Two bridgehead invasions of *Xylella fastidiosa* subsp. *multiplex* in France

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Abstract

Of American origin, a wide diversity of *Xylella fastidiosa* strains belonging to different subspecies have been reported in Europe since 2013 and its discovery in Italian olive groves. Strains from the subspecies *multiplex* (ST6 and ST7) were first identified in France in 2015 in urban and natural areas. To trace back the most probable introduction scenario, the molecular evolution rate of this subspecies was estimated at 3.2165×10^{-7} substitutions per site per year, based on heterochronous genome sequences collected worldwide. This rate allowed the dating of the divergence between French and American strains in 1987 for ST6 and in 1971 for ST7. The development of a new VNTR-13 scheme allowed tracing the spread of the bacterium in France, hypothesizing an American origin. Our results suggest that both sequence types were initially introduced and spread in PACA; then they were introduced in Corsica in two waves from the PACA bridgehead populations.

Teaser

Tipdating and ABC analyses on genomic and microsatellite data were combined to provide scenarios for *X. fastidiosa* introduction in France.

Introduction

Worldwide global food security is threatened by emerging plant diseases, which frequency is increasing as a consequence of the globalization of plant material exchanges, crop intensification and global climate change (*1*). Many emerging infectious diseases result from

geographical expansion following accidental introduction and can be considered as biological invasions (*2*). Our ability to anticipate, prevent and mitigate emerging infectious diseases depends on a better understanding of current pathogen distribution over space and time, invasion routes, conditions favoring their emergence and population reservoirs (*3*).

Xylella fastidiosa is a phytopathogenic genetically diverse bacterial species including two largely divergent lineages. One lineage bears two subspecies, *fastidiosa* and *multiplex*, originating from Central and North America, respectively (*4*, *5*). These subspecies include strains pathogenic on a wide host range, with some plants being common hosts of both subspecies (*6*). Extensive intersubspecific homologous recombination was experimentally demonstrated between strains of these two subspecies (*7*), and this phenomenon was previously speculated to be at the origin of host range expansion in these taxa, especially for the strains infecting mulberry and blueberry (*8*). The other lineage is composed of one highly diverse subspecies, *pauca*, known to originate from South America, where main economic hosts are citrus and coffee plants (*9*). MultiLocus Sequence Typing (MLST), which consists in partial sequencing of seven housekeeping genes and leads to sequence type (ST) number attribution, is the reference method used to type *X. fastidiosa* at an infrasubspecific level (*10*).

X. fastidiosa first detection in Europe was reported from natural settings in Italy in 2013 (*11*). Since then, the bacterium has devastated thousands of hectares of olive groves in Apulia, Italy, leading to a severe socio-economic crisis (*12*). This species is considered as one of the most dangerous plant-pathogenic bacteria worldwide (*13*). *X. fastidiosa* has a very wide host range, with 655 known host plant species worldwide (*6*). Its host range includes plants of major socio-economic interest such as grapevine, citrus, coffee and olive trees, but also fruit and forest trees, ornamental plants, shade trees, and wild species, making *X. fastidiosa* a global threat. For these reasons, *X. fastidiosa* is a priority quarantine pathogen in the European Union (EU), meaning that it is of mandatory declaration and eradication, with the exception of areas where the bacterium is established, and where eradication has been considered as unfeasible (*14*, *15*). In EU, these areas are Corsica in France, Apulia in Italy, and the Balearic Islands in Spain (*14*, *16*).

Over short distances, the dissemination of the bacterium results mostly from the movements of insect vectors. Indeed, transmission by sap-feeding insect vectors of the families of Aphrophoridae, Cicadellidae, Cercopidae, and Cicadidae is the only natural way of transmission among plants (*17*). Over long distances, human activities are responsible for the dispersal of this pathogen through the trade of infected plant material. In the recent past, this bacterium has been introduced in Taiwan via infected grapevine for planting (*18*). Trade of ornamental coffee plants is the presumed means of introduction of the strain decimating Apulia's olive trees from Central America (*19*). Several lines of evidence indicate that earlier on, *X. fastidiosa* strains responsible for the Pierce's disease of grapevine, that still represents a strong constraint on vineyards in California, were introduced from Central America via infected coffee plants (*4*). The low diversity of *X. fastidiosa* observed in California in comparison to Central America

confirmed this hypothesis (*4*, *20*), which was reinforced by historical data documenting the importation of coffee plants from Nicaragua to Los Angeles around 1855 (*21*). Transport of infected *Prunus* was the likely vector of the introduction of strains from the subspecies *multiplex* in Southern Brazil (*22*). The introduced population then diversified in the United-States and served as reservoir for introductions in Taiwan and Europe (*23*).

In France, a first suspicion of *X. fastidiosa* infection dates back to 1989, when a grapevine plant was found infected in the Languedoc region (*24*). Then, in 2010 in the Saint-Emilion area, genomic signatures of *X. fastidiosa* were found in the microbiota of a grapevine plant (*25*). However, it was not until 2013 that the presence of *X. fastidiosa* subsp. *pauca* (ST53) was officially identified, in Europe, in the Apulia, in Italy (*11*). The link between this identification and the disastrous decline of olive trees in Apulia and the previous detections on contained coffee plants (France, Netherlands, Italy, Switzerland, Germany) prompted pest risk assessments in other European countries (*13*). In 2015, monitoring led to the discovery in France of the subspecies *multiplex* (ST6, ST7) and *pauca* (ST53) (*26*). Then, in the Balearic Islands (Spain) the subspecies *fastidiosa* (ST1), *multiplex* (ST7 and ST81) and *pauca* (ST80) were detected (*27*). The subspecies *multiplex* ST6 was then identified in continental Spain in 2017, a close genotype (ST87) was detected in Tuscany (Italy) and ST7 was reported from Portugal in 2018 (*28*, *29*). All these records of different sequence types in distant areas are clear indications of various independent introductions of *X. fastidiosa* strains in Europe (*26*). Most sequence types (except ST76, ST80, ST81 and ST87) had previously been described in the Americas that hence represents their most probable area of origin and source of introduction in Europe. These hypotheses were tested and confirmed by a first analysis of a limited number of strains from most EU outbreaks (*29*).

In France, *X. fastidiosa* was detected in three regions, i.e. Corsica, Provence-Alpes-Côte d'Azur (PACA) and Occitanie. Most foci were infected by ST6 or ST7, clustering in *X. fastidiosa* subsp. *multiplex* (*26*). In 2018, while a large number of foci were detected all over Corsica (354 foci), in the Corsican bush and in urban areas; and on a large range of endemic or introduced plant species (39 hosts), a limited number (166 foci) of mostly urban foci were reported in PACA on a range of 25 species, from which 15 plant species were not reported infected in Corsica. Hence, situations seem having different histories.

MLST is one of the most popular technique to genotype pathogenic bacteria. It was widely used to resolve the epidemic spread of pathogens both in human, animals and plants (*30*–*32*). Nevertheless, in some cases this method lacks resolution (*33*, *34*) and MultiLocus Variable number of tandem repeat Analysis (MLVA) may then be preferred. MLVA is based on the analysis of rapidly evolving markers allowing to study recent events and discriminate individuals with more resolution than MLST (*35*). MLVA allowed deciphering population genetic structure in the monomorphic bacteria *Xanthomonas citri* pv. *citri* and *Xanthomonas citri* pv. *viticola* (*34*, *36*) and to infer their invasion routes using Approximate Bayesian Computation (ABC) (*36*).

Assuming an exogenous origin of *X. fastidiosa* subsp. *multiplex* in France, our aim was to decipher the most probable scenario of introduction of ST6 and ST7 in Corsica and PACA regions, on the basis of the plant material gathered in the frame of the official French monitoring plan. We mainly based our study on MLVA to take advantage of both the large sample collection and the capacity of these markers to monitor recent evolutionary events. Genome data were used to date the divergence of French *X. fastidiosa* subsp. *multiplex* strains from their American relatives. Bayesian methodologies were used to infer the number of introductions and the most probable scenario of population evolution and spread in these two French regions, Corsica and PACA.

Results

A low polymorphism within ST6 and ST7 genome sequences but enough temporal signal to date divergence time

A set of 49 *X. fastidiosa* subsp. *multiplex* strains isolated from plants between 2015 and 2018 in France and six strains isolated in USA between 1995 and 2011 were available for sequencing. With all genome sequences publicly available at the time of analysis, a total of 82 genome sequences of *X. fastidiosa* subsp. *multiplex* were analyzed (Table S1). Most genome sequences (85.4%) were Illumina dye sequences. Average genome length was 2,520,537 bp, with a mean N50 and L50 of 354,785 bp and 7.28, respectively. The dataset comprised strains of diverse geographical origin (Brazil n=1, France n=52, Italy n=3, Spain n=12, USA n=14) spanning 36 years of evolution (isolated between 1983 to 2018). The length of their core genome alignment was 1,679,574 bp, in which 16,739 single nucleotide polymorphisms (SNPs) were detected. After removal of regions with evidence of recombination 13,818 SNPs only originating from mutation events were kept.

Considering ST6 and ST7 strains genome clustering from all geographic origins revealed patterns in partial discordance with traditional MLST grouping (Fig. S1). While all French and American ST6 strains clustered in a homogeneous cluster, as expected from MLST, Spanish ST6 strains were scattered within the ST7 cluster grouping all the French ST7 strains, the three American ST7 strains, and one of the Spanish ST81 strain. The two other Spanish ST81 strains were intermediate between French ST7 and the Spanish ST6 strains. American, Italian and Brazilian *X. fastidiosa* subsp. *multiplex* strains of other sequence types grouped into three other clusters (Fig. S1). Similar groupings were observed by plotting the core genome SNPs from mutation on a heatmap (Fig. S2). A range of 560 to 586 SNPs differentiated French ST7 strains from Spanish ST81 strains, 613 to 643 SNPs from Spanish ST6 strains, and 674 to 709 SNPs from USA ST7 strains, when a range of 899 to 912 SNPs differentiated French from Spanish ST6 strains. Moreover, draft genomes of French strains were quite homogeneous with 37 SNPs and 48 SNPs issued from mutations for the 23 ST6 and the 29 ST7 strains, respectively. SNPs were distributed all over the genome sequences. Six ST6 genome sequences (CFBP 8418, CFBP 8431, CFBP 8435, CFBP 13586, CFBP 13623 and CFBP 13742) and five ST7 genome sequences (CFBP 8416, CFBP 8434, CFBP 13552, CFBP 13585 and CFBP 13631) all isolated

in Corsica, France, between 2015 and 2017 did not show any polymorphism. The strains were isolated from different foci, in central-west Corsica for ST6 and in southern Corsica for ST7. The low polymorphism observed in the core genome and the absence of sub-structuration within ST6 or ST7 genome sequences were not compatible with any further population genetics analysis aiming at reconstructing the pathways of the emergence of *X. fastidiosa* at a regional scale in French territories based only on these data.

In contrast, the complete set of 82 genome sequences, isolated all over the world, was proved suitable for investigate the timing of *X. fastidiosa* subsp. *multiplex* divergence (Table S1.). Analyzing the linear regression of sample age against root-to-tip distance (Fig. S3) and performing a date randomization test (DRT) with BEAST (*37*) (Fig. S4) revealed a sufficient temporal signal at the whole-tree scale. Therefore, the dataset could be used to coestimate evolutionary rates with ancestral divergence times with a tip-based calibration approach.

At the scale of the genome, the mean substitution rate for *X. fastidiosa* subsp. *multiplex* was inferred at 3.2165×10^{-7} substitutions per site per year (95% Highest Posterior Density [HPD] $1.5468 \times 10^{-7} – 5.2043 \times 10^{-7}$ substitutions per site per year). The standard deviation of the uncorrelated log-normal relaxed clock calculated by BEAST was 1.020, suggesting moderate variation in rates among branches. The divergence between French and American ST6 strains was estimated in 1987 (1974 to 1994 95% HPD) (Fig. 1). Then the divergence between these strains and the Spanish ST81 strains was estimated in 1425 (766 to 1914 95% HPD). The one between ST7 French and American strains was estimated in 1971 (1924 to 1994 95% HPD). This time to the most recent common ancestor (TMRCA) was due to the USA RAAR6Butte strain, as the TMRCA with the two other ST7 USA strains (M12 and Griffin-1) is older (=1510; 991 to 1911 95% HPD). The split between Spanish ST6 strains and ST7 strains was estimated in 1027 (120 to 1743 95% HPD). The divergence between the group of ST7 and Spanish ST6 strains and the group of ST81 and ST6 French and American strains was estimated in 755 (-397 to 1540 95% HPD).

Better genotyping resolution with MLVA within *X. fastidiosa* subsp *multiplex*

To elucidate the scenario that led to the establishment of *X. fastidiosa* subsp. *multiplex* in Corsica and PACA, variable number of tandem repeats (VNTRs) were used to complement the relatively low information gained from SNP calling. *In silico* analysis of the *X. fastidiosa* subsp. *multiplex* strain M12 genome sequence led to the identification of 113 VNTR loci, with repeat units ranging from 4 bp to 44 bp in size. After further investigations on a subcollection of 46 genome sequences representing the known diversity of *X. fastidiosa* (10 *X. fastidiosa* subsp. *multiplex*, 18 *X. fastidiosa* subsp. *fastidiosa*, 18 *X. fastidiosa* subsp. *pauca*) (*38*) and then on a panel test of 16 strains from the present study, only three VNTR loci were retained to complete the set of 10 VNTR loci previously proposed by Lin *et al*. (2005) and Francisco *et al*. (2017) (Table 1) (*39*, *40*). These 13 VNTR loci were present in all *X. fastidiosa* genome sequences examined, were not redundant with each other, were highly polymorphic, had a TR unit size ranging from 4 bp to 12 bp and a total array sizes from 77 to 360 bp. Among these 13 VNTR

loci, all were chromosomic and six were intergenic (Table 1). Moreover, *in silico* analyses on the WGS database of bacteria from NCBI revealed that specific amplifications were exclusively obtained on all *X. fastidiosa* genome sequences and on no other genome sequence (date of analysis: 2018-08-22). The 110 other TR loci detected were not further considered, as 39 were imperfect motifs or had incomplete repetitions, 10 were redundant with previously published VNTRs, and 61 had a low allelic diversity or did not allowed to discriminate between ST6 and ST7 as examined on the 10 *X. fastidiosa* subsp. *multiplex* genome sequences.

The VNTR-13 scheme was specifically developed to type the subspecies *multiplex*. All 13 VNTR loci were successfully amplified and typed on our collection of 68 French and American *X. fastidiosa* subsp. *multiplex* strains (Table S2) and on the DNAs of 18 Spanish *X. fastidiosa* subsp. *multiplex* strains (Table S3). Interestingly, each VNTR locus was also successfully amplified on the 27 DNAs of *X. fastidiosa* strains belonging to nine different sequence types of *X. fastidiosa* subsp. *fastidiosa* and *pauca* (Table S2). Of particular interest, and consistent with SNP data, strains belonging to ST6 were scattered into two clusters, one grouping French and American ST6 strains, and the other grouping ST6 strains from Spain (Fig. S5). The MLVA accurately resolved the different haplotypes in our international strain collection as the haplotype accumulation curve reached a plateau with more than 95% of the haplotypes detected with nine or more markers (Fig. S6).

Efficient genotyping of the VNTR-13 scheme on both *X. fastidiosa* subsp. *multiplex* isolated strains and DNA extracted from plants

Besides a conventional use on isolated strains, VNTR genotyping was attempted directly on large sets of DNA samples extracted from frozen infected plant material. Genotyping conditions were thus optimized by: i) multiplexing the primers by four according to their annealing temperature (Table 1); ii) selecting a highly efficient DNA polymerase, meaning the least affected by PCR inhibitors. Platinum™ Taq DNA Polymerase (ThermoFisher) was selected as it allowed amplification of some VNTR loci (ASSR-9, ASSR-16, GSSR-4) in bacterial suspensions at ten times lower concentrations than GoTaq® G2 Flexi DNA Polymerase (i.e. concentrations as low as 10^3 to 10^4 CFU.mL^{-1}); and iii) setting sample DNA aliquot volume to 2 µL per 20 µL-total volume reaction to maximize target presence and amplification, as no inhibitory effect was noticed (data not shown).

The MLVA proved to have an excellent ability to genotype *X. fastidiosa* from isolated strains as well as from DNA extracted from plant sample. In fact, we had at our disposal 13 pairs of isolated strains and DNAs extracted from the same original plant samples for a total of five different plant species (*Acacia dealbata*, *Euryops chrysanthemoides*, *Medicago sativa*, *Polygala myrtifolia*, and *Prunus avium*) (Table S4). An identical VNTR profile was obtained for each member of these 13 pairs, indicating that VNTR amplification from DNA extracted from plant material was efficient and was not affected by DNA extraction efficiency and/or quality. From this point, each of these 13 pairs was considered as one sample.

VNTR-13 scheme revealed that French *X. fastidiosa* split into four groups of strains

In France, from 2015 to 2018, among the plant samples tested in the framework of the French surveillance and officially declared to be *X. fastidiosa* infected, 917 samples had a Cq < 32 (the amplification limit Cq of the MLVA), which corresponded to approximately 5.10^5 *X. fastidiosa* cells per gram of plant. Depending on the availability of frozen samples and in order to avoid the analysis of several samples from the same foci, a selection of samples was made to maximize the number of foci and plant species analyzed and resulted in a set of 534 samples for the MLVA. A total of 396 samples were successfully genotyped for all 13 loci (184 ST6 and 212 ST7; 43.18% of the French *X. fastidiosa* samples and 74.16% of the tested samples) (Table 2, Table S4). The loci were all highly polymorphic across the French dataset with a number of alleles ranging from 7 to 21 and a number of TRs ranging from 1 to 30 (Table 3). Simpson's diversity index ranged from 0.52 to 0.88 and allelic richness from 3.82 to 15.73. For the VNTR loci ASSR-19, XFSSR-40 and XFSSR-58, all possible allele sizes of the allelic range were observed within the collection. For the VNTR loci ASSR-9, ASSR-11, ASSR-12, ASSR-16, COSS-1, GSSR-7, OSSR-16, OSSR-19, XFSSR-37 the observed diversity of TR sizes did not cover the entire allelic range as one to three TR sizes were not observed, indicating either missing infected samples in the evolution path or large mutation steps (Table S4). MLVA accurately resolved the different haplotypes from the French outbreaks as more than 95% of the haplotypes were detected with 12 markers (Fig. S6). The discriminatory power of the MLVA was 0.9969, showing a very high level of discrimination. The distribution of allele frequencies for each of the 13 VNTR loci indicated that some allelic forms were specific of each sequence type, with 34 allelic forms strictly specific to ST6 and 46 allelic forms strictly specific to ST7 (Table S5). Moreover, for 10 VNTR loci (ASSR-11, ASSR-12, ASSR-16, ASSR-19, GSSR-4, OSSR-16, OSSR-19, XFSSR-37, XFSSR-40, and XFSSR-58) different allelic profiles were observed between the two sequence types (Fig. S7). The distribution of allele frequencies for each of the 13 VNTR loci did not indicate differences between samples isolated in Corsica or PACA or their host plant (data not shown).

For a minority of 13 French *X. fastidiosa* infected plant samples, several peaks were observed on the electrophoregrams on 3 up to 12 amplified loci (data not shown), and this was confirmed in at least two independent analyses. As some alleles were, for now, specific of ST6 or ST7 (e.g., for ASSR-16: 29 TR=ST6, 24 TR=ST7), these results revealed the presence of co-infections by several strains in these plants and for some of them potentially by several sequence types.

MLVA allowed observing a large haplotype diversity within French ST6 and ST7 *X. fastidiosa* as 320 haplotypes were delineated. The 184 ST6 samples were genotyped in 148 haplotypes, while the 212 ST7 samples were genotyped in 172 other haplotypes, and no VNTR profile was shared between these two sequence types (Table S4). ST6 samples were grouped into four clonal complexes (*i.e.*, networks grouping haplotypes differing from their closest neighbor at a single VNTR locus). The founder haplotype (#309) of the main clonal complex grouped 11

samples from three plant species (*P. myrtifolia*, *Lavandula* x *allardii*, *Calicotome villosa*), and was linked, in this clonal complex, to 95 samples that were all sampled in Corsica (Fig. 2). ST7 samples grouped into 15 clonal complexes. The founder haplotype (#138) of the main clonal complex comprised 15 samples of three plant species (*P. myrtifolia*, *Genista* x *spachiana*, *Helichrysum italicum)* and was linked to 88 samples, of which 86 were isolated in Corsica and only two in PACA. The other 17 smaller clonal complexes grouped from two to eight samples that were sampled in a same region, with the exception of one clonal complex that grouped haplotype #163 sampled in PACA and haplotype #165 sampled in Corsica. The remaining 167 samples differed by at least two loci (=163 haplotypes, 80 ST6 haplotypes and 83 ST7 haplotypes) or by three and more loci (=36 ST6 haplotypes and 32 ST7 haplotypes). This high number of singletons differing by at least two loci from the clonal complexes originated from the evolution of all VNTRs but OSSR-16 for ST6 samples and ASSR-16, GSSR-4 and XFSSR-58 for ST7 samples (Table S4).

Due to the nature of the data that mostly came from official monitoring programs, which aim is the eradication of any infected plant and not population genetics studies, it was impossible to analyze the impact of the host and year of sampling on the minimum spanning tree (MST) structuration. Nevertheless, the presence of infected samples from 2015 in distal parts of evolutionary branches and of founder haplotypes sampled in 2017 (Fig. 2) suggests that sampling was carried out in an already diversified population. Regarding host plants, a large majority (69.95%) of our dataset was made of myrtle-leaf milkwort plants (*P. myrtifolia*), while Spanish broom (*Spartium junceum*) accounted for 7.07% of the samples and then all remaining 23 plant species each accounted for less than 3.78% of the samples, which was highly imbalanced and did not allow the analysis of MST structuration relative to host species. Moreover, 4.68% of the haplotypes were identified in more than one plant species, indicating that haplotypes did not face intrinsic dispersal barriers.

On the basis of genetic clustering analyses (DAPC and STRUCTURE) and geographical information, we validated the clustering of all 396 samples into four clusters that were, as expected, also supported (p-value < 0.05) by R_{ST} and F_{ST} pairwise comparisons (Table S6). Because DAPC and STRUCTURE analyses led to almost identical groupings (Fig. 3, Fig. S8), the multivariate analysis of population subdivision method of the DAPC was used, as it does not rely on an underlying population genetics model (*41*), in contrast to the model-based clustering algorithm of STRUCTURE. As expected, ST6 and ST7 strains from plant samples were always separated in different clusters. We tested increasing numbers of clusters from k=2 upwards, and for k>6, F-statistics (R_{ST} and F_{ST}) did not validate the groupings. For k=4, cluster 1 was mainly composed of ST6 samples from Corsica (135 Corsica and two PACA); cluster 2 grouped the rest of the 47 ST6 samples (19 Corsica and 28 PACA); cluster 3 was mainly composed of the ST7 samples from Corsica (110 Corsica and eight PACA); and cluster 4 grouped the remaining 94 ST7 samples mainly sampled from PACA (19 Corsica and 75 PACA) (Fig. 3). In the 20 independent DAPC runs, all 396 samples, except 16, were consistently assigned to a single DAPC cluster (Table S4). For these 16 remaining samples, the 11 ST6

samples, all from PACA, were most often (i.e. in 70% of the runs) assigned to DAPC cluster 2 (mix geographical origin), and less frequently to DAPC cluster 1 (i.e. in 30% of the runs). The five ST7 samples from Corsica and PACA were most often (i.e. in 80 % of the runs) assigned to DAPC cluster 4, and less frequently to DAPC cluster 3 (i.e. in 20 % of the runs). All samples grouped in clonal complexes by MST analysis clustered together at k=4 by DAPC analysis. For lower and higher values of k (two to six) each ST6 and ST7 group of samples were gradually divided from one to three clusters. At k=6, two of the three ST6 clusters grouped both samples isolated in Corsica and PACA regions, without any obvious clustering in relation to host or year of isolation. Moreover, comparing these clusters and the MST, the main ST6 clonal complex containing 95 samples was divided into two clusters. Regarding ST7, the three clusters grouped samples isolated from both regions. MST algorithm and DAPC and STRUCTURE provided coherent clustering for k=4 and this clustering made biological sense (clustering mainly coherent with geographical origin of the strain or potential dissemination of haplotypes), so it was used as a first basis for further analyses.

Bridgehead introductions of *X. fastidiosa* subsp. *multiplex* ST6 and ST7 in Corsica from PACA

We inferred the routes of dissemination of *X. fastidiosa* subsp. *multiplex* in France using Approximate Bayesian Computation, beginning with the definition of a set of evolutionary scenarios that may explain the observed data. Firstly, in order to keep tested scenarios as simple as possible, we analyzed ST6 and ST7 French samples separately, because there was no known element indicating that these different strains were introduced simultaneously into France and tip-dating provided different dates of divergence for French ST6 and ST7 strains from their American relatives. Secondly, we had to define groups of strains likely to have shared common history (in sexual species, these would be populations, but in bacteria this step is not trivial). In each cluster previously defined by DAPC, samples originating from distinct regions were split as subgroups when the corresponding populations were differentiated based on R_{ST} and F_{ST} pairwise comparisons, with a p-value < 0.05 (Table S4 and S6). Moreover, analysis of molecular variance evaluated that the majority of the genetic variance occurred within the subgroups (ST6: 63.99%, ST7: 78.12%) (Table S7). As a result, three groups were defined for each sequence type (Table S4, Fig. 4). For ST6, the DAPC cluster 1 grouping samples mostly from Corsica (135 samples) and a few from PACA (two samples) was named ST6_C1P1. The DAPC cluster 2 was separated into two subgroups: one named ST6_C2, grouping the 19 samples originating from Corsica and another one named ST6_P2 grouping the 28 samples originating from PACA. For ST7, the DAPC cluster 3 grouping samples mostly from Corsica (110 samples) and a few from PACA (eight samples) was named ST7_C1P1. The DAPC cluster 4 was separated into two subgroups, one, named ST7_C2, composed of the 19 samples originating from Corsica, and another one, named ST7_P2, composed of the 75 samples originating from PACA.

The number of scenarios with three French populations, one outgroup population and possible non-sampled (ghost) populations is huge, making it impossible to perform a single analysis to

answer our question. To cope with this complexity, we adopted a two-step approach composed of i) a bottom-up stage in which population from a same sequence type were analyzed two by two in three different analyses, which aimed at deciphering histories between pairs of French populations (Fig. S9A), and ii) a top-down stage confronting three-population scenarios not excluded by the bottom-up stage (Fig. S9B).

On the three **French ST6 populations** (C1P1, C2, and P2), after bottom-up approach, no scenario (topology × combination of populations) achieved sufficiently high posterior probability and low prior error rate to be considered as the best scenario to reconstruct the evolutionary history of the ST6 French populations in regards to their USA counterparts. However, some scenarios had so low posterior probabilities ($p<0.05$) that they could be ruled out (Table S8). Specifically, scenarios 2 and 6 testing the possibility of only one French population were ruled out for all combinations of populations, confirming that the French ST6 samples did group into three populations (Fig. S9A).

Scenarios not excluded during this first stage were used in the top-down approach to elaborate scenarios of the evolutionary history of the three French ST6 populations (Fig. S9B). Considering all combinations of populations, 30 scenarios were confronted (Fig. S10). Scenario II.7 was selected in the abcrf analysis as the most probable scenario with 9.9% of the votes and the highest posterior probability (0.26 – 0.37) (Table S8). In this scenario, ST6 strains would have been first introduced in PACA (P2 population). Then population C1P1 would have diverged from this initial focus, and would thus represent the first established population in Corsica. A second independent population (C2) would have diverged later on from the first established P2 population in PACA, and established in Corsica (Fig. S10). However, it should be tempered by the fact that this selected scenario also presented a high prior error rate (0.72) (Table S8).

The following most probable scenarios received a low number of votes. The second and third best scenario were III.I.16 and II.9 with respectively 5.8% and 5.7% of votes (Table S8). These two scenarios had a close topology to scenario II.7, as both considered an introduction in PACA (P2), from which the population C2 from Corsica would have diverged. Moreover, on the 30 scenarios confronted, the seven scenarios testing the hypothesis that the Corsican population C2 would have diverged from the P2 population from PACA totalized 35.9% of the votes, giving more strength to this event.

Similarly, on the three **French ST7 populations** (C1P1, C2, and P2), the bottom-up approach did not allow to identified the best scenario, but allowed ruling out scenarios 2 and 6, thereby confirming that the French ST7 samples did group into three populations (Fig. S9A, Table S8). In addition, scenarios 1 and 9 that tested independent and successive introductions of each French populations from the American ancestor were also excluded. It is however interesting to note that similar scenarios (5 and 10) including an unsampled population between the American ancestor and the French ones were not ruled out. In contrast, scenarios 11 and 12 that were slight variations of previous scenarios 1 and 9 including unsampled populations between

the American ancestor and each French populations were ruled out. Altogether, six scenarios (n°3, 4, 5, 7, 8 and 10, Fig. S9A) were kept for further consideration after this bottom-up approach.

Moving to the top-down approach, based on the results of the bottom-up approach scenarios that tested independent introductions (class I in Fig. S9B) and those testing two independent introductions, one of which was responsible for a bridgehead invasion of the third population (class III.I and III.II in Fig. S9B), were consequently not considered. This left us with two closely related topologies to be tested (Fig. S9B and Fig. S11), i.e., scenarios testing the introduction in France of one population subsequently responsible for two independent bridgehead invasions, (class II in Fig S10B), and scenarios considering that the first introduction lead to two successive bridgehead invasions (class IV in Fig S10B). Considering all combinations of populations, 12 scenarios were confronted. Scenario II.1 was selected in the abcrf analysis as the most likely scenario with 17.5% of the votes and with the highest posterior probability (0.41 – 0.50) (Table S8). In this scenario, ST7 strains would have been first introduced in PACA (P2 population). Then population C1P1 would have diverged from this initial focus, and would thus represent the first established population in Corsica. A second independent population (C2) would have diverged later on from the first established P2 population in PACA, and established in Corsica (Fig. S11). However, it should be tempered by the fact that this well supported scenario also presented a high prior error rate (0.70 – 0.71) (Table S8).

Then scenarios having the highest number of votes were scenario IV.27 and scenario IV.25, to which respectively 12.4% and 10.9% of the votes were attributed (Table S8). Both had a close topology to the best scenario, as they considered that a first population would have been introduced in PACA (P2), from which populations C1P1 and C2 would have diverged but from two successive bridgehead invasions (C1P1 then C2 or C2 then C1P1) instead of two independent divergence events. Moreover, among the 12 scenarios confronted, the four scenarios testing the hypothesis that the population from PACA (P2) was the first one introduced in France and from which the other two population diverged totalized 53.24% of the votes, giving more strength to this event.

Discussion

While natural spreading capacities of *X. fastidiosa* depend on the activity of the sap-sucking insects that vector this bacterium from plant to plants, the detection of strains outside their areas of origin since the end of the 19th century illustrates the effectiveness of its human-assisted transmission, as elegantly demonstrated for *X. fastidiosa* strains introduced in the Balearic islands (*42*). The introduction of infected but asymptomatic plants for planting of species not cultivated in Europe, such as coffee plants, or of various ornamental species is now considered one, if not the main pathway for introduction of *X. fastidiosa* (*13*). The introduction of the subspecies *fastidiosa* in California would have been the first example (*4*, *21*) and the introduction of *X. fastidiosa* subsp. *pauca* strain ST53 into Apulia, Italy, the most recent one

(*29*). It is within this framework that we have sought to reconstruct the invasive scenario of *X. fastidiosa* subsp. *multiplex* ST6 and ST7 in France.

