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RESEARCH ARTICLE

Inferring the Evolutionary History of the Plant Pathogen *Pseudomonas syringae* from Its Biogeography in Headwaters of Rivers in North America, Europe, and New Zealand

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ABSTRACT Nonhost environmental reservoirs of pathogens play key roles in their evolutionary ecology and in particular in the evolution of pathogenicity. In light of recent reports of the plant pathogen *Pseudomonas syringae* in pristine waters outside agricultural regions and its dissemination via the water cycle, we have examined the genetic and phenotypic diversity, population structure, and biogeography of *P. syringae* from headwaters of rivers on three continents and their phylogenetic relationship to strains from crops. A collection of 236 strains from 11 sites in the United States, in France, and in New Zealand was characterized for genetic diversity based on housekeeping gene sequences and for phenotypic diversity based on measures of pathogenicity and ice nucleation activity. Phylogenetic analyses revealed several new genetic clades from water. The genetic structure of *P. syringae* populations was not influenced by geographic location or water chemistry, whereas the phenotypic structure was affected by these parameters. Comparison with 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. The abundance and diversity in water relative to crops suggest that adaptation to the freshwater habitat has played a nonnegligible role in the evolutionary history of *P. syringae*. We discuss how adaptation to the water cycle is linked to the epidemiological success of this plant pathogen.

IMPORTANCE Many pathogens have life cycles that involve survival and multiplication in nonhost environmental habitats. For human pathogens, numerous studies have revealed how adaptation to environmental habitats is linked to the evolution of their pathogenicity and emergence of pathogens. For plant pathogens, the link between adaptation to nonhost habitats and pathogenicity has not been explored. Here we have examined the genetic and phenotypic diversity of the plant pathogen *Pseudomonas syringae* in headwaters of rivers on three continents and compared it to that of strains from crops. This model pathogen was chosen because it is widely abundant in habitats associated with the water cycle and in particular in pristine waters outside agricultural regions. This work reveals that there is considerable exchange of populations between freshwater and agricultural habitats and that those in the former contribute considerably to the diversification of *P. syringae*.

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There is mounting evidence that the ecology of pathogens in their nonhost environmental reservoirs can have a significant impact on their ability to cause disease in their hosts. This has been demonstrated for human pathogens, such as *Vibrio cholerae*, with a marked capacity to survive and proliferate in environmental reservoirs (1, 2). Other examples include *Legionella pneumophila* (3), *Pseudomonas aeruginosa* (4), the *Burkholderia cepacia* complex (5), and *Cryptococcus neoformans* (6). Environmental reservoirs play three key roles in the evolutionary ecology of these pathogens (7). First, survival and proliferation in environmental reservoirs ensure a competitive advantage in the absence of the host. Second, genes for virulence factors can be acquired in these reservoirs. Third, some virulence factors also have roles in adaptation to the conditions of the environmental reservoirs and are

thereby positively selected in the reservoirs in the absence of interaction with the primary host. In the quest to elucidate the foundation of parasitic fitness, this emerging insight has oriented research toward questions concerning the basis of adaptability to the environment—in complement to questions about specialization to the host (5).

For plant pathogens, there has been relatively little investigation of the impact of their ecology in environmental (nonagricultural) reservoirs on parasitic fitness. Although environmental reservoirs of many plant pathogens are known, they have been ignored in studies of the evolution of parasitic fitness—which have been almost exclusively agrocentric (7). For example, we have very little perspective on the relative genetic diversity of plant pathogens in environmental versus agricultural habitats, whereas

TABLE 1 Origins of strains of *P. syringae* from water and characteristics of the water sampled

Country, region, date, and stream	Latitude, longitude (altitude [m])	Site code	Conductivity (μ S)	Population density (log CFU/liter)		Strain codes
				<i>P. syringae</i>	Total mesophilic bacteria	
France, Alpes-de-Haute-Provence County						
3 April 2007						
Sauze, east branch	44°20'40"N, 6°40'54"E (2,100)	10.1	522	4.30	7.25	SZ002—SZ030
Sauze, west branch	44°20'40"N, 6°40'48"E (2,100)	11.1	1,105	3.00	7.30	SZ031—SZ054
31 May 2007						
Sauze, east branch	44°20'40"N, 6°40'54"E (2,100)	10.2	339	2.16	5.55	SZ085—SZ113
Sauze, west branch	44°20'40"N, 6°40'48"E (2,100)	11.2	352	1.56	5.62	SZ115—SZ125
Sauze, source	44°20'11"N, 6°40'15"E (2,500)	12	232	1.85	5.51	SZ127—SZ145
France, Hautes-Alpes County, 31 May 2007, Rioul Mounal, source	44°32'09"N, 6°42'12"E (2,100)	0	102	1.83	6.79	UB410—UB429
France, Lozère County, 23 April 2007, Tarn, near source	44°22'44"N, 3°47'41"E (1,300)	21	20	2.65	7.24	TA001—TA022
France, Aveyron County, 24 April 2007, Viaur, near source	44°15'35"N, 2°59'10"E (900)	22	87	3.03	6.82	Vi003—Vi024
United States, Park County, MT, 12 August 2007, Pine Creek	45°29'15"N, 110°30'00" W (1,865)	33	68	2.75	5.84	USA001—USA019
United States, Grand Teton National Park, WY, 14 August 2007						
Pilgrim Creek	43°55'42"N, 110°33'42"W (2,140)	37	200	2.69	6.82	USA087—USA108
Cascade Creek	43°45'54"N, 110°45'00" W (2,200)	40	43	2.84	6.32	USA031—USA053
New Zealand, Central Otago, South Island, 16 November 2007, Schoolhouse Creek						
	45°12'05.14"S, 168°59'09"E (677)	42	1.42	3.45	5.81	AI001—AI134
4 March 2009, Commissioners Creek	45°14'50.41"S, 168°55'53"E (800)	43	1.49	4.03	5.92	AL005—AL039

for human pathogens such as *V. cholerae*, autochthonous environmental isolates are known to have more extensive genetic diversity than strains from clinical contexts, which tend to be primarily clonal (8). Similarly, the genotypes of strains of *P. aeruginosa* in open oceans are, surprisingly, distinct from those from all other habitats of this bacterium (9). Furthermore, we have no clear sense of the biogeographic distribution of plant pathogens in environmental habitats. For *V. cholerae*, it is known that the distribution of genotypes in water is markedly influenced by temperature and the extent of eutrophication (8). For both *V. cholerae* and *P. aeruginosa*, geographic location in ocean waters relative to the coast has a notable influence on the genetic structure of their populations (10, 11). In contrast, environmental and clinical strains of *Legionella* spp. manifest similar degrees of genetic diversity and the distribution of these genotypes does not have an obvious geographic pattern (12).

The plant pathogen *Pseudomonas syringae* is emerging as an opportune model for exploring ecology in environmental habitats. Our recent discovery of its abundance in substrates associated with the water cycle, and in particular its frequent presence in alpine rivers and lakes (13), provides a unique occasion to characterize this unknown diversity. The objectives of this work were to determine the genetic diversity and major phenotypic properties (pathogenicity and ice nucleation activity) of populations of *P. syringae* in river headwaters—upstream from agricultural regions on three continents—and to evaluate the biogeographical

relationships among these populations and their relatedness to strains collected from disease epidemics. Via this approach, we attempted to gain novel insight into the evolutionary history of this bacterium that might not be perceived from studies of its direct relationship with crops.

