

Non-agricultural reservoirs contribute to emergence and evolution of crop pathogens

Where do new variants of plant pathogens come from? For the past 60 years, the concept of gene-for-gene co-evolution of plants and pathogens has been the predominant framework for understanding the emergence new plant pathogens. This concept describes a process of natural selection that leads to changes in population structure of the pathogen. However, a missing element in this concept of emergence is how the diversity - on which natural selection operates - arises. Random mutations, horizontal gene transfer, and recombination clearly mold the genomes of plant pathogens to various degrees. However, the relative importance of these processes for plant pathogens and where and when they occur are most often unknown.



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A recent paper in *New Phytologist* (2), by researchers from INRA in Avignon, Virginia Tech in the US and the University of Exeter in the UK, provides the first clear illustration that non-agricultural habitats are reservoirs of strains of potential pathogens that accumulate and recombine genes for a wide range of effectors (traits that allow bacteria to disarm the defense mechanisms of the plant).

In the example presented in this work, close relatives of epidemic strains of the tomato pathogen *Pseudomonas syringae* pv. tomato (*Pto*) were found in snowpack and streams in sub-alpine regions of the southern French Alps and in pristine regions of New Zealand's South Island. *Pto*-relatives in the non-agricultural habitats were pathogenic on tomato in laboratory tests but also had wider host ranges than *Pto* strains from disease epidemics. Although the strains from non-agricultural habitats had effector repertoires that were similar to *Pto* strains from disease epidemics, they had a remarkably greater variability in the combinations of alleles of the effector genes and revealed recombination.

The authors speculate that a series of stochastic events leads to the encounter of a given environmental strain with cultivated plants and to its eventual emergence in disease epidemics. *P. syringae* is readily spread among different habitats by wind, streamflow and rainfall, hence there are likely to be regular encounters of which a few occasionally lead to significant bacterial multiplication. Agricultural practices favor further spread of the emerging population.

Authors of a commentary in the same issue of *New Phytologist* (1) propose that the role of non-agricultural habitats as reservoirs and bastions of diversification is not unique to *P. syringae*. These authors reiterate previous calls to expand our knowledge of the life history and ecology of plant pathogens as a means to understand pathogen emergence (4, 6).

The strains of *P. syringae* used for this study came from the collection maintained at the Plant Pathology Research Unit of INRA in Avignon. Over the past decade, this collection has been set-up to allow comparison of populations from crops and natural habitats, leading to the discovery that aquatic habitats and the whole of the water cycle play important roles in the evolution and ecology of this bacterium (3, 5, 7). The *Pto*-like strains from environmental habitats were chosen from the 1600 strains for which the phylogenetic situation has been identified among the 7000 strains in the collection. The collection is now being used to evaluate the potential of emergence of new variants of bacterial canker of kiwi and will be used to obtain insight into emergence of other important diseases caused by *P. syringae* such as apricot canker and cantaloupe blight.

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