First, we estimated the divergence time of strains from the main lineages present in France (ST6 and ST7) from their American relatives and from the ST6 and ST81 Spanish strains. Divergence date between French and American ST6 strains was estimated in 1987 (1974 to 1994 95% HPD), while divergence date between French and American ST7 strains was estimated a little earlier in 1971 (1924 to 1994 95% HPD). Moreover, very few SNPs were detected between French strains sharing the same sequence type, confirming recent introductions, even if divergence time is not synonymous to introduction time, but here represent the lower bounds of introduction. The period of divergence of ST6 and ST7 French strains from US counterparts corresponds to the 70's-80's, a period during which alien plants were massively introduced in Corsica (*43*). To our knowledge, no such data about alien species trade, in particular from the only other known place of occurrence of *X. fastidiosa* subsp. *multiplex* ST6 and ST7, the USA, could be recovered to document potential introductions in PACA. The period of time for *X. fastidiosa* introduction into France inferred from analysis of genomic data is highly consistent with a previous evaluation dating it in 1985 (1978 to 1993 95% HPD) (*44*). That study used a mechanistic-statistical approach based on spatio-temporal modelling of the French surveillance plan data and the assumption of a hidden compartment limiting the exhaustiveness of the sampling (*44*). This study did not take into account the genetic diversity of the pathogen and considered the subspecies *multiplex* no matter its sequence type, as a whole, which explains the fact that only one date of introduction was proposed. In contrast, our results are not consistent with estimates from the recent study of Moralejo *et al* (2020), which dated the introduction in Corsica of *X. fastidiosa* subsp. *multiplex* in 2000 (*42*). Actually, in this study only three Corsican strains all isolated in 2015 were analyzed and strains where clustered by region during analysis without taking into account the presence of the two genetic lineages, ST6 and ST7, both present in Corsica. In our study, the dating of the French strains, make them the earlier ones that would have occurred in Europe, before the introduction of ST1 in 1993 and of ST81 in 1995 in the Balearic Islands, of ST6 in 2005 in mainland Spain and of ST53 in Apulia (*20*, *42*). We also confirmed the polyphyly of the French and Spanish ST6 strains previously observed (*29*). These two groups of strains differed by 899 to 912 SNPs and their divergence date traced back to the divergence between ST6/ST81 and ST7 estimated in 755 (-397 to 1540 95% HPD). At the time of this study no strain or genome of Spanish ST7 strains was available, which impeded their inclusion in our study.

In order to specify the invasive scenario of ST6 and ST7 introductions and further dissemination over the French territory, genomic data were used. All the 49 *X. fastidiosa* subsp. *multiplex* strains isolated in France from plant were sequenced and together with publicly available sequences they allowed the extraction of a core genome of 1,679,574 bp containing 16,739 SNPs. These data are in line with those previously obtained by Landa *et al*. (2020), in which the core genome of 21 *X. fastidiosa* subsp. *multiplex* strains was estimated at 1,569,508 bp, containing 5,630 core SNPs (*29*). But these data are surprisingly in contrast with those of

Vanhove *et al*. (2019) in which the core genome of 23 strains of *X. fastidiosa* subsp. *multiplex* was estimated at 736,868 bp containing 37,485 SNPs (*20*). Differences may rely on the use of different methodologies as Vanhove *et al.,* (2019) study analyzed mapped raw reads data on reference and both Landa's *et al.,* (2020) and our study analyzed assembled genomes which is more precise.

The molecular evolutionary rates of *X. fastidiosa* subsp. *multiplex* was evaluated using tip-calibrating approach at 3.2165×10^{-7} substitutions per site per year (1.5468×10^{-7} – 5.2043×10^{-7} 95% HPD). This estimation is congruent with those previously estimated for the subspecies *pauca* (7.62×10^{-7} substitutions per site per year, 95 Confidence Interval (CI): 1.027×10^{-7} to 1.454×10^{-6}) and for the subspecies *fastidiosa* (6.38×10^{-7} substitutions per site per year, 95 CI: 3.9277×10^{-7} to 9.0912×10^{-7} and 7.71×10^{-7} substitutions per site per year, 95 CI: 1.20×10^{-7} to 1.69×10^{-6} substitutions per site per year) (*20*, *42*, *45*). Moreover, the mean substitution rate estimated in our study is consistent with those of several human and animal bacterial pathogens estimated within a similar time period (*46*).

To trace back the most probable invasive scenario for ST6 and ST7 strains in France, we developed a MLVA typing scheme, composed of 13 VNTRs adapted for analyses at small evolutionary scales. Another strength of our analysis comes from the fact that it was specifically developed and optimized to study the diversity of the subspecies *multiplex*. We made use of discriminant existing VNTR loci (*39*, *40*) and coupled them to three newly identified VNTR loci, the only ones that we found to complement the observed diversity in our collection of *X. fastidiosa* subsp. *multiplex* strains. This relatively limited number of examined loci (13) should however be analyzed with regards to the small size of *X. fastidiosa* genome. Another strength of our MLVA scheme is that it has been developed and optimized to be directly usable on genomic DNA extracted from fresh or frozen infected plant material, as it has already shown to be possible for Italian samples infected with *X. fastidiosa* subsp. *pauca* ST53 (*47*). Our study further confirms the interest of such direct genotyping techniques.

MLVA highlighted substantial diversity within each sequence type as three subgroups of samples were defined that partially fitted with the geographical location of samples. One subgroup was composed of both PACA and Corsican samples, and the other two were exclusively composed of samples from PACA or Corsica regions. These groups however clustered samples from various plant species. On the one hand such genetic structures are highly indicative of a long distance spread of the pathogen by human activities for the two groups mixing geographical origins of strains, i.e. lacking spatial structuration. Human activities are often associated with fortuitous introductions of pathogens into yet free areas that turned out to be responsible for high losses (*48*). On the other hand, the two other groups of each sequence type that are highly spatially structured are indicative of a more local dissemination that can result from human activities but also, as it overcomes host barrier, from the activity of insect vectors, the only natural means of dispersion of *X. fastidiosa*. In Corsica, *Philaenus spumarius* was identified as a potential vector of *X. fastidiosa* ST6 and ST7 strains (*49*).

From an American origin, a first ST6_P2 population would have been introduced in PACA and have spread within this region, where it was found on ornamental plants in urban contexts. Contemporary samples are clustered in a limited area around cities Antibes and Nice. Then, a population, named C1P1, diverged from this bridgehead initial population. This divergent population also established in PACA but individuals were also introduced in western Corsica, where they established. This introduction is most likely attributable to the trade of infected plants, i.e. *P. myrtifolia*, as it is known that plantings of this ornamental species were multiplied in a few places in Tuscany, Italy and PACA and were subsequently moved to Corsica (*50*). Other hosts identified within this group both come from Corsican bush and ornamentals. In western Corsica the founders of this group were mainly found around the city of Ajaccio. Finally, the last population, named C2, found only in Corsica would have diverged from the bridgehead population established in PACA and spread around Zonza in eastern Corsica. For now, ABC analysis did not fully validate all these scenarios, but the hypothesis according to which the Corsican C2 population would have diverged from the population P2 of PACA is the most likely to have happened.

A very similar scenario was found as the most probable for ST7, the differences rely mostly in places of occurrence, with co-location of ST6 and ST7 infected samples in some places. In Corsica the ST7_C1P1 population coming from the P2 population from PACA established in Southern Corsica and then Corsican C2 population, also coming from the P2 population, spread around Ajaccio, but also in distant places in the Northern and Western parts of Corsica. This larger distribution over the Corsican territory is congruent with an older introduction, estimated here as 16 years earlier for the ST7 strains (1971), than the ST6 one (1987). Here again, ABC analysis did not fully validate the entire scenario, but the hypothesis according to which the population P2 from PACA was the first established in France, from which the two other diverged is the most likely to have happened. Bridgehead effect is a concept first developed for eukaryote invasive species (*51*) and recently applied to phytopathogenic bacteria (*36*). Here, we suspect that trade of infected myrtle leaf milkwort (the species representing 69.95% of the samples detected infected over the reference period, from which founder haplotypes of all clonal complexes were detected) represents all initial migration events that served later on as a reservoir for local dissemination by plant movement or insect vectors, which would explain the identification of same haplotypes in plants of different species.

P. myrtifolia is a bush native to South Africa, genetically bred in Florida in the 1980's, before being sold to Europe (*50*, *52*). Moreover, the first identification of ST6 and ST7 of *X. fastidiosa* subsp. *multiplex* were made in the Eastern and South-Eastern USA (*10*). In Europe the three largest countries that produce *P. myrtifolia* cuttings are Italy, Spain and then Portugal (*50*). In Corsica, the trade of plants is unilateral and plants from southern Europe are sold to PACA, which serves as an importer for Corsica or are sold directly to Corsica. In fact, when the *X. fastidiosa* detections arose in 2015 in Corsica, the origins of the first infected *P. myrtifolia* plants were Italy (8 plants), PACA (2 plants) and Spain (1 plant) (*50*). Furthermore, the dates of diversification of the French ST6 and ST7 strains compared to their American counterparts, in

1987 and 1971 respectively, correspond to a period of massive introduction of exotic plants, particularly in Corsica (*43*). Unfortunately, no such data were found for the PACA area plant trade. All these elements are in line with the best scenario that we obtained and could validate the myrtle leaf milkwort as the initial vector of *X. fastidiosa* subsp. *multiplex* in France. The climate all over France is supposed to be favorable for the spread and survival of *X. fastidiosa* subsp. *multiplex* (*53*). A spread to other areas in France or the discovery of *X. fastidiosa* in other places, such as recently reported in Occitanie (*28*), should be anticipated, as the probable presence of *X. fastidiosa* in Corsica and PACA for half a century has been overlooked. Indeed, in Corsica, sampling was quite exhaustive, as most infected samples grouped in clonal complexes that are biologically meaningful groups of single locus variants epidemiologically related. In contrast, most PACA infected samples grouped in several small clonal complexes and singletons that could not be linked as several evolutionary steps were lacking. Further sampling in PACA would allow refining the scenario we presented here.

Materials and Methods

Bacterial strains and growth conditions

A collection of 95 *Xylella fastidiosa* strains (Table S2) was used in this study. Dr Leonardo De la Fuente (Auburn University, AL, USA) kindly provided 12 *X. fastidiosa* strains isolated in the USA. The Plant Health Laboratory (Anses LSV, Angers, France) shared 39 strains of *X. fastidiosa* subsp. *multiplex*. All strains were preserved by the French Collection of Plant-Associated Bacteria (CIRM-CFBP. International Centre of Microbial Resource (CIRM) - French Collection for Plant-associated Bacteria. INRAE. https://doi.org/10.15454/E8XX-4Z18). Strains were grown on BCYE medium (*10*) or modified PWG medium (*54*) at 28°C for one to two weeks.

DNA extraction and DNA sample collections used for MLVA

Bacterial suspensions were prepared from fresh cultures in sterile distilled water, adjusted at $OD_{600\ nm}$ = 0.1 ($1x10^8$ $CFU.mL^{-1}$), boiled for 20 min, cooled on ice and centrifuged at 10,000 g during 10 min. DNAs from the 18 Spanish *X. fastidiosa* strains (Table S3) were kindly provided by Dr Blanca Landa (Institute for Sustainable Agriculture, Córdoba, Spain) and were extracted using CTAB protocol (*10*). A collection of 357 DNAs from *X. fastidiosa* subsp. *multiplex* infected French plant samples (Table 2, Table S4) was used in this study. These infected samples were collected in Corsica and in PACA between 2015 and 2018 in the framework of the national official surveillance strategy for *X. fastidiosa* and other dedicated sampling campaigns and were declared infected based on positive Harper's qPCR test at Cq<38 (*10*). Plant samples were finely chopped in distilled water, optionally sonicated (*54*), and incubated 15 min at room temperature before DNA extraction using CTAB or QuickPick™ SML Plant DNA Kit (Bio-Nobile, Turku, Finland) as described in PM7/24 (*10*). The DNA samples were stored at -20°C before analysis.

DNA extraction and whole-genome sequencing

Highly concentrated bacterial suspensions of the 48 strains to be sequenced by Illumina HiSeq X (Table S1) were prepared from fresh cultures in 5 mL of ultrapure sterile water. The genomic DNA was extracted using the Wizard® Genomic DNA Purification Kit (Promega), following the manufacturer's recommendations. DNA was rehydrated in 100 µL of ultrapure sterile water. Quality and quantity of extracted DNA were verified using a NanoDrop ND-100 Spectrophotometer (Thermofisher) and a Qubit Fluorometer 1.0 (Invitrogen). Library preparation and sequencing were performed on Illumina HiSeq 4000 platform (BGI, Hong Kong). For the seven strains sequenced using the PacBio technology, DNA was extracted from fresh cultures in 10 mL of ultrapure sterile water following Mayjonade *et al*.'s recommendations (*55*). Library preparation and sequencing were performed at the GeT-PlaGe core facility, INRAE Toulouse, according to the manufacturer's instructions "Shared protocol-20kb Template Preparation Using BluePippin Size Selection system (15kb size Cutoff)". At each step, DNA was quantified using the Qubit dsDNA HS Assay Kit (Life Technologies). DNA purity was tested using the NanoDrop (Thermofisher) and size distribution and degradation assessed using the Fragment analyzer (AATI) High Sensitivity Large Fragment 50kb Analysis Kit. Purification steps were performed using 0.45X AMPure PB beads (PacBio). 10µg of each DNA was purified then sheared at 40kb using the megaruptor1 system (diagenode). Using SMRTBell template Prep Kit 1.0 (PacBio), a DNA and END damage repair step was performed on 5µg of each sample. Then blunt hairpin adapters were ligated to the libraries. The libraries were treated with an exonuclease cocktail to digest unligated DNA fragments. A size selection step using a 10kb cutoff was performed on the BluePippin Size Selection system (Sage Science) with 0.75% agarose cassettes, Marker S1 high Pass 15-20kb. Conditioned Sequencing Primer V2 was annealed to the size-selected SMRTbells. The annealed libraries were then bound to the P6-C4 polymerase using a ratio of polymerase to SMRTbell at 10:1. Then after a magnetic bead-loading step (OCPW), 7 SMRTbell libraries were sequenced on 7 SMRTcell on RSII instrument at 0.2nM with a 360 min movie.

Design and development of the VNTR-13 scheme

The complete genome sequence of the M12 strain of *X. fastidiosa* subsp. *multiplex* isolated from *Prunus dulcis* in the USA in 2003 (GenBank accession number NC_010513.1) was screened for the presence of candidate TR loci using Tandem Repeat Finder 4.09 (https://tandem.bu.edu/trf/trf.html). Parameters were set as follows: total length in a range of 50–500 bp and TR length ≤ 44 bp. Other parameters were set as default. The identified loci were analyzed for (i) presence in 10 *X. fastidiosa* subsp. *multiplex* (*38*) using BLASTn, (ii) absence of redundancy with the previously published set of VNTR loci (*39*, *40*), and (iii) existence of polymorphism in the 10 *X. fastidiosa* subsp *multiplex* genome sequences by manual checking. Three novel VNTR loci (XFSSR-37, XFSSR-40 and XFSSR-58) were retained for further analyses to complete the set of 10 previously published VNTR loci (nine VNTR loci previously designed by Lin *et al*. (2005) and one VNTR locus designed by Francisco *et al*.

(2017), Table 1). The 150 bp flanking regions of these VNTR loci were extracted from the 10 genome sequences of *X. fastidiosa* subsp *multiplex*. Oligonucleotide primers were designed in their homologous segments using Primer3 2.3.4 (*56*). The specificity of all 13 VNTR primer pairs was tested *in silico* using PrimerSearch (Val Curwen, Human Genome Mapping Project, Cambridge, UK) on the 154,478 bacterial Whole Genome Shotgun (WGS) sequences available in the NCBI database (as on August 22, 2018). The primer pair sets were tested using Amplify to verify the absence of dimer and cross-amplification (*57*).

VNTR-13 scheme genotyping

Primers were tested by PCR using 16 strains of *X. fastidiosa* as a "panel test" (Table S2). Primer pair multiplexing was done according to the annealing temperature. Finally, all forward primers were labeled with one of the fluorescent dyes (6-FAM, HEX, ATTO550 and ATTO565) (Eurofins) at their 5' end. To optimize VNTR amplification protocol for direct use in plant material, the efficiency of two Taq polymerases (Platinum™ Taq DNA Polymerase, Invitrogen, and GoTaq® G2 Flexi DNA Polymerase, Promega) were compared, as well as the impact of the DNA volume (1 µL and 2 µL) added to the reaction mix on ASSR-9, ASSR-16 and GSSR-4 VNTR loci amplification. Tests were run on DNA extracted from maceration of healthy *Polygala myrtifolia* samples (0.2 $g.ml^{-1}$) spiked with CFBP 8416 strain suspensions ranging from 1×10^2 to 1×10^6 $CFU.mL^{-1}$. These tests allowed the determination of the limit of VNTR genotyping directly in plant extract as a function of Cq, as spiked solutions were all tested with the Harper's qPCR test (*58*). Finally, the PCRs were performed in a 20 µL-final volume containing 1X PCR buffer (no magnesium chloride) (Invitrogen), 1.5 mM of magnesium chloride (Promega), 0.2 mM of each dNTP, 0.2 µM of each primer (Promega), 1U of Platinum® Taq DNA Polymerase (Invitrogen) and 2 µL of sample DNA or 1 µL of boiled bacterial suspension. The optimal PCR conditions were 5 min at 95°C, followed by 35 cycles of 30 s at 95°C, 30 s at the annealing temperature (Table 1) and 30 s at 72°C, and ended by 10 min at 72°C.

To test VNTR typing repeatability the strain CFBP 8416 was included as a control in each series of amplification. For samples previously detected infected by *X. fastidiosa* with the Harper's qPCR test at Cq values below 27, VNTRs were amplified in multiplex formats and 2.4 µL of PCR products were mixed with 9.35 µL of Hi-Di formamide (Sigma-Aldrich) and 0.15 µL of Genescan 500 Liz internal line size standard (Applied Biosystems) for capillary electrophoresis using an ABI PRISM 3130 genetic analyzer (Applied Biosystems): injection of 16 sec at 1.2 kvolts, voltage steps 20 nk, interval of 15 sec, data delay time of 60 sec, run of 12000 sec at 15 kvolts,. For samples with Cq values equal at 27 or lower than 32, VNTRs were amplified in simplex assays and products were visualized on 1% agarose gel electrophoresis in Tris-borate-EDTA buffer. PCR products were multiplexed by four for capillary electrophoresis.

Data scoring

Electrophoregrams were analyzed using Geneious 9.1.8 software (Biomatters) and peaks were first automatically detected using the predict peaks mode. Each ladder and VNTR peaks were then carefully checked by eye and artefacts or small peaks were corrected. The reproducibility of the entire experiment was checked by amplifying and sequencing the strain CFBP 8416 in each run. Sets of 13 VNTRs were sequenced for the strains CFBP 8416, CFBP 8417, and CFBP 8418 to confirm TR sequence length, length of the repeat flanking region, and the number of repeats. The number of repeats in each locus was calculated based on the fragment sizes using Geneious 9.1.8 software (Biomatters).

MLVA analyses and statistics

MSTs were drawn and clonal complexes analyzed using the algorithm recommended for MLVA data combining global optimal Euclidean and goeBURST distances in PHYLOViZ v2.0 (*59*). Haplotypes differing one another by only one locus (single-locus variant, SLV) were grouped in clonal complexes. The discriminatory power of the MLVA was calculated using http://insilico.ehu.es/mini_tools/discriminatory_power/index.php. Data were analyzed using two different methods in order to infer population structure and assign samples to clusters. Bayesian clustering approach (STRUCTURE 2.3.4 software) (*60*) was applied with 10 independent runs, performed for K=1 to 10, with a burn-in period of 100,000 iterations followed by 500,000 Monte Carlo Markov Chain (MCMC) replicates. This analysis was completed with the Discriminant Analysis of Principal Components (DAPC), which was used as it does not rely on any assumption about the population genetic model (*41*). DAPC analyses were conducted on 20 independent k-means runs in order to verify the stability of the clustering. Analyses were performed using a single individual per haplotype with the adegenet package from the R software (*61*). Simpson's index of diversity using BioNumerics 7.6 (Applied Maths) and allelic richness using Fstat 2.9.4 (*62*) were calculated to access the discriminatory power of each VNTR. Using the groups defined by DAPC, the number of alleles and their frequency distribution were determined using GenAlEx 5.5.1 (*63*). Genetic differentiation of the DAPC groups was estimated using F_{ST} and R_{ST} with Arlequin 3.5.2.2 (*64*). Using the same software an analysis of molecular variance was performed. The individuals were grouped according to the groups established for DIYABC analysis. Spatial representation of the distribution of the French samples and their genetic clustering on the French territory were made using the R package maptools (*65*).

Approximate Bayesian Computation (ABC) analysis

We investigated whether the French emergence of *X. fastidiosa* subsp. *multiplex* was the result of multiple independent introduction events or the result of one or a few events that subsequently spread. First, we conducted a scenario choice using ABC. This method consists in generating a large number of datasets, simulated under each of the tested scenarios, and measuring the similarity between the simulated data and the real data with statistics (*66*). The

posterior probability of each scenario is then obtained from its occurrence in the simulations that are the closest to the real dataset using a post-sampling adjustment (*66*). To decipher the scenario of introduction of *X. fastidiosa* subsp. *multiplex* in France, we first used an ABC approach which is implemented in the DIYABC software v2.1 (*67*). Then, the machine learning tool ABC random forest (ABC-rf), implemented in the R package "abcrf" (*68*) was used to analyzed DIYABC results, as it is the most robust and offers a larger discriminative power among competing scenarios (*68*, *69*).

Data were analyzed independently per sequence type number (ST6 and ST7). As *X. fastidiosa* subsp. *multiplex* ST6 and ST7 were previously known to occur only in the USA, the American ST6 Dixon strain and the American ST7 M12 and Griffin strains were used as representatives of ancestral populations, from which the French strains were linked. All MLVA data from French infected samples and strains were used to run ABC analyses. Four genetic groups were defined for ST6 and ST7 strains, using results previously obtained from DAPC and STRUCTURE clustering analysis, goeBURST tree topology, historical and geographical information. For both sequence type analyses, three French populations were defined, one grouping both Corsica and PACA samples (named C1P1), one grouping exclusively Corsica samples (named C2) and one grouping exclusively PACA samples (named P2). Based on these assumptions and data, the number of possible scenarios to test was estimated at 30, without taking into account the existence of unsampled population(s). In order to limit the number of scenarios analyzed in each run, a Nested strategy was followed. Populations were first compared by a bottom-up approach, in which scenarios were composed only of American strain(s) and two French populations. Then, the following analyses used the conclusions obtained from previous analyses and allowed to eliminate assumptions. Second, all French populations were simultaneously compared in a top-down approach, in which each scenario topology was analyzed separately. For a detailed description of the scenarios analyzed and software parameters read "Supplemental material".

Genome assembly, alignment and SNP calling

A total of 82 genome sequences of *X. fastidiosa* subsp. *multiplex* was analyzed in this study (Table S1), including 27 publicly available genome sequences (NCBI on 16/12/2019) and 55 genome sequences of strains that were sequenced in this study (49 from France and 6 from USA). Genome assembly was performed with SOAPdenovo version 2.04, SOAPGapCloser version 1.12 (*70*) and Velvet version 1.2.02. (*71*). The 82 genome sequences were aligned using the strain M12 as a reference with Parsnp tool v1.2 from Harvest suite (*72*) to obtain *X. fastidiosa* subsp. *multiplex* core genome. The matrix of SNPs was extracted using Gingr tool v1.3 from Harvest suite (*72*). Detection of recombinant sequences within the core genome alignment was performed using ClonalFrame (*73*), running three independent MCMCs of 50,000 iterations, a burn-in length of 10,000 iterations and iteration samples every 100 iterations. The recombinant events detected were discarded from the SNP matrix using R scripts (M. Mariadassou and D. Merda pers. comm.) sourcing the "ape" (*74*) and "coda" packages (*75*).

Population structure

To infer population structure, the fastStructure program based on a Bayesian clustering approach was run on the whole core SNPs alignment (*76*). Ten independent runs were performed for K=1 to 10, with a MCMC of 1,000,000 iterations. The other parameters were set as default. Then a heat map was drawn using the gplots package (*77*) of R software on SNPs only issued from mutation events.

Molecular Tip dating

The no-recombining core genome of the 82 strains, spanning 36 years of evolution (1983 to 2018) was used to investigate the presence of temporal signal thanks to two different tests. At first, a Maximum Likelihood (ML) tree was constructed with RAxML 8.2.4 (*78*) using a rapid Bootstrap analysis, a General Time-Reversible model of evolution following a Γ distribution with four rate categories (GTRGAMMA) and 1,000 alternative runs. A linear regression test between sample age and root-to-tip distances was computed at each internal node of the ML tree using Phylostems (*79*). Temporal signal was considered present at nodes displaying a significant positive correlation. Secondly, a date-randomisation test (*80*) was performed with 40 independent date-randomised datasets built with the R package "TipDatingBeast" (*81*). The "RandomCluster" function allowed to randomized the isolation dates of samples per cluster of 10 years (1983-1989; 1990-1999; 2000-2009; 2010-2018). Results were generated using the "PlotDRT" function. Temporal signal was considered present when there was no overlap between both the inferred root height and substitution rate 95% HPD of the initial dataset and that of the date-randomized datasets. Tip-dating inferences were performed using the Bayesian MCMC method implemented in BEAST v2.6.1 (*37*). Leaf heights were constrained to be proportional to sample ages. Flat priors (i.e., uniform distributions) were applied both for the substitution rate (10^{-12} to 10^{-2} substitutions/site/year) and for the age of all internal nodes in the tree. We also considered a general time reversible (GTR) substitution model with a Γ distribution and invariant sites (GTR+G+I), an uncorrelated relaxed log-normal clock to account for variations between lineages, and a tree prior for demography of coalescent Bayesian skyline. Six independent chains were run for 200,000,000 step and sampled every 20,000 steps, after a discarded burn-in of 10%. Convergence, sufficient sampling and mixing were verified by visual inspection of the posterior samples using Tracer v1.7.1 (*37*). Parameter estimation was based on the samples combined from the six different chains. The six tree output files were merged using LogCombiner software v2.6.1 after a 20% burn-in period and the best supported tree was drawn using the maximum clade credibility method implemented in Tree-Annotator software v2.6, after a 10% burn-in period (*37*). In parallel, Bayesian skyline analysis was performed to observe effective population size along time using Tracer v1.7.1 (*37*).

References

1. S. Savary, L. Willocquet, Modeling the Impact of Crop Diseases on Global Food Security. *Annual Review of Phytopathology*. **58**, 313–341 (2020).

2. P. K. Anderson, A. A. Cunningham, N. G. Patel, F. J. Morales, P. R. Epstein, P. Daszak, Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. *Trends in Ecology & Evolution*. **19**, 535–544 (2004).

3. C. Bonneaud, L. A. Weinert, B. Kuijper, Understanding the emergence of bacterial pathogens in novel hosts. *Phil. Trans. R. Soc. B*. **374**, 20180328 (2019).

4. L. Nunney, X. Yuan, R. Bromley, J. Hartung, M. Montero-Astúa, L. Moreira, B. Ortiz, R. Stouthamer, Population genomic analysis of a bacterial plant pathogen: novel insight into the origin of Pierce's disease of grapevine in the U.S. *PLoS ONE*. **5**, e15488 (2010).

5. L. Nunney, D. Hopkins, L. Morano, S. Russell, R. Stouthamer, Intersubspecific Recombination in Xylella fastidiosa Strains Native to the United States: Infection of Novel Hosts Associated with an Unsuccessful Invasion. *Applied and Environmental Microbiology*. **80**, 1159–1169 (2014).

6. EFSA, A. Delbianco, D. Gibin, L. Pasinato, M. Morelli, Update of the Xylella spp. host plant database – systematic literature search up to 30 June 2021. *EFSA Journal*. **20**, e07039 (2022).

7. P. P. Kandel, R. P. P. Almeida, P. A. Cobine, L. De La Fuente, Natural Competence Rates Are Variable Among Xylella fastidiosa Strains and Homologous Recombination Occurs In Vitro Between Subspecies fastidiosa and multiplex. *MPMI*. **30**, 589–600 (2017).

8. L. Nunney, E. L. Schuenzel, M. Scally, R. E. Bromley, R. Stouthamer, Large-Scale Intersubspecific Recombination in the Plant-Pathogenic Bacterium Xylella fastidiosa Is Associated with the Host Shift to Mulberry. *Appl Environ Microbiol*. **80**, 3025–3033 (2014).

9. L. Nunney, X. Yuan, R. E. Bromley, R. Stouthamer, Detecting Genetic Introgression: High Levels of Intersubspecific Recombination Found in Xylella fastidiosa in Brazil. *Appl. Environ. Microbiol.* **78**, 4702–4714 (2012).

10. EPPO, PM 7/24 (4) Xylella fastidiosa. *EPPO Bulletin*. **49**, 175–227 (2019).

11. M. Saponari, D. Boscia, F. Nigro, G. P. Martelli, Identification of DNA sequences related to Xylella fastidiosa in oleander, almond and olive trees exhibiting leaf scorch symptoms in Apulia (southern Italy). *Journal of Plant Pathology*. **95**, 659–668 (2013).

12. M. Saponari, A. Giampetruzzi, G. Loconsole, D. Boscia, P. Saldarelli, Xylella fastidiosa in Olive in Apulia: Where We Stand. *Phytopathology*. **109**, 175–186 (2019).

13. EFSA, C. Bragard, K. Dehnen-Schmutz, F. D. Serio, P. Gonthier, M. A. Jacques, J. A. J. Miret, A. F. Justesen, A. MacLeod, C. S. Magnusson, P. Milonas, J. A. Navas-Cortés, R. Potting, P. L. Reignault, H.-H. Thulke, W. van der Werf, A. V. Civera, J. Yuen, L. Zappalà, D. Boscia, D. Chapman, G. Gilioli, R. Krugner, A. Mastin, J. R. S. Lopes, A. Simonetto, S. White, J. C. Abrahantes, A. Delbianco, A. Maiorano, O. Mosbach-Schulz, G. Stancanelli, M. Guzzo, S. Parnell, Update of the Scientific Opinion on the risks to plant health posed by Xylella fastidiosa in the EU territory. *EFSA Journal*. **17**, e05665 (2019).

14. EPPO, EPPO A2 List of pests recommended for regulation as quarantine pests - version 2018-09 - (2018), (available at https://www.eppo.int/ACTIVITIES/plant_quarantine/A2_list).

15. European Commission, Commission Delegated Regulation (EU) 2019/1702 of 1 August 2019 supplementing Regulation (EU) 2016/2031 of the European Parliament and of the Council by establishing the list of priority pests. *Official Journal of the European Union* (2019) (available at http://data.europa.eu/eli/reg_del/2019/1702/oj/eng).

16. European Commission, Commission implementing regulation (EU) 2020/1201 of 14 August 2020 as regards measures to prevent the introduction into and the spread within the Union of Xylella fastidiosa (Wells et al.). *Official Journal of the European Union* (2020).

17. R. Krugner, M. S. Sisterson, E. A. Backus, L. P. Burbank, R. A. Redak, Sharpshooters: a review of what moves Xylella fastidiosa. *Austral Entomology*. **58**, 248–267 (2019).

18. C. C. Su, C. J. Chang, C. M. Chang, H. T. Shih, K. C. Tzeng, F. J. Jan, C. W. Kao, W. L. Deng, Pierce's Disease of Grapevines in Taiwan: Isolation, Cultivation and Pathogenicity of Xylella fastidiosa. *Journal of Phytopathology*. **161**, 389–396 (2013).

