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AN ARCHETYPICAL EPIPHYTE IN THE HYDROSPHERE: BIOGEOGRAPHY OF *PSEUDOMONAS SYRINGAE* IN RIVER SOURCE WATERS.

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Over the past few years there has been an explosion of interest in the interaction of air-borne micro-organisms with atmospheric processes. This interest has been founded on the unique capacity of a few micro-organisms such as *P. syringae* to catalyze the freezing of super-cooled water at temperatures warmer than those of the numerically dominant mineral-based ice nucleators in the atmosphere. Furthermore, *P. syringae* has been detected by several authors in clouds and has recently been shown to be prevalent in niches and substrates associated with the water cycle. As will be illustrated in the presentation at this meeting by P. Amato, the important contribution of the phyllosphere microbial community to the composition of aerosols – both in terms of numbers and functional groups – is that it opens novel research questions on a range of impacts that plant canopies can have on climate processes.

In light on the potential link that *P. syringae* has with the water cycle – as a participant and possibly as a critical player – we explored its biogeography as if it were principally an aquatic bacterium rather than an epiphyte. 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 or wild plants. 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 suggesting a role for endemism. 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 (found in all substrates investigated in this and other studies) 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*. Furthermore, given the overall abundance and genetic diversity of *P. syringae* outside of its association with diseased plants, it could be argued that pathogenicity *per se* has a relatively minor role in the fitness of this species and hence in its overall life history.