New Phytologist

Forum

Commentary

What a wild plant pathosystem reveals about local adaptation between hosts and pathogens and the implications for cultivated plant pathosystems under climate change

Local adaptation applied to phytopathology is evidenced by a higher mean fitness of plant pathogens – practically, a higher infectivity – on local hosts than on foreign hosts, or by a higher mean fitness of local pathogens than foreign pathogens on local hosts (Kaltz & Shykoff, 1998). Fungal pathogens are generally considered to locally adapt to host plant populations, and host plants also locally adapt to the pathogen population, while both partners adapt to local abiotic conditions, particularly climate. As a result, both partners may evolve local adaptations to each other within their particular environment, yielding lower infection rates in co-evolved populations if hosts are locally adapted or higher infection rates if pathogens are locally adapted (Gandon, 2002). This dynamic results in complex patterns within wild plant pathosystems (WPP), which are the focus of extensive research in functional ecology. Although the principles and mechanisms examined in this context may manifest differently in crop plant pathosystems (CPP) studied by phytopathologists and agronomists, understanding them remains crucial for developing effective disease management strategies at the scale of entire agroecosystems, which encompass both cultivated and uncultivated compartments that are increasingly recognised as interacting (Lebeda & Burdon, 2023).

> *'. . . crop plant pathosystems often exhibit a type of co-evolution in which pathogens tend to dominate, prompting humans to frequently shift varieties or management practices instead of seeking long-term ecological balance.'*

In the article 'Local adaptation of both plant and pathogen: an arms-race compromise in switchgrass rust' recently published in *New Phytologist*, VanWallendael *et al.* (2025; doi: 10.1111/nph.70313) examined the local adaptation of switchgrass (*Panicum virgatum*) and its leaf rust pathogen (*Puccinia novopanici*) along a latitudinal gradient in North America. Both host and pathogen exhibit local adaptation: the host to environmental conditions and the pathogen to host populations. To show this, the authors relied on a replicated multiyear 'host reciprocal transplant' experimental design – an original framework where the biotic environment (the host) is transplanted rather than the adapting pathogen population – and conducted a comprehensive body of associated analyses. This framework is derived from the classic ecological concept of 'common gardens', which, when applied to WPP or CPP, typically involves transplanting pathogens to different host populations, either in the field or under controlled laboratory conditions (Kawecki & Ebert, 2004). Switchgrass genotypes were moved between ecoregions, each having its own endemic rust population, avoiding the common pitfalls of pathogen local adaptation research and retaining essential local biotic and abiotic contexts. VanWallendael *et al.* (2025) found evidence of pathogen local adaptation, as sufficiently differentiated field conditions and pathogen populations across sites led to observable differences in infectivity. The *P. virgatum*–*P. novopanici* system appears particularly well-suited for studies of pathogen–host co-adaptation because switchgrass is consistently infected by rust, and the genetic diversity of the pathogen is structured into distinct populations that correspond to host ecotypes locally adapted to different ecoregions. The host plant itself varies not only in terms of rust resistance (VanWallendael *et al.*, 2020) but also in tolerance to abiotic factors, such as cold.

Initially, there was little evidence to suggest that a 'host transplantation' strategy could be effective, but the experimental design used was particularly well conceived. Laine (2007) was among the first evolutionary ecologists to provide a comparative analysis of host vs pathogen transplantation under controlled conditions in a specific WPP model, the *Podosphaera plantaginis*–*Plantago lanceolata* system, and found that pathogen transplantation was the most conclusive. Field studies often lack the sensitivity to detect average population infectivity in interactions governed by strain-specific resistance. Furthermore, because pathogen transmission potential can be influenced by abiotic factors and genotype-by-environment interactions, it has been suggested that studies in controlled conditions aimed at detecting local adaptation in pathogens should incorporate relevant environmental variation. Laine (2007) questioned the reliability of 'aggressiveness' as a trait for detecting local adaptation. Although it is theoretically a good indicator, the proxies used to estimate it can differ depending on whether the experimental study is conducted in the field or under controlled conditions. For example, in field studies, aggressiveness may be measured as disease 'incidence' – the proportion of infected leaves per individual – whereas in controlled conditions it is often assessed using disease 'severity' indices, such as the percentage of

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leaf area covered by symptoms, sometimes accounting for spore production and thus transmission potential. The latter measure approaches the ecological concept of fitness. Choosing the appropriate metric remains a challenge for plant disease epidemiologists, as it is highly pathosystem-specific and shaped by the experimental context of the study. VanWallendael *et al.* (2025) measured rust severity by incorporating temporal disease dynamics using the area under the disease progress curve metric, which is a well-established and robust approach. Moreover, the authors addressed the sources of bias in disease severity ratings, which varied across years and among assessors at different sites, by using best linear unbiased predictions (BLUPs), a method employed in linear mixed models to estimate random effects. BLUPs were calculated for each genotype and subsequently used as phenotypic inputs to test for local adaptation and to perform genome-wide association studies (GWAS).