19. A. Giampetruzzi, M. Saponari, G. Loconsole, D. Boscia, V. N. Savino, R. P. P. Almeida, S. Zicca, B. B. Landa, C. Chacón-Diaz, P. Saldarelli, Genome-Wide Analysis Provides Evidence on the Genetic Relatedness of the Emergent Xylella fastidiosa Genotype in Italy to Isolates from Central America. *Phytopathology*. **107**, 816–827 (2017).

20. M. Vanhove, A. C. Retchless, A. Sicard, A. Rieux, H. D. Coletta-Filho, L. D. L. Fuente, D. C. Stenger, R. P. P. Almeida, Genomic Diversity and Recombination among Xylella fastidiosa Subspecies. *Appl. Environ. Microbiol.* **85**, e02972-18 (2019).

21. J. M. Guinn, *A History of California and an Extended History of Los Angeles and Environs: Also Containing Biographies of Well Known Citizens of the Past and Present* (Historic Record Company, 1915), vol. 1.

22. L. R. Nunes, Y. B. Rosato, N. H. Muto, G. M. Yanai, V. S. da Silva, D. B. Leite, E. R. Gonçalves, A. A. de Souza, H. D. Coletta-Filho, M. A. Machado, S. A. Lopes, R. C. de Oliveira, Microarray Analyses of Xylella fastidiosa Provide Evidence of Coordinated Transcription Control of Laterally Transferred Elements. *Genome Res*. **13**, 570–578 (2003).

23. A. I. Castillo, I. Bojanini, H. Chen, P. P. Kandel, L. De La Fuente, R. P. P. Almeida, Allopatric Plant Pathogen Population Divergence following Disease Emergence. *Appl Environ Microbiol*. **87**, e02095-20 (2021).

24. D. Boubals, La maladie de Pierce arrive dans les vignobles d'Europe. *Prog. Agric. Vitic.*, 85–87 (1989).

25. G. Martins, B. Lauga, C. Miot-Sertier, A. Mercier, A. Lonvaud, M.-L. Soulas, G. Soulas, I. Masneuf-Pomarède, Characterization of Epiphytic Bacterial Communities from Grapes, Leaves, Bark and Soil of Grapevine Plants Grown, and Their Relations. *PLOS ONE*. **8**, 1–9 (2013).

26. N. Denancé, B. Legendre, M. Briand, V. Olivier, C. de Boisseson, F. Poliakoff, M.-A. Jacques, Several subspecies and sequence types are associated with the emergence of Xylella fastidiosa in natural settings in France. *Plant Pathol*. **66**, 1054–1064 (2017).

27. D. Olmo, A. Nieto, D. Borras, M. Montesinos, F. Adrover, A. Pascual, P. A. Gost, B. Quetglas, A. Urbano, J. de Dios Garcia, M. Pilar Velasco-Amo, C. Olivares-Garcia, O. Beidas, A. Juan, E. Marco-Noales, M. Gomila, J. Rita, E. Moralejo, B. B. Landa, Landscape Epidemiology of Xylella fastidiosa in the Balearic Islands. *Agronomy-Basel*. **11**, 473 (2021).

28. EPPO Global Database. *https://gd.eppo.int/reporting/article-6447*, (available at https://gd.eppo.int/reporting/article-6447).

29. B. Landa, A. Castillo, A. Giampetruzzi, A. Kahn, M. Román-Écija, M. P. Velasco-Amo, J. Navas-Cortés, E. Marco-Noales, S. Barbé, E. Moralejo, H. Coletta-Filho, P. Saldarelli, M. Saponari, R. Almeida, Emergence of a Plant Pathogen in Europe Associated with Multiple Intercontinental Introductions. *Appl. Environ. Microbiol.* **86**, 1–15 (2020).

30. C. van der Veer, M. Himschoot, S. M. Bruisten, Multilocus sequence typing of Trichomonas vaginalis clinical samples from Amsterdam, the Netherlands. *BMJ Open*. **6**, e013997 (2016).

31. S. A. Vollmer, A. Bormane, R. E. Dinnis, F. Seelig, A. D. M. Dobson, D. M. Aanensen, M. C. James, M. Donaghy, S. E. Randolph, E. J. Feil, K. Kurtenbach, G. Margos, Host migration impacts on the phylogeography of Lyme Borreliosis spirochaete species in Europe. *Environmental Microbiology*. **13**, 184–192 (2011).

32. R. M. Gonçalves, M. I. Balbi-Peña, J. M. Soman, A. C. Maringoni, G. Taghouti, M. Fischer-Le Saux, P. Portier, Genetic diversity of Curtobacterium flaccumfaciens revealed by multilocus sequence analysis. *Eur J Plant Pathol*. **154**, 189–202 (2019).

33. M. C. J. Maiden, Multilocus Sequence Typing of Bacteria. *Annu. Rev. Microbiol.* **60**, 561–588 (2006).

34. M. A. S. V. Ferreira, S. Bonneau, M. Briand, S. Cesbron, P. Portier, A. Darrasse, M. A. S. Gama, M. A. G. Barbosa, R. de L. R. Mariano, E. B. Souza, M.-A. Jacques, Xanthomonas citri pv. viticola Affecting Grapevine in Brazil: Emergence of a Successful Monomorphic Pathogen. *Front. Plant Sci.* **10**, 1–18 (2019).

35. L. M. Schouls, H. G. J. van der Heide, L. Vauterin, P. Vauterin, F. R. Mooi, Multiple-Locus Variable-Number Tandem Repeat Analysis of Dutch Bordetella pertussis Strains Reveals Rapid Genetic Changes with Clonal Expansion during the Late 1990s. *J Bacteriol*. **186**, 5496–5505 (2004).

36. A. Leduc, Y. N. Traoré, K. Boyer, M. Magne, P. Grygiel, C. C. Juhasz, C. Boyer, F. Guerin, I. Wonni, L. Ouedraogo, C. Vernière, V. Ravigné, O. Pruvost, Bridgehead invasion of a monomorphic plant pathogenic bacterium: Xanthomonas citri pv. citri, an emerging citrus pathogen in Mali and Burkina Faso. *Environmental Microbiology*. **17**, 4429–4442 (2015).

37. R. Bouckaert, T. G. Vaughan, J. Barido-Sottani, S. Duchêne, M. Fourment, A. Gavryushkina, J. Heled, G. Jones, D. Kühnert, N. D. Maio, M. Matschiner, F. K. Mendes, N. F. Müller, H. A. Ogilvie, L. du Plessis, A. Popinga, A. Rambaut, D. Rasmussen, I. Siveroni, M. A. Suchard, C.-H. Wu, D. Xie, C. Zhang, T. Stadler, A. J. Drummond, BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLOS Computational Biology*. **15**, e1006650 (2019).

38. N. Denancé, M. Briand, R. Gaborieau, S. Gaillard, M.-A. Jacques, Identification of genetic relationships and subspecies signatures in Xylella fastidiosa. *BMC Genomics*. **20**, 1–21 (2019).

39. H. Lin, E. L. Civerolo, R. Hu, S. Barros, M. Francis, M. A. Walker, Multilocus simple sequence repeat markers for differentiating strains and evaluating genetic diversity of Xylella fastidiosa. *Applied and environmental microbiology*. **71**, 4888–4892 (2005).

40. C. S. Francisco, P. C. Ceresini, R. P. P. Almeida, H. D. Coletta-Filho, Spatial Genetic Structure of Coffee-Associated Xylella fastidiosa Populations Indicates that Cross Infection Does Not Occur with Sympatric Citrus Orchards. *Phytopathology*. **107**, 395–402 (2017).

41. T. Jombart, S. Devillard, F. Balloux, Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. *BMC Genetics*. **11**, 1–15 (2010).

42. E. Moralejo, M. Gomila, M. Montesinos, D. Borràs, A. Pascual, A. Nieto, F. Adrover, P. A. Gost, G. Seguí, A. Busquets, J. A. Jurado-Rivera, B. Quetglas, J. de D. García, O. Beidas, A. Juan, M. P. Velasco-Amo, B. B. Landa, D. Olmo, Phylogenetic inference enables reconstruction of a long-overlooked outbreak of almond leaf scorch disease (Xylella fastidiosa) in Europe. *Commun Biol*. **3**, 1–13 (2020).

43. D. Jeanmonod, A. Natali, Les xénophytes de Corse: un danger pour la flore indigène. *Lagascalia, 19 (1-2), 783-792.* (1997).

44. S. Soubeyrand, P. de Jerphanion, O. Martin, M. Saussac, C. Manceau, P. Hendrikx, C. Lannou, Inferring pathogen dynamics from temporal count data: the emergence of Xylella fastidiosa in France is probably not recent. *New Phytol*. **219**, 824–836 (2018).

45. M. Vanhove, A. Sicard, J. Ezennia, N. Leviten, R. P. P. Almeida, Population structure and adaptation of a bacterial pathogen in California grapevines. *Environmental Microbiology*. **22**, 2625–2638 (2020).

46. S. Duchêne, K. E. Holt, F.-X. Weill, S. Le Hello, J. Hawkey, D. J. Edwards, M. Fourment, E. C. Holmes, Genome-scale rates of evolutionary change in bacteria. *Microb Genom*. **2**, 1–12 (2016).

47. A. Mazzaglia, Y. J. Rahi, M. C. Taratufolo, M. Tatì, S. Turco, S. Ciarroni, V. Tagliavento, F. Valentini, A. M. D'Onghia, G. M. Balestra, A new inclusive MLVA assay to investigate genetic variability of Xylella fastidiosa with a specific focus on the Apulian outbreak in Italy. *Scientific Reports*. **10**, 10856 (2020).

48. A. Santini, A. Liebhold, D. Migliorini, S. Woodward, Tracing the role of human civilization in the globalization of plant pathogens. *The ISME Journal*. **12**, 647–652 (2018).

49. A. Cunty, B. Legendre, P. de Jerphanion, V. Juteau, A. Forveille, J.-F. Germain, J.-M. Ramel, P. Reynaud, V. Olivier, F. Poliakoff, Xylella fastidiosa subspecies and sequence types detected in Philaenus spumarius and in infected plants in France share the same locations. *Plant Pathology*. **69**, 1798–1811 (2020).

50. G. Chauvel, A. Cruaud, B. Legendre, J.-F. Germain, J.-Y. Rasplus, Mission d'expertise sur Xylella fastidiosa en Corse (3 au 11 août 2015) (2015).

51. N. Miller, A. Estoup, S. Toepfer, D. Bourguet, L. Lapchin, S. Derridj, K. S. Kim, P. Reynaud, L. Furlan, T. Guillemaud, Multiple Transatlantic Introductions of the Western Corn Rootworm. *Science*. **310**, 992–992 (2005).

52. W. Van Der, Polygala myrtifolia L. *Population Genetics of Plant Pathogens* (2003), (available at plantZafrica.com).

53. M. Godefroid, A. Cruaud, J.-C. Streito, J.-Y. Rasplus, J.-P. Rossi, Xylella fastidiosa: climate suitability of European continent. *Sci Rep*. **9**, 8844 (2019).

54. E. Dupas, M. Briand, M.-A. Jacques, S. Cesbron, Novel Tetraplex Quantitative PCR Assays for Simultaneous Detection and Identification of Xylella fastidiosa Subspecies in Plant Tissues. *Front. Plant Sci.* **10**, 1–15 (2019).

55. B. Mayjonade, J. Gouzy, C. Donnadieu, N. Pouilly, W. Marande, C. Callot, N. Langlade, S. Muños, Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. *BioTechniques*. **61**, 203–205 (2016).

56. T. Koressaar, M. Remm, Enhancements and modifications of primer design program Primer3. *Bioinformatics*. **23**, 1289–1291 (2007).

57. W. R. Engels, Contributing software to the internet: the amplify program. *Trends in Biochemical Sciences*. **18**, 448–450 (1993).

58. S. J. Harper, L. I. Ward, G. R. G. Clover, Development of LAMP and real-time PCR methods for the rapid detection of Xylella fastidiosa for quarantine and field applications. *Phytopathology*. **100**, 1282–1288 (2010).

59. M. Nascimento, A. Sousa, M. Ramirez, A. P. Francisco, J. A. Carriço, C. Vaz, PHYLOViZ 2.0: providing scalable data integration and visualization for multiple phylogenetic inference methods. *Bioinformatics*. **33**, 128–129 (2017).

60. M. J. Hubisz, D. Falush, M. Stephens, J. K. Pritchard, Inferring weak population structure with the assistance of sample group information. *Molecular Ecology Resources*. **9**, 1322–1332 (2009).

61. T. Jombart, adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics*. **24**, 1403–1405 (2008).

62. J. Goudet, FSTAT Version 2.9.4.: A Program to Estimate and Test Population Genetics Parameters. *Available from URL: http://www2.unil.ch/popgen/softwares/fst ?at.htm.* (2005).

63. R. Peakall, P. E. Smouse, GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics*. **28**, 2537–2539 (2012).

64. L. Excoffier, H. E. L. Lischer, Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Mol Ecol Resour*. **10**, 564–567 (2010).

65. R. Bivand, N. Lewin-Koh, E. Pebesma, E. Archer, A. Baddeley, N. Bearman, H.-J. Bibiko, S. Brey, J. Callahan, G. Carrillo, Package 'maptools.' **0.9-9** (2019).

66. M. A. Beaumont, W. Zhang, D. J. Balding, Approximate Bayesian Computation in Population Genetics, 12 (2002).

67. J.-M. Cornuet, P. Pudlo, J. Veyssier, A. Dehne-Garcia, M. Gautier, R. Leblois, J.-M. Marin, A. Estoup, DIYABC v2.0: a software to make approximate Bayesian computation inferences about population history using single nucleotide polymorphism, DNA sequence and microsatellite data. *Bioinformatics*. **30**, 1187–1189 (2014).

68. P. Pudlo, J.-M. Marin, A. Estoup, J.-M. Cornuet, M. Gautier, C. P. Robert, Reliable ABC model choice via random forests. *Bioinformatics*. **32**, 859–866 (2016).

69. A. Fraimout, V. Debat, S. Fellous, R. A. Hufbauer, J. Foucaud, P. Pudlo, J.-M. Marin, D. K. Price, J. Cattel, X. Chen, M. Deprá, P. François Duyck, C. Guedot, M. Kenis, M. T. Kimura, G. Loeb, A. Loiseau, I. Martinez-Sañudo, M. Pascual, M. Polihronakis Richmond, P. Shearer, N. Singh, K. Tamura, A. Xuéreb, J. Zhang, A. Estoup, Deciphering the routes of invasion of Drosophila suzukii by means of ABC random forest. *Mol Biol Evol*, msx050 (2017).

70. R. Luo, B. Liu, Y. Xie, Z. Li, W. Huang, J. Yuan, G. He, Y. Chen, Q. Pan, Y. Liu, J. Tang, G. Wu, H. Zhang, Y. Shi, Y. Liu, C. Yu, B. Wang, Y. Lu, C. Han, D. W. Cheung, S.-M. Yiu, S. Peng, Z. Xiaoqian, G. Liu, X. Liao, Y. Li, H. Yang, J. Wang, T.-W. Lam, J. Wang, SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. *Gigascience*. **1**, 18 (2012).

71. D. R. Zerbino, E. Birney, Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* **18**, 821–829 (2008).

72. T. J. Treangen, B. D. Ondov, S. Koren, A. M. Phillippy, The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. *Genome Biology*. **15**, 524 (2014).

73. X. Didelot, D. Falush, Inference of Bacterial Microevolution Using Multilocus Sequence Data. *Genetics*. **175**, 1251–1266 (2007).

74. E. Paradis, J. Claude, K. Strimmer, APE: Analyses of Phylogenetics and Evolution in R language. *Bioinformatics*. **20**, 289–290 (2004).

75. M. Plummer, N. Best, K. Cowles, K. Vines, CODA: convergence diagnosis and output analysis for MCMC. *R News*. **6**, 7–11 (2006).

76. A. Raj, M. Stephens, J. K. Pritchard, fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. *Genetics*. **197**, 573–589 (2014).

77. Warnes, Bolker, Bonebakker, Gentleman, Liaw, Lumley, Maechler, Magnusson, Moeller, Schwartz, Venables, gplots: Various R Programming Tools for Plotting Data. *R package version 3.0.1.1* (available at https://CRAN.R-project.org/package=gplots).

78. A. Stamatakis, RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. **30**, 1312–1313 (2014).

79. A. Doizy, A. Prin, G. Cornu, F. Chiroleu, A. Rieux, "Phylostems: a new graphical tool to investigate temporal signal of heterochronous sequences at various evolutionary scales" (2020), p. 2020.10.19.346429, , doi:10.1101/2020.10.19.346429.

80. S. Duchêne, D. Duchêne, E. C. Holmes, S. Y. W. Ho, The Performance of the Date-Randomization Test in Phylogenetic Analyses of Time-Structured Virus Data. *Molecular Biology and Evolution*. **32**, 1895–1906 (2015).

81. A. Rieux, C. E. Khatchikian, tipdatingbeast: an r package to assist the implementation of phylogenetic tip-dating tests using beast. *Molecular Ecology Resources*. **17**, 608–613 (2017).

References Supplementary Materials

82. J.-M. Cornuet, V. Ravigné, A. Estoup, Inference on population history and model checking using DNA sequence and microsatellite data with the software DIYABC (v1.0). BMC Bioinformatics. 11, 401 (2010).

83. J.-M. Cornuet, F. Santos, M. A. Beaumont, C. P. Robert, J.-M. Marin, D. J. Balding, T. Guillemaud, A. Estoup, Inferring population history with DIY ABC: a user-friendly approach to approximate Bayesian computation. Bioinformatics. 24, 2713–2719 (2008).

References Supplementary Tables

84. A. Bhattacharyya, S. Stilwagen, N. Ivanova, M. D'Souza, A. Bernal, A. Lykidis, V. Kapatral, I. Anderson, N. Larsen, T. Los, G. Reznik, E. Selkov, T. L. Walunas, H. Feil, W. S. Feil, A. Purcell, J.-L. Lassez, T. L. Hawkins, R. Haselkorn, R. Overbeek, P. F. Predki, N. C. Kyrpides, Whole-genome comparative analysis of three phytopathogenic Xylella fastidiosa strains. Proc. Natl. Acad. Sci. U.S.A. 99, 12403–12408 (2002).

85. J. Chen, G. Xie, S. Han, O. Chertkov, D. Sims, E. L. Civerolo, Whole Genome Sequences of Two Xylella fastidiosa Strains (M12 and M23) Causing Almond Leaf Scorch Disease in California. J Bacteriol. 192, 4534 (2010).

86. C. Van Horn, C.-J. Chang, J. Chen, De Novo Whole-Genome Sequence of Xylella fastidiosa subsp. multiplex Strain BB01 Isolated from a Blueberry in Georgia, USA. Genome Announc. 5, e01598-16 (2017).

87. A. Giampetruzzi, M. P. Velasco-Amo, E. Marco-Noales, M. Montes-Borrego, M. Román-Écija, I. Navarro, A. Monterde, S. Barbé, R. P. P. Almeida, P. Saldarelli, M. Saponari, V. Montilon, V. N. Savino, D. Boscia, B. B. Landa, Draft Genome Resources of Two Strains ("ESVL" and "IVIA5901") of Xylella fastidiosa Associated with Almond Leaf Scorch Disease in Alicante, Spain. Phytopathology. 109, 219–221 (2019).

88. J. Chen, H. Huang, C.-J. Chang, D. C. Stenger, Draft Genome Sequence of Xylella fastidiosa subsp. multiplex Strain Griffin-1 from Quercus rubra in Georgia. Genome Announc. 1, e00756-13 (2013).

89. A. Giampetruzzi, G. D'Attoma, S. Zicca, R. Abou Kubaa, D. Rizzo, D. Boscia, P. Saldarelli, M. Saponari, Draft Genome Sequence Resources of Three Strains (TOS4, TOS5, and TOS14) of Xylella fastidiosa Infecting Different Host Plants in the Newly Discovered Outbreak in Tuscany, Italy. Phytopathology. 109, 1516–1518 (2019).

Acknowledgments

We thank Quentin Beaurepère for technical support, Muriel Bahut (ANAN technical facility, SFR QUASAV, Angers, FR) for DNA extraction automation and VNTRs sequencing, CIRM-CFBP (Beaucouzé, INRAE, France http://www6.inra.fr/cirm_eng/CFBP -Plant-Associated-Bacteria) for strain preservation and supply, Jérôme Gouzy (CATI BARIC) for the genome assembly pipeline, Mahendra Mariadassou and Déborah Merda for script sharing. We also thank Leonardo de la Fuente (Auburn University, AL, USA) and LSV-ANSES for sharing

strains, Blanca L. Landa (Institute for Sustainable Agriculture, Córdoba, Spain) for sharing DNA; Valérie Oliver and Françoise Poliakoff for information related to the analysis of plant samples and strains in the framework of official surveillance, Marina Blanc for preliminary experiments on VNTR design, Laetitia Hugo from CNBC and François Casabianca from Corsican INRAE center for facilitating samplings, and Charles Manceau for co-writing the initial project providing ED funding support.

Funding

INRAE SPE division and ANSES (ED salary).

European Union's Horizon 2020 research and innovation program under grant agreement 727987 XF-ACTORS (*Xylella fastidiosa* Active Containment Through a Multidisciplinary-Oriented Research Strategy) (SC, MAJ). The present work reflects only the authors' view and the EU funding agency is not responsible for any use that may be made of the information it contains.

XyleCor funded by the SPE division of INRAE (MAJ).

Sap Alien project funded by the RFI Objectif Végétal (ND salary)

France Génomique National infrastructure, funded as part of "Investissement d'avenir" program managed by Agence Nationale pour la Recherche (contract ANR-10-INBS-09) and by the GET-PACBIO program (« Programme operationnel FEDER-FSE MIDI-PYRENEES ET GARONNE 2014-2020 ») (CD, CLR).

European Union (European Regional Development Fund, ERDF contract GURDT I2016-1731-0006632), Conseil Régional de La Réunion and Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD) (AR, OP, VR).

Agence Nationale pour la Recherche JCJC MUSEOBACT contrat ANR-17-CE35-0009-01(AR).

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Competing interests:

All other authors declare they have no competing interests.

Data and materials availability:

Strains of *X. fastidiosa* were deposited at the CIRM-CFBP (International Centre of Microbial Resource (CIRM) - French Collection for Plant-associated Bacteria. INRAE. https://doi.org/10.15454/E8XX-4Z18). Genome sequences were deposited at NCBI under the accession numbers listed in Table S1.

All data are available in the main text or the supplementary materials.

Figures

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Fig. S7. Allele frequencies at each VNTR locus per sequence type for the 396 French *X. fastidiosa* infected samples. At each locus, colors represent the set of haplotypes.

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Tables

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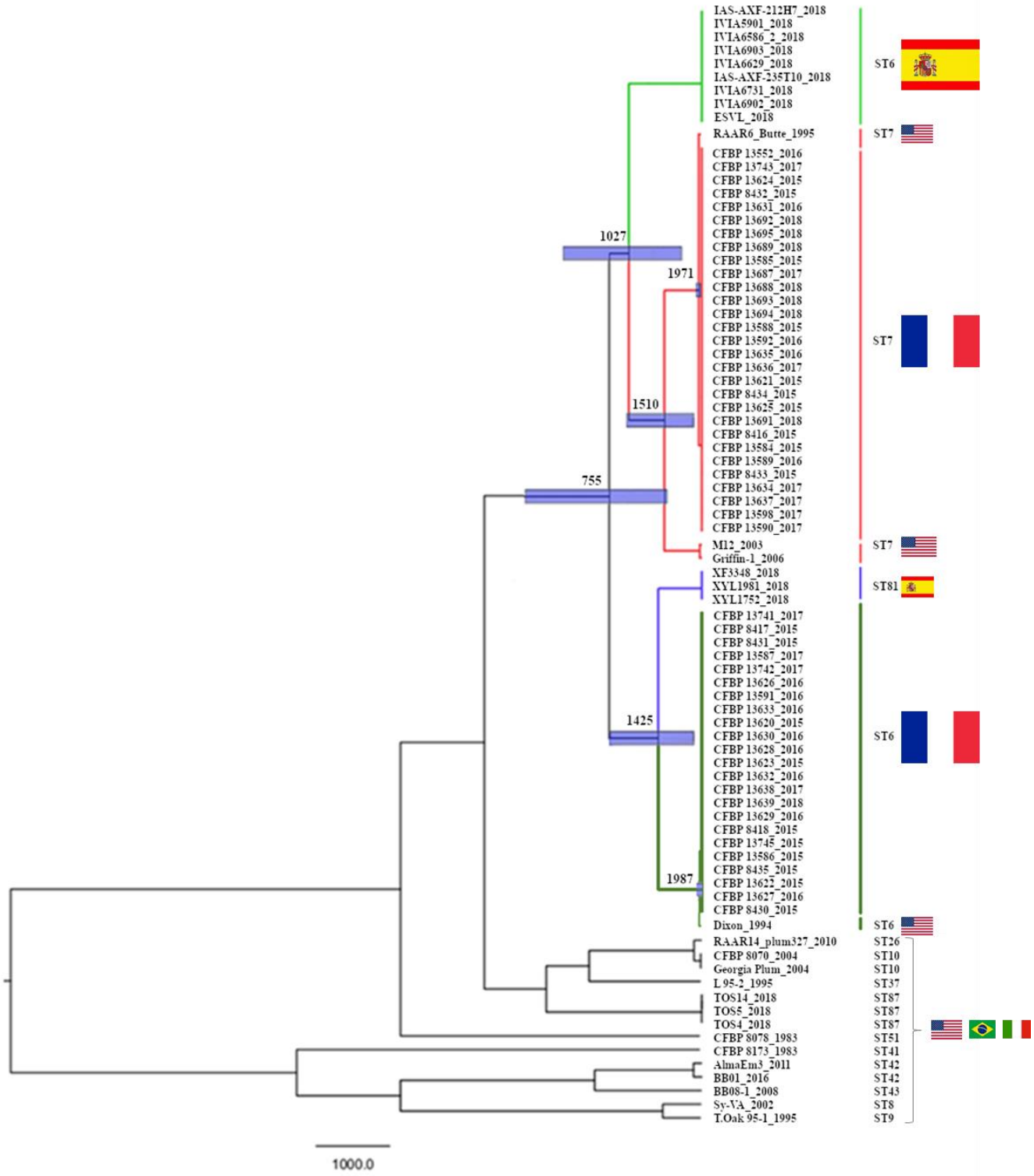

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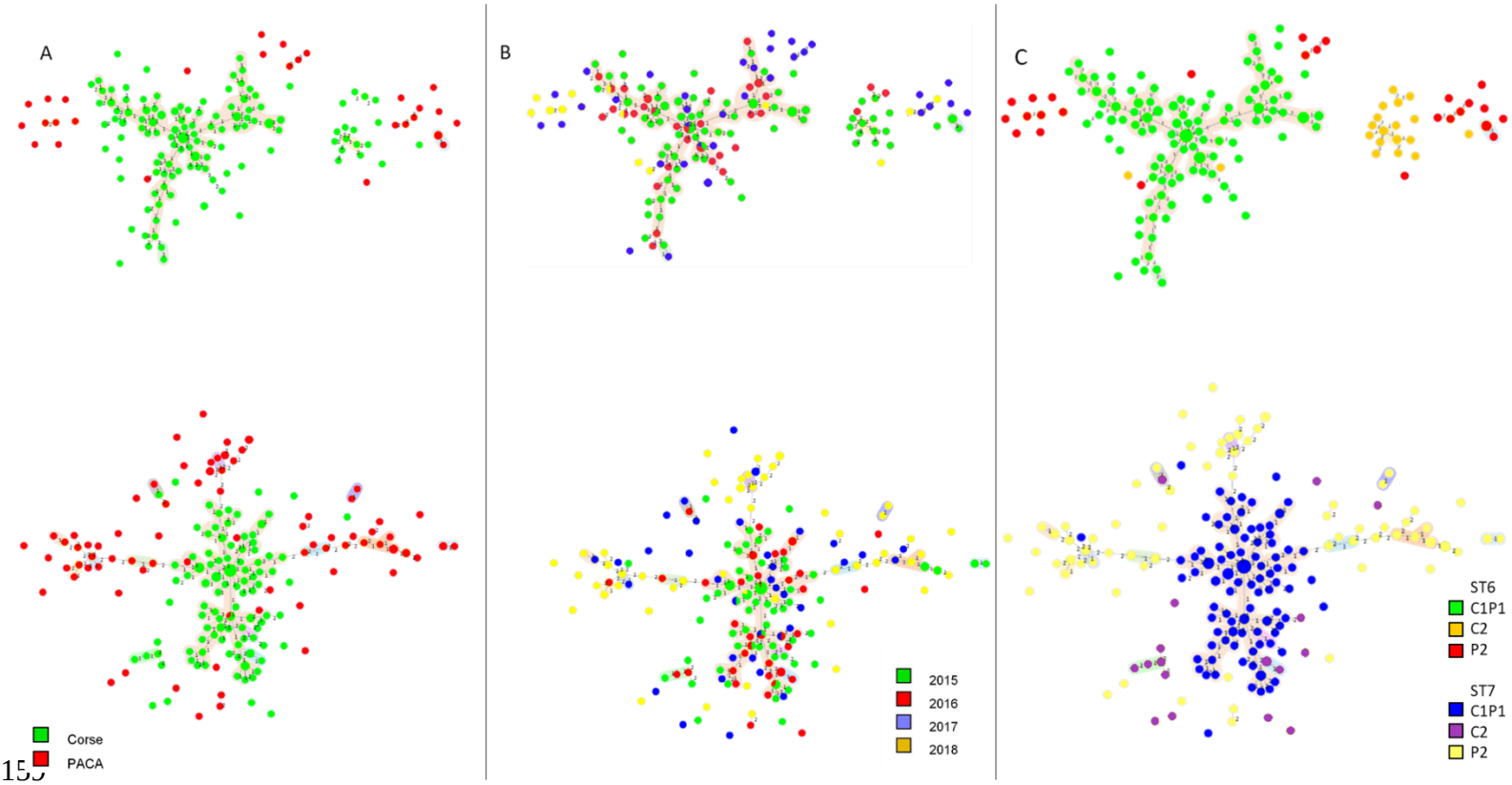

