to reproduce sexually, is lower.

On the allopatric host, the conclusion about the pathogen stability at the inter-annual scale was somewhat different, since a significant increase in the mean lesion size was observed (isolates corresponding to the intra-annual scale were not checked on the allopatric host). This shows the possibility for the pathogen to evolve at the inter-annual scale, for a given aggressiveness trait and on a given host.

In conclusion, Suffert *et al.*'s [2] study emphasizes the importance of the experimental design in terms of sampling time scale and host genotype choice to analyze the pathogen adaptation to its host plants. It provides also an interesting scenario, at the crossroad of the pathogen's reproduction regime, niche partitioning and epidemiological processes, to interpret these contrasted results. Pathogen adaptation to plant cultivars with major-effect resistance genes is usually fast, including in the wheat-*Z. tritici* system [3]. Therefore, this study will be of great help for future studies on pathogen adaptation to plant partial resistance genes and on strategies of deployment of such resistance at the landscape scale.

## References

- [1] Penczykowski RM, Laine A-L and Koskella B. 2016. Understanding the ecology and evolution of host–parasite interactions across scales. *Evolutionary Applications*, 9: 37–52. doi: [10.1111/eva.12294](https://doi.org/10.1111/eva.12294)
- [2] Suffert F, Goyeau H, Sache I, Carpentier F, Gelisse S, Morais D and Delestre G. 2017. Epidemiological trade-off between intra- and interannual scales in the evolution of aggressiveness in a local plant pathogen population. *bioRxiv*, 151068, ver. 3 of 12th November 2017. doi: [10.1101/151068](https://doi.org/10.1101/151068)
- [3] Brown JKM, Chartrain L, Lasserre-Zuber P and Saintenac C. 2015. Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. *Fungal Genetics and Biology*, 79: 33–41. doi: [10.1016/j.fgb.2015.04.017](https://doi.org/10.1016/j.fgb.2015.04.017)

## Appendix

Reviews by Benoît Moury and an anonymous referee: <http://dx.doi.org/10.24072/pci.evolbiol.100039>