RESULTS

***P. syringae* is ubiquitous in river source waters.** *P. syringae* was detected at concentrations of ca. 50 to 10⁴ CFU/liter in rivers at all 11 sites sampled and constituted generally less than 10⁻³ of the total cultural bacteria in these water samples (Table 1). All of the strains characterized here had phenotypic traits compatible with *P. syringae* (production of a fluorescent pigment and absence of cytochrome *c* oxidase and arginine dihydrolase). Genotyping confirmed this identification as indicated below. Ninety-six percent of the strains also induced a hypersensitive response (HR) in tobacco. The rivers in this study represent sources of irrigation water in southeastern and southwestern France, in the northwestern United States, and in southern New Zealand. These data complement previous observations of *P. syringae* in river source waters in other geographic regions, viz, the Po River in Italy (13). These population density values are probably underestimates in that they do not account for variants of *P. syringae* that cannot grow on the culture medium used here.

TABLE 2 Genetic variability within and between clades of *P. syringae*^a

Clade ^b	No. of strains	Mean variability within clade	Mean variability between clades												
			Group 1	Group 2a	Group 2b	Group 3	Group 4	SZ030	USA102	TA003	TA002	CC1524			
Group 1	16	1.45													
Group 2a	23	0.79	8.71												
Group 2b	38	0.92	9.13	2.81											
Group 3	6	1.20	7.85	5.96	6.62										
Group 4	3	0.18	8.45	8.44	8.69	8.16									
SZ030	7	1.03	8.98	3.53	3.71	6.46	8.63								
USA102	3	1.61	9.75	9.46	9.61	9.22	8.16	9.80							
TA003	4	1.25	10.08	9.78	9.78	9.72	9.89	9.69	2.99						
TA002	4	2.3	10.00	10.52	10.96	9.85	9.82	10.51	10.53	10.67					
CC1524	6	1.01	10.74	11.20	11.67	10.73	11.68	11.46	11.19	11.53	7.37				
UB246	2	0.60	13.74	13.89	14.17	14.13	14.88	14.07	13.02	13.78	14.28	14.21			

^a Variability is expressed as the percent difference in the 1,885-base-long concatenated partial sequences of the *cts*, *gapA*, *gyrB*, and *rpoD* genes.

^b Clades refer to branches on the phylogenetic tree in Fig. 1.

Strains of *P. syringae* from rivers represent clades that have not been detected previously. The phylogenetic trees resulting

from the neighbor-joining approach and from the maximum-likelihood approach were strictly identical in terms of the grouping of strains and their placement in the trees. Results here refer to the phylogeny based on the neighbor-joining approach.

Clades of *P. syringae* were differentiated based on phylogenetic analysis of 1,885 bp of concatenated *cts*, *gapA*, *gyrB*, and *rpoD* gene sequences (Fig. 1) such that the maximum genetic difference between strains in a single clade was not greater than 2.3%. This criterion is consistent with the genetic variability in previously described clades of *P. syringae* (groups 1 to 5) (47, 63) and places the reference strains in the expected clades. Based on this criterion, strains in group 2 could be differentiated into two clades, with each clade having less than 1% genetic variation within it and with a mean genetic distance of 2.8% between clades (Fig. 1). Otherwise, each clade was more than 3.5% different from the other clades (Table 2). In water, nine clades that have not been previously described were identified (the USA102 clade, the TA003 clade, the TA002 clade, the CC1524 clade, the UB246 clade, and four clades that were represented by only one strain each, i.e., UB370, USA032, TA020, and TA006). Twenty-three strains used for phylogenetic analyses fell into these nine clades. Among these, 74% induced an HR in tobacco. Strains that did not induce an HR in tobacco included three of four strains in the TA002 clade, one strain in the CC1524 clade, and both strains in the UB246 clade.

Interestingly, several identical concatenated sequence types were identified among the strains for which the four genes were sequenced. Strains CC0457 (isolated from diseased cantaloupe during an epidemic of bacterial blight near Avignon, France, in 2003) and AI116 (from water at site 42 in New Zealand) had identical concatenated sequences. Strains USA001 (from water at site 33 in the United States), USA109 (from water at site 37 in the United States), and CC1429 (isolated from an epilithic biofilm at site 33 in the United States in 2004) (15) also had identical concatenated sequences.

The *P. syringae* metapopulation is composed of three ecotypes: water strains, crop strains, and ubiquitous strains. Further analyses of the structure of populations from water and from crops were based on the sequences of the *cts* gene only. When the phylogeny based on four housekeeping genes described above was compared to a tree constructed based solely on the sequence of the *cts* gene, strains were clustered identically. The use of the *gyrB*, *rpoD*, and *gapA* sequences in addition to that of *cts* led to the

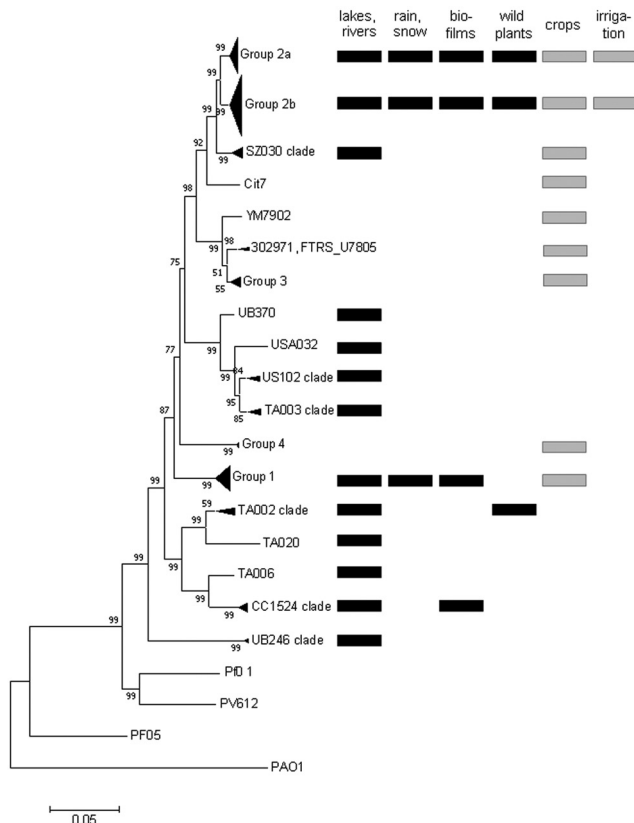


FIG 1 Neighbor-joining phylogenetic tree constructed on the basis of the concatenated sequences of the four housekeeping gene fragments *gapA*, *cts*, *gyrB*, and *rpoD* (1,885 bases) for 120 strains of *P. syringae* and 4 strains of similar species (*P. viridiflava*, *P. fluorescens*, and *P. aeruginosa*). The tree was rooted on *P. aeruginosa* PAO1. Bootstrap scores are indicated at each node, and a ruler for 5% dissimilarity of the concatenated sequences is presented below the tree. Names of branches indicated as groups correspond to the genomic groups reported previously (47, 63). Names of branches indicated as clades correspond to genomic groups not reported previously. For the part of the tree containing *P. syringae* strains, the substrates from which the strains on each branch were isolated are indicated. Substrates collected in nonagricultural environments are indicated by black rectangles, and those from agricultural environments are indicated by gray rectangles.