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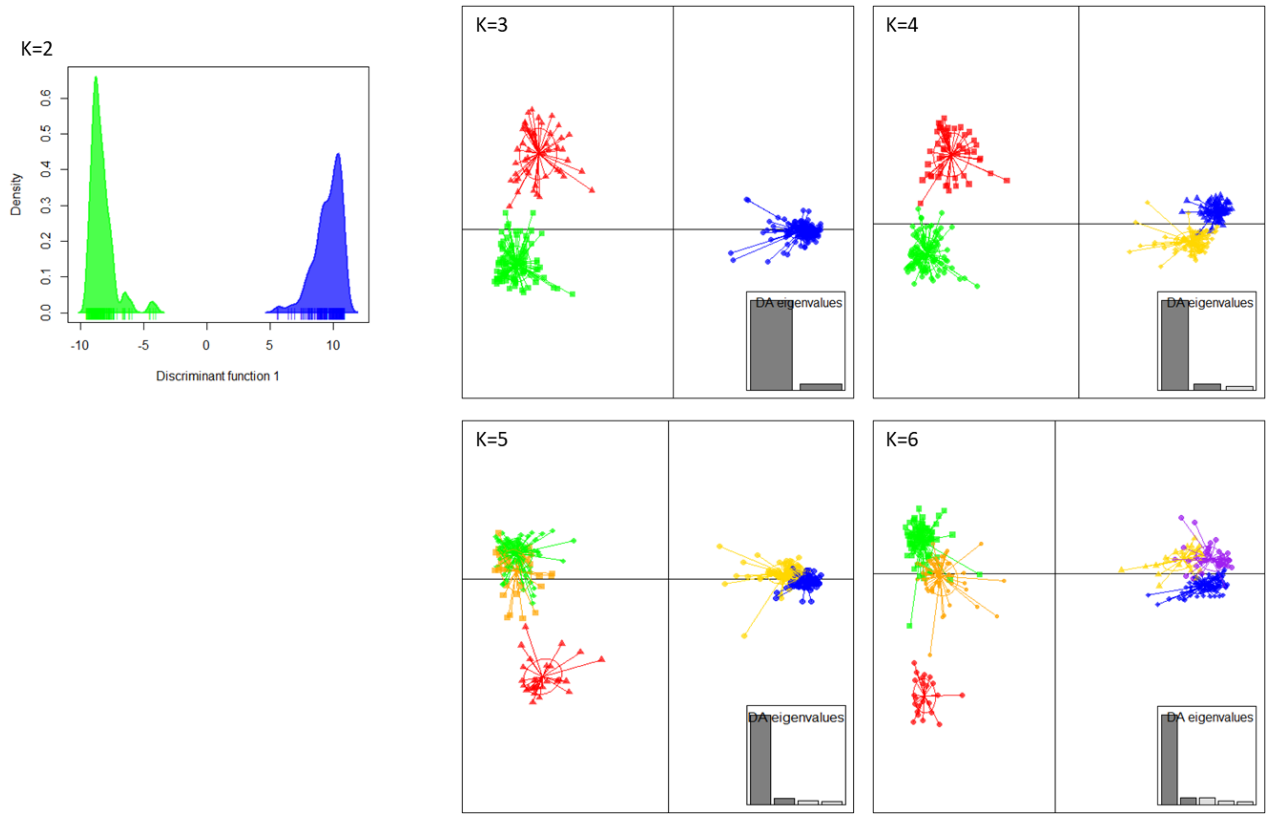

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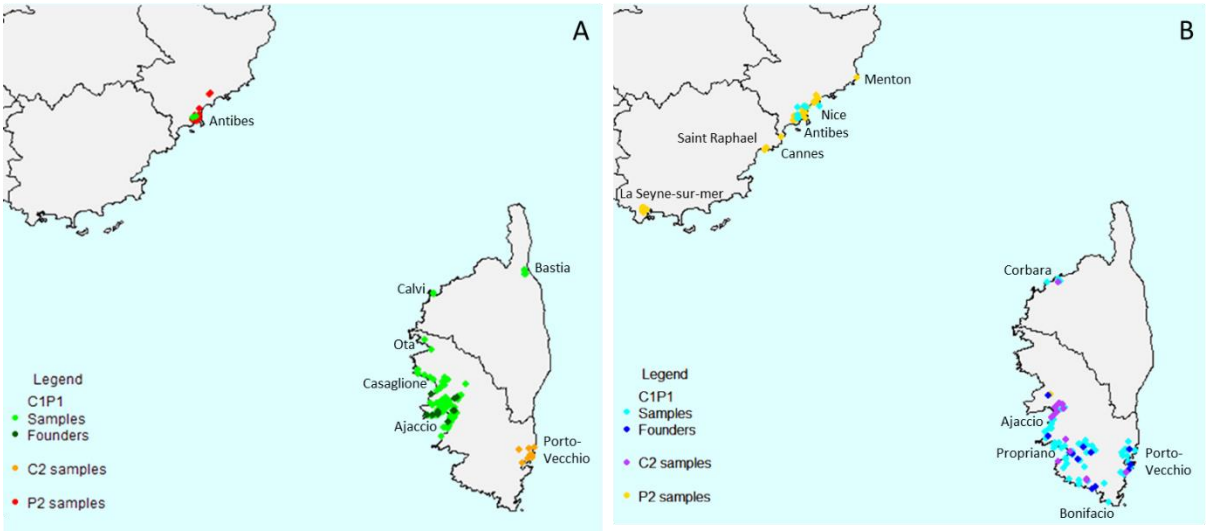

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1178 **Table 1. Nomenclature, location, function and genetic diversity of the 13 TR loci.**

Locus	Primers	Repeat motif	Number of motif repetition	On the M12 genome sequences		Multiplexing annealing temperature (°C)	On the 10 genome sequences of *X. fastiosa* subsp. *multiplex*			Reference
				Location	Coordinates (start - end)		Number of alleles	Range of repetition number	Simpson's diversity index	
ASSR-11	ATTO550 - AGAGGCAACGCAGGAACAG GTGAGTTATATCGGTGCAGCAG	ACGCATC	14	Hypothetical protein	2,074,633 - 2,074,920	53	6	3 - 14	0.18	Lin et al., 2005
ASSR-16	ATTO565 - TTAATCAACAACGCTTATCC TCGCAGTAGCCAGTATAC	GCTCCGGTTCTA	19	1,4-beta-cellobiosidase CDS	658,561 - 658,173	53	8	8 - 29	0.16	Lin et al., 2005
COSS-1	6-FAM - GAAACAAGATGGCGGTTGC CATTTAAACGGGCGGCATA	ATTGCTG	2	Non coding	18,250 - 18,484	53	7	1 - 11	0.16	Francisco et al., 2017
OSSR-19	HEX - GCTGTGAACTTCCATCAATCC GCAAGTAGGGGTAAATGTGAC	CAGGATCA	7	adenylosuccinate lyase CDS	967,661 - 967,412	53	6	3 - 11	0.2	Lin et al., 2005
GSSR-7	ATTO550 - ATCATGTCGTGTCGTTTC CAATAAAGCACCGAATTAGC	AGCAAC	11	Non coding	19,289 - 19,595	55	8	9 - 25	0.14	Lin et al., 2005
OSSR-16	ATTO565 - GCAAATAGCATGTACGAC GTGTTGTGTATGTGTTGG	CTGCTA	9	Non coding	593,243 - 593,502	55	6	7 - 17	0.24	Lin et al., 2005
XFSSR-37	HEX - CACCTGCAACGAACACCAAT	CTGATGTG	8	hydroxyacylglutathione	1,421,433 - 1,421,644	55	4	3 - 12	0.3	This study

	TTCAGTTGGTGTTGCAGGTC			hydrolase CDS						
XFSSR-58	6-FAM - CCCTAGCAAAACAATACTGCCA GGTATGTGCTGTGTGGTTGG	AAGGGGC	7	Non coding	1,997,325 - 1,997,556	55	6	3 - 12	0.22	This study
ASSR-9	6-FAM - GGTTGTCGGGCTCATTCC TTGTCACAGCATCACTATTCTC	CAAGTAC	9	Non coding	949,863 - 950,106	57	6	3 - 15	0.22	Lin et al., 2005
ASSR-12	ATTO565 - TGCTCATTGTGGCGAAGG CGCAACGTGCATTCATCG	GATTCAG	9	Hypothetical protein	2,116,062 - 2,115,798	57	7	4 - 14	0.16	Lin et al., 2005
ASSR-19	ATTO550 - CGCCGACTGTCTATGTGAC TTCCTAGCAATGGCAATGTTG	ACAACG	3	Hypothetical protein	2,075,410 - 2,075,699	57	7	2 - 12	0.16	Lin et al., 2005
GSSR-4	HEX - GCGTTACTGGCGACAAAC GCTCGTTCCTGACCTGTG	ATCC	4	Hypothetical protein	1,702,352 - 1,702,608	57	3	3 - 5	0.38	Lin et al., 2005
XFSSR-40	6-FAM - ACACACTCACACTGTCCGAT GGGTTAGGAGTTGGTGTCGA	ACAGCAAT	5	Non coding	1,513,631 - 1,513,860	60	6	3 - 11	0.2	This study

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Table 2. Characteristics of the 396 French strains and plant samples used in this study.

Summary per host of isolation	Corsica	PACA	Total
Acacia sp.	/	1	1
Artemisia arborescens	1	/	1
Calicotome villosa	15	/	15
Cistus spp.	5	/	5
Convolvulus cneorum	/	3	3
Coronilla spp.	1	4	5
Cytisus villosus	2	/	2
Euryops chrysanthemoides	/	8	8
Genista spp.	6	/	6
Grevillea juniperina	/	1	1
Hebe sp.	1	/	1
Helichrysum spp.	12	3	15
Lavandula spp.	7	1	8
Lonicera japonica	/	1	1
Medicago sativa	/	1	1
Metrosideros excelsa	1	/	1
Pelargonium spp.	5	/	5
Phagnalon saxatile	1	/	1
Polygala myrtifolia	205	72	277
Prunus spp.	3	3	6
Quercus suber	1	/	1
Rosa canina	1	/	1
Spartium junceum	16	12	28
Veronica spp.	/	2	2
Westringia fruticosa	/	1	1
Summary per year of isolation			
2015	166	14	180
2016	75	4	79
2017	34	39	73
2018	8	56	64
Summary per sequence type			
ST6	154	30	184
ST7	129	83	212

Table 3. Genetic diversity based on 13 VNTRs in the 396 French samples.

Locus	Nb of alleles	Nb of repetition min - max	Simpson's diversity index (1-D)	Allelic richness
ASSR-11	11	5 - 16	0.69	7.79
ASSR-16	7	22 - 30	0.52	8.41
COSS-1	11	1 - 12	0.76	5.25
OSSR-19	11	3 - 14	0.64	4.28
GSSR-7	19	10 - 29	0.88	13.46
OSSR-16	21	6 - 29	0.75	9.45
XFSSR-37	8	1 - 10	0.56	6.88
XFSSR-58	8	4 - 11	0.54	6.71
ASSR-9	13	5 - 18	0.82	4.98
ASSR-12	7	7 - 14	0.62	7.86
ASSR-19	8	7 - 14	0.74	3.82
GSSR-4	7	8 - 21	0.52	15.73
XFSSR-40	8	5 - 12	0.73	6.1

Supplementary materiel and methods

Scenarios

The bottom-up approach consisted in searching for the most probable topology for each population combination of the American ancestor and two French populations in presence or not of an unsampled (ghost) population. Altogether this lead to three independent analyses and in each analysis, 10 to 12 topologies were tested (Fig. S9 A). A total of 30 scenarios (combination of population choice and topology) were analyzed for ST6 and 36 for ST7 in this bottom-up approach.

Topologies 1, 5, 9, 10, 11 and 12 assumed that the French populations were introduced separately from two events. Topologies 2 and 6 hypothesizes that samples which belonged to the same population may have been mistakenly separated into two populations. Topologies 3, 4, 7 and 8 assumed that a first population was introduced in France and that a bridgehead invasion was responsible for the emergence of the second French populations. Topologies 5, 6, 7, 8, 10, 11 and 12 assumed that one or two populations may have been unsampled (named ghost population).

The top-down approach consisted in searching for the most probable population combinations for each possible topology. A total of 5 topologies were tested for each of the three French ST6 and ST7 populations (six combinations) (Fig. S9 B). The topologies differed by the number of independent introductions and divergence events. However, based on the results of the bottom-up approach, a number of scenario were considered statistically impossible and were not tested in the top-down approach.

In consequence, from the six possible population combinations all were tested for ST6, for a total of 30 scenarios (Fig. S10) and only two topologies for ST7 for a total of 12 scenarios (Fig. S11).

Class 1 topology (I) assumed three independent introductions in France from a source population. Class 2 topology (II) assumed that one population was introduced in France and is responsible for two independent bridgehead invasions. Class 3 topologies (III.I and III.II) assumed that two independent introductions occurred and one of them was responsible for a bridgehead invasion of the third population. Class 4 topology (IV) assumed that one population was first introduced and was responsible for two successive bridgehead invasions.

Choice and validation of priors

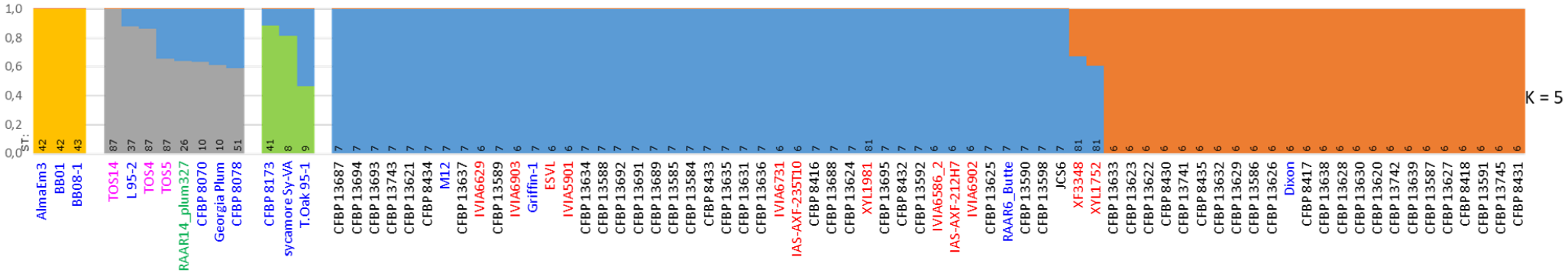
For the DiyABC analyses, parameters were drawn in the prior distribution described in Table S9. Due to the lack of knowledge concerning the bacterium population biology (population effective sizes, date of founder event, existence and duration of a bottleneck, for example), a log uniform distribution with large ranges was chosen. Parameters for microsatellite mutation models were set by default following a stepwise mutation model (82). Other parameters of the mutation models were set by default at "0" and all summary statistics were selected.

Prior choices were validated by performing a principal component analysis (PCA) implemented in DiyABC, in the space of summary statistics for all simulated datasets (106 per scenario) with parameter values drawn from the prior parameters. The observed dataset was projected as a supplementary individual to determine by visual check whether it fell within the variability of simulated data (82).

Simulations and posterior probability estimation

A total of 106 simulations were performed for each competing scenario using DiyABC software (83). Because the DiyABC lack of discriminative power among competing scenarios, abcrf were used to estimate best scenarios or the rejected one, using the R package "abcrf" (68). Following Pudlo et al., 2016 abcrf treatments were processed on reference tables including 104 simulations per scenario (68). In the constructed random-forests the number of trees was fixed at n=1000. For each abcrf analysis the best scenario, its prior error rates and its posterior probability were evaluated over 10 replicate runs of the same reference table. Moreover, for the bottom-up approach, an event was rejected when less than 50/1000 (<5%) of votes were attributed to it. Scripts published by Fraimout *et al*., 2017 were optimized to fit our dataset (69).

Fig. S1. Genome clustering by FastSTRUCTURE software for K=5. Color bars represent groups identified by Bayesian clustering. ST numbers are indicated above strain codes. Color names represents their country of origin of strains: black for France, blue for USA, green for Brazil, purple for Italy and red for Spain.



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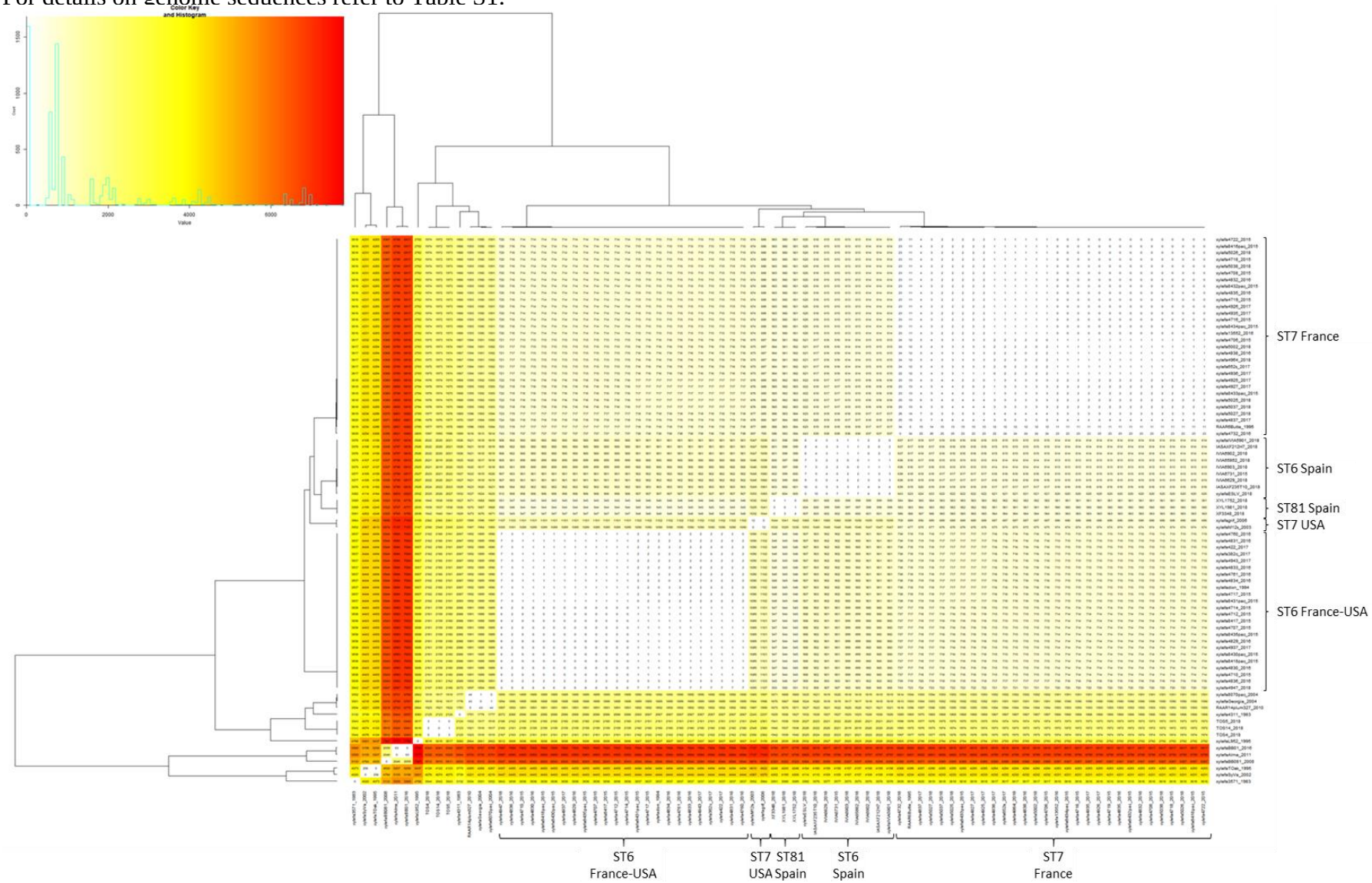

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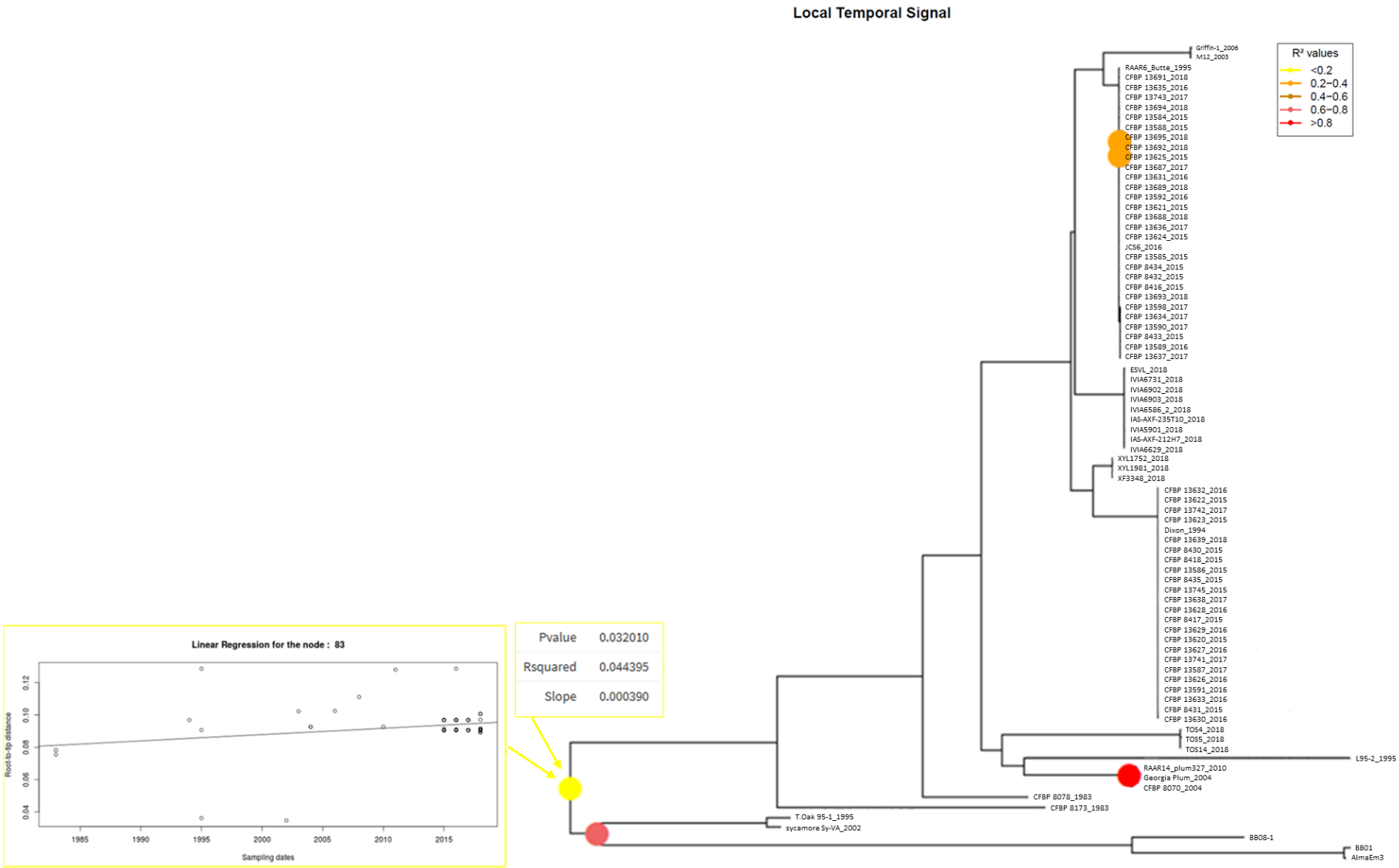

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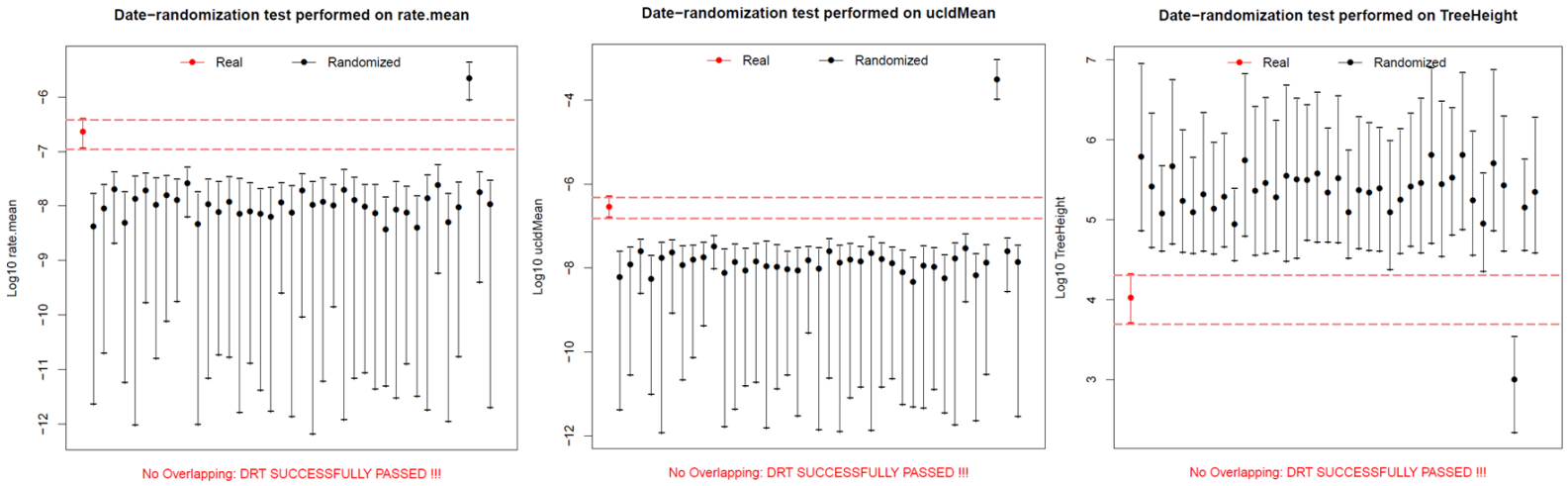

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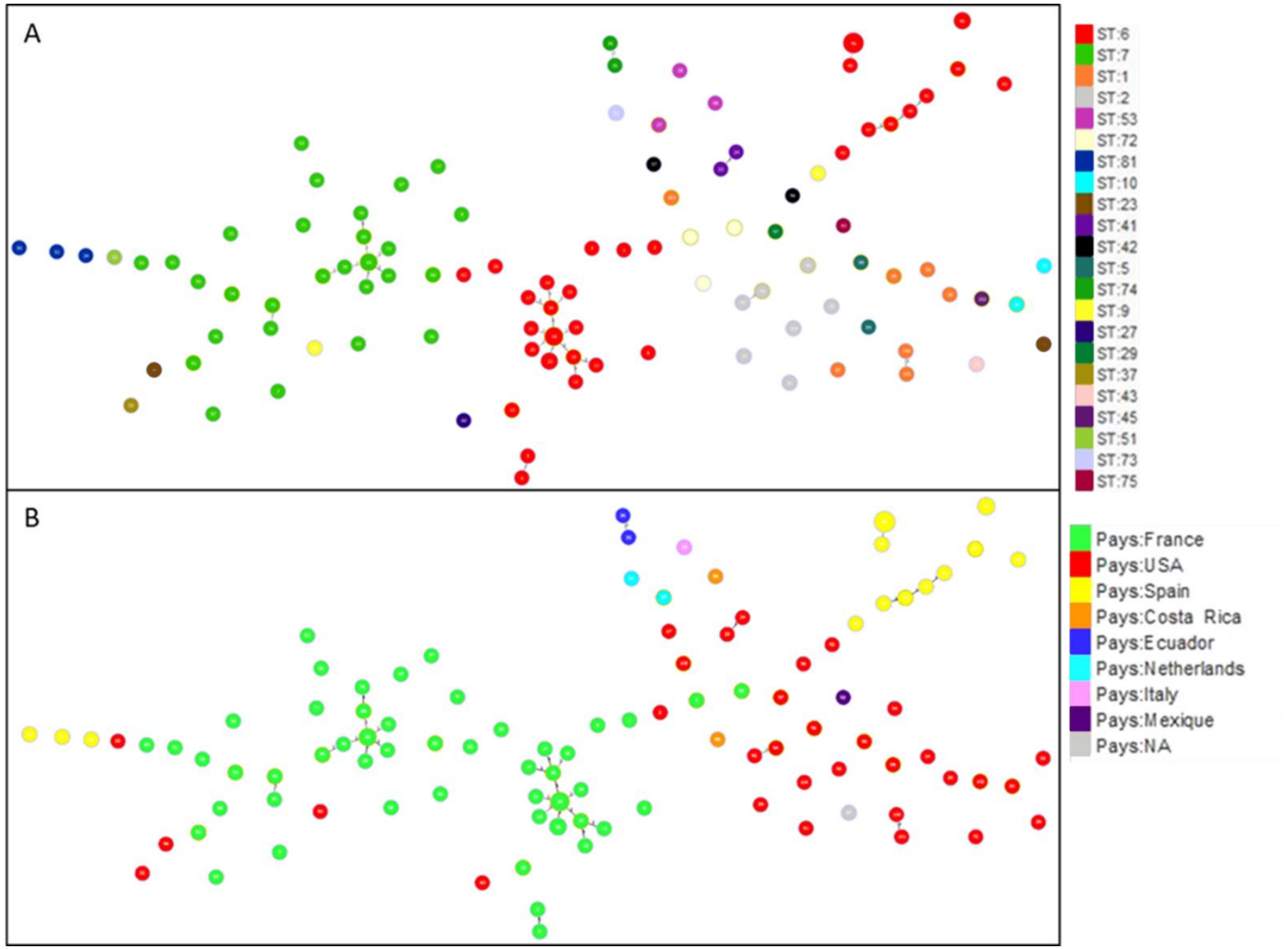

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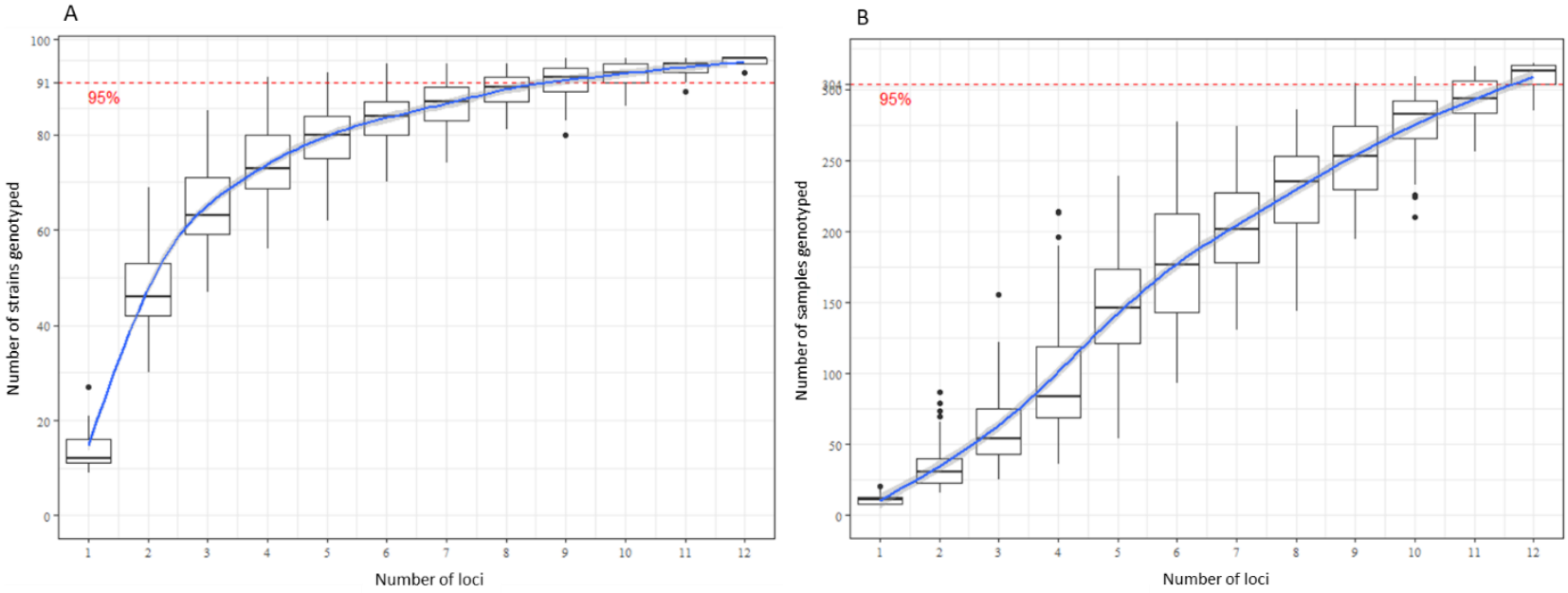

