HAL
open science

Limitation of gene flow by distance in the common yellow jasmine (Chrysojasminum fruticans, Oleaceae): implications for the study of its mating strategies

Aurore Puyoou, Hervé Gryta, Anne-Laure Fuchs, Pierrick Blanchard, Laure Civeyrel, Pierre-Olivier Cheptou, Mathilde Dufaÿ, Julia Dupin, Patricia Jargeat, Emilie Lecompte, et al.

To cite this version:

Aurore Puyoou, Hervé Gryta, Anne-Laure Fuchs, Pierrick Blanchard, Laure Civeyrel, et al.. Limitation of gene flow by distance in the common yellow jasmine (Chrysojasminum fruticans, Oleaceae): implications for the study of its mating strategies. Botanical Journal of the Linnean Society, In press, 10.1093/botlinnean/boad035 . hal-04133393

HAL Id: hal-04133393

https://hal.science/hal-04133393

Submitted on 19 Jun 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

The Linnean Society of London
BOTANICAL Journal of the Linnean Society

Limitation of gene flow by distance in the common yellow jasmine (Chrysojasminum fruticans, Oleaceae): implications for the study of its mating strategies

Journal:	*Botanical Journal of the Linnean Society*
Manuscript ID	BOTJLS-Jan-2023-4211-ART.R1
Manuscript Type:	Original Article
Date Submitted by the Author:	14-Apr-2023
Complete List of Authors:	Puyoou, Aurore; Université Paul Sabatier - Complexe Scientifique de Rangueil, UMR5174, Laboratoire Evolution et Diversité Biologique Gryta, Hervé; Université Toulouse III Paul Sabatier, UMR5174, Laboratoire Evolution et Diversité Biologique Fuchs, Anne-Laure; Université Toulouse III Paul Sabatier, UMR5174, Laboratoire Evolution et Diversité Biologique Blanchard, Pierrick; Université Toulouse III Paul Sabatier, UMR5174, Laboratoire Evolution et Diversité Biologique Cheptou, Pierre-Olivier; CEFE, CNRS Civeyrel, Laure; Université Toulouse III Paul Sabatier, UMR5174, Laboratoire Evolution et Diversité Biologique Dufay, Mathilde; Université Montpellier Faculté des Sciences de Montpellier, UMR5175, CEFE (Centre d'Ecologie Fonctionnelle et Evolutive) Dupin, Julia; Universite Paul Sabatier, Laboratoire Evolution et Diversite Biologique, UMR 5174 Jargeat, Patricia; Université Toulouse III Paul Sabatier, UMR5174, Laboratoire Evolution et Diversité Biologique Lecompte, Emilie; Université Toulouse III Paul Sabatier, UMR5174, Evolution & Diversité Biologique Besnard, Guillaume; CNRS, Université Paul Sabatier, EDB, Laboratoire Evolution & Diversité Biologique
Keywords:	cpDNA < Genetics, gene flow < Genetics, genetic differentiation < Genetics, genetic structure < Genetics, microsatellites < Genetics, mitochondria < Genetics, self-incompatibility < Genetics, Mediterranean < Geography

SCHOLARONE™
Manuscripts

Limitation of gene flow by distance in the common yellow jasmine (*Chrysojasminum fruticans*, Oleaceae): implications for the study of its mating strategies

Running title: Population genetics of a yellow jasmine

AUTHORS:

Aurore Puyoou[1], Hervé Gryta[1], Anne-Laure Fuchs[1], Pierrick Blanchard[1], Pierre-Olivier Cheptou[2], Laure Civeyrel[1], Mathilde Dufay[2], Julia Dupin[1], Patricia Jargeat[1], Emilie Lecompte[1], Guillaume Besnard[1]*

[1]*Laboratoire Evolution et Diversité Biologique (EDB), UMR 5174, CNRS, IRD, Université Toulouse Paul Sabatier, 31062 Toulouse, France*

[2]*CEFE (Centre d'Ecologie Fonctionnelle et Evolutive), UMR 5175, CNRS, Université de Montpellier, Université Paul Valéry, EPHE, IRD, 34293 Montpellier, France*

* Corresponding author: Guillaume Besnard, guillaume.besnard@univ-tlse3.fr

PDF Proof

ABSTRACT

The common yellow jasmine (*Chrysojasminum fruticans*; Oleaceae) is a distylous shrub occurring in the wild in southwestern Europe and the Mediterranean Basin. Little is known about the genetics of its populations and such information would be necessary to investigate its spread and mating strategies. Here, the organization of its genetic diversity was investigated among and between 13 populations from southern France, including a 35-years old experimental plot ('CEFE', CNRS Montpellier). Markers (microsatellites and indels) were developed to screen polymorphisms in nuclear, chloroplast, and mitochondrial genomes. Low linkage disequilibrium was observed between chloroplast and mitochondrial haplotypes likely resulting from paternal leaks in their inheritance as reported in other species of tribe Jasmineae. Yet, analyses of 36 progenies issued from parents with distinct chloroplast and/or mitochondrial DNA haplotypes only revealed a maternal contribution. Natural populations of *C. fruticans* are moderately to highly differentiated at the regional scale with a strong isolation-by-distance pattern detected on nuclear data, indicating limited gene flow. An isolated site ('Moulis'), located on the marginal distribution area, was remarkably genetically depauperate and highly differentiated from other populations. Further studies on the variation of mating strategies in *C. fruticans* should consider populations with contrasting patterns of genetic diversity. The artificial 'CEFE' population also offers opportunities for experiments in a closed system.