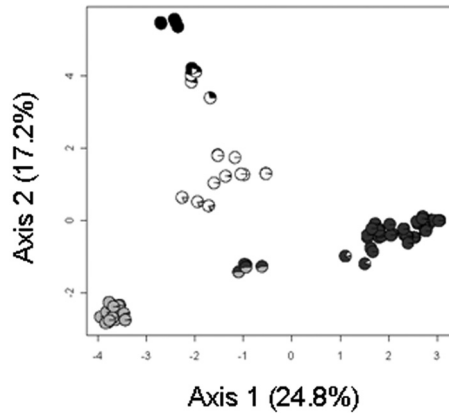


FIG 2 PCA performed on 88 haplotypes of *P. syringae*, followed by a non-hierarchical classification with clustering based on Ward's method. For each strain, the probability of assignment to each of the four clusters obtained with the STRUCTURE software is reported on the PCA using a pie chart legend as follows: cluster 1, black; cluster 2, white; cluster 3, light gray; cluster 4, dark gray.

placement of strains UB370, TA006, and TA020 into clades that were distinct from their neighbors. Otherwise, all of the clades in both trees were identical. Hence, we used the *cts* sequences only, thereby allowing us to incorporate more strains into the subsequent analyses.

Haplotypes of the *cts* sequences of 236 strains from water were compared to those of 87 strains from epidemics by exploiting, for the latter, sequences available in public databases and those for some crop strains in our collection. The 323 strains split into 88 unique haplotypes (G/N [genetic richness, i.e., the total number of multilocus genotypes, G , divided by the total number of samples, N] = 0.37), 44 of which were represented by a single strain, and the dominant haplotype was represented by 54 strains. Of the 88 haplotypes analyzed, 21 represented strains from crops only, 59 represented strains from water only, and 8 represented strains from water and crops. To separate haplotypes into homogeneous groups, clustering was performed with STRUCTURE for 1 to 11 clusters (K). Two optimal numbers of clusters were identified, $k = 2$ and $k = 4$, based on the ΔK statistic of Evanno et al. (16). A subsequent principal-component analysis (PCA), followed by clustering based on Ward's method, revealed four clusters of *P. syringae* strains (Fig. 2). Axes 1 and 2 of the PCA accounted, respectively, for 24.8% and 17.2% of the total genetic variability. The clusters discriminated by multivariate analysis were in perfect agreement with the clusters inferred by using the Bayesian clustering algorithm with $k = 4$ (Fig. 2). Assuming a threshold of $Q > 0.8$ for assignment to a cluster, about 88% of the distinct haplotypes clearly belonged to only one cluster, indicating that the four clusters were highly divergent.

Clusters 2, 3, and 4 were composed of haplotypes representing strains from water and from crops (Fig. 3). Seven haplotypes that had equal probabilities of belonging to cluster 3 and cluster 4 represented strains from crops. Haplotypes in cluster 1, or that were equally likely to belong to clusters 1 and 2, represented strains from water only. Three of the strains in cluster 1 were also included in the phylogenetic analysis presented above. These strains all belonged to the CC1524 clade (Fig. 1). Likewise, the relationship between clades and the other clusters could be determined based on strains used in both the phylogenetic and cluster

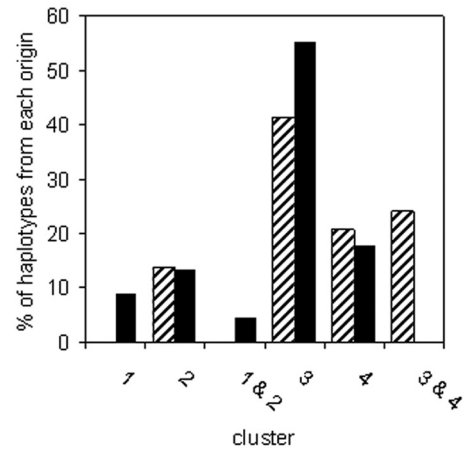


FIG 3 Distribution of *cts* haplotypes of *P. syringae* into four genetic clusters inferred with the Bayesian clustering algorithm of the STRUCTURE software. The frequency of haplotypes assigned to each of the clusters is indicated for haplotypes of strains from crops (hatched bars) and of strains from water (solid black bars). Of the 88 haplotypes analyzed, 78 were assigned to clusters with probabilities of inferred ancestry between 0.70 and 0.99. Three haplotypes were assigned at equal probabilities (ca. 0.50) to clusters 1 and 2, and seven haplotypes were assigned at equal probabilities to clusters 3 and 4.

analyses. Cluster 2 was composed of strain USA032 and strains in the USA102 and TA003 clades but also included strain SZ131 in the UB246 clade. Cluster 3 was composed of strains in groups 2a and 2b and the SZ030 clade. Cluster 4 was composed of strains in group 1. Strains that had equal probabilities of being in cluster 3 and cluster 4 were in group 3. Strain TA020 and strains in the TA002 clade had equal probabilities of being in cluster 1 and cluster 2.

Results of both clustering and phylogenetic analyses were coherent in terms of the co-occurrence and separation of genetic groups of *P. syringae* between water and crops. Water harbored genotypes not found among the strains from crops analyzed here. These genotypes corresponded to cluster 1 haplotypes: the CC1524 and TA002 clades and strain TA020 (Fig. 1). Furthermore, phylogenetic analysis based on all four housekeeping gene sequences indicated that crop strains in cluster 2 were not part of the USA102, TA003, and UB246 clades, even though they had similar *cts* sequences. Hence, the latter three clades contained no representatives from crops. Among these five clades, the CC1524 and TA002 clades harbored strains from other nonagricultural substrates (Fig. 1). Likewise, crops harbored a genotype not detected among the water strains: group 3, which comprises reference strain 1448A. Strains in groups 1, 2a, and 2b were found in water and in crops. These clades were widespread among numerous substrates, and groups 2a and 2b, in particular, were detected in all of the substrates from which isolations have been made in this and previous studies (13, 15).

The genetic structure of *P. syringae* populations in water is not markedly influenced by geographic location. The partial *cts* sequences of the 236 strains from water analyzed here revealed 67 haplotypes. For each of the three major regions where water was sampled (France, the United States, and New Zealand), 40 to 70% of the combined samples from that region constituted haplotypes specific to the region and 13 to 27% was composed of haplotypes shared by all three major regions (Fig. 4). Overall, not more than

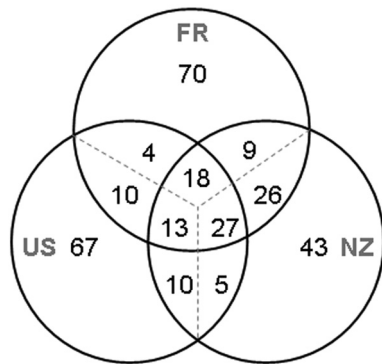


FIG 4 Frequency of haplotypes of *P. syringae* from water unique to the region sampled (France [FR], New Zealand [NZ], or the United States [US]) and in common between and among these regions. Frequency is expressed as the percentage of the total number of strains in the pooled samples from each region. Haplotypes were identified in terms of partial sequences of the *cts* gene.