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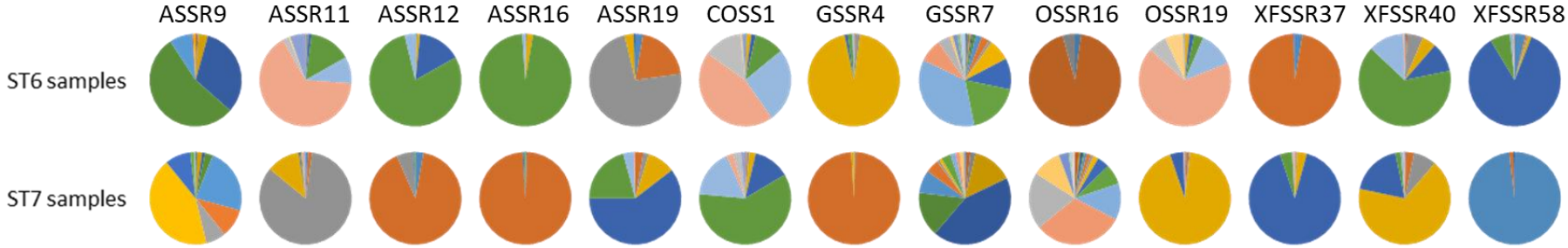

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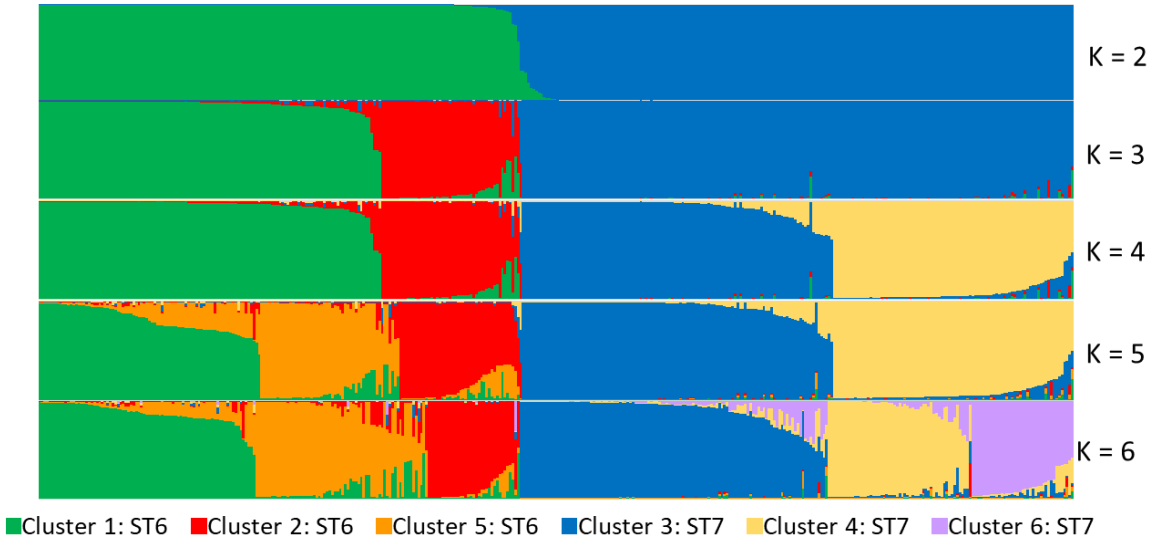

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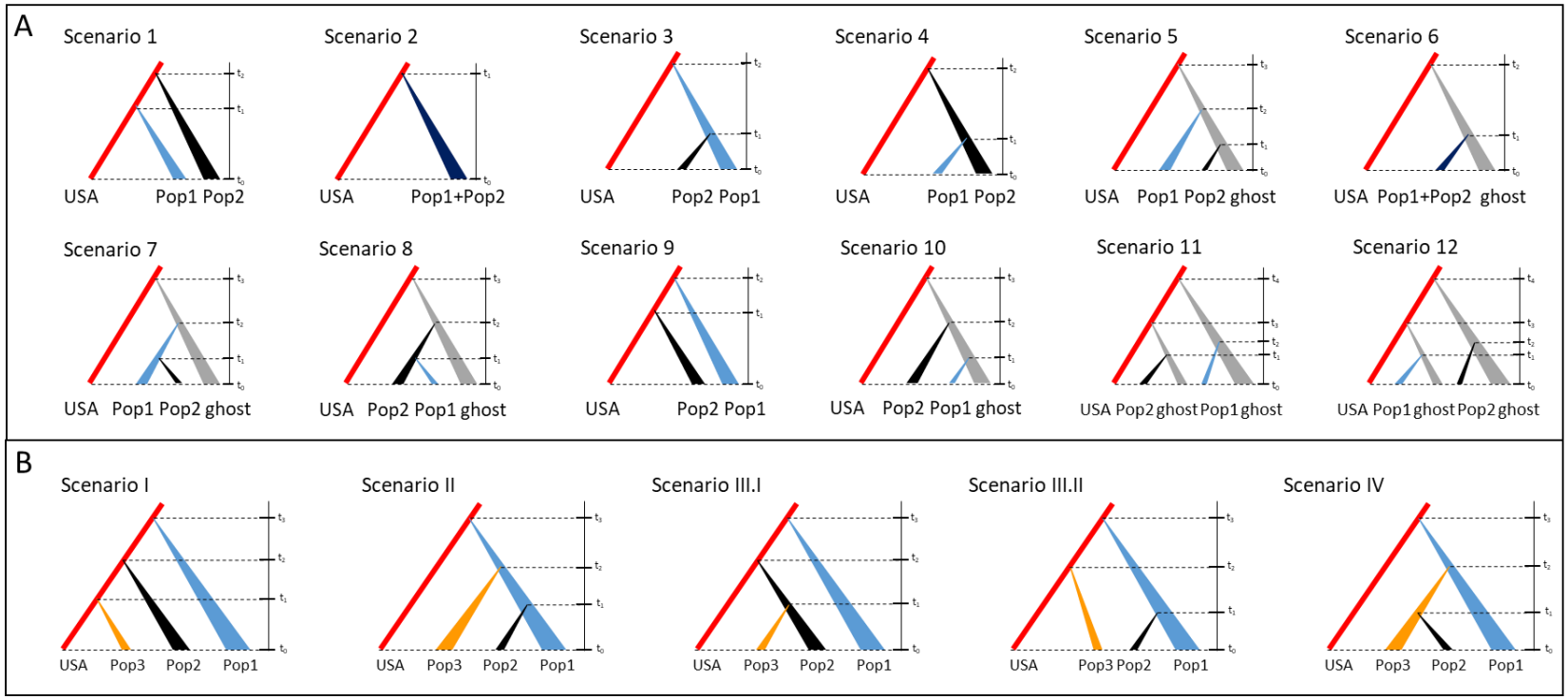

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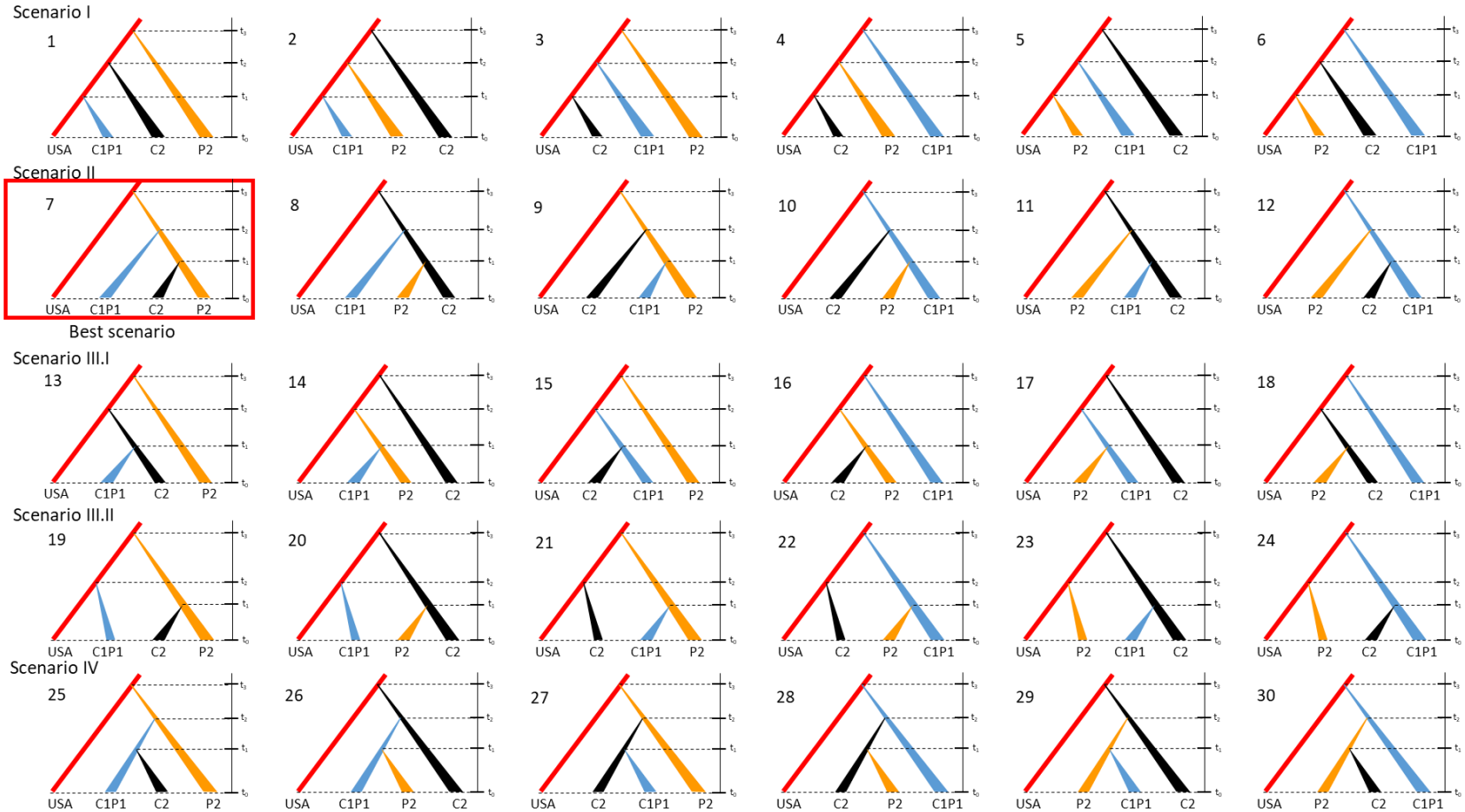

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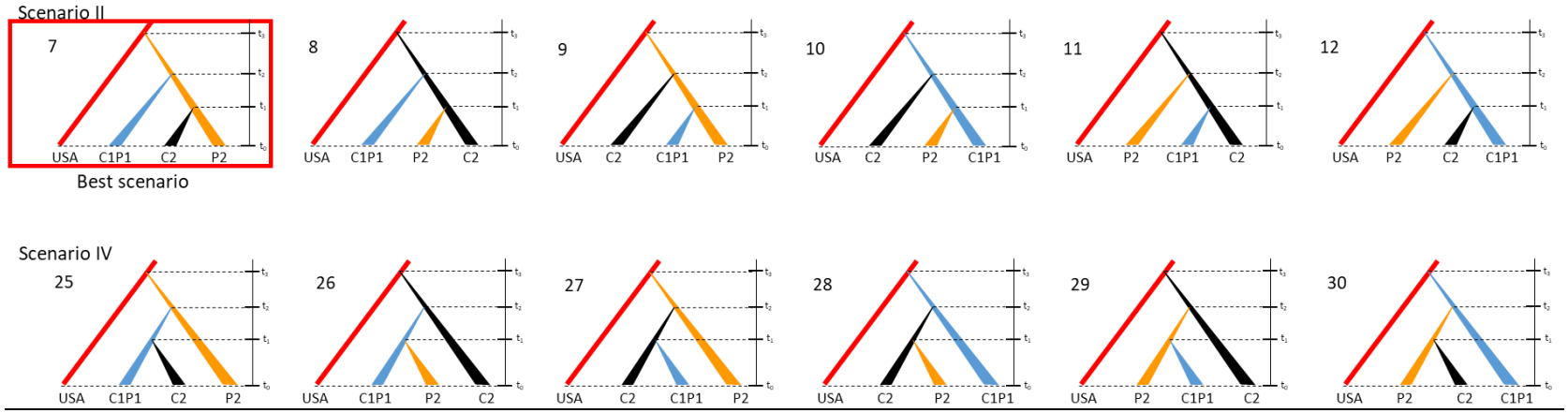

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Table S6. Genetic differentiation of the clusters of X. fastidiosa subsp. multiplex estimated by RST (bellow the diagonal) and FST (above the diagonal) pairwise comparisons for A) the DAPC k=4 groups; B) the three ST6 clusters used in ABC analyses; C) the three ST7 clusters used in ABC analyses. All pairwise population comparisons were significantly different (P<0.05) after 1,000 permutations.

Table S7. Hierarchical AMOVA for A) ST6 X. fastidiosa subsp. multiplex DiyABC groups and B) ST7 X. fastidiosa subsp. multiplex DiyABC groups.

Table S8. Percentage of votes obtained for each scenario using abcrf. A) results of the ST6 bottom-up analyses; B) results of the ST6 top-down analyses; C) results of the ST7 bottom-up analyses; D) results of the ST7 top-down analyses.

Table S9. Distribution of prior parameters used for the DiyABC analyses.

Table S1. List of the 82 *X. fastidiosa* genome sequences used in this study.

CFBP strain code	Other strain code	ST	Host plant	Place of isolation	Year of isolation	Contig number	sequencing method	N50	L50	Accession	Reference
CFBP 13551	Dixon	6	*Prunus dulcis*	USA (California)	1994	32		201792	4	AAAL00000000	Bhattacharyya et al., 2002
CFBP 13552	JCS6	7	*Polygala myrtifolia*	France (Corse)	2016	136	Illumina Hiseq X	97172	8	JAJKBE000000000	This study
CFBP 13584	LSV 47.06	7	*Polygala myrtifolia*	France (Corse)	2015	134	Illumina Hiseq X	97172	8	JAJKBD000000000	This study
CFBP 13585	LSV 47.08	7	*Polygala myrtifolia*	France (Corse)	2015	142	Illumina Hiseq X	97164	8	JAJKBC000000000	This study
CFBP 13586	LSV 47.10	6	*Lavandula X allardii*	France (Corse)	2015	275	Illumina Hiseq X	96039	9	JAJKBB000000000	This study
CFBP 13587	LSV 49.43	6	*Prunus cerasus*	France (PACA)	2017	278	Illumina Hiseq X	96969	9	JAJKBA000000000	This study
CFBP 13588	LSV 47.22	7	*Polygala myrtifolia*	France (Corse)	2015	139	Illumina Hiseq X	97172	8	JAJKAZ000000000	This study
CFBP 13589	LSV 47.32	7	*Spartium junceum*	France (PACA)	2016	149	Illumina Hiseq X	98320	8	JAJKAY000000000	This study
CFBP 13590	LSV 49.27	7	*Coronilla glauca*	France (PACA)	2017	186	Illumina Hiseq X	97172	8	JAJKAX000000000	This study
CFBP 13591	LSV 48.34	6	*Polygala myrtifolia*	France (Corse)	2016	273	Illumina Hiseq X	96039	9	JAJKAW000000000	This study
CFBP 13592	LSV 48.35	7	*Prunus dulcis*	France (Corse)	2016	157	Illumina Hiseq X	96972	8	JAJKAV000000000	This study
CFBP 13598	LSV 49.25	7	*Acacia dealbata*	France (PACA)	2017	159	Illumina Hiseq X	97172	8	JAJKAU000000000	This study
CFBP 13620	LSV 47.12	6	*Polygala myrtifolia*	France (PACA)	2015	295	Illumina Hiseq X	96961	9	JAJKAT000000000	This study
CFBP 13621	LSV 47.16	7	*Polygala myrtifolia*	France (Corse)	2015	142	Illumina Hiseq X	96972	8	JAJKAS000000000	This study
CFBP 13622	LSV 47.17	6	*Polygala myrtifolia*	France (Corse)	2015	292	Illumina Hiseq X	93226	9	JAJKAR000000000	This study
CFBP 13623	LSV 47.14	6	*Lavandulla angustifolia*	France (Corse)	2015	277	Illumina Hiseq X	93663	9	JAJKAQ000000000	This study
CFBP 13624	LSV 47.18	7	*Polygala myrtifolia*	France (Corse)	2015	138	Illumina Hiseq X	119392	7	JAJKAP000000000	This study
CFBP 13625	LSV 47.19	7	*Polygala myrtifolia*	France (Corse)	2015	125	Illumina Hiseq X	97172	8	JAJKAO000000000	This study
CFBP 13626	LSV 47.60	6	*Helichrysum italicum*	France (Corse)	2016	272	Illumina Hiseq X	93671	9	JAJKAN000000000	This study
CFBP 13627	LSV 47.61	6	*Calicotome villosa*	France (Corse)	2016	269	Illumina Hiseq X	118458	8	JAJKAM000000000	This study
CFBP 13628	LSV 48.29	6	*Lavandula sp*.	France (Corse)	2016	264	Illumina Hiseq X	96961	9	JAJKAL000000000	This study
CFBP 13629	LSV 48.30	6	*Polygala myrtifolia*	France (Corse)	2016	268	Illumina Hiseq X	96033	8	JAJKAK000000000	This study
CFBP 13630	LSV 48.31	6	*Cistus monspeliensis*	France (Corse)	2016	259	Illumina Hiseq X	109545	8	JAJKAJ000000000	This study
CFBP 13631	LSV 48.32	7	*Cistus monspeliensis*	France (Corse)	2016	145	Illumina Hiseq X	97172	8	JAJKAI000000000	This study
CFBP 13632	LSV 48.33	6	*Lavandula stoechas*	France (Corse)	2016	245	Illumina Hiseq X	109551	8	JAJKAH000000000	This study
CFBP 13633	LSV 48.36	6	*Rosa canina*	France (Corse)	2016	264	Illumina Hiseq X	96039	8	JAJKAG000000000	This study
CFBP 13634	LSV 48.37	7	*Westrigia fruticosa*	France (PACA)	2017	121	Illumina Hiseq X	98560	8	JAJKAF000000000	This study
CFBP 13635	LSV 48.38	7	*Cistus creticus*	France (Corse)	2016	117	Illumina Hiseq X	97172	8	JAJKAE000000000	This study
CFBP 13636	LSV 49.26	7	*Coronilla glauca*	France (PACA)	2017	154	Illumina Hiseq X	97178	8	JAJKAD000000000	This study
CFBP 13637	LSV 49.36	7	*Polygala myrtifolia*	France (PACA)	2017	144	Illumina Hiseq X	97178	8	JAJKAC000000000	This study
CFBP 13638	LSV 49.37	6	*Euryops chrysanthemoïdes*	France (PACA)	2017	278	Illumina Hiseq X	96039	9	JAJKAB000000000	This study
CFBP 13639	LSV 49.47	6	*Prunus avium*	France (PACA)	2018	532	Illumina Hiseq X	78416	10	JAJKAA000000000	This study
CFBP 13677	AlmaEm3	42	*Vaccinium corymbosum*	USA (Georgia)	2011	139	Illumina Hiseq X	97040	9	JAJJZZ000000000	This study
CFBP 13679	Georgia Plum	10	*Prunus sp*.	USA (Georgia)	2004	316	Illumina Hiseq X	91004	11	JAJJZY000000000	This study
CFBP 13683	BB08-1	43	*Vaccinium 'Windsor'*	USA (Florida)	2008	143	Illumina Hiseq X	114067	7	JAJJZX000000000	This study
CFBP 13684	L 95-2	37	*Lupinus villosus*	USA (Florida)	1995	228	Illumina Hiseq X	80724	9	JAJJZW000000000	This study
CFBP 13685	T.Oak 95-1	9	*Quercus cerris*	USA	1995	141	Illumina Hiseq X	99853	10	JAJJZV000000000	This study
CFBP 13687	LSV 49.35	7	*Medicago sativa*	France (PACA)	2017	140	Illumina Hiseq X	97172	8	JAJJZU000000000	This study
CFBP 13688	LSV 50.26	7	*Convolvulus cneorum*	France (PACA)	2018	132	Illumina Hiseq X	97178	8	JAJJZT000000000	This study
CFBP 13689	LSV 50.38	7	*Prunus dulcis*	France (Corse)	2018	129	Illumina Hiseq X	97172	8	JAJJZS000000000	This study
CFBP 13691	LSV 50.02	7	*Polygala myrtifolia*	France (PACA)	2018	167	Illumina Hiseq X	93300	9	JAJJZR000000000	This study
CFBP 13692	LSV 50.27	7	*Convolvulus cneorum*	France (PACA)	2018	137	Illumina Hiseq X	97150	8	JAJJZQ000000000	This study
CFBP 13693	LSV 49.64	7	*Polygala myrtifolia*	France (PACA)	2018	133	Illumina Hiseq X	97166	8	JAJJZP000000000	This study
CFBP 13694	LSV 50.25	7	*Euryops chrysanthemoïdes*	France (PACA)	2018	149	Illumina Hiseq X	93413	9	JAJJZO000000000	This study
CFBP 13695	LSV 50.37	7	*Helichrysum italicum*	France (PACA)	2018	137	Illumina Hiseq X	96972	8	JAJJZN000000000	This study
CFBP 13741		6	*Polygala myrtifolia*	France (Corse)	2017	251	Illumina Hiseq X	109591	8	JAJJZM000000000	This study
CFBP 13742		6	*Polygala myrtifolia*	France (Corse)	2017	263	Illumina Hiseq X	118458	8	JAJJZL000000000	This study
CFBP 13743		7	*Helichrysum italicum*	France (Corse)	2017	132	Illumina Hiseq X	97582	8	JAJJZK000000000	This study
CFBP 13744	M12	7	*Prunus dulcis*	USA (California)	2003	1		2475130	1	NC_010513	Chen et al., 2010
CFBP 13745	LSV 47.07	6	*Polygala myrtifolia*	France (Corse)	2015	272	Illumina Hiseq X	96961	9	JAJJZJ000000000	This study
CFBP 8070	LSV 40.38	10	*Prunus spp*	USA (Georgia)	2004	5	PacBio RS II	2074959	1	JAJKGN000000000	This study
CFBP 8078	LSV 43.11	51	*Vinca* sp.	USA (Florida)	1983	190	Illumina MiSeq	87559	10	PHFS00000000	Denancé et al., 2019

CFBP 8173	LSV 40.39	41	*Prunus salicina*	USA (Georgia)	1983	58	Illumina Hiseq 2000	106692	7	NZ_AUAJ00000000	DOE Joint Genome Institute 2013
CFBP 8416	LSV 46.77	7	*Polygala myrtifolia*	France (Corse)	2015	128	Illumina MiSeq	113891	6	LUYC00000000	Denancé et al., 2017
CFBP 8417	LSV 46.78	6	*Spartium junceum*	France (Corse)	2015	256	Illumina MiSeq	118419	8	LUYB00000000	Denancé et al., 2017
CFBP 8418	LSV 46.79	6	*Spartium junceum*	France (Corse)	2015	271	Illumina MiSeq	96035	9	LUYA00000000	Denancé et al., 2017
CFBP 8430	LSV 47.11	6	*Polygala myrtifolia*	France (PACA)	2015	4	PacBio RS II	2716895	1	JAJKGO000000000	This study
CFBP 8431	LSV 47.13	6	*Prunus cerasifera*	France (Corse)	2015	2	PacBio RS II	1987931	1	JAJKGP000000000	This study
CFBP 8432	LSV 47.15	7	*Polygala myrtifolia*	France (PACA)	2015	1	PacBio RS II	2560653	1	CP087991	This study
CFBP 8433	LSV 47.20	7	*Cistus monspeliensis*	France (Corse)	2015	1	PacBio RS II	2496778	1	CP087992	This study
CFBP 8434	LSV 47.21	7	*Pelargonium sp*.	France (Corse)	2015	2	PacBio RS II	1939023	1	JAJKGQ000000000	This study
CFBP 8435	LSV 47.23	6	*Coronilla valentina*	France (Corse)	2015	3	PacBio RS II	2672324	1	JAJKGR000000000	This study
	BB01	42	*Vaccinium corymbosum*	USA (California)	2016	83	Illumina MiSeq	96868	10	MPAZ00000000	Van Horn et al., 2017
	ESVL	6	*Prunus dulcis*	Spain (Alicante)	2018	133	Illumina HiSeq 4000	103116	7	QPQV00000000	Giampetruzzi et al., 2019
	Griffin-1	7	*Quercus ruba*	USA (Georgia)	2006	84	454	74017	12	AVGA00000000	Chen et al., 2013
	IAS-AXF-212H7	6	*Prunus dulcis*	Spain (Alicante)	2018	336	Illumina HiSeq 4000	103609	7	VCPQ00000000	Landa et al., 2020
	IAS-AXF-235T10	6	*Prunus dulcis*	Spain (Alicante)	2018	432	Illumina HiSeq 4000	103901	7	VCQO00000000	Landa et al., 2020
	IVIA5901	6	*Prunus dulcis*	Spain (Alicante)	2018	1	Nanopore MiniION	2559157	1	GCA_004023395.2	Giampetruzzi et al., 2019
	IVIA6586_2	6	*Helichrysum italicum*	Spain (Alicante)	2018	341	Illumina HiSeq 4000	96774	8	VDCM00000000	Landa et al., 2020
	IVIA6629	6	*Rhamnus alaternus*	Spain (Alicante)	2018	1099	Illumina HiSeq 4000	96774	8	VCPM00000000	Landa et al., 2020
	IVIA6731	6	*Helichrysum italicum*	Spain (Alicante)	2018	422	Illumina HiSeq 4000	98660	7	VCPN00000000	Landa et al., 2020
	IVIA6902	6	*Prunus dulcis*	Spain (Alicante)	2018	1584	Illumina HiSeq 4000	94781	9	VCPO00000000	Landa et al., 2020
	IVIA6903	6	*Prunus dulcis*	Spain (Alicante)	2018	534	Illumina HiSeq	103089	7	VCPP00000000	Landa et al., 2020
	RAAR14_plum327	26	*Prunus domestica*	Brazil (Veranopolis)	2010	192	Illumina HiSeq 4000	96594	8	VDDF00000000	Landa et al., 2020
	RAAR6_Butte	7	*Prunus dulcis*	USA (California)	1995	140	Illumina HiSeq 4000	128621	7	VDDE00000000	Landa et al., 2020
	sycamore Sy-VA	8	*Platanus occidentalis*	USA (Virginia)	2002	128	454	119240	7	JMHP00000000	Guan et al., 2014
	TOS14	87	*Spartium junceum*	Italy (Tuscany)	2018	80	Illumina NovaSeq	193588	4	SMTJ00000000	Giampetruzzi et al., 2019
	TOS4	87	*Prunus dulcis*	Italy (Tuscany)	2018	77	Illumina NovaSeq	178266	4	SMTH00000000	Giampetruzzi et al., 2019
	TOS5	87	*Polygala myrtifolia*	Italy (Tuscany)	2018	72	Illumina NovaSeq	178266	4	SMTI00000000	Giampetruzzi et al., 2019
	XF3348	81	*Prunus dulcis*	Spain (Mallorca)	2018	392	Illumina HiSeq 4000	102161	7	VDCL00000000	Landa et al., 2020
	XYL1752	81	*Prunus dulcis*	Spain (Mallorca)	2018	422	Illumina HiSeq 4000	98273	9	VDCK00000000	Landa et al., 2020
	XYL1981	81	*Ficus carica*	Spain (Mallorca)	2018	353	Illumina HiSeq 4000	96968	9	VDCJ00000000	Landa et al., 2020

Table S2. List of the 95 *X. fastidiosa* strains used in this study and their VNTR allelic profile.

* CFBP refers to strains from the CIRM-CFBP (https://www6.inra.fr/cirm_eng/CFBP -Plant-Associated-Bacteria); LSV to strains isolated by the Plant Health Laboratory at ANSES, † NA: not available, ‡ the 16 strains used as "panel test" to set up the MLVA scheme.

