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Insights into the evolutionary history of the plant pathogen *Pseudomonas syringae* from its biogeography in river headwaters

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The discovery of the abundance of *Pseudomonas syringae* in substrates associated with the water cycle, in particular alpine rivers and lakes, has provided the occasion to explore the ecology of this plant pathogen in contexts where a crop host is not apparently exerting a selection pressure. From a study of the biogeographical relationships of *P. syringae* in river headwaters upstream from agricultural regions on three continents, we have obtained unique insight into the evolutionary history of this bacterium. A collection of 236 strains from 11 sites in the USA, in France and in New Zealand was characterized for genetic diversity based on housekeeping gene sequences and for phenotypic diversity based on pathogenicity and ice nucleation activity. Water harbored several new genetic clades not previously observed among strains from crops. Populations on all continents were dominated by a few haplotypes and hence population structure was not significantly influenced by geographic location. However up to 70% of the haplotypes in the populations on each continent were unique to each site. Comparison with 87 strains from crops revealed that the metapopulation of *P. syringae* is structured into three genetic ecotypes: a crop-specific type, a water-specific type, and an abundant ecotype found in both habitats. Aggressiveness of strains was significantly and positively correlated with ice nucleation activity. Furthermore, the ubiquitous genotypes were the most aggressive on average. This work reveals that there is considerable exchange of populations between freshwater and agricultural habitats and that the former contribute considerably to the diversification of *P. syringae*.

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