50% of the haplotypes collected in each region were also found elsewhere. Nevertheless, F_{ST} analyses of the interaction of genetic population structure and geography revealed few significant differences among sites (Fig. 5). With the exception of the populations at site 43 and at the second sampling date for site 10 (31 May 2007), all populations were similar to at least one other population (within or across regions), in terms of the relative proportions of the different haplotypes and their overall genetic relatedness. The significant differences observed between the two samples at site 10 were due to loss of diversity in the sample obtained on the second

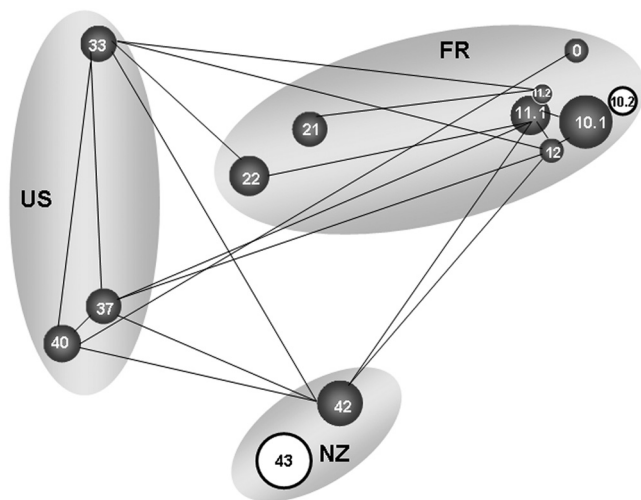


FIG 5 Genetic similarity of populations of *P. syringae*, based on partial sequences of the *cts* gene, in terms of the sites and dates of isolation from water. Populations are represented by circles whose size is proportional to the relative concentration of the *P. syringae* population (number of bacteria per liter) in the waters that were sampled. The numbers in the circles correspond to the sampling sites listed in Table 1. The regional origins of samples are indicated by the gray ovals (US, United States; FR, France; NZ, New Zealand). Within the U.S. and France regions, the physical distance between populations shown is roughly proportional to their real geographic distance. The genetic structures of populations linked by black lines are not significantly different ($P > 0.05$) based on an F_{ST} test. The structures of those not linked by black lines are significantly different ($P \leq 0.05$). The structures of the populations circled in black are significantly different from those of all of the other populations in this study.

TABLE 3 Average aggressiveness and ice nucleation activity phenotypes of strains of *P. syringae* in waters from different origins

Source ^a	No. of strains	Aggressiveness ^b	Ice nucleation activity ^d
0	13	1.64 (A) ^c	-6.2 (AB) ^e
10.1	15	0.08 (C)	-7.2 (B)
10.2	14	1.68 (A)	-4.7 (A)
11.1	14	0.23 (C)	-7.1 (B)
11.2	10	0.72 (ABC)	-5.2 (A)
12	11	0.29 (BC)	-6.3 (AB)
21	13	0.13 (C)	-6.1 (AB)
22	15	1.10 (ABC)	-5.3 (A)
33	10	1.56 (AB)	-5.8 (AB)
37	10	0.48 (ABC)	-4.9 (A)
40	10	0.64 (ABC)	-5.8 (AB)
42	70	1.02 (ABC)	-5.4 (A)

^a Sources are described in Table 1. Phenotypes of strains from site 43 were not determined.

^b Shown is the overall mean disease severity (on a scale of 0 to 4), for all strains tested per source, as indexed on 12 cantaloupe cotyledons per strain.

^c Mean severity values followed by the same letters were not significantly different ($P \leq 0.05$) based on Tukey's honest significant difference test.

^d Shown is the overall mean temperature, for all strains tested per source, at which ice nucleation was induced by the suspensions of 10^6 cells tested per strain.

^e Mean temperatures followed by the same letter are not significantly different ($P \leq 0.05$) based on the least significant difference test. (No significant differences were revealed with Tukey's honest significant difference test.)

date relative to that obtained on the first date: the samples obtained on both dates had two haplotypes in common, but the sample obtained on the first date had four additional haplotypes not detected in that obtained on the first date, whereas the sample from the second date had an additional haplotype not detected in that from the first date. It is interesting that this corresponded to a 100-fold reduction in the density of the *P. syringae* population at this site between the two sampling dates. At adjacent sampling site 11, there was a 25-fold reduction in population density between the two dates but this did not lead to a significant change in population structure. The differences in population structure at New Zealand sites 42 and 43 were more striking than the temporal differences observed at French site 10. At site 42, 19 haplotypes were detected; at site 43, 11 haplotypes were detected, of which only 4 were also detected at site 42. Furthermore, about 30% of the population at site 43 was composed of strains with haplotypes unique to that site.

The phenotypic structure of *P. syringae* populations in water is influenced by geographic location. The origin of water samples had a significant effect on the aggressiveness of *P. syringae* populations on cantaloupe seedlings. This significant influence was observed for aggressiveness expressed as the mean absolute disease severity on cotyledons, the mean disease severity relative to that induced by control strain CC0094, and the mean frequency of cotyledons with a score of ≥ 1 . A one-way analysis of variance (ANOVA) revealed a significant effect of sample origin on mean disease severity for the samples in Table 1 ($P = 3.38 \times 10^{-8}$). The sites with the lowest average aggressiveness of strains were all French sites (10.1, 11.1, and 21) (Table 3). However, the populations at sites 10 and 11 experienced marked increases in average aggressiveness between the first and second sampling dates, and for site 10, this increase was significant. Likewise, one-way ANOVA indicated that sample origin had a significant effect on the average temperature at which strains catalyzed freezing, as measured for suspensions of 10^4 ($P = 0.023$) and 10^6 ($P = 0.036$) cells. Here we present mean freezing temperatures for suspensions of 10^6 cells. These temperatures were

TABLE 4 Aggressiveness on cantaloupe seedlings and ice nucleation activity of strains in each of the *cts* haplotype clusters of *P. syringae*

Cluster ^a	No. of strains	Mean disease severity score ^b	% of strains with disease severity score of >2 ^c	Mean freezing temp (°C) ^d	% of strains freezing at ≥ -5°C ^e
1	20	0.23	5.0B	-6.90	20.0B
2	19	0.35	5.3B	-5.26	73.7A
3	121	1.20	30.0A	-4.97	80.2A
4	43	0.46	0.0B	-7.47	27.9B

^a Clusters of *cts* haplotypes were inferred with the Bayesian clustering algorithm of the STRUCTURE software.

^b Shown is the mean disease severity after 7 days of incubation of 12 inoculated cotyledons per strain. ANOVA indicated a significant effect of cluster on mean disease severity ($P < 0.001$).