Taxonomic position	CFBP strain code*	Other strain code	ST	Host plant of isolation	Place of isolation	Year of isolation	XFSSR allelic profile												
							ASSR-11	ASSR-16	COSS-1	OSSR-19	GSSR-7	OSSR-16	XFSSR-37	XFSSR-58	ASSR-9	ASSR-12	ASSR-19	GSSR-4	XFSSR-40
Xylella fastidiosa subsp. fastidiosa	CFBP 13349	ATCC 35876	2	*Ambrosia artemifolia*	USA (Florida)	1983	7	26	8	10	24	11	10	12	2	3	2	24	8
	CFBP 13354	ICMP 15197	2	*Vitis vinifera*	USA (Florida)	1987	4	29	5	3	15	9	12	14	2	3	2	26	9
	CFBP 13676	Temecula 1	1	*Vitis vinifera*	USA (California)	1998	9	25	11	3	16	8	5	8	2	6	2	17	7
	CFBP 13686	MED PRI 047	5	*Nerium oleander*	USA (Texas)	NA	7	27	1	7	17	13	2	14	16	10	2	24	4
	CFBP 7969	LMG 15553	2	*Vitis rotundifolia*	USA (North Carolina)	1985	8	27	1	5	19	7	12	11	2	3	2	24	8
	CFBP 7970	LMG 17159	2	*Vitis vinifera*	USA (Florida)	1987	8	27	1	5	12	8	12	14	2	3	2	26	9
	CFBP 8069	PD89.1	1	*Vitis* sp.	NA†	NA	4	28	4	6	9	7	12	10	2	12	2	22	7
	CFBP 8071‡	LSV 40.41	1	*Prunus dulcis*	USA (California)	1987	7	23	6	10	23	14	7	7	2	7	2	16	7
	CFBP 8073‡	LSV 42.09	75	*Coffea canephora*	Mexique	2012	7	27	1	5	30	13	8	13	2	13	2	56	8
	CFBP 8077‡	LSV 42.36	5	*Nerium oleander*	USA (California)	1995	8	23	1	6	18	12	2	8	2	7	2	24	4
	CFBP 8082	LMG 9064	2	*Ambrosia artemifolia*	USA (Florida)	1983	9	27	1	10	24	11	10	12	2	3	2	24	8
	CFBP 8083	LMG 15554	2	*Vitis vinifera*	USA (North Carolina)	1985	7	28	1	5	17	7	12	12	2	3	2	24	6
	CFBP 8084‡	LMG 15098	29	*Mulberry* sp.	USA (Georgia)	NA	8	28	1	5	19	11	5	5	2	8	2	19	10
	CFBP 8174	ICMP 6576	1	*Vitis vinifera*	USA (California)	NA	9	23	1	6	27	6	11	7	2	7	2	16	12
	CFBP 8175	ICMP 8729	1	*Vitis vinifera*	USA (Florida)	NA	9	23	1	6	31	6	11	7	2	7	2	16	12
	CFBP 8176	ICMP 8730	2	*Vitis vinifera*	USA (Florida)	NA	8	27	1	5	16	9	12	14	2	3	2	26	9
	CFBP 8177	ICMP 8731	1	*Vitis vinifera*	USA (Florida)	NA	8	23	1	6	23	14	7	7	2	7	2	16	8
	CFBP 8351	LSV 46.26	1	*Vitis* sp.	USA (California)	1993	4	28	7	8	23	13	8	8	2	6	2	16	12
	CFBP 8356	LSV 46.27	72	*Coffea arabica*	Costa Rica	2015	9	22	4	10	28	16	3	3	2	10	2	13	6
	CFBP 8419	LSV 46.39	72	*Coffea arabica*	France	2015	10	29	7	3	18	4	3	3	2	12	2	12	7
	CFBP 8478	LSV 46.28	72	*Coffea arabica*	France	2015	8	27	1	5	14	4	3	3	2	10	2	12	10
Xylella fastidiosa subsp. multiplex	CFBP 13551‡	Dixon	6	*Prunus dulcis*	USA (California)	1994	10	29	7	10	20	8	3	5	11	12	9	17	9
	CFBP 13552‡	JCS6	7	*Polygala myrtifolia*	France (Corsica)	2016	7	24	9	7	14	22	8	4	15	8	11	9	8
	CFBP 13677	AlmaEm3	42	*Vaccinium corymbosum*	USA (Georgia)	2011	7	24	5	3	9	11	3	9	8	6	2	17	2
	CFBP 13678	ALS6	27	*Prunus dulcis*	USA (California)	NA	7	24	6	13	24	14	3	7	13	10	8	14	8
	CFBP 13679	Georgia Plum	10	*Prunus* sp.	USA (Georgia)	2004	25	27	10	14	26	11	8	10	9	10	9	9	5
	CFBP 13680	GIL GRA 274 EXT	23	*Helianthus annuus*	USA (Texas)	NA	8	19	10	2	23	18	5	9	12	3	11	9	5
	CFBP 13681	LLA FAL 718 A	23	*Iva angustifolia*	USA (Texas)	NA	2	27	10	10	10	21	11	10	12	5	9	10	6
	CFBP 13682	VAL VAL 072 EXT	42	*Ambrosia trifida*	USA (Texas)	NA	8	27	1	5	24	10	5	5	9	5	2	14	5
	CFBP 13683	BB08-1	43	*Vaccinium windsor*	USA (Florida)	2008	7	24	8	12	15	11	5	7	10	5	2	11	7
	CFBP 13684	L 95-2	37	*Lupinus villosus*	USA (Florida)	NA	23	29	10	2	12	10	2	7	11	3	13	19	5
	CFBP 13685	T.Oak 95-1	9	*NA*	USA (Florida)	NA	7	25	1	5	15	12	4	6	15	8	4	26	3
	CFBP 13690	UVA 519-1B	45	*Cercis* sp.	USA (Texas)	NA	9	23	7	8	15	11	8	8	2	5	9	11	4
	CFBP 13741		6	*Polygala myrtifolia*	France (Corsica)	2017	12	27	10	11	12	7	3	8	11	14	9	17	10
	CFBP 13742		6	*Polygala myrtifolia*	France (Corsica)	2017	12	29	11	11	22	7	3	8	11	13	9	17	10
	CFBP 13743		7	*Helichrysum italicum*	France (Corsica)	2017	7	24	7	7	14	22	6	4	15	8	11	9	8
	CFBP 8068‡	LNPV 00.54	41	*Ulmus elm*	USA (Washington DC)	NA	15	32	11	5	25	8	7	8	3	7	12	8	4
	CFBP 8070	LSV 40.38	10	*Prunus* sp.	USA (Georgia)	2004	2	27	7	10	25	11	8	4	9	10	9	9	5
	CFBP 8076‡	LSV 42.31	9	*Quercus rubra*	USA (Washington DC)	NA	7	27	11	6	20	12	5	6	9	6	8	27	5
	CFBP 8078‡	LSV 43.11	51	*Vinca* sp.	USA (Florida)	1983	7	21	5	5	11	7	7	4	7	4	8	9	6
	CFBP 8173‡	LSV 40.39	41	*Prunus* sp.	USA (Georgia)	1983	15	32	11	5	24	8	7	8	3	7	12	8	4
	CFBP 8416	LSV 46.77	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	7	7	14	22	7	4	15	8	11	9	8
	CFBP 8417‡	LSV 46.78	6	*Spartium junceum*	France (Corsica)	2015	12	29	9	11	21	7	3	8	11	13	9	17	11
	CFBP 8418	LSV 46.79	6	*Spartium junceum*	France (Corsica)	2015	12	29	9	11	22	7	3	8	11	13	9	18	11
	CFBP 8430	LSV 47.11	6	*Polygala myrtifolia*	France (PACA)	2015	11	29	8	13	17	7	3	9	11	12	8	17	9
	CFBP 8431‡	LSV 47.13	6	*Prunus cerasifera*	France (Corsica)	2015	12	29	9	7	22	7	3	8	11	13	9	17	10
	CFBP 8432‡	LSV 47.15	7	*Polygala myrtifolia*	France (PACA)	2015	7	24	12	7	16	25	7	4	12	8	12	9	9
	CFBP 8433‡	LSV 47.20	7	*Cistus monspeliensis*	France (Corsica)	2015	7	24	6	7	16	16	7	4	13	8	12	9	9
	CFBP 8434‡	LSV 47.21	7	*Pelargonium* sp.	France (Corsica)	2015	7	24	7	7	13	23	10	4	15	8	12	9	8
	CFBP 8435‡	LSV 47.23	6	*Coronilla valentina*	France (Corsica)	2015	12	29	9	7	22	7	3	8	11	13	9	17	10
	CFBP 13584	LSV 47.06	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	8	7	14	20	7	4	15	8	11	9	8
	CFBP 13745	LSV 47.07	6	*Polygala myrtifolia*	France (Corsica)	2015	12	29	9	11	22	7	3	8	11	13	9	17	10
	CFBP 13585	LSV 47.08	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	7	7	14	22	7	4	15	8	11	9	8
	CFBP 13586	LSV 47.10	6	*Lavandula* X *allardii*	France (Corsica)	2015	12	29	9	11	22	7	3	8	11	13	9	17	10
	CFBP 13620	LSV 47.12	6	*Polygala myrtifolia*	France (PACA)	2015	11	29	8	13	17	7	3	8	11	12	8	17	9

	CFBP 13623	LSV 47.14	6	*Lavandula angustifolia*	France (Corsica)	2015	12	29	10	11	28	7	3	8	11	13	9	17	10
	CFBP 13621	LSV 47.16	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	5	7	14	22	7	4	15	8	11	9	8
	CFBP 13622	LSV 47.17	6	*Polygala myrtifolia*	France (Corsica)	2015	12	29	9	12	22	7	3	8	10	13	9	17	10
	CFBP 13624	LSV 47.18	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	9	7	15	22	7	4	15	8	11	9	8
	CFBP 13625	LSV 47.19	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	4	7	13	23	7	5	16	8	8	9	8
	CFBP 13588	LSV 47.22	7	*Polygala myrtifolia*	France (Corsica)	2015	7	24	7	7	15	23	7	4	15	9	11	9	10
	CFBP 13589	LSV 47.32	7	*Spartium junceum*	France (PACA)	2016	7	24	5	7	15	21	7	4	13	8	10	9	9
	CFBP 13626	LSV 47.60	6	*Helichrysum italicum*	France (Corsica)	2016	12	29	9	11	15	7	3	8	11	13	9	17	10
	CFBP 13627	LSV 47.61	6	*Calicotome villosa*	France (Corsica)	2016	12	29	9	11	22	7	3	8	11	13	9	17	10
	CFBP 13628	LSV 48.29	6	*Lavandula* sp.	France (Corsica)	2016	12	29	9	11	24	7	3	8	13	13	9	17	10
	CFBP 13629	LSV 48.30	6	*Polygala myrtifolia*	France (Corsica)	2016	12	29	9	11	21	7	3	8	11	13	9	17	10
	CFBP 13630	LSV 48.31	6	*Cistus monspeliensis*	France (Corsica)	2016	10	29	7	10	21	7	3	9	11	13	8	17	10
	CFBP 13631	LSV 48.32	7	*Cistus monspeliensis*	France (Corsica)	2016	7	24	7	7	16	21	7	4	15	8	11	9	8
	CFBP 13632	LSV 48.33	6	*Lavandula stoechas*	France (Corsica)	2016	10	29	7	10	20	7	3	9	11	12	8	15	10
	CFBP 13591	LSV 48.34	6	*Polygala myrtifolia*	France (Corsica)	2016	12	29	10	11	22	7	3	8	11	13	9	17	10
	CFBP 13592	LSV 48.35	7	*Prunus dulcis*	France (Corsica)	2016	7	24	7	7	14	22	7	4	16	8	8	9	7
	CFBP 13633	LSV 48.36	6	*Rosa canina*	France (Corsica)	2016	12	29	9	11	20	8	3	8	11	13	9	17	10
	CFBP 13634	LSV 48.37	7	*Westrigia fructicosa*	France (PACA)	2017	7	24	7	8	15	22	7	4	16	8	11	9	8
	CFBP 13635	LSV 48.38	7	*Cistus creticus*	France (Corsica)	2017	7	24	7	7	16	29	7	4	15	8	11	9	8
	CFBP 13598	LSV 49.25	7	*Acacia dealbata*	France (PACA)	2017	7	24	7	7	16	12	7	4	13	8	13	9	8
	CFBP 13636	LSV 49.26	7	*Coronilla glauca*	France (PACA)	2017	7	24	8	7	17	24	7	4	12	8	12	9	12
	CFBP 13590	LSV 49.27	7	*Coronilla glauca*	France (PACA)	2017	6	24	7	7	16	25	7	4	13	8	13	9	11
	CFBP 13687	LSV 49.35	7	*Medicago sativa*	France (PACA)	2017	8	24	6	7	13	22	7	4	12	8	11	9	9
	CFBP 13637	LSV 49.36	7	*Polygala myrtifolia*	France (PACA)	2017	7	24	8	7	14	23	7	4	12	8	12	9	9
	CFBP 13638	LSV 49.37	6	*Euryops chrysanthemoïdes*	France (PACA)	2017	12	29	8	13	24	7	3	8	9	13	8	17	10
	CFBP 13587	LSV 49.43	6	*Prunus cerasus*	France (PACA)	2017	16	29	8	11	19	7	1	8	10	13	7	17	7
	CFBP 13639	LSV 49.47	6	*Prunus avium*	France (PACA)	2018	7	24	7	11	19	7	7	8	10	13	8	17	7
	CFBP 13693	LSV 49.64	7	*Polygala myrtifolia*	France (PACA)	2018	7	24	8	7	22	20	7	4	12	8	11	9	6
	CFBP 13691	LSV 50.02	7	*Polygala myrtifolia*	France (PACA)	2018	8	25	6	7	18	18	6	5	12	9	11	9	7
	CFBP 13694	LSV 50.25	7	*Euryops chrysanthemoïdes*	France (PACA)	2018	8	22	5	3	25	19	6	4	14	9	11	9	9
	CFBP 13688	LSV 50.26	7	*Convolvulus cneorum*	France (PACA)	2018	7	24	8	7	17	22	7	4	12	8	12	9	8
	CFBP 13692	LSV 50.27	7	*Convolvulus cneorum*	France (PACA)	2018	16	29	7	7	21	18	7	4	12	9	12	9	9
	CFBP 13695	LSV 50.37	7	*Helichrysum italicum*	France (PACA)	2018	12	24	8	8	19	24	7	4	12	8	11	9	9
	CFBP 13689	LSV 50.38	7	*Prunus dulcis*	France (Corsica)	2018	12	28	9	11	14	22	7	4	16	8	8	9	7
Xylella fastidiosa subsp. pauca	CFBP 8072	LSV 41.03	74	*Coffea arabica*	Ecuador	2012	4	24	6	7	4	4	4	8	2	15	2	51	1
	CFBP 8074	LSV 42.10	74	*Coffea arabica*	Ecuador	2012	4	24	6	7	4	11	4	8	2	15	2	56	1
	CFBP 8402	LSV 47.29	53	*Olea europaea*	Italy (Apulia)	2014	2	18	10	13	4	27	3	11	2	4	2	7	1
	CFBP 8495	PD 7202	53	*Coffea arabica*	The Netherlands	2015	2	16	5	13	4	24	3	9	2	4	2	7	1
	CFBP 8498	PD 7211	73	*Coffea arabica*	The Netherlands	2015	2	31	8	3	4	8	2	12	2	12	2	60	1
		LSV 47.33	53	*Coffea arabica*	Costa Rica	2016	9	15	5	8	4	29	1	6	2	4	2	7	1

Table S3. List of the 18 Spanish *X. fastidiosa* subsp. *multiplex* strain DNAs used in this study and their VNTR allelic profile.

Strain code	ST	Host plant	Place of isolation	Year of isolation	XFSSR allelic profile												
					COSS-1	OSSR-19	ASSR-	ASSR-16	XFSSR-58	XFSSR-37	GSSR-7	OSSR-16	ASSR-9	GSSR-4	ASSR-19	ASSR-12	XFSSR-40
AXF 120	6	*Prunus dulcis*	Spain (Alicante, La Vall Alcala)	2018	8	7	4	33	6	10	35	4	18	12	9	6	6
AXF 183	6	*Prunus dulcis*	Spain (Alicante, Polop)	2018	8	7	4	33	6	10	36	6	18	12	9	6	7
AXF 213	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	33	6	16	13	7	6	8
AXF 26	6	*Prunus dulcis*	Spain (Alicante, Xalo)	2018	9	7	4	33	6	9	36	6	17	12	7	6	8
AXF 45	6	*Prunus dulcis*	Spain (Alicante, Benissa)	2018	8	7	4	33	6	9	34	6	9	12	10	6	9
AXF 51	6	*Prunus dulcis*	Spain (Alicante, Alcalali)	2018	10	7	4	33	6	9	36	6	17	12	7	6	8
AXF 82	6	*Prunus dulcis*	Spain (Alicante, Castell de Castells)	2018	9	7	4	33	6	9	34	6	17	12	7	6	8
AXF 87	6	*Prunus dulcis*	Spain (Alicante, Benifato)	2018	10	7	4	33	6	9	36	6	18	12	7	6	8
IAS-AXF212H7	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	35	6	18	13	7	6	8
IAS-AXF235T1	6	*Prunus dulcis*	Spain (Alicante, El Castell de Guadalest	2018	8	7	4	33	6	6	42	7	19	12	9	6	8
IAS-AXF235T10	6	*Prunus dulcis*	Spain (Alicante, El Castell de Guadalest	2018	8	7	4	33	6	6	42	7	19	12	9	6	8
IAS-AXF64H11	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	33	6	16	13	7	6	8
IAS-AXF64T12	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	33	6	16	13	7	6	8
IAS-AXF64T13	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	33	6	16	13	7	6	8
IAS-AXF64T14	6	*Prunus dulcis*	Spain (Alicante, Benimantell)	2018	9	7	4	33	6	9	33	6	16	13	7	6	8
XF3348	81	*Prunus dulcis*	Spain (Mallorca)	2018	7	5	4	23	6	2	11	12	7	13	11	9	5
XYL1752	81	*Prunus dulcis*	Spain (Menorca)	2018	9	6	6	22	6	2	12	13	6	13	11	9	5
XYL1981	81	*Ficus carica*	Spain (Mallorca)	2018	9	6	6	23	6	2	15	7	6	13	11	9	5

Table S4. List of the 396 *X. fastidiosa* subsp. *multiplex* -infected French plant samples used in this study and their VNTR allelic profile.

* 13 pairs of isolated strains and the DNA extracted from the same original plant sample, † the 16 samples for which DAPC clustering differed over the 20 runs, ‡ the samples collected by the DGAL in the framework of the national official surveillance strategy.

Sample code	ST	Host plant	Place of sampling	Year of isolation	Ct with Harper's qPCR test	XFSSR allelic profile													Haplotype number	Cluster Number in DAPC for k=4	ABC groups
						ASSR-11	ASSR-16	COSS-1	OSSR-19	GSSR-7	OSSR-16	XFSSR-37	XFSSR-58	ASSR-9	ASSR-12	ASSR-19	GSSR-4	XFSSR-40			
2015_1053.7‡	ST6	*Polygala myrtifolia*	Corsica, Albitreccia	2015	26.49	12	29	9	11	23	7	3	8	11	13	9	17	10	316	1	ST6_C1P1
2015_1067.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	25.58	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2015_1188.11‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	26.34	10	29	9	11	22	7	3	8	10	13	9	17	10	284	1	ST6_C1P1
2015_1268.12‡	cysG_7	*Polygala myrtifolia*	Corsica, Sainte Lucie de Tallano	2015	26.86	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_1268.9‡	ST7	*Polygala myrtifolia*	Corsica, Fozzano	2015	23.35	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_1273.1‡	ST6	*Spartium junceum*	Corsica, Alata	2015	24.81	12	29	9	11	21	7	3	8	11	13	9	17	11	304	1	ST6_C1P1
2015_1298.1‡	cysG_3	*Polygala myrtifolia*	Corsica, Appietto	2015	25.25	12	29	9	11	14	7	3	8	11	13	9	17	10	294	1	ST6_C1P1
2015_1298.6‡	ST6	*Polygala myrtifolia*	Corsica, Calcatoggio	2015	21.40	13	29	9	11	21	7	3	5	11	13	10	17	6	222	1	ST6_C1P1
2015_1298.7‡	cysG_3	*Polygala myrtifolia*	Corsica, Bastelicaccia	2015	24.61	12	29	10	11	21	7	3	4	11	13	9	17	10	6	1	ST6_C1P1
2015_1344.1‡	ST6	*Hebe* sp.	Corsica, Pietrosella	2015	30.07	10	29	8	11	22	7	3	8	10	13	9	17	10	211	1	ST6_C1P1
2015_1350.1‡	ST7	*Genista* X *spachiana*	Corsica, Coti-Chiavari	2015	25.25	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_1381.1‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2015	21.63	12	29	9	11	22	7	3	7	11	13	9	17	10	292	1	ST6_C1P1
2015_1396.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	23.22	12	29	10	11	22	7	3	8	11	13	9	17	10	9	1	ST6_C1P1
2015_1396.10‡	cysG_7	*Polygala myrtifolia*	Corsica, Sartene	2015	26.98	7	24	7	7	15	22	7	4	15	8	11	9	8	158	3	ST7_C1P1
2015_1396.2‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	24.37	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_1396.5‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	24.18	7	24	7	7	14	20	7	4	15	8	12	9	8	130	3	ST7_C1P1
2015_1396.8‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	23.11	12	29	5	11	24	7	3	8	7	14	9	17	9	46	1	ST6_C1P1
2015_1489.12‡	cysG_3	*Polygala myrtifolia*	Corsica, Lecci	2015	26.99	10	29	7	11	21	7	3	8	11	13	8	17	10	96	2	ST6_C2
2015_1527.1‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	25.14	7	24	7	7	14	23	3	4	15	8	11	9	8	108	3	ST7_C1P1
2015_1581.2‡	ST6	*Polygala myrtifolia*	Corsica, Appietto	2015	28.27	12	29	9	11	21	7	3	8	11	13	9	17	11	304	1	ST6_C1P1
2015_1581.5‡	cysG_3	*Polygala myrtifolia*	Corsica, Villanova	2015	27.51	12	29	9	11	21	7	3	8	10	13	9	17	10	302	1	ST6_C1P1
2015_1581.7‡	cysG_3	*Polygala myrtifolia*	Corsica, Casaglione	2015	25.85	11	29	10	11	24	7	3	8	12	13	9	17	11	3	1	ST6_C1P1
2015_1627.2‡	cysG_3	*Polygala myrtifolia*	Corsica, Zonza	2015	30.94	10	29	7	11	22	7	3	8	11	12	8	17	10	97	2	ST6_C2
2015_1627.3‡	cysG_3	*Polygala myrtifolia*	Corsica, Zonza	2015	30.15	10	29	8	10	22	7	3	8	11	12	8	17	7	201	2	ST6_C2
2015_1627.6‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	26.62	10	29	10	10	20	7	3	8	11	12	8	17	10	1	2	ST6_C2
2015_1659.34‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	25.73	10	29	9	11	22	7	3	8	10	13	9	17	10	284	1	ST6_C1P1
2015_1659.6‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	26.13	10	29	9	11	22	7	3	8	10	13	9	17	10	284	1	ST6_C1P1
2015_1659.61‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	24.41	10	29	9	11	22	7	3	8	10	13	9	17	10	284	1	ST6_C1P1
2015_1659.65‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	22.13	10	29	9	11	22	7	3	8	10	13	9	17	10	284	1	ST6_C1P1
2015_1725.3‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	25.01	7	24	7	7	16	21	7	4	15	8	11	9	7	167	3	ST7_C1P1
2015_1732.1‡	ST7	*Polygala myrtifolia*	Corsica, Bastelicaccia	2015	26.22	7	24	6	7	17	7	7	4	14	8	9	9	8	63	4	ST7_C2
2015_1754.3‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	24.00	7	24	7	7	10	21	7	4	15	7	11	9	8	111	3	ST7_C1P1
2015_1782.5‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	23.38	10	29	7	10	20	7	3	9	11	12	8	17	11	91	2	ST6_C2
2015_1809.1‡	ST7	*Polygala myrtifolia*	Corsica, Figari	2015	28.36	10	24	7	7	15	22	7	4	10	8	13	9	8	103	3	ST7_C1P1
2015_1809.3‡	ST7	*Polygala myrtifolia*	Corsica, Pianottoli Caldarello	2015	25.39	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_1829.3‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	24.94	10	29	9	11	21	7	3	8	10	13	9	17	10	283	1	ST6_C1P1
2015_1850.2‡	ST6	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	28.28	10	29	8	11	21	7	3	4	10	12	8	17	10	210	2	ST6_C2
2015_1861.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	26.05	12	30	9	11	22	7	3	8	11	13	10	17	10	235	1	ST6_C1P1
2015_1861.11‡	ST7	*Polygala myrtifolia*	Corsica, Bastelicaccia	2015	24.89	7	24	6	7	19	17	7	4	13	8	12	9	8	64	4	ST7_C2
2015_1861.2‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	26.95	12	29	9	11	19	7	3	8	10	13	9	19	10	296	1	ST6_C1P1
2015_1861.4‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	26.00	12	29	8	11	23	7	3	8	10	13	9	17	11	226	1	ST6_C1P1
2015_1922.1‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	26.81	10	29	7	10	18	7	3	8	10	12	8	17	10	84	2	ST6_C2
2015_1925.5‡	ST6	*Polygala myrtifolia*	Corsica, Afa	2015	25.61	12	29	10	11	22	7	3	8	11	13	9	17	10	9	1	ST6_C1P1
2015_1925.6‡	ST6	*Polygala myrtifolia*	Corsica, Cuttoli-Corticchiato	2015	28.33	12	29	9	11	21	7	3	8	10	13	9	15	10	301	1	ST6_C1P1
2015_1939.1‡	ST6	*Polygala myrtifolia*	Corsica, Vero	2015	24.56	12	29	9	11	23	7	3	8	11	12	9	17	10	315	1	ST6_C1P1
2015_1939.2‡	ST6	*Polygala myrtifolia*	Corsica, Peri	2015	24.70	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2015_1980.1‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	23.17	7	24	8	7	14	22	7	4	14	8	11	9	7	254	3	ST7_C1P1
2015_1980.2‡	ST7	*Polygala myrtifolia*	Corsica, Viggianello	2015	24.57	7	24	6	7	14	22	7	4	16	8	11	9	8	56	3	ST7_C1P1
2015_1980.4‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	23.40	7	24	7	7	13	23	7	4	17	8	11	9	11	121	3	ST7_C1P1
2015_2107.3‡	cysG_7	*Quercus suber*	Corsica, Grosseto-Prugna	2015	27.62	7	24	7	7	13	22	7	4	15	8	12	9	8	120	3	ST7_C1P1
2015_2141.3‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2015	30.09	12	29	9	11	23	8	3	8	12	13	9	17	7	319	1	ST6_C1P1
2015_2141.4‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2015	28.90	9	29	9	11	20	8	3	8	10	13	9	17	10	101	1	ST6_C1P1
2015_2141.9‡	cysG_7	*Polygala myrtifolia*	Corsica, Olmeto	2015	26.85	7	24	7	7	14	22	8	4	16	8	11	9	8	181	3	ST7_C1P1
2015_2151.5‡	ST6	*Polygala grandiflora nana*	Corsica, Bastelicaccia	2015	28.60	12	29	9	11	21	8	3	8	11	13	9	17	10	307	1	ST6_C1P1
2015_2155.1‡	ST6	*Polygala* sp.	PACA, Nice	2015	31.61	11	29	8	13	17	7	3	8	11	12	8	17	9	238	2	ST6_P2
2015_2155.2‡	ST6	*Polygala* sp.	PACA, Nice	2015	18.93	11	29	8	13	17	7	3	8	11	12	8	17	9	238	2	ST6_P2
2015_2155.4/CFBP 13620*‡	ST6	*Polygala* sp.	PACA, Nice	2015	19.08	11	29	8	13	17	7	3	8	11	12	8	17	9	238	2	ST6_P2
2015_2155.5‡	ST6	*Polygala* sp.	PACA, Nice	2015	29.94	11	29	9	12	25	7	3	8	12	7	8	17	11	95	2	ST6_P2
2015_2166.2‡	cysG_7	*Polygala myrtifolia*	Corsica, Olmeto	2015	25.66	7	24	8	7	14	22	8	4	15	8	11	9	8	275	3	ST7_C1P1
2015_2171.2‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	26.73	12	29	10	11	22	7	3	8	11	13	9	17	11	10	1	ST6_C1P1
2015_2192.9‡	ST7	*Polygala myrtifolia*	Corsica, Lecci	2015	27.85	7	24	8	7	14	22	7	4	15	8	12	9	8	256	3	ST7_C1P1
2015_2272.3‡	ST7	*Polygala myrtifolia*	Corsica, Santa Maria Figanielle	2015	27.77	7	24	7	7	16	20	7	4	16	8	11	9	8	166	3	ST7_C1P1
2015_2298.3‡	ST7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	26.10	7	24	12	7	17	25	7	4	12	8	12	9	9	38	4	ST7_P2

2015_2298.5‡	ST7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	25.00	7	24	12	7	16	25	7	4	12	8	12	9	9	37	4	ST7_P2
2015_2306.13‡	ST7	*Polygala myrtifolia*	Corsica, Appietto	2015	23.58	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_2306.14‡	cysG_3	*Polygala myrtifolia*	Corsica, Calcatoggio	2015	26.26	12	29	9	11	21	7	3	8	11	13	9	17	7	305	1	ST6_C1P1
2015_2306.15‡	cysG_3	*Polygala myrtifolia*	Corsica, Cargese	2015	29.57	12	29	8	11	22	7	3	8	10	13	9	17	10	220	1	ST6_C1P1
2015_2306.16‡	cysG_3	*Polygala myrtifolia*	Corsica, Vico	2015	28.27	12	29	10	11	23	7	3	8	11	13	9	17	10	12	1	ST6_C1P1
2015_2306.18/CFBP 13621*‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	24.09	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_2306.2/CFBP 13622*‡	ST6	*Polygala myrtifolia*	Corsica, Peri	2015	22.16	12	29	9	12	22	7	3	8	10	13	9	17	10	47	1	ST6_C1P1
2015_2306.22/CFBP 13624*‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	23.85	7	24	9	7	15	22	7	4	15	8	11	9	8	24	3	ST7_C1P1
2015_2306.35†‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	29.78	7	24	9	7	15	19	7	4	14	9	11	9	8	25	4	ST7_C2
2015_2306.4‡	cysG_3	*Polygala myrtifolia*	Corsica, Biguglia	2015	26.74	12	29	10	12	27	7	3	8	12	13	9	17	10	15	1	ST6_C1P1
2015_2306.6‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	24.44	7	24	7	7	14	21	7	4	15	7	11	9	8	134	3	ST7_C1P1
2015_2318.1‡	ST7	*Pelargonium* sp.	Corsica, Porto-Vecchio	2015	25.12	7	24	7	7	15	22	7	4	15	8	11	9	8	158	3	ST7_C1P1
2015_2368.3‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	20.02	7	24	7	7	14	23	7	4	15	9	11	9	8	147	3	ST7_C1P1
2015_2451.17‡	ST6	*Polygala myrtifolia*	Corsica, Eccica-Suarella	2015	24.50	12	29	9	11	20	7	3	8	11	13	9	17	10	299	1	ST6_C1P1
2015_2451.3‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	25.08	7	24	7	7	15	22	7	4	15	8	11	9	8	158	3	ST7_C1P1
2015_2451.4‡	ST6	*Polygala myrtifolia*	Corsica, Bastelicaccia	2015	23.61	12	29	7	11	23	7	3	8	11	13	9	17	10	99	1	ST6_C1P1
2015_2451.6‡	cysG_7	*Polygala myrtifolia*	Corsica, Bastelicaccia	2015	24.49	7	24	6	7	17	24	7	4	13	8	12	9	8	62	4	ST7_C2
2015_2451.7‡	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2015	24.22	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2015_2451.9‡	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2015	25.41	12	29	8	11	24	7	3	7	11	13	9	17	7	213	1	ST6_C1P1
2015_2471.4‡	ST6	*Pelargonium graveolens*	Corsica, Bastelicaccia	2015	27.37	12	25	9	11	22	7	1	8	11	13	9	17	10	287	1	ST6_C1P1
2015_2498.6‡	ST7	*Polygala myrtifolia*	Corsica, San Gavino Di Carbini	2015	25.76	7	24	8	8	13	23	7	4	15	8	11	9	8	281	3	ST7_C1P1
2015_2600.1‡	ST7	*Pelargonium* sp.	Corsica, Sollacaro	2015	24.94	8	24	8	7	14	23	7	4	16	8	12	9	8	278	4	ST7_C2
2015_2601.2‡	cysG_7	*Polygala myrtifolia*	Corsica, Sollacaro	2015	25.38	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_2601.3‡	ST7	*Polygala myrtifolia*	Corsica, Sollacaro	2015	26.04	7	24	7	7	14	24	7	4	15	8	11	9	8	150	3	ST7_C1P1
2015_2601.5‡	ST7	*Polygala myrtifolia*	Corsica, Viggianello	2015	23.45	7	24	7	7	15	22	7	4	16	8	10	9	8	159	3	ST7_C1P1
2015_2601.6‡	ST7	*Polygala myrtifolia*	Corsica, Viggianello	2015	24.09	7	24	7	7	15	21	7	4	16	8	11	9	8	156	3	ST7_C1P1
2015_2601.8‡	ST7	*Polygala myrtifolia*	Corsica, San Gavino Di Carbini	2015	23.58	7	24	7	7	15	22	7	4	15	8	11	9	8	158	3	ST7_C1P1
2015_2664.1‡	ST6	*Spartium junceum*	Corsica, Calvi	2015	27.71	10	29	9	11	21	7	3	8	10	13	9	17	10	283	1	ST6_C1P1
2015_2681.1‡	cysG_7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	22.43	7	24	10	7	14	24	7	4	12	8	12	9	9	26	4	ST7_P2
2015_2681.2‡	cysG_7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	21.81	7	24	10	7	14	24	7	4	12	8	12	9	9	26	4	ST7_P2
2015_2681.3‡	cysG_7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	23.53	7	24	10	7	14	24	7	4	12	8	12	9	9	26	4	ST7_P2
2015_2681.4‡	cysG_7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	20.65	7	24	10	7	15	24	7	4	12	8	12	9	9	27	4	ST7_P2
2015_2681.5‡	cysG_7	*Polygala* sp.	PACA, Saint Laurent du Var	2015	22.54	7	24	10	7	15	24	7	4	12	8	12	9	9	27	4	ST7_P2
2015_2682.1‡	ST7	*Polygala myrtifolia*	PACA, La Seyna-sur-Mer	2015	30.81	8	24	5	7	13	25	7	4	12	8	11	9	8	52	4	ST7_P2
2015_2768.1‡	ST6	*Metrosideros excelsa*	Corsica, Appietto	2015	30.30	12	29	9	11	22	7	3	8	12	12	9	17	11	314	1	ST6_C1P1
2015_2769.2‡	ST6	*Polygala myrtifolia*	Corsica, Calvi	2015	25.32	10	29	9	9	22	7	3	8	10	13	9	17	10	21	1	ST6_C1P1
2015_2792.1‡	cysG_7	*Spartium junceum*	Corsica, Zonza	2015	26.75	7	24	7	7	14	21	7	4	16	8	10	9	8	135	3	ST7_C1P1
2015_2793.16‡	cysG_7	*Polygala myrtifolia*	Corsica, Belvedere-Campomoro	2015	27.68	7	24	7	7	14	21	7	4	12	12	8	17	10	131	4	ST7_C2
2015_2793.2‡	cysG_3	*Polygala myrtifolia*	Corsica, Zonza	2015	29.86	10	29	6	9	21	7	3	8	15	12	11	9	8	82	2	ST6_C2
2015_2793.3‡	cysG_7	*Polygala myrtifolia*	Corsica, Viggianello	2015	26.83	7	24	7	7	14	18	7	4	15	8	11	9	8	124	3	ST7_C1P1
2015_2793.4‡	cysG_7	*Polygala myrtifolia*	Corsica, Coti-Chiavari	2015	25.30	7	24	7	7	14	21	5	4	14	8	11	9	7	109	3	ST7_C1P1
2015_2793.8‡	cysG_7	*Polygala myrtifolia*	Corsica, Lecci	2015	31.97	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_2794.1‡	cysG_3	*Polygala myrtifolia*	Corsica, Furiani	2015	28.83	12	29	10	12	27	7	3	9	11	13	9	17	10	18	1	ST6_C1P1
2015_2794.2‡	cysG_3	*Polygala myrtifolia*	Corsica, Cargese	2015	25.76	13	29	8	11	21	7	3	8	8	13	9	19	8	229	1	ST6_C1P1
2015_2794.3‡	cysG_3	*Polygala myrtifolia*	Corsica, Arro	2015	27.68	13	29	8	11	22	7	3	10	10	13	7	17	11	228	1	ST6_C1P1
2015_2811.1‡	cysG_3	*Polygala myrtifolia*	Corsica, Sant Andrea d'Orcino	2015	27.54	12	29	9	11	21	7	3	8	11	13	9	17	10	303	1	ST6_C1P1
2015_2811.3‡	cysG_3	*Polygala myrtifolia*	Corsica, Coggia	2015	30.94	12	29	12	11	21	7	3	8	11	13	9	17	10	36	1	ST6_C1P1
2015_2832.1‡	cysG_7	*Polygala myrtifolia*	Corsica, Sartene	2015	25.73	7	24	7	7	14	20	7	4	15	8	11	9	9	129	3	ST7_C1P1
2015_2832.6‡	cysG_7	*Polygala myrtifolia*	Corsica, Monacia d'Aullene	2015	23.98	7	24	7	7	14	13	7	4	15	8	10	9	8	122	3	ST7_C1P1
2015_2856.7‡	cysG_7	*Polygala myrtifolia*	Corsica, Sainte Lucie de Tallano	2015	28.01	7	24	7	7	14	22	7	8	15	8	11	9	8	183	3	ST7_C1P1
2015_559.1‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	20.26	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_601.1‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	26.96	7	24	7	7	14	25	7	4	15	8	11	9	8	152	3	ST7_C1P1
2015_601.2/CFBP 13584*‡	ST7	*Polygala myrtifolia*	Corsica, Belvedere-Campomoro	2015	26.05	7	24	8	7	14	20	7	4	15	8	11	9	8	253	3	ST7_C1P1
2015_646.11‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	26.67	10	29	7	10	21	7	3	8	11	12	8	17	10	88	2	ST6_C2
2015_646.14‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	24.86	7	24	7	7	13	22	7	4	15	8	11	9	8	119	3	ST7_C1P1
2015_743.1‡	ST6	*Polygala myrtifolia*	Corsica, Alata	2015	25.88	12	29	10	11	24	7	3	11	11	13	9	17	8	5	1	ST6_C1P1
2015_743.5‡	ST7	*Polygala myrtifolia*	Corsica, Belvedere-Campomoro	2015	22.15	7	24	7	7	15	23	8	4	15	8	11	9	8	182	3	ST7_C1P1
2015_743.9‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2015	22.43	12	29	10	11	24	7	3	8	11	13	9	17	10	13	1	ST6_C1P1
2015_746.1‡	ST6	*Polygala myrtifolia*	Corsica, Alata	2015	22.48	12	29	9	11	21	7	3	8	11	13	9	17	10	303	1	ST6_C1P1
2015_746.2‡	ST6	*Polygala myrtifolia*	Corsica, Peri	2015	21.79	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2015_746.3/CFBP 13585*‡	ST7	*Polygala myrtifolia*	Corsica, Sartene	2015	20.19	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_770.11‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	22.59	7	24	7	7	14	23	7	4	15	8	11	9	8	146	3	ST7_C1P1
2015_770.13‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	23.75	7	24	7	7	15	17	7	4	17	8	11	9	8	154	3	ST7_C1P1
2015_770.21‡	ST7	*Polygala myrtifolia*	Corsica, Cauro	2015	22.93	7	24	7	8	15	23	7	4	16	7	11	9	8	197	3	ST7_C1P1
2015_770.22‡	ST6	*Polygala myrtifolia*	Corsica, Cauro	2015	24.64	12	29	9	11	19	7	3	8	11	13	8	17	10	297	1	ST6_C1P1
2015_770.5‡	ST6	*Polygala myrtifolia*	Corsica, Cargese	2015	25.80	12	29	9	11	22	7	3	8	11	13	8	19	10	313	1	ST6_C1P1
2015_770.9‡	ST6	*Polygala myrtifolia*	Corsica, Alata	2015	25.89	12	29	8	11	22	7	3	8	11	13	9	17	10	223	1	ST6_C1P1
2015_791.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	24.55	12	29	5	11	22	7	3	8	11	13	9	17	10	45	1	ST6_C1P1
2015_791.2‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	22.58	12	29	8	11	22	8	3	8	10	13	9	17	11	225	1	ST6_C1P1
2015_791.3‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	22.34	12	29	8	11	22	7	3	8	10	13	9	17	10	220	1	ST6_C1P1
2015_791.4‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	21.12	12	29	5	11	20	7	3	8	10	13	9	17	9	44	1	ST6_C1P1