VanWallendael *et al.* (2025) elegantly used previous knowledge on the local adaptation of switchgrass to northern and southern climatic regions of the United States (VanWallendael *et al.*, 2020, 2022) as well as a detailed study of the genetic structuring of the *P. novopanici* population to detect local adaptation of the pathogen to its host and to identify the underlying genetic architecture of resistance by GWAS. Rust populations differ between the northern and southern regions and are locally adapted to northern and southern switchgrass populations. A genome scan of nucleotide diversity identified several genomic regions associated with this adaptation, potentially indicating loci involved in local adaptation to the host or abiotic factors. To disentangle biotic from abiotic factors, one approach could be to use bioclimatic variables from sampling sites as proxies for unmeasured phenotypes in genotype–environment association analyses, aiming to detect loci specifically associated with variation in these climatic variables (e.g. Alvarado *et al.*, 2022; Lasky *et al.*, 2023; Feurtey *et al.*, 2023). VanWallendael *et al.* (2025) revealed a polygenic basis of resistance in both northern and southern switchgrass populations, with few shared resistance loci, as indicated by the lack of overlap among the top SNPs identified by GWAS in the two regions. These results suggest that both the host and pathogen are adapted to each other and that they are locally adapted to their abiotic environment. Selective pressures from biotic and abiotic factors acting on hosts and pathogens clearly influence one another and shape the genetic architecture of resistance in the host and pathogenicity in the pathogen. It is worth noting the emerging use of the co-genome-wide association study (co-GWAS or joint-GWAS) approach, which enables the identification of interconnected genomic regions in both the pathogen and host (Märkle *et al.*, 2021), offering significant potential for uncovering signatures of co-adaptation.

The current challenge for research on CPP lies in deciphering the adaptation of pathogen populations to interconnected pressures of selection, including host plant resistance and a changing climate, particularly high temperatures and humidity (Romero *et al.*, 2022). Crop varieties are bred to perform optimally within specific ecoregions, but they are typically much more genetically uniform, deployed over larger spatial scales, and cultivated for shorter periods than wild plant populations. Crucially, it is not possible to define a zone of origin or local environment for varieties bred by crossing lines with often highly diverse origins. Genetically heterogeneous landraces can be assigned an intermediate status between WPP and CPP, making them particularly relevant in the context of adaptation studies. However, these studies may be constrained by tightly managed disease pressures or, in some cases, by the absence of disease altogether. Thus, upon reading the article by VanWallendael *et al.* (2025), phytopathologists working on CPP might wonder whether host transplant experiments could shed light on adaptive dynamics with practical implications for managing diseases in widely cultivated crops under changing climatic conditions. Although plant pathogens are expected to become locally adapted (Gandon & Michalakis, 2002), a key difference between CPP and WPP is that host species and varieties in conventional agrosystems change rapidly. This frequent turnover can lead to a lack of strong spatial or temporal genetic structure in some pathogen populations, particularly in cereal rusts, where long-distance migration plays a major role (Hovmøller *et al.*, 2023), preventing the establishment of stable, dynamic interactions (Burdon & Laine, 2019). The large-scale deployment of selected crop varieties can be likened to abrupt and short-lived transplants, lacking coevolution and often replaced within a few years. For interactions governed by strain-specific resistance, standard field transplant experiments may lack the sensitivity to detect the average virulence or aggressiveness of local pathogen populations, especially when rapid evolutionary changes are driven by shifting resistance gene pressures (e.g. Fontyn *et al.*, 2022). However, the host transplantation approach could be valuable in certain situations, particularly where local varieties (especially genetically heterogeneous landraces) have been cultivated over long periods and where pathogen populations are stable (e.g. Ali *et al.*, 2021). Perennial crops, such as fruit trees, coffee, and grapevines, may also offer favourable conditions for such investigations, as they allow for the possibility of long-term coevolution (e.g. Rodrigues *et al.*, 2022). Interestingly, in cases involving strong interactions between wild and cultivated compartments, such as the involvement of alternate hosts, as in rusts (e.g. *Puccinia graminis*; Rodriguez-Algaba *et al.*, 2022), or alternative hosts that act as reservoirs (e.g. *Claviceps purpurea*; Douhan *et al.*, 2008), host reciprocal transplant could help test the local adaptation of the pathogen population to these secondary hosts. When possible, host transplantation should be preferred over pathogen transplantation (i.e. field inoculation with 'exotic strains'). Transplanting host plants typically poses fewer regulatory, ethical, and experimental complications than transplanting pathogens, for example, by allowing contamination of a trial with a local inoculum, avoiding the need to consider the reduction of local pathogen population complexity, or to apply the inoculum manually when disease pressure is naturally high. Moreover, for many obligate biotrophic pathogens that cannot be cultured outside their hosts, direct transplantation is particularly challenging.

In conclusion, VanWallendael *et al.* (2025) showed that the coevolutionary arms race between switchgrass and its leaf rust pathogen did not result in a clear winner. This can be interpreted as a form of equilibrium that may be characteristic of the WPP. By contrast, CPP often exhibit a type of coevolution in which pathogens tend to dominate, prompting humans to frequently shift varieties or management practices instead of seeking long-term ecological balance. Disease management in agroecosystems could benefit from studies like that of VanWallendael *et al.* (2025) from both a conceptual and methodological standpoint. The primary objective was to determine whether the local context has a greater influence on parasite infectivity or host susceptibility. Plant pathologists interested in such questions are encouraged to engage with the WPP community, which held its fourth conference in 2024 (https://wildplantpath.net/).

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