^c The frequency of highly aggressive strains is expressed as the percentage of strains inducing a mean disease severity of 2 (on a scale of 0 to 4) on cantaloupe seedlings. Percentages followed by the same letter are not significantly different ($P > 0.05$) based on a pairwise Fisher exact test of the total number of strains in each phenotype category.

^d Shown is the mean warmest freezing temperature of 10^6 cells of each strain tested in each cluster. ANOVA indicated a significant effect of cluster on mean freezing temperature ($P < 0.001$).

^e The frequency of highly ice nucleation active strains is expressed as the percentage of strains freezing at -5°C or at warmer temperatures. Percentages followed by the same letter are not significantly different ($P > 0.05$) based on a pairwise Fisher exact test of the total number of strains in each phenotype category.

the coldest for French samples 10.1 and 11.1 (Table 3). As for disease severity, the mean freezing temperature increased significantly—by 2°C or more—by the second sampling date at both of these sites. It is interesting that the change in phenotypic profile at site 10 corresponded to a significant change in genetic population structure but for site 11 it did not.

Water conductivity has a significant impact on the aggressiveness and ice nucleation activity, but not on the genetic structure, of populations. To evaluate the impact of overall water chemistry on the structure of *P. syringae* populations, water samples were categorized based on low conductivity (<100 μS), medium conductivity (100 to 500 μS), and high conductivity (>500 μS). For genotypic characterization, the analysis was based on 134, 73, and 29 strains in each category, respectively, and for phenotypic characterization, analyses were based on 102, 73, and 29 strains in each category, respectively; F_{ST} analysis indicated that there was no significant effect of water conductivity on the genetic structure of *P. syringae* populations (AMOVA, among-group variation V_G , $P = 0.421$). However, one-way analyses of variance showed that there was a significant effect of conductivity for all phenotypic variables (all measures of aggressiveness and ice nucleation activity) ($P < 0.05$). Tukey's honest significant difference test showed that the effect of conductivity was due to a significantly reduced aggressiveness on cantaloupe and reduced ice nucleation activity of strains from waters with high conductivity. The mean severity of disease caused by strains from water with low and medium conductivity was 0.93 and 1.05, respectively, but for strains from water with high conductivity, the mean disease severity was 0.15. Likewise, the mean temperature of ice nucleation activity for suspensions of 10^6 cells of strains from low- and high-conductivity waters was -5.5°C and -5.3°C, respectively, whereas for strains from high-conductivity waters it was -7.1°C.

There is a significant interaction among phylogenetic relatedness, aggressiveness, and ice nucleation activity for *P. syringae* strains from water. Genetic clusters of *P. syringae*, identified with Bayesian clustering as described above, had a significant effect on aggressiveness on cantaloupe and on ice nucleation activity (one-way ANOVA, $P < 0.001$ for all measures of these phenotypes). Strains in cluster 3 induced the overall highest mean severity. In particular, 30% of the strains in this cluster induced disease on cantaloupe with a mean severity score of 2 or greater. This frequency was significantly greater ($P < 0.05$) than that of any of the other clusters (Table 4). Likewise, on average, cluster 3 strains induced freezing at warmer temperatures than strains in the other clusters (Table 4). Clusters 2 and 3 had significantly higher fre-

quencies of strains that could induce freezing at -5°C or at warmer temperatures ($P < 0.05$).

There was also a significant positive correlation between the temperature at which strains induced ice nucleation and their aggressiveness on cantaloupe. Based on Pearson's product-moment correlation, the warmest temperature of ice nucleation for suspensions of 10^6 cells increased significantly with aggressiveness in terms of the mean disease score per strain ($R = 0.274$, $P = 7.21 \times 10^{-5}$), the mean disease score per strain as a fraction of the score for the control strain (CC0094) used in each series of inoculation ($R = 0.296$, $P = 1.67 \times 10^{-5}$), and the frequency of diseased plants per strain ($R = 0.292$, $P = 2.14 \times 10^{-5}$). Spearman's rank correlation also indicated that these correlations were significant ($P < 3 \times 10^{-5}$ for all correlations). Correlations with ice nucleation activity in suspensions of 10^4 cells indicated identical significant trends.

To further evaluate the relationship between ice nucleation activity and aggressiveness on cantaloupe, strains were attributed to classes based in the intensity of these traits. Strains in aggressiveness class 0 (nonvirulent strains) did not cause symptoms on more than 1 of the 12 seedlings inoculated per strain. Strains in aggressiveness class 1 caused disease on two to eight seedlings. Strains in aggressiveness class 2 caused disease on 9 or more of the 12 seedlings. Likewise, strains in ice nucleation activity class 0 had no detectable capacity to induce freezing at temperatures warmer than -9°C in a population of 10^6 cells; those in ice nucleation activity class 1 had at least 1 cell among 10^6 able to catalyze ice formation at -6 to -9°C, and those in class 2 had at least 1 cell among 10^6 able to catalyze ice formation at -2 to -5°C. A contingency table of the number of strains in each of the paired classes further illustrates the significant relationship between ice nucleation activity and aggressiveness (Table 5). Nonvirulent strains had equal probabilities of being in any of the three classes of ice nucleation activity, whereas strains that were not ice nucleation active were rarely virulent on cantaloupe.

DISCUSSION

The whole of the population biology of *P. syringae* reported to date concerns populations associated with plants, and in particular with plant canopies. Natural populations of *P. syringae* on plant canopies are generally dominated by strains that are pathogenic to the cropped plants in the locality studied (17–20), illustrating the selective pressure of plants in the apparent diversity and structure of populations of plant pathogens. By exploring the diversity of *P. syringae* populations in freshwater, a habitat where this bacterium is ubiquitous and likely to be subjected to selective forces

TABLE 5 Contingency table of the relationship of aggressiveness on cantaloupe to the ice nucleation activity of 203 water strains of *P. syringae*

Aggressiveness class ^a	No. of strains in ice nucleation activity class ^b :		
	0	1	2
0	24	22	37
1	3	10	35
2	6	12	54

^a Strains in aggressiveness class 0 (nonvirulent strains) did not cause symptoms on more than 1 of the 12 seedlings inoculated per strain, strains in aggressiveness class 1 caused disease on 2 to 8 seedlings, and strains in aggressiveness class 2 caused disease on 9 or more of the 12 seedlings.

^b Strains in ice nucleation activity class 0 had no detectable capacity to induce freezing at temperatures warmer than -9°C in a population of 10^6 cells. Strains in ice nucleation activity class 1 had at least 1 cell among 10^6 able to catalyze ice formation at -6 to -9°C . Strains in class 2 had at least 1 cell among 10^6 able to catalyze ice formation at -2 to -5°C . $P = 0.0000$, Fisher's exact test.

quite different from those engendered by plants, we have revealed four major insights into its population biology that also give clues to its evolutionary history and strategies for adaptation.