2015_791.5‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	26.39	12	29	8	11	22	7	3	8	10	13	9	17	10	220	1	ST6_C1P1
2015_791.8‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	22.87	7	29	9	11	20	7	3	8	10	12	9	17	10	199	1	ST6_C1P1
2015_826.11‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	25.86	10	29	7	10	19	7	3	8	11	12	8	17	10	85	2	ST6_C2
2015_826.18‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	23.04	10	29	7	10	19	7	3	9	11	14	8	17	10	89	2	ST6_C2
2015_826.2‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	26.23	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_826.4‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	25.30	7	24	7	7	14	22	7	4	13	8	11	9	8	136	3	ST7_C1P1
2015_834.13‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	25.41	10	29	7	10	19	7	3	8	12	12	8	21	8	86	2	ST6_C2
2015_834.14‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	24.15	10	29	7	10	20	7	3	4	12	12	8	17	5	83	2	ST6_C2
2015_834.7‡	ST6	*Polygala myrtifolia*	Corsica, Zonza	2015	24.45	10	29	7	10	20	7	3	8	12	12	8	17	10	87	2	ST6_C2
2015_912.3‡	ST6	*Polygala myrtifolia*	Corsica, Alata	2015	26.86	12	27	9	11	22	7	3	8	10	13	9	17	10	289	1	ST6_C1P1
2015_917.1‡	ST6	*Spartium junceum*	Corsica, Alata	2015	18.08	12	29	9	11	22	7	3	8	11	13	9	18	11	312	1	ST6_C1P1
2015_942.2‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	19.92	7	24	7	7	16	16	7	4	15	8	12	9	8	164	3	ST7_C1P1
2015_961.2‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	26.83	9	24	7	7	14	22	7	4	15	8	11	9	8	193	3	ST7_C1P1
2015_961.4‡	ST7	*Polygala myrtifolia*	Corsica, Serra Di Ferro	2015	22.95	7	24	7	7	15	22	7	4	14	8	11	9	8	157	3	ST7_C1P1
2015_969.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	25.03	12	29	9	11	20	7	3	8	11	13	9	17	10	299	1	ST6_C1P1
2015_969.3‡	ST6	*Polygala myrtifolia*	Corsica, Cargese	2015	27.47	12	29	9	11	24	7	3	8	11	13	9	17	11	248	1	ST6_C1P1
2015_969.4‡	ST6	*Polygala myrtifolia*	Corsica, Ota	2015	25.16	12	29	8	11	20	7	3	8	10	13	8	17	10	214	1	ST6_C1P1
2015_969.6‡	ST6	*Polygala myrtifolia*	Corsica, Sarrola Carcopino	2015	27.66	12	29	9	11	24	7	3	8	11	13	9	17	10	320	1	ST6_C1P1
2015_973.3‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2015	25.74	12	29	10	11	10	7	3	8	11	11	9	17	10	7	1	ST6_C1P1
2015_973.7‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	25.50	7	24	7	7	13	22	7	4	15	8	11	9	8	119	3	ST7_C1P1
2015_981.10‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	25.04	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2015_981.15‡	ST7	*Polygala myrtifolia*	Corsica, Eccica-Suarella	2015	22.34	7	24	7	7	14	21	7	4	15	8	10	9	8	133	3	ST7_C1P1
2015_981.16‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2015	24.47	12	29	8	11	22	7	3	8	10	13	9	17	10	220	1	ST6_C1P1
2015_981.17‡	ST7	*Polygala myrtifolia*	Corsica, Pietrosella	2015	23.43	7	24	7	7	14	21	7	4	15	8	10	9	8	133	3	ST7_C1P1
2015_981.20‡	ST7	*Polygala myrtifolia*	Corsica, Albitreccia	2015	24.08	8	24	7	7	14	22	7	4	15	8	11	9	8	191	3	ST7_C1P1
2015_981.21‡	ST7	*Polygala myrtifolia*	Corsica, Coti-Chiavari	2015	23.40	7	24	7	7	13	22	7	4	15	8	11	9	8	119	3	ST7_C1P1
2015_981.22‡	ST7	*Polygala myrtifolia*	Corsica, Cauro	2015	23.35	7	24	7	7	13	22	7	4	15	8	11	9	8	119	3	ST7_C1P1
2015_981.24‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2015	25.55	12	29	9	11	22	7	3	4	11	13	9	17	10	291	1	ST6_C1P1
2015_981.25‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2015	23.99	12	29	9	11	16	7	3	9	12	13	9	17	10	246	1	ST6_C1P1
2015_981.4‡	ST7	*Polygala myrtifolia*	Corsica, Grossa	2015	26.14	7	24	7	7	13	22	7	4	15	8	11	9	8	119	3	ST7_C1P1
2015_981.6‡	ST7	*Polygala myrtifolia*	Corsica, Grossa	2015	24.05	7	24	7	7	15	23	7	4	16	8	11	9	8	162	3	ST7_C1P1
2015_981.9‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2015	26.20	7	24	7	7	14	19	7	4	15	8	11	9	8	127	3	ST7_C1P1
2016_110.1‡	ST7	*Polygala myrtifolia*	Corsica, Monacia d'Aullene	2016	31.05	7	24	6	7	14	23	7	4	9	8	10	9	8	58	4	ST7_C2
2016_110.2‡	ST7	*Polygala myrtifolia*	Corsica, Monacia d'Aullene	2016	30.14	7	24	6	7	14	23	7	4	9	8	10	9	8	58	4	ST7_C2
2016_110.3‡	ST7	*Polygala myrtifolia*	Corsica, Monacia d'Aullene	2016	27.71	7	24	6	7	14	23	7	4	9	8	10	9	6	57	4	ST7_C2
2016_110.4‡	ST7	*Polygala myrtifolia*	Corsica, Monacia d'Aullene	2016	28.62	7	24	6	7	14	23	7	4	9	8	10	9	8	58	4	ST7_C2
2016_135.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2016	25.20	12	29	8	11	22	7	3	8	10	13	9	17	8	221	1	ST6_C1P1
2016_138.1‡	ST6	*Calicotome villosa*	Corsica, Ajaccio	2016	24.38	12	29	6	8	22	7	3	8	11	13	9	17	10	81	1	ST6_C1P1
2016_145.2‡	ST6	*Polygala myrtifolia*	Corsica, Cauro	2016	24.73	12	29	9	11	22	7	3	9	11	13	9	17	10	245	1	ST6_C1P1
2016_145.3‡	ST6	*Polygala myrtifolia*	Corsica, Cauro	2016	24.50	12	29	9	11	21	7	3	8	12	13	9	17	10	306	1	ST6_C1P1
2016_169.1‡	ST6	*Calicotome villosa*	Corsica, Ajaccio	2016	24.55	12	29	9	11	19	7	3	8	11	13	9	17	10	298	1	ST6_C1P1
2016_173.1‡	ST7	*Calicotome villosa*	Corsica, Pietrosella	2016	24.60	7	24	7	7	11	21	7	4	15	8	11	9	8	113	3	ST7_C1P1
2016_185.1‡	ST7	*Helichrysum italicum*	Corsica, Fozzano	2016	23.33	7	24	7	7	14	20	7	4	15	8	11	9	8	128	3	ST7_C1P1
2016_202.3‡	ST7	*Calicotome villosa*	Corsica, Coti-Chiavari	2016	28.50	7	24	7	7	16	23	7	4	15	8	11	9	8	170	3	ST7_C1P1
2016_223.1‡	ST7	*Genista corsica*	Corsica, Serra Di Ferro	2016	23.02	6	24	8	7	14	22	7	4	15	8	11	9	7	250	3	ST7_C1P1
2016_224.1‡	ST6	*Polygala myrtifolia*	Corsica, Biguglia	2016	26.01	12	29	10	12	28	7	3	8	11	13	9	17	10	16	1	ST6_C1P1
2016_24.1‡	cysG_3	*Pelargonium sp.*	Corsica, Coti-Chiavari	2016	31.32	12	29	9	11	22	7	3	8	11	13	9	17	9	311	1	ST6_C1P1
2016_252.2‡	ST7	*Helichrysum italicum*	Corsica, Cauro	2016	18.90	7	24	7	7	14	21	7	4	15	8	10	9	8	133	3	ST7_C1P1
2016_253.4‡	ST7	*Calicotome villosa*	Corsica, Cauro	2016	26.95	7	24	7	7	14	24	7	4	15	8	11	9	8	150	3	ST7_C1P1
2016_254.1‡	ST7	*Cytisus villosus Pourr.*	Corsica, Cauro	2016	23.36	7	24	7	7	22	21	7	4	15	8	10	9	8	176	3	ST7_C1P1
2016_269.2‡	ST7	*Calicotome villosa*	Corsica, Cauro	2016	29.06	7	24	7	7	14	23	7	4	15	8	10	9	8	145	3	ST7_C1P1
2016_281.1‡	ST7	*Helichrysum italicum*	Corsica, Porto-Vecchio	2016	24.13	7	24	7	7	14	19	7	4	15	8	10	9	7	126	3	ST7_C1P1
2016_282.1‡	ST7	*Genista corsica*	Corsica, Porto-Vecchio	2016	29.67	7	24	7	6	14	23	7	4	15	8	10	9	6	102	3	ST7_C1P1
2016_303.1†‡	ST7	*Phagnalon saxatile*	Corsica, Ocana	2016	29.11	7	24	7	7	16	19	7	4	13	8	13	9	8	165	4	ST7_C2
2016_308.4‡	ST7	*Helichrysum italicum*	Corsica, Pianottoli Caldarello	2016	21.63	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
2016_311.1‡	ST6	*Helichrysum italicum*	Corsica, Cargese	2016	19.97	12	29	8	11	22	8	3	8	10	13	9	17	10	224	1	ST6_C1P1
2016_327.1‡	ST6	*Spartium junceum*	Corsica, Afa	2016	26.62	12	29	10	8	21	7	3	8	11	13	9	17	9	28	1	ST6_C1P1
2016_332.10‡	ST7	*Calicotome villosa*	Corsica, Cauro	2016	24.88	7	24	7	7	13	21	7	4	12	13	9	17	10	116	4	ST7_C2
2016_332.5‡	ST7	*Calicotome villosa*	Corsica, Cauro	2016	31.44	7	24	8	7	15	23	7	4	15	8	10	9	8	263	3	ST7_C1P1
2016_346.18‡	ST7	*Calicotome villosa*	Corsica, Coti-Chiavari	2016	25.91	7	24	7	7	13	22	7	4	14	8	11	9	8	117	3	ST7_C1P1
2016_348.1‡	ST7	*Genista corsica*	Corsica, Sartene	2016	24.99	7	24	8	7	14	23	7	4	15	8	11	9	8	258	3	ST7_C1P1
2016_351.1‡	ST6	*Spartium junceum*	Corsica, Ajaccio	2016	22.84	12	29	10	11	22	7	3	8	11	13	9	17	10	9	1	ST6_C1P1
2016_353.3‡	ST6	*Calicotome villosa*	Corsica, Calcatoggio	2016	24.96	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2016_354.1‡	ST6	*Helichrysum italicum*	Corsica, Calcatoggio	2016	19.56	12	29	9	11	20	6	1	8	11	13	9	17	10	293	1	ST6_C1P1
2016_379.1‡	ST6	*Calicotome villosa*	Corsica, Ambiegna	2016	23.98	12	29	8	11	23	7	3	6	10	13	9	17	11	212	1	ST6_C1P1
2016_390.1‡	ST7	*Calicotome villosa*	Corsica, Grossa	2016	24.30	7	24	7	7	14	20	7	4	15	8	11	9	8	128	3	ST7_C1P1
2016_40.1‡	cysG_7	*Spartium junceum*	Corsica, Grosseto-Prugna	2016	30.42	7	24	6	7	16	24	7	4	13	8	12	9	8	61	4	ST7_C2
2016_40.2‡	cysG_3	*Spartium junceum*	Corsica, Grosseto-Prugna	2016	22.62	12	29	9	9	22	7	3	8	11	14	9	17	10	20	1	ST6_C1P1
2016_40.3‡	cysG_3	*Spartium junceum*	Corsica, Grosseto-Prugna	2016	21.93	12	29	9	11	21	7	3	8	12	13	9	17	10	306	1	ST6_C1P1
2016_40.5‡	ST7	*Spartium junceum*	Corsica, Grosseto-Prugna	2016	23.89	7	24	6	7	17	23	8	4	10	9	12	9	8	65	4	ST7_C2
2016_400.1/CFBP 13629*‡	ST6	*Polygala myrtifolia*	Corsica, Appietto	2016	23.17	12	29	9	11	21	7	3	8	11	13	9	17	10	303	1	ST6_C1P1

2016_403.1‡	ST6	*Spartium junceum*	Corsica, Alata	2016	24.07	12	29	10	11	22	7	3	8	12	13	9	17	10	11	1	ST6_C1P1
2016_461.2‡	ST7	*Lavandula angustifolia*	Corsica, Loreto-Di-Tallano	2016	26.59	7	24	8	7	14	22	7	4	15	8	11	9	8	255	3	ST7_C1P1
2016_462.1‡	ST6	*Calicotome villosa*	Corsica, San Gavino Di Carbini	2016	30.14	11	29	7	10	20	7	3	8	11	12	8	17	11	93	2	ST6_C2
2016_500.1‡	ST6	*Polygala myrtifolia*	Corsica, Biguglia	2016	29.49	12	29	10	12	29	7	3	8	11	13	9	17	11	17	1	ST6_C1P1
2016_514.1‡	ST7	*Helichrysum italicum*	Corsica, Olmiccia	2016	25.29	7	24	7	8	14	22	7	4	15	9	11	9	8	194	3	ST7_C1P1
2016_534.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2016	23.85	12	29	8	11	22	7	3	9	10	13	9	17	10	227	1	ST6_C1P1
2016_540.1‡	ST7	*Artemisia arborescens*	Corsica, Bonifacio	2016	30.35	7	24	7	7	14	23	7	4	5	8	11	9	5	149	3	ST7_C1P1
2016_603.1‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2016	22.65	12	29	9	12	21	7	3	4	11	13	9	17	8	55	1	ST6_C1P1
2016_61.11‡	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2016	26.94	11	29	9	11	20	7	3	8	11	13	9	17	10	285	1	ST6_C1P1
2016_61.13‡	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2016	21.76	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2016_61.2‡	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2016	26.66	12	29	8	11	21	7	3	8	10	13	9	17	10	215	1	ST6_C1P1
2016_61.3‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2016	23.11	12	29	9	9	21	7	3	9	11	13	9	17	10	2	1	ST6_C1P1
2016_61.9‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2016	21.39	12	29	8	11	21	7	3	8	10	13	9	17	10	215	1	ST6_C1P1
2016_645.1‡	ST6	*Lavandula* sp.	Corsica, Ambiegna	2016	24.62	12	29	9	11	23	7	3	8	9	13	7	17	10	318	1	ST6_C1P1
2016_706.1‡	ST7	*Polygala myrtifolia*	PACA, La Seyna-sur-Mer	2016	27.31	8	24	6	7	14	23	7	4	12	8	11	9	8	78	4	ST7_P2
2016_72.1‡	ST7	*Spartium junceum*	Corsica, Ajaccio	2016	25.99	7	24	6	7	16	23	7	4	13	8	12	9	8	60	4	ST7_C2
2016_740.1‡	ST6	*Polygala myrtifolia*	Corsica, Villanova	2016	27.14	11	29	10	13	22	7	3	8	11	11	9	17	9	19	2	ST6_C2
2016_742.1‡	ST7	*Spartium junceum*	PACA, Theoule sur Mer	2016	21.50	7	24	8	7	15	15	9	4	12	8	12	9	8	276	4	ST7_P2
2016_762.1‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2016	28.01	7	24	8	7	14	23	7	4	16	8	11	9	8	259	3	ST7_C1P1
2016_764.1‡	ST7	*Polygala myrtifolia*	PACA, Mougins	2016	22.69	8	24	7	7	13	24	7	4	14	8	12	9	8	188	4	ST7_P2
2016_799.1‡	ST7	*Calicotome villosa*	Corsica	2016	22.17	7	24	7	7	14	22	7	4	16	8	8	9	7	142	3	ST7_C1P1
2016_821.4‡	ST6	*Helichrysum italicum*	Corsica, Osani	2016	18.59	12	27	9	11	21	6	1	8	11	13	9	17	10	288	1	ST6_C1P1
2016_828.2‡	ST7	*Helichrysum italicum*	Corsica, Santa Maria Figanielle	2016	23.96	7	24	7	7	14	22	7	4	17	8	11	9	8	143	3	ST7_C1P1
2016_83.1‡	ST7	*Spartium junceum*	Corsica, Propriano	2016	29.24	7	24	7	7	14	23	7	4	15	8	11	9	8	146	3	ST7_C1P1
2016_830.1‡	ST7	*Cytisus villosus*	Corsica, Mela	2016	29.32	7	24	7	7	14	23	7	4	15	9	11	9	9	148	3	ST7_C1P1
2016_836.1‡	ST6	*Lavandula* sp.	Corsica, Arbori	2016	26.02	12	30	1	11	22	7	3	8	10	13	9	17	11	31	1	ST6_C1P1
2016_841.1‡	ST6	*Cistus creticus*	Corsica, Arbori	2016	24.82	12	29	10	11	20	7	3	8	12	13	9	17	9	8	1	ST6_C1P1
2016_848.3‡	ST7	*Helichrysum italicum*	Corsica, Santa Maria Figanielle	2016	25.00	7	24	7	7	14	22	7	4	15	8	11	9	9	139	3	ST7_C1P1
2016_85.1‡	ST7	*Polygala myrtifolia*	Corsica, Santa Reparata Di Balagna	2016	30.35	7	24	7	7	14	22	7	4	16	8	11	9	7	140	3	ST7_C1P1
2017_101.1‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2017	24.18	7	24	9	7	15	22	7	4	15	8	11	9	8	24	3	ST7_C1P1
2017_101.2‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2017	26.48	7	24	8	7	14	23	7	4	15	8	11	9	8	258	3	ST7_C1P1
2017_101.3‡	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2017	26.04	7	24	7	7	16	21	7	4	15	8	9	9	8	169	3	ST7_C1P1
2017_15	ST7	*Spartium junceum*	Corsica, Corbara	2017	24.96	7	24	7	7	14	16	7	4	16	8	8	9	7	123	3	ST7_C1P1
2017_183.1‡†	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	25.94	16	29	8	11	18	7	3	8	10	13	7	17	7	231	2	ST6_P2
2017_213.1‡	ST6	*Polygala myrtifolia*	Corsica, Bastelicaccia	2017	23.96	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2017_322.1†‡	ST7	*Polygala myrtifolia*	PACA, Biot	2017	19.20	7	24	7	7	15	20	7	4	13	8	13	9	8	155	4	ST7_P2
2017_324.1/CFBP 13598*†‡	ST7	*Acacia dealbata*	PACA, Villeneuve Loubet	2017	25.63	7	24	7	7	16	12	7	4	13	8	13	9	8	163	4	ST7_P2
2017_326.1‡	ST7	*Spartium junceum*	PACA, Villeneuve Loubet	2017	24.36	7	24	8	7	27	21	7	4	14	8	11	9	9	274	4	ST7_P2
2017_326.2‡	ST7	*Spartium junceum*	PACA, Villeneuve Loubet	2017	25.84	7	24	7	7	15	15	7	4	14	8	11	9	10	153	3	ST7_C1P1
2017_328.1‡	ST7	*Polygala* sp.	PACA, Villeneuve Loubet	2017	27.22	7	24	7	8	21	21	7	4	12	8	11	9	9	198	4	ST7_P2
2017_328.2‡	ST7	*Polygala* sp.	PACA, Villeneuve Loubet	2017	24.17	7	24	7	8	21	21	7	4	12	8	11	9	9	198	4	ST7_P2
2017_328.3†‡	ST6	*Polygala* sp.	PACA, Antibes	2017	27.38	7	29	7	7	20	7	3	8	10	13	7	17	7	184	2	ST6_P2
2017_328.4†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	30.79	16	29	8	10	16	8	3	4	9	13	9	17	7	205	2	ST6_P2
2017_337.1‡	ST6	*Polygala myrtifolia*	Corsica, Sarrola Carcopino	2017	27.58	12	29	8	11	21	7	3	8	10	13	9	17	11	216	1	ST6_C1P1
2017_337.2‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2017	24.20	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
2017_357.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2017	28.34	12	29	9	11	23	7	3	8	11	13	9	17	11	317	1	ST6_C1P1
2017_357.3‡	ST7	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2017	26.08	7	24	6	7	17	7	8	4	13	8	11	9	8	66	4	ST7_C2
2017_357.4‡	ST6	*Polygala myrtifolia*	Corsica, Bastelicaccia	2017	25.10	12	29	9	11	22	7	3	8	10	13	9	17	10	308	1	ST6_C1P1
2017_357.5‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2017	26.96	11	29	9	11	23	7	3	8	11	13	9	17	10	286	1	ST6_C1P1
2017_374.1‡	ST7	*Polygala myrtifolia*	Corsica, Pietrosella	2017	31.11	7	24	7	7	14	24	7	4	16	8	11	9	8	151	3	ST7_C1P1
2017_374.2‡	ST7	*Polygala myrtifolia*	Corsica, Pietrosella	2017	30.16	7	24	7	7	14	21	7	4	15	7	10	9	9	132	3	ST7_C1P1
2017_374.3‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2017	29.04	12	29	10	9	29	7	3	8	12	13	10	17	10	29	1	ST6_C1P1
2017_374.4‡	ST6	*Polygala myrtifolia*	Corsica, Pietrosella	2017	30.73	12	29	8	11	21	8	3	8	10	13	9	17	11	218	1	ST6_C1P1
2017_38	ST6	*Polygala myrtifolia*	Corsica, Vignola	2017	25.16	12	27	10	11	12	7	3	8	11	14	9	17	10	4	1	ST6_C1P1
2017_392.1‡	ST6	*Polygala myrtifolia*	Corsica, Cargese	2017	27.45	12	29	8	11	22	7	3	8	10	13	10	17	10	219	1	ST6_C1P1
2017_42	ST6	*Polygala myrtifolia*	Corsica, Vignola	2017	22.91	12	29	10	11	22	7	3	8	11	13	9	17	10	9	1	ST6_C1P1
2017_500.1‡	ST6	*Polygala myrtifolia*	Corsica, Afa	2017	28.16	12	29	9	12	22	7	3	8	11	13	9	17	11	40	1	ST6_C1P1
2017_500.2‡	ST6	*Polygala myrtifolia*	Corsica, Afa	2017	26.45	12	29	6	11	21	6	3	8	12	13	9	17	12	54	1	ST6_C1P1
2017_500.3‡	ST6	*Polygala myrtifolia*	Corsica, Afa	2017	28.20	12	29	9	12	16	7	3	8	11	13	9	17	10	49	1	ST6_C1P1
2017_501.1‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	24.69	11	29	8	8	22	7	3	8	10	14	8	15	10	279	2	ST6_P2
2017_501.3†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	22.38	16	29	8	10	23	7	3	8	10	13	9	17	10	209	2	ST6_P2
2017_515.1/CFBP 13687*‡	ST7	*Medicago sativa*	PACA, La Seyna-sur-Mer	2017	21.99	8	24	6	7	13	22	7	4	12	8	11	9	9	74	4	ST7_P2
2017_527.1†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	28.33	15	29	8	10	20	7	3	8	10	13	9	17	9	204	2	ST6_P2
2017_527.2‡	ST7	*Polygala myrtifolia*	PACA, Antibes	2017	29.69	7	24	8	8	16	22	7	4	12	8	12	9	8	282	4	ST7_P2
2017_527.3/CFBP 13637*‡	ST7	*Polygala myrtifolia*	PACA, Antibes	2017	27.80	7	24	8	7	14	23	7	4	12	8	12	9	9	257	4	ST7_P2
2017_528.1/CFBP 13638*‡	ST6	*Euryops chrysanthemoides*	PACA, Antibes	2017	23.52	12	29	8	13	25	7	3	8	9	13	8	17	10	242	2	ST6_P2
2017_550.1‡	ST7	*Polygala myrtifolia*	Corsica, Sartene	2017	30.10	7	24	7	7	13	20	7	4	15	8	11	9	9	115	3	ST7_C1P1
2017_552.1‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	25.44	16	29	8	10	19	7	3	8	10	12	10	17	9	207	2	ST6_P2
2017_563.1‡	ST6	*Polygala myrtifolia*	Corsica, Furiani	2017	29.15	12	29	9	12	27	7	3	9	11	13	9	17	10	39	1	ST6_C1P1
2017_564.1‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	29.62	11	29	8	13	21	7	3	8	10	12	8	17	10	239	2	ST6_P2
2017_564.2‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	27.78	12	29	8	14	23	7	3	8	10	14	8	17	9	243	2	ST6_P2