First, populations of *P. syringae* in water contain genetic clades not previously reported for strains from crops. These clades, for the most part, are closer to the root of the phylogenetic tree than the previously reported clades. Most of the strains in these clades induce hypersensitivity in tobacco, suggesting that they have type III secretion systems. In other words, they have the cellular structures that effectively inject some effectors into plants, signaling that they are pathogens, thereby inducing a resistance response in the plants (14). However, their low aggressiveness on cantaloupe suggests that they do not have sufficient molecular arms to cause much disease in this plant species. It is possible that these new clades are, in fact, associated with crops and have not yet been reported or that they are below current detection levels. Alternatively, they could be pathogens of plants not grown as crops. The focus of plant pathology has been mostly limited to cultivated plants. As cultivated plants are a minority in the plant kingdom, pathogens of noncrop plants could have easily been overlooked.

Second, the overall genetic structure of *P. syringae* populations in water is not significantly affected by geographic location. Sequencing of more genes of the strains studied here might contribute nuances to this initial observation. But based on the data as presented, there seems to be a considerable force contributing to the pandemics of lines of this bacterium, most likely via transport with the water cycle (13). This is well illustrated by the numerous haplotypes found both in water and on crops and in particular by the presence of apparent clones such as AI116 and CC0457 found in both water in New Zealand and crops in France. Nevertheless, 43% to 70% of the combined populations from each continent contained haplotypes of the *cts* gene that were unique to that continent. These haplotypes were not dominant and thereby did not have a significant impact on overall population structure. However, we cannot rule out the possibility that the haplotypes labeled as unique to a location are indeed unique and not simply present at a low concentration elsewhere. If some haplotypes are found only in one location while others are spread around the world, then it would suggest that two different mechanisms might be responsible for the dispersion of *P. syringae*. Both could be linked with the water cycle. But one would be responsible for dispersion over short distances (explaining the high percentage of

haplotypes unique to a continent or a sampling site) and one would be responsible for dispersion over large distances (explaining why the same haplotype can be found on different continents). Nevertheless, these unique haplotypes reveal a role for endemism of water-borne populations of *P. syringae*, thereby supporting the notion that freshwater habitats are not simply passive reservoirs of *P. syringae* but play a role in the evolution of this bacterium. Water chemistry had an impact on genetic population structure only when there were marked shifts in chemistry, such as in the early spring in the French Alps. Water chemistry can vary, depending on the residence time of the water emerging from the water table into mountain streams and the geologic context (21). Hence, the specific biogeography portrayed in this study could fluctuate across seasons in some geographic contexts.

Third, there is a link between the phylogeny and pathogenicity of *P. syringae*. This was revealed by the significant effect of the *cts* haplotype cluster on aggressiveness on cantaloupe. The strains in cluster 3, in particular, were the most aggressive on cantaloupe. Previously, we demonstrated that aggressiveness on cantaloupe was positively correlated with the number of plant species in *P. syringae*'s host range (22). The strains most aggressive on cantaloupe were virulent on up to 10 other plant species. The correlation we observed was highly significant (for Pearson's product-moment correlation, $P < 0.0001$; not reported in the original publication). We have confirmed this trend with an independent test of the host range of 31 strains of *P. syringae* on 15 plant species (data not shown; for Pearson's product-moment correlation, $P = 9.1 \times 10^{-7}$). Hence, the intensity of symptoms induced on cantaloupe (i.e., aggressiveness) is an indication of the relative extent of the host range of strains. The more aggressive strains tend to be more polyvalent in their host range than the less aggressive strains. This leads to the surprising observation that strains in group 2 (which corresponds to cluster 3) are found in a wide diversity of agricultural (crops, irrigation water) and nonagricultural (snow, rain, lakes and rivers, epilithic biofilms, wild plants) substrates and are also effective pathogens with broad host ranges. Among the strains in this group for which we have host range data, CC0094, CFBP1906, and CC0125 were reported to be virulent on 7, 9, and 10 plant species, respectively (22). This suggests that strains of *P. syringae* in group 2, in particular, have accumulated factors favoring both extended host range and saprophytic ubiquity. It is likely that these factors would be dual-use pathogenicity factors, such as broad-spectrum toxins (7). Based on observations from other pathosystems, we might have expected to observe a fitness cost of aggressiveness and broad host range. For instance, a *Turnip mosaic virus* isolate avirulent on the turnip line containing the resistance gene *TuRB01* outcompeted virulent isolates in coinoculation experiments in a susceptible host background (23). A similar situation was recently well illustrated in the interaction between *Potato virus Y* and the pepper resistance gene *Pvr4* (24). Fitness costs have been reported for fungal plant pathogens such as *Leptosphaeria maculans* (25) and *Melampsora lini* (26). For the bacterium *Xanthomonas oryzae* pv. *oryzae*, virulent strains obtained through mutagenesis caused shorter lesions than the wild-type strain on a rice line containing no resistance genes (27). However, other authors have reviewed numerous examples where a pathogen's multiplication is not negatively correlated to its aggressiveness (28). For *P. syringae*, we observed that a sensitivity to water conductivity above $500 \mu\text{S}$ might be associated with a fitness cost for high levels of aggressiveness. This might imply that the

factors involved in broad host range and general saprophytic fitness in group 2 involve regulation of membrane and cell wall permeability to ions and that this regulation is more constrained in clades with limited host range and environmental distribution. This fitness cost might also be markedly different from the cost of host-specific virulence. In other clades of *P. syringae*, strains might be aggressive on a very limited number of plant species (such as in group 3) and the underlying mechanisms of virulence could severely preclude their fitness as saprophytes, thereby contributing to their limited spread among habitats. In this light, it is interesting to note the recent emergence of strains of *P. syringae* in group 3 that are highly aggressive on horse chestnut (29). These strains have a limited host range and fall into a clade that seems to be particularly adapted to woody species.

Fourth, ice nucleation activity and pathogenicity are also linked; *viz.*, there is a very low probability for strains to be aggressive on cantaloupe, and hence to have a broad host range in light of the arguments above, if they are not ice nucleation active. This link is likely the result of dissemination being facilitated by ice nucleation activity. We have previously presented evidence that ice nucleation activity is a sort of active dissemination mechanism ensuring that bacteria, which are otherwise aerodynamically ultralight and tend to remain suspended in the air, are deposited with falling precipitation formed by freezing of atmospheric water drops (13). Airborne dissemination and subsequent fallout would favor encounters with a wide variety of habitats where virulence factors could be acquired or where lines with phenotypes permitting a large host range are positively selected. Initial contact with plant cellular contents might have been facilitated by the induction of frost damage to plants, which would have positively selected for ice nucleation in those strains able to grow on the released nutrients (30). It is interesting that the host range of *P. syringae* is also positively correlated with the range of carbon sources strains can use for growth (31). This scenario would suppose that the ancestors of modern *P. syringae* were effectively ice nucleation active but not plant pathogenic. The sequenced alleles of the ice nucleation gene of bacteria are highly conserved and found only in the gammaproteobacteria (32). The known ice nucleation species containing this gene are on disparate branches of the phylogenetic tree of the pseudomonads (33), and there is evidence that the gene derives from a common ancestor of these species (32). The type III secretion system essential for pathogenicity in *P. syringae* and in many other Gram-negative bacteria is also widely prevalent across divergent lineages of the pseudomonads, as well as outside this group. However, the gene cluster for the type III secretion system is on a pathogenicity island flanked by remnants of mobile genetic elements indicative of acquisition by horizontal gene transfer (14). The sequence diversity between alleles of the genes in this pathogenicity cluster suggests that the clusters evolved independently after acquisition (14). If ice nucleation activity is a driver of diversification of plant pathogenicity in *P. syringae*, has it played this role in other plant-pathogenic species? Only a very few pathovars in the quintessential plant-associated genus *Xanthomonas*, for example, are ice nucleation active, and this genus is composed mostly of host-specific strains with virtually no reports of its presence in other substrates. *P. fluorescens* and *Pantoea agglomerans* are widespread and frequently associated with plants, yet only a few strains of the former have been reported as ice nucleation active, in contrast to the latter. It is difficult to speculate on the originality of this evolutionary strategy without fully comparative observations of other bac-

teria. Furthermore, it could also be possible that there are metabolic or regulatory links between ice nucleation activity and pathogenicity that lead to compatibility or incompatibility of these traits in the same individual. However, this question has not been explored.

Taken as a whole, our results suggest that the freshwater habitat has a considerable impact on the biology and population structure of *P. syringae*. To assess the importance of freshwater habitats in the life history of this bacterium, a comparison of the sizes of the total metapopulation of *P. syringae* in water relative to that in association with plants would be useful. These population sizes would be indicators of comparative fitness in these two environments. We can only make rough estimates based on existing data on abundance on plant surfaces and in water, neither of which accounts fully for spatial heterogeneity. To make this calculation, we can exploit measures of the total leaf surface on Earth (10^9 km²) (34), the percentage of this leaf surface in biomes compatible with *P. syringae* ecology (ca. 10% in cropland plus 30% elsewhere) (35), and the total freshwater reserves in lakes and rivers (175,000 km³) (36). If we use mean values for *P. syringae* density on nondiseased plants and in water of 100 to 10⁴ cells/cm² (13) and 1,000 cells/liter (reported here), respectively, then the total planetary population of *P. syringae* associated with plants would be roughly 10²⁰ to 10²² cells, whereas that in freshwater would be a total of 10²⁰ cells. Disease on plants might have only a small impact on the total plant-associated population if we consider that a hectare of diseased leaves with 10⁸ cells/cm² of leaf would represent a total of only 10¹⁶ *P. syringae* cells. On the other hand, the size of the population in freshwater might be even greater if we consider that groundwater represents 100 times more volume than surface waters (lakes and rivers) (36, 37), and in many regions groundwater contributes significantly to stream flow and lake volume (38). Glaciers also hold a volume of freshwater 100 times that of surface waters, but it is unknown if they harbor *P. syringae* populations that fall with snow. These rough calculations suggest that the total planetary population of *P. syringae* in water is of a size comparable to that on crops.

The considerable effort to sequence the full genomes of numerous strains of *P. syringae* is motivated by the need to understand the molecular basis of the adaptation of this bacterium to the habitat of plants and its capacity to cause disease (39–42). Intense bioinformatic investigation has been invested in identifying effectors implicated in pathogenesis (43, 44). The fundamental objective of these investigations is to understand the evolutionary history of pathogenicity in *P. syringae*. The practical objective is to gain insight into targets for methods to control disease. However, as mentioned in the introduction, the epidemiological success of pathogens with significant environmental reservoirs is linked to their capacity to persist in the environment. Furthermore, virulence factors in many human pathogens can have dual uses in both environmental and parasitic fitness, and there are also numerous examples of such dual-use factors in plant pathogens (7). Given the overall abundance and genetic diversity of *P. syringae* outside 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. If this is the case, it does not take away from the economic importance of this bacterium as a plant pathogen and the need to control disease. However, this point of view could reorient genomic analyses to be more globally encompassing of the ensemble of mechanisms involved in the epidemiological success of *P. syringae*.

MATERIALS AND METHODS

Bacterial strains. *P. syringae* was isolated from the water samples described in Table 1. All sites except site 22 are at source waters of rivers at altitudes above agriculture or in conservation zones where land was not cultivated. Cultivated fields (pasture) bordered site 22. Up to 1,500 ml of water was collected at each site in sterile plastic bottles that were rinsed once with the site water before the definitive sample was collected. The conductivity of the water at French and U.S. sites was measured on-site with a Consort C561 portable electrochemical analyzer (Consort nv, Turnhout, Belgium), and that of water from New Zealand sites was measured with a Bio-Rad model EG-1 Econo Gradient Monitor (Hercules, CA) in the laboratory. Water was kept in a cooler and transported to the laboratory within 12 h after sampling. To isolate *P. syringae*, water samples were filtered across nitrocellulose filters (0.22- μ m pore diameter), the material collected on the filters was resuspended in filtrate to concentrate the captured bacteria by a factor of 100, and this concentrated suspension was diluted plated (10 replicates per dilution) on KBC medium (45) as described previously (13). One replicate per dilution of the original water sample was also plated on 10% strength tryptic soy agar to estimate the size of the total mesophilic bacterial population as described previously (13). After 4 to 5 days of incubation at 22 to 25°C, fluorescent colonies on KBC medium were randomly collected from a single dilution, purified, and tested for traits compatible with the *P. syringae* species (absence of cytochrome *c* oxidase and of the enzyme arginine dihydrolase) (13). According to our previous experience, at least 98% of the strains characterized with these initial tests prove to be *P. syringae* when subjected to molecular and other biochemical characterizations (13, 15). Strains were stored in nutrient broth containing 40% glycerol at -80°C .

Strain CC0094 of *P. syringae* from cantaloupe (22) was used as a reference strain for phenotypic tests. For genotypic comparisons, sequences of housekeeping genes (described below) of a wide range of *P. syringae* strains were collected and are described in the sections concerning phylogenetics and population genetics.

Phenotypic characterization of strains. Strains were characterized for their pathogenicity and ice nucleation activity. The capacity to induce an HR in tobacco was determined by infiltrating fully developed leaves of plants of *Nicotiana tabacum* L. cv. Samsun at the 10-leaf stage (bacterial suspensions of 48-h cultures at ca. 1×10^8 CFU/ml). Aggressiveness on cantaloupe plants (*Cucumis melo* var. *cantalupensis* Naud. cv. Védraçais) was quantified by injecting 50- μ l volumes of bacterial suspensions (prepared in the same way as for hypersensitivity tests) into the junction of the cotyledons of 12 plants at the cotyledon stage (ca. 10 days after sowing). Strains were tested in blocks of up to 30 chosen in random order to distribute the effect of the inoculation date across the different origins of the strains. Strain CC0094 was used as the positive control for all blocks. Plants were incubated for 7 days in a growth chamber at 25°C during the daylight period (16 h) and 18°C at night (8 h). Disease was noted throughout incubation, and disease scores at 7 days were used for analysis. The notation scores were 0 (no symptoms), 1 (one cotyledon wilted or discolored), 2 (both cotyledons wilted or discolored), 3 (both cotyledons completely wilted and upper stem of plant collapsed), and 4 (plant collapsed at base and entire plant fallen on soil surface). Mean absolute aggressiveness and mean aggressiveness relative to that of reference strain CC0094 were calculated for each strain. Ice nucleation activity at -2°C to -8°C was determined for three 30- μ l drops of aqueous bacterial suspensions per strain containing a total of 10^4 and 10^6 cells per drop as described previously (15). Bacterial suspensions were prepared in the same way as for inoculation of plants and were then kept at 4°C for 1 h before testing. The ice nucleation activity at each concentration and at each temperature was considered positive if at least two of the three drops froze.