2017_564.3‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	29.49	10	29	8	13	23	7	3	8	10	12	8	17	10	237	2	ST6_P2
2017_564.4‡	ST7	*Polygala myrtifolia*	PACA, Antibes	2017	30.81	7	24	8	7	12	19	7	4	14	8	12	9	8	252	4	ST7_P2
2017_575.1‡	ST7	*Polygala myrtifolia*	PACA, Nice	2017	28.42	7	24	7	7	13	13	7	4	15	8	11	9	8	114	3	ST7_C1P1
2017_575.4‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2017	31.84	12	29	7	11	15	7	3	8	10	13	8	17	8	98	1	ST6_C1P1
2017_601.1‡	ST6	*Polygala myrtifolia*	PACA, Vallauris	2017	30.51	11	29	9	13	16	7	3	8	10	12	8	17	9	34	2	ST6_P2
2017_601.2‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	30.47	7	24	7	7	14	23	7	4	14	8	12	9	9	144	4	ST7_P2
2017_601.3‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	28.21	8	24	7	7	13	23	6	4	15	8	11	9	8	185	3	ST7_C1P1
2017_601.4‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	28.56	8	24	6	7	13	22	7	4	15	8	13	9	7	76	4	ST7_P2
2017_601.5‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	29.41	7	24	7	7	11	20	7	4	18	8	11	9	7	112	3	ST7_C1P1
2017_607.1‡	ST7	*Polygala myrtifolia*	PACA, Menton	2017	20.52	7	24	8	7	17	24	7	4	13	8	13	9	9	271	4	ST7_P2
2017_615.1‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	27.26	7	24	8	7	15	27	7	4	15	8	11	9	8	266	3	ST7_C1P1
2017_615.2‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	26.30	8	24	7	7	15	24	7	4	13	8	12	9	6	192	4	ST7_P2
2017_615.3‡	ST6	*Polygala myrtifolia*	PACA, Vallauris	2017	27.81	12	29	7	9	13	7	3	10	10	13	10	17	8	200	1	ST6_C1P1
2017_621.1‡	ST7	*Euryops chrysanthemoides*	PACA, Ollioules	2017	27.95	8	24	3	7	13	23	7	4	12	8	11	9	8	41	4	ST7_P2
2017_625.2‡	ST6	*Polygala myrtifolia*	Corsica, Peri	2017	25.42	12	29	9	11	22	7	3	8	11	13	9	17	11	310	1	ST6_C1P1
2017_625.3‡	ST6	*Polygala myrtifolia*	Corsica, Peri	2017	29.07	12	29	8	10	20	7	3	8	11	13	9	17	10	202	1	ST6_C1P1
2017_631.1‡	ST7	*Polygala myrtifolia*	PACA, Vallauris	2017	28.73	7	24	7	7	14	23	7	4	15	8	11	9	8	146	3	ST7_C1P1
2017_633.1/CFBP 13639*†‡	ST6	*Prunus avium*	PACA, Antibes	2017	30.51	16	29	8	11	19	7	7	8	10	13	8	17	7	233	2	ST6_P2
2017_77	ST7	*Genista corsica*	Corsica, Rocapina	2017	26.07	7	24	7	7	14	22	8	4	15	8	11	9	8	180	3	ST7_C1P1
2017_78	ST7	*Polygala myrtifolia*	Corsica, Pont de l'Oso	2017	23.96	7	24	7	8	14	27	7	4	15	8	10	9	8	195	3	ST7_C1P1
2017_XF24	cysG_7	*Genista corsica*	Corsica, Sartene	2017	28.80	7	24	7	7	14	21	8	4	15	8	11	9	8	179	3	ST7_C1P1
2017_XF32	cysG_3	*Polygala myrtifolia*	Corsica, Ajaccio	2017	24.89	12	29	8	11	21	7	3	8	10	13	9	17	7	217	1	ST6_C1P1
2017_XF41	cysG_7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2017	26.22	7	24	7	7	14	22	7	4	16	8	11	9	8	141	3	ST7_C1P1
2018_176.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2018	27.56	12	29	8	12	22	7	3	8	10	13	9	17	10	234	1	ST6_C1P1
2018_182.1‡	ST7	*Polygala myrtifolia*	PACA, Saint Laurent du Var	2018	28.35	7	24	6	7	18	18	6	5	12	9	12	9	7	68	4	ST7_P2
2018_192.1‡	cysG_3	*Helichrysum italicum*	PACA, Nice	2018	29.16	11	29	8	13	29	7	3	8	9	12	8	17	10	240	2	ST6_P2
2018_222.1‡	ST7	*Polygala myrtifolia*	PACA, Villeneuve Loubet	2018	31.55	7	24	8	7	17	25	7	4	13	8	11	9	7	272	4	ST7_P2
2018_225.1‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2018	25.36	11	29	9	13	23	7	3	8	11	13	8	17	10	33	2	ST6_P2
2018_226.1†‡	ST7	*Euryops chrysanthemoides*	PACA, Villeneuve Loubet	2018	29.75	7	24	5	7	25	20	6	4	15	9	11	9	9	50	4	ST7_P2
2018_226.3‡	ST7	*Euryops chrysanthemoides*	PACA, Villeneuve Loubet	2018	27.15	7	24	7	7	25	21	7	4	12	8	11	9	9	178	4	ST7_P2
2018_283.1‡	ST7	*Helichrysum italicum*	PACA, Villeneuve Loubet	2018	27.69	7	24	5	8	21	7	7	4	12	8	11	9	9	53	4	ST7_P2
2018_284.1‡	ST7	*Euryops chrysanthemoides*	PACA, Villeneuve Loubet	2018	27.12	7	24	7	7	14	19	7	4	13	8	12	9	9	125	4	ST7_P2
2018_287.1‡	ST7	*Spartium junceum*	PACA, Toulon	2018	29.07	8	24	7	7	13	23	7	4	12	8	11	9	8	187	4	ST7_P2
2018_287.2‡	ST7	*Spartium junceum*	PACA, La Seyna-sur-Mer	2018	31.85	8	24	7	7	13	26	7	4	13	8	11	9	8	189	4	ST7_P2
2018_288.1‡	ST7	*Polygala myrtifolia*	PACA, La Seyna-sur-Mer	2018	26.17	8	24	6	7	13	22	7	4	13	8	12	9	8	75	4	ST7_P2
2018_316.1†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2018	28.55	16	29	8	10	22	7	3	8	9	13	9	17	9	208	2	ST6_P2
2018_316.2‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2018	29.13	10	29	8	13	22	7	3	8	10	12	8	17	8	236	2	ST6_P2
2018_316.4‡	ST7	*Polygala myrtifolia*	PACA, Antibes	2018	29.94	7	24	8	7	16	22	7	4	14	8	9	9	8	267	4	ST7_P2
2018_316.5†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2018	26.72	16	29	8	10	19	6	1	8	10	13	9	17	9	206	2	ST6_P2
2018_323.2†‡	ST6	*Polygala myrtifolia*	PACA, Antibes	2018	27.60	16	29	8	11	19	7	3	8	9	13	9	17	9	232	2	ST6_P2
2018_369.1†‡	cysG_3	*Polygala myrtifolia*	PACA, Antibes	2018	25.80	16	29	7	10	19	7	3	4	10	13	9	17	9	94	2	ST6_P2
2018_390.1‡	ST7	*Polygala myrtifolia*	PACA, La Seyna-sur-Mer	2018	28.74	8	24	6	7	14	23	7	4	12	8	11	8	8	77	4	ST7_P2
2018_390.2‡	ST7	*Polygala myrtifolia*	PACA, Ollioules	2018	27.42	8	24	6	7	13	23	6	4	11	8	11	9	9	69	4	ST7_P2
2018_391.1‡	ST7	*Spartium junceum*	PACA, Ollioules	2018	21.49	8	24	6	7	13	19	7	4	12	8	11	9	9	72	4	ST7_P2
2018_410.1‡	ST7	*Spartium junceum*	PACA, Ollioules	2018	28.27	8	24	6	7	11	23	7	4	11	7	11	9	8	70	4	ST7_P2
2018_410.2‡	ST7	*Spartium junceum*	PACA, Ollioules	2018	23.35	8	24	6	7	13	14	7	4	11	8	11	9	8	71	4	ST7_P2
2018_410.3‡	ST7	*Spartium junceum*	PACA, Ollioules	2018	25.19	8	24	7	7	13	28	7	4	12	8	12	9	8	190	4	ST7_P2
2018_410.4‡	ST7	*Spartium junceum*	PACA, Ollioules	2018	26.11	8	24	6	7	14	24	7	4	11	8	11	9	8	79	4	ST7_P2
2018_410.5‡	ST7	*Spartium junceum*	PACA, Toulon	2018	29.13	8	24	6	7	13	21	7	4	12	8	11	9	8	73	4	ST7_P2
2018_422.1‡	ST7	*Coronilla glauca*	PACA, Mougins	2018	26.00	8	24	7	7	13	22	7	4	14	8	12	9	8	186	4	ST7_P2
2018_437.1‡	ST6	*Lonicera japonica*	PACA, Villeneuve Loubet	2018	28.92	13	29	8	10	19	7	3	9	10	13	8	17	9	203	2	ST6_P2
2018_438.1‡	ST7	*Grevillea juniperina*	PACA, Villeneuve Loubet	2018	28.13	7	24	10	5	15	24	7	4	12	8	12	9	8	23	4	ST7_P2
2018_486.1‡	ST7	*Polygala myrtifolia*	PACA, Toulon	2018	19.96	8	24	8	7	12	22	7	4	12	8	11	9	8	277	4	ST7_P2
2018_511.1‡	ST7	*Euryops chrysanthemoides*	PACA, Theoule sur Mer	2018	24.89	7	24	7	7	15	23	7	4	13	8	10	9	9	160	4	ST7_P2
2018_545.1‡	ST6	*Polygala myrtifolia*	Corsica, Ajaccio	2018	28.04	11	29	9	11	20	7	3	8	11	13	9	17	10	285	1	ST6_C1P1
2018_626.2‡	ST7	*Polygala myrtifolia*	PACA, Antibes	2018	29.16	7	24	8	7	15	23	7	4	12	8	12	9	7	262	4	ST7_P2
2018_626.3‡	ST7	*Polygala myrtifolia*	PACA, Nice	2018	29.22	7	24	8	7	14	24	7	4	12	8	11	9	9	260	4	ST7_P2
2018_626.4‡	ST7	*Polygala myrtifolia*	PACA, Nice	2018	30.76	7	24	8	7	14	24	7	4	12	8	12	9	9	261	4	ST7_P2
2018_627.1‡	ST7	*Euryops chrysanthemoides*	PACA, Antibes	2018	31.96	7	24	8	7	17	23	7	4	12	8	12	9	8	269	4	ST7_P2
2018_65.1‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	23.59	5	24	8	7	23	20	7	4	12	8	11	9	6	249	4	ST7_P2
2018_65.2‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	20.96	5	24	8	7	23	20	7	4	12	8	11	9	6	249	4	ST7_P2
2018_65.3‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	21.75	7	24	7	7	21	21	7	4	12	8	12	9	9	173	4	ST7_P2
2018_65.4/CFBP 13693*‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	20.99	7	24	8	7	22	20	7	4	12	8	11	9	6	273	4	ST7_P2
2018_666.1‡	ST7	*Polygala myrtifolia*	PACA, Nice	2018	21.51	6	24	7	7	14	24	7	4	12	8	10	9	8	105	4	ST7_P2
2018_683.1‡	ST6	*Prunus dulcis*	PACA, Antibes	2018	27.25	9	29	7	12	17	7	3	8	10	12	8	17	10	100	2	ST6_P2
2018_684.1‡	ST7	*Polygala myrtifolia*	PACA, Le Cannet	2018	24.26	8	24	6	7	12	22	8	4	15	8	12	9	8	80	4	ST7_P2
2018_700.1‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	24.48	7	24	7	7	22	21	7	4	12	8	11	9	9	175	4	ST7_P2
2018_700.2‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	25.44	7	24	7	7	21	21	7	4	12	8	12	9	9	173	4	ST7_P2
2018_716.1‡	ST7	*Veronica* sp.	PACA, Villeneuve Loubet	2018	30.70	7	24	4	7	14	22	7	4	11	8	14	9	8	42	3	ST7_C1P1
2018_716.2‡	cysG_7	*Veronica elliptica*	PACA, Villeneuve Loubet	2018	30.21	7	24	8	5	15	23	7	4	12	8	12	9	8	244	4	ST7_P2
2018_717.1‡	ST7	*Convolvulus cneorum*	PACA, Villeneuve Loubet	2018	22.93	7	24	8	7	12	19	7	4	11	9	12	9	8	251	4	ST7_P2

2018_721.1‡	ST7	*Lavandula x intermedia*	PACA, Villeneuve Loubet	2018	29.19	7	24	8	7	15	24	7	4	12	8	13	9	8	264	4	ST7_P2
2018_727.1‡	ST6	*Polygala myrtifolia*	Corsica, Grosseto-Prugna	2018	28.28	12	29	9	11	19	7	3	8	11	13	9	17	10	298	1	ST6_C1P1
2018_736.1‡	cysG_7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	26.86	7	24	7	7	23	21	7	4	13	8	11	9	9	177	4	ST7_P2
2018_765.1‡	ST7	*Polygala myrtifolia*	PACA, Nice	2018	25.94	7	24	8	7	15	24	7	4	13	7	10	9	8	265	4	ST7_P2
2018_794.1‡	ST7	*Polygala myrtifolia*	PACA, Saint Raphael	2018	21.60	7	24	7	7	22	20	7	4	12	8	11	9	10	174	4	ST7_P2
2018_795.1‡	ST7	*Coronilla glauca*	PACA, Saint Raphael	2018	20.57	7	24	7	7	21	20	7	4	12	8	11	9	9	172	4	ST7_P2
2018_851.1‡	ST6	*Polygala myrtifolia*	Corsica, Alata	2018	30.56	11	29	12	10	23	7	3	9	11	13	9	17	10	35	2	ST6_C2
2018_860.1‡	ST7	*Polygala myrtifolia*	Corsica, Sartene	2018	24.44	7	24	7	7	14	22	7	4	14	8	11	9	8	137	3	ST7_C1P1
2018_860.2‡	ST7	*Polygala myrtifolia*	Corsica, Sartene	2018	28.30	7	24	7	7	15	22	7	4	15	8	11	9	8	158	3	ST7_C1P1
2018_860.3‡	ST7	*Polygala myrtifolia*	Corsica, Propriano	2018	28.69	7	24	7	7	13	22	7	4	15	8	11	9	7	118	3	ST7_C1P1
CFBP 13552	ST7	*Polygala myrtifolia*	Corsica, Porto-Vecchio	2016	na	7	24	9	7	14	22	8	4	15	8	11	9	8	22	3	ST7_C1P1
CFBP 13586	ST6	*Lavandula X allardii*	Corsica, Ajaccio	2015	na	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
CFBP 13587†	ST6	*Prunus cerasus*	PACA, Antibes	2017	na	16	29	8	11	19	7	1	8	10	13	7	17	7	230	2	ST6_P2
CFBP 13588	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	na	7	24	7	7	15	23	7	4	15	9	11	9	8	161	3	ST7_C1P1
CFBP 13589	ST7	*Spartium junceum*	PACA, Afa	2016	na	7	24	5	7	15	21	7	4	13	8	10	9	9	51	4	ST7_P2
CFBP 13590	ST7	*Coronilla glauca*	PACA, Villeneuve Loubet	2017	na	6	24	7	7	16	25	7	4	13	8	13	9	11	106	4	ST7_P2
CFBP 13591	ST6	*Polygala myrtifolia*	Corsica	2016	na	12	29	10	11	22	7	3	8	11	13	9	17	10	9	1	ST6_C1P1
CFBP 13592	ST7	*Prunus dulcis*	Corsica	2016	na	7	24	7	7	14	22	7	4	16	8	8	9	7	142	3	ST7_C1P1
CFBP 13623	ST6	*Lavandula angustifolia*	Corsica, Ajaccio	2015	na	12	29	10	11	28	7	3	8	11	13	9	17	10	14	1	ST6_C1P1
CFBP 13625	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	na	7	24	4	7	13	23	7	5	16	8	8	9	8	43	4	ST7_C2
CFBP 13626	ST6	*Helichrysum italicum*	Corsica	2016	na	12	29	9	11	15	7	3	8	11	13	9	17	10	295	1	ST6_C1P1
CFBP 13627	ST6	*Calicotome villosa*	Corsica	2016	na	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
CFBP 13628	ST6	*Lavandula* sp.	Corsica	2016	na	12	29	9	11	24	7	3	8	13	13	9	17	10	247	1	ST6_C1P1
CFBP 13630	ST6	*Cistus monspeliensis*	Corsica	2016	na	10	29	7	10	21	7	3	9	11	13	8	17	10	92	2	ST6_C2
CFBP 13631	ST7	*Cistus monspeliensis*	Corsica	2016	na	7	24	7	7	16	21	7	4	15	8	11	9	8	168	3	ST7_C1P1
CFBP 13632	ST6	*Lavandula stoechas*	Corsica	2016	na	10	29	7	10	20	7	3	9	11	12	8	15	10	90	2	ST6_C2
CFBP 13633	ST6	*Rosa canina*	Corsica	2016	na	12	29	9	11	20	8	3	8	11	13	9	17	10	300	1	ST6_C1P1
CFBP 13634	ST7	*Westrigia fructicosa*	PACA, Alpes-Maritimes	2017	na	7	24	7	8	15	22	7	4	16	8	11	9	8	196	3	ST7_C1P1
CFBP 13635	ST7	*Cistus creticus*	Corsica	2017	na	7	24	7	7	16	29	7	4	15	8	11	9	8	171	3	ST7_C1P1
CFBP 13636	ST7	*Coronilla glauca*	PACA, Villeneuve Loubet	2017	na	7	24	8	7	17	24	7	4	12	8	12	9	12	270	4	ST7_P2
CFBP 13688	ST7	*Convolvulus cneorum*	PACA, Villeneuve Loubet	2018	na	7	24	8	7	17	22	7	4	12	8	12	9	8	268	4	ST7_P2
CFBP 13689	ST7	*Prunus dulcis*	Corsica, Corbara	2018	na	12	28	9	11	14	22	7	4	16	8	8	9	7	290	4	ST7_C2
CFBP 13691	ST7	*Polygala myrtifolia*	PACA, Saint Laurent du Var	2018	na	7	24	6	7	18	18	6	5	12	9	11	9	7	67	4	ST7_P2
CFBP 13692	ST7	*Convolvulus cneorum*	PACA, Villeneuve Loubet	2018	na	16	29	7	7	21	18	7	4	12	9	12	9	9	104	4	ST7_P2
CFBP 13694	ST7	*Euryops chrysanthemoides*	PACA, Villeneuve Loubet	2018	na	8	22	5	3	25	19	6	4	14	9	11	9	9	48	4	ST7_P2
CFBP 13695	ST7	*Helichrysum italicum*	PACA, Villeneuve Loubet	2018	na	12	24	8	8	19	24	7	4	12	8	11	9	9	280	4	ST7_P2
CFBP 13741	ST6	*Polygala myrtifolia*	Corsica, Vignola	2017	na	12	27	10	11	12	7	3	8	11	14	9	17	10	4	1	ST6_C1P1
CFBP 13742	ST6	*Polygala myrtifolia*	Corsica, Vignola	2017	na	12	29	11	11	22	7	3	8	11	13	9	17	10	30	1	ST6_C1P1
CFBP 13743	ST7	*Helichrysum italicum*	Corsica, Propriano	2017	na	7	24	7	7	14	22	6	4	15	8	11	9	8	110	3	ST7_C1P1
CFBP 13745	ST6	*Polygala myrtifolia*	Corsica, Fontanaccia Bastelicaccia	2015	na	12	29	9	11	22	7	3	8	11	13	9	17	10	309	1	ST6_C1P1
CFBP 8416	ST7	*Polygala myrtifolia*	Corsica, Propriano	2015	na	7	24	7	7	14	22	7	4	15	8	11	9	8	138	3	ST7_C1P1
CFBP 8417	ST6	*Spartium junceum*	Corsica, Alata	2015	na	12	29	9	11	21	7	3	8	11	13	9	17	11	304	1	ST6_C1P1
CFBP 8418	ST6	*Spartium junceum*	Corsica, Alata	2015	na	12	29	9	11	22	7	3	8	11	13	9	18	11	312	1	ST6_C1P1
CFBP 8430	ST6	*Polygala myrtifolia*	PACA, Nice	2015	na	11	29	8	13	17	7	3	9	11	12	8	17	9	241	2	ST6_P2
CFBP 8431	ST6	*Prunus cerasifera*	Corsica, Afa	2015	na	12	29	9	7	22	7	3	8	11	13	9	17	10	32	1	ST6_C1P1
CFBP 8432	ST7	*Polygala myrtifolia*	PACA, Saint Laurent du Var	2015	na	7	24	12	7	16	25	7	4	12	8	12	9	9	37	4	ST7_P2
CFBP 8433	ST7	*Cistus monspeliensis*	Corsica, Grosseto-Prugna	2015	na	7	24	6	7	16	16	7	4	13	8	12	9	9	59	4	ST7_C2
CFBP 8434	ST7	*Pelargonium* sp.	Corsica, Propriano	2015	na	7	24	7	7	13	23	10	4	15	8	12	9	8	107	3	ST7_C1P1
CFBP 8435	ST6	*Coronilla valentina*	Corsica, Peri	2015	na	12	29	9	7	22	7	3	8	11	13	9	17	10	32	1	ST6_C1P1

Table S5. Summary of private allele frequencies of ST6 and ST7 samples.

Pop	Locus	Allelic profile	Frequence
ST6	ASSR-11	11	0.092
ST6	ASSR-11	13	0.022
ST6	ASSR-11	15	0.005
ST6	ASSR-16	25	0.005
ST6	ASSR-16	27	0.022
ST6	ASSR-16	30	0.011
ST6	COSS-1	1	0.005
ST6	COSS-1	11	0.005
ST6	OSSR-19	9	0.033
ST6	OSSR-19	10	0.125
ST6	OSSR-19	12	0.065
ST6	OSSR-19	13	0.065
ST6	OSSR-19	14	0.005
ST6	GSSR-7	20	0.109
ST6	GSSR-7	24	0.043
ST6	GSSR-7	28	0.011
ST6	GSSR-7	29	0.016
ST6	OSSR-16	6	0.022
ST6	OSSR-16	8	0.043
ST6	XFSSR-37	1	0.027
ST6	XFSSR-58	6	0.005
ST6	XFSSR-58	7	0.011
ST6	XFSSR-58	9	0.071
ST6	XFSSR-58	10	0.011
ST6	XFSSR-58	11	0.005
ST6	ASSR-9	7	0.005
ST6	ASSR-9	8	0.005
ST6	ASSR-12	11	0.011
ST6	ASSR-12	14	0.038
ST6	ASSR-19	7	0.027
ST6	GSSR-4	15	0.016
ST6	GSSR-4	18	0.011
ST6	GSSR-4	19	0.016
ST6	GSSR-4	21	0.005
ST7	ASSR-11	5	0.009
ST7	ASSR-11	6	0.014
ST7	ASSR-11	8	0.118
ST7	ASSR-16	22	0.005
ST7	ASSR-16	24	0.986
ST7	ASSR-16	28	0.005
ST7	COSS-1	3	0.005
ST7	COSS-1	4	0.009
ST7	OSSR-19	3	0.005
ST7	OSSR-19	5	0.009
ST7	OSSR-19	6	0.005
ST7	GSSR-7	11	0.014
ST7	OSSR-16	12	0.005
ST7	OSSR-16	13	0.009
ST7	OSSR-16	14	0.005
ST7	OSSR-16	15	0.009
ST7	OSSR-16	16	0.014
ST7	OSSR-16	17	0.009
ST7	OSSR-16	18	0.019
ST7	OSSR-16	19	0.042
ST7	OSSR-16	20	0.071
ST7	OSSR-16	21	0.127
ST7	OSSR-16	22	0.316
ST7	OSSR-16	23	0.198
ST7	OSSR-16	24	0.104
ST7	OSSR-16	25	0.033
ST7	OSSR-16	26	0.005
ST7	OSSR-16	27	0.009
ST7	OSSR-16	28	0.005
ST7	OSSR-16	29	0.005
ST7	XFSSR-37	5	0.005
ST7	XFSSR-37	6	0.033
ST7	XFSSR-37	8	0.042
ST7	XFSSR-37	9	0.005
ST7	XFSSR-37	10	0.005
ST7	ASSR-9	5	0.005
ST7	ASSR-9	14	0.071
ST7	ASSR-9	16	0.09
ST7	ASSR-9	17	0.014
ST7	ASSR-9	18	0.005
ST7	ASSR-12	8	0.906
ST7	ASSR-12	9	0.057
ST7	ASSR-19	12	0.208
ST7	ASSR-19	13	0.038
ST7	ASSR-19	14	0.005
ST7	GSSR-4	8	0.005

Table S6. Genetic differentiation of the clusters of *X. fastidiosa* subsp. *multiplex* estimated by RST (bellow the diagonal) and FST (above the diagonal) pairwise comparisons for A) the DAPC k=4 groups; B) the three ST6 clusters used in ABC analyses; C) the three ST7 clusters used in ABC analyses.

All pairwise population comparisons were significantly different (P<0.05) after 1,000 permutations.

A)

RST \ **FST**	Cluster 1: ST6	Cluster 2: ST6	Cluster 3: ST7	Cluster 4: ST7
Cluster 1: ST6	/	**0.3186**	**0.7309**	**0.6302**
Cluster 2: ST6	0.0992	/	**0.6574**	**0.5109**
Cluster 3: ST7	0.9557	0.9441	/	**0.2099**
Cluster 4: ST7	0.9039	0.8608	0.1981	/

B)

RST \ **FST**	Cluster C1P1	Cluster C2	Cluster P2
Cluster C1P1	/	**0.429**	**0.3377**
Cluster C2	0.199	/	**0.2122**
Cluster P2	0.1447	0.157	/

C)

RST \ **FST**	Cluster C1P1	Cluster C2	Cluster P2
Cluster C1P1	/	**0.2707**	**0.2341**
Cluster C2	0.2723	/	**0.0965**
Cluster P2	0.2442	0.0602	/

Table S7. Hierarchical AMOVA for A) ST6 *X. fastidiosa* subsp. *multiplex* DiyABC groups and B) ST7 *X. fastidiosa* subsp. *multiplex* DiyABC groups.

A) ST6: C1P1 - C2 - P2

Source of variation	d.f.	Sum of scares	Variance components	Percentage of variation
Among population	2	92.873	1.17077	36.01
Within populations	181	376.632	2.08084	63.99
Total	183	469.505	3.25161	

B) ST7: C1P1 - C2 - P2

Source of variation	d.f.	Sum of scares	Variance components	Percentage of variation
Among population	2	74.199	0.59253	21.88
Within populations	209	442.117	2.11539	78.12
Total	211	516.316	2.70792	

Table S8. Percentage of votes obtained for each scenario using abcrf. A) results of the ST6 bottom-up analyses; B) results of the ST6 top-down analyses; C) results of the ST7 bottom-up analyses; D) resul the ST7 top-down analyses.

A)

Analyses	Posterior probability	Best scenario	Percentage of votes attributed to each scenario										Prior error rate
			Sc1	Sc2	Sc3	Sc4	Sc5	Sc6	Sc7	Sc8	Sc9	Sc10	
C1P1_C2	0.39 - 0.47	9	11.8 - 20.1	0.3 - 0.7	6.3 - 10.7	6.8 - 13.6	3.5 - 19.8	0.1 - 0.6	4.3 - 7.1	5.4 - 8.5	**20.5 - 29.1**	3.5 - 14.4	0.66
C1P1_P2	0.38 - 0.47	(70%) - 9 (30%)	7.5 - 12.8	0.4 - 1.5	5.9 - 11.1	**15.6 - 24.1**	0.0 - 17.7	0.3 - 0.8	4.1 - 7.7	11.3 - 15.5	**15.0 - 21.7**	5.8 - 15.2	0.64 - 0.65
C2_P2	0.34 - 0.42	(80%) - 9 (20%)	10.3 - 17.1	1.1 - 2.6	8.1 - 12.1	**14.5 - 24.3**	8.3 - 13.7	0.4 - 2.1	4.5 - 10.1	9.8 - 15.8	**12.5 - 20.4**	7.8 - 13.3	0.67

B)

Posterior probability	Best scenario	Percentage of vote attributed to each scenario														
		Sc1	Sc2	Sc3	Sc4	Sc5	Sc6	Sc7	Sc8	Sc9	Sc10	Sc11	Sc12	Sc13	Sc14	Sc15
0.26 - 0.37	7	4.5 - 6.7	2.9 - 7.0	2.8 - 5.4	1.8 - 3.3	3.4 - 4.6	2.1 - 3.3	**8.5 - 11.3**	3.8 - 5.9	4.2 - 6.4	1.4 - 2.6	2.1 - 4.2	1.5 - 3.2	0.9 - 3.0	1.1 - 2.7	0.7 - 2.2

Sc16	Sc17	Sc18	Sc19	Sc20	Sc21	Sc22	Sc23	Sc24	Sc25	Sc26	Sc27	Sc28	Sc29	Sc30	Prior error rate
4.0 - 8.8	0.6 - 1.5	2.6 - 5.3	2.3 - 4.1	1.3 - 2.6	2.5 - 4.3	0.8 - 2.4	2.7 - 4.2	1.6 - 2.7	2.2 - 3.7	1.2 - 2.1	3.0 - 6.3	0.9 - 2.4	2.0 - 4.2	3.0 - 4.5	0.72

C)

Analyses	Posterior probability	Best scenario	Percentage of votes attributed to each scenario												Prior error rate
			Sc1	Sc2	Sc3	Sc4	Sc5	Sc6	Sc7	Sc8	Sc9	Sc10	Sc11	Sc12	
C1P1_C2	0.43 - 0.50	8	0.0-1.2	0.2-2.6	6.2-11.8	16.2-21.4	10.6-15.8	0.2-1.2	8.4-19.4	**26.0-34.2**	0.2-2.6	6.2-11.0	0.0-0.6	0.0-0.6	0.67 - 0.68
C1P1_P2	0.45 - 0.54	8	0.0-1.0	0.0-1.8	6.2-10.2	13.8-18.6	10.2-15.8	0.0-1.2	10.8-21.2	**29.6-41.4**	0.2-1.2	8.0-13.0	0.0-0.6	0.0-0.4	0.65 - 0.66
C2_P2	0.43 - 0.52	(70%) - 8 (20%)	0.2-1.8	1.0-4.4	10.8-21.0	9.8-18.4	3.8-10.4	1.6-5.0	**21.6-29.2**	**16.6-26.4**	0.0-1.2	7.4-13.6	0.0-0.6	0.0-0.6	0.67 - 0.68

D)

Posterior probability	Best scenario	scenario												Prior error rate
		Sc1	Sc2	Sc3	Sc4	Sc5	Sc6	Sc7	Sc8	Sc9	Sc10	Sc11	Sc12	
0.41 - 0.50	1	**14.8 - 20.2**	6.0 - 10.6	8.2 - 14.4	1.6 - 4.4	6.4 - 12.6	4.8 - 9.0	9.4 - 13.0	2.0 - 3.8	10.0 - 15.8	2.2 - 6.0	4.4 - 7.8	5.0 - 10.8	0.70 - 0.71

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Table S9. Distribution of prior parameters used for the DiyABC analyses.

Parameters	Parameters name	Priors
Population effective size of the ancestral American population and the unsampled population	$N_{USA,}$ N_{ghost}	Loguniform [10^3 - 10^6]
Population effective size of the French populations	N_{C1}, N_{C2}, N_{P1}, N_{P2}, N_{C1P1}	Loguniform [10^2 - 10^4]
Founder event of the French populations	t_1, t_2, t_3, t_4	Loguniform [5 - $5x10^2$]
Founder event of the unsampled population	t_{ghost}	Loguniform [$5x10^1$ - 10^4]
Duration of the bottleneck	db1, db2, db3, db4	Uniform [0-20]
Population effective size of the French populations at bottleneck time	Nb_{C1}, Nb_{C2}, Nb_{P1} Nb_{P2},Nb_{C1P1}	Uniform [1-10^2]
Mean mutation rate	$M\mu_{mic}$	Uniform [10^{-6} - 10^{-3}]
Individual locus mutation rate	$M\ \mu L_{oc}$	Gamma [10^{-7} - 10^{-2}]