Genotyping of strains. Genotyping was based on sequences of regions of four genes of the core genome, *rpoD*, *gyrB*, *cts* (*glt*), and *gapA* (*gap1*). PCR amplifications were performed as previously described (13), using primers described by Yamamoto et al. (46) for *rpoD* and *gyrB* and primers described by Sarkar and Guttman (47) for *cts* and *gapA*. For numerous

strains, these primers for *gapA* were not appropriate. Hence, for some strains, the *gapA* sequence was amplified with primers developed for us by Boris Vinatzer, Virginia Tech, Blacksburg (personal communication). These were *gapA230F* (5'-GTC AGY GCC ATY CGC AAY C-3') and *gapA942R* (5'-AAA ACS CCC AYT CGT TGT C-3'). Amplified products were electrophoresed and purified as described previously (13). Forward and reverse sequencing was conducted by Eurofins MWG Operon (Ebersberg, Germany) and by the Waikato DNA Sequencing Facility (Department of Biological Sciences at the University of Waikato, Hamilton, New Zealand) with the sequencing primers described previously (46, 47).

Phenotypic analyses. The objective of the phylogenetic analysis was to determine the phylogenetic context of water strains relative to the genetic diversity of *P. syringae* for the ensemble of habitats from which it has been isolated. We reconstructed phylogenetic relationships for 121 strains of *P. syringae*, 3 strains of *P. fluorescens*, and 1 strain of *P. viridiflava*, including strains used in a previous phylogenetic analysis (13). The present analysis included 44 water strains from this study, as well as strains from crops and all other substrates from which we have isolated this bacterium (see Table S1 in the supplemental material). DNA sequences obtained from the PCR products corresponding to the *rpoD*, *gyrB*, *cts*, and *gapA* gene fragments were aligned with the ClustalW routine and cut to equal lengths with DAMBE, version 5.1.1 (48). Two approaches were used for the phylogenetic analyses. For the first approach, phylogenetic trees were constructed from the concatenated sequences according to the neighbor-joining method in MEGA, version 3.1 (49), based on the Tamura-Nei model with gamma correction and 1,000 bootstrap replicates as employed by Sarkar and Guttman (47). To choose from among the hundreds of water strains, preliminary trees were constructed based only on *cts* sequences. We attempted to (i) avoid including multiple strains that were likely to be within the previously described genomic groups, in particular, groups 1 to 5 (47, 50), where we have already demonstrated the presence of strains from water and other substrates (13) and (ii) include strains in new phylogenetic groups. Criteria for choosing strains were based on a preliminary analysis of the variability of each gene sequence within genetic groups 1 to 5. Hence, only a few representatives of water strains that were less than 1.8% divergent in their *cts* sequence from strains in groups 1 to 5 (and therefore likely to fall into one of these known groups) were included in the phylogenetic tree. For those that were more than 1.8% divergent, the other three housekeeping genes were sequenced and incorporated into the tree. For the second approach, the alignment was analyzed using the DataMonkey Facility, a web server of the HyPhy package (51), to select an appropriate substitution model. Phylogenetic relationships among alleles were then reconstructed using maximum-likelihood methods as implemented in PHYML 3.0 (52), available online (<http://www.atgc-montpellier.fr/phyml>), using HKY85 as the most appropriate substitution model. All other settings were set to default.

Clustering analyses. Strains of *P. syringae* from water and crops were clustered on the basis of their genetic relatedness, in terms of *cts* sequences, using two different individual-based clustering methods: a Bayesian algorithm and a multivariate analysis. Sequences of 87 strains from crops and 236 strains from water were aligned and cut to a length of 411 bases. Strains from crops were those indicated in Table S1 in the supplemental material under the headings "strains used for phylogenetic analyses" (of crop and agricultural origin) and "strains used for population structure analyses." Redundant sequences were eliminated, thereby leading to the identification of 88 haplotypes among the total of 323 sequences. The sequences of these haplotypes were converted into the Structure format using xmf2struct, which was developed by Didelot and Falush and is available at the ClonalFrame website (<http://www2.warwick.ac.uk/fac/sci/statistics/staff/research/didelot/clonalframe/>).

The Bayesian clustering approach was performed using the software STRUCTURE 2.3 (53, 54). The method assumes that each locus is at Hardy-Weinberg equilibrium and independent of the others, but this Bayesian algorithm has proved to be robust in response to deviations from these assumptions and has been successfully used in partially asexual or-

ganisms such as bacteria (55), aphids (56), and fungal and oomycete plant pathogens (57–59). Using the admixture model, we estimated the number of genetic clusters (K) to which the isolates should be assigned to be between $k = 1$ and $k = 10$ with 10 repeats. For all simulations, we did not force the model with predefined allele frequencies for source clusters. Runs were based on 200,000 iterations after a burn-in period of 100,000 iterations. We followed the method developed by Evanno et al. (16), which uses the distribution of maximum likelihoods to identify the number of genetically homogeneous clusters (K).

The optimal number of clusters was further evaluated by a PCA using the procedure available in the package *ade4* (60) for the statistical freeware R version 2.7.2 (R Foundation for Statistical Computing, 2008). PCA has the advantage over the Bayesian clustering algorithm implemented in STRUCTURE because it does not require assumptions such as the Hardy-Weinberg equilibrium or the absence of linkage disequilibrium between loci (60). PCA was followed by a clustering analysis using the classical Ward method available in R, which is a hierarchical method designed to optimize minimum variance within clusters.

Analysis of population structure. The genetic structures of the *P. syringae* populations in water at the different sampling sites were compared based on an F_{ST} test (61) using Arlequin software version 3.11 developed by the Population and Molecular Genetics Laboratory at the University of Bern, Bern, Switzerland (<http://cmpg.unibe.ch/software/arlequin3/>) (62). Calculations of F_{ST} were based on the frequency of each of the 88 different 411-base-long haplotypes of the partial *cts* sequences observed for each of the 13 different dates and sites of sampling (Table 1). AMOVA analyses were conducted to determine the effect of general geographic location (United States, France, New Zealand), of specific location, and of water conductivity (low conductivity, less than 200 μ S; medium conductivity, 200 to 500 μ S; high conductivity, >500 μ S) by assigning each population to the appropriate group. Pairwise comparisons were based on 100 permutations, 100,000 steps in the Markov chain, and 10,000 dememorization steps. The phenotypic structures of *P. syringae* populations from water were compared via parametric (ANOVA) and nonparametric (χ^2) tests using the Statistica software package (StatSoft, Maison-Alfort, France) to determine the effects of geographic location, water chemistry (as indicated above), and genetic cluster.

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SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <http://mbio.asm.org/lookup/suppl/doi:10.1128/mBio.00107-10/-/DCSupplemental>

TABLE S1, DOC file, 0.19 MB.

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