ADDITIONAL KEYWORDS: Chloroplast genome – Heterostyly – IBD – Jasmineae – Microsatellite – Mitochondrial genome – Organelle paternal leakage – Population genetics – Self-incompatibility.

PDF Proof

INTRODUCTION

Many ecological and evolutionary processes directly depend on how genetic diversity is structured within and among natural populations. For instance, levels of genetic variation and patterns of gene flow among populations determine both the opportunity for selection and the geographical scale at which selection can act (Slatkin, 1987; Sork, 2016). In plants, this mainly depends on dispersal strategies of pollen and seeds, but also on cross-compatibilities between individuals (Barrett, 2002; Charlesworth, 2006). Beyond the acknowledged usefulness of population genetics descriptors for applied purposes, such as conservation biology, describing the distribution of genetic diversity in a species also constitutes the first step of many basic research studies, in particular those that investigate the ecology and evolution of reproductive systems.

The common yellow jasmine [*Chrysojasminum fruticans* (L.) Banfi; Oleaceae] is a distylous shrub, which is the only native European species of Jasmineae, the sister lineage of the olive tribe or Oleeae (Wallander and Albert, 2000; Dupin *et al.*, 2020). In various members of Oleeae, a homomorphic self-incompatibility (SI) system with only two groups (di-allelic SI: DSI) has been discovered. This unusual DSI, compared to highly diversified SI (see for instance Bush *et al.*, 2010), asks the question of its maintenance as well as its potential role in the evolution of separate sexes in Oleaceae (Vassiliadis *et al.*, 2000; Saumitou-Laprade *et al.*, 2010; Vernet *et al.*, 2016; Billiard *et al.*, 2015). In addition, a breakdown of the same DSI system has been documented in some individuals of one Oleeae species (de Cauwer *et al.*, 2021). No information of the genetic structure is currently available in the common yellow jasmine, and more generally in any species of Jasmineae. Such data has both practical and theoretical importance: (i) studying levels of variation will help in defining molecular markers and identifying populations of potential interest; (ii) measurements of heterozygosity should provide some indirect insight on the mating system and on possible breakdown of the DSI; and

(iii) patterns of gene flow through both seed and pollen may help us to infer geographical scale at which evolutionary processes take place.

Our study species (*C. fruticans*) occurs in the wild in southwestern Europe and the Mediterranean Basin (Dommée, Thompson & Cristini, 1992; Olesen *et al.,* 2003; Banfi, 2014). It is generally found on dry and sunny soils of hillsides, often rocky with a slight preference for limestone, leading to a heterogeneous and fragmented habitat. The species is a small rhizomatous semi-evergreen shrub with slightly fragrant yellow flowers, which appear from April to June, and small black berries (0.5 cm in diameter) in the autumn. Individuals of *C. fruticans* either have "pin" flowers (long style and low anthers = longistylous) or "thrum" flowers (short style and high anthers = brevistylous), and reciprocal crosses mostly occur between the two morphs (Dommée, Thompson & Cristini, 1992; Gutián, Gutián & Medrano, 1998). Pollination and seed dispersal are respectively mediated by numerous insects of different orders (Thompson, 2001) and by birds (Puech, 1986). A generalist pollination system that may impede specialization of the plant to particular pollinators has been notably described by Thompson (2001). On the other hand, no study has specifically documented fruit dispersal of *C. fruticans*, but its frequent occurrence in abandoned cultivated areas and firebreaks suggests an efficient spread at the local scale (e.g. Debussche, Escarré & Lepart, 1982). Although pollinated by an insect community and its fruits spread by birds, the dispersal of the common yellow jasmine should be limited by geographic distance due to its occurrence in a fragmented habitat. A strong structure of its genetic diversity among populations is therefore expected, but gene flow measured on the organellar genomes or on the nuclear genome should not be impacted in the same way due to their different transmission modes (Petit *et al.*, 2005).

In this study, we thus aim at describing the population genetics of *Chrysojasminum fruticans* in southern France, in particular the isolation by distance (IBD) and the genetic differentiation between populations. Patterns of genetic diversity on different genomic

PDF Proof

compartments were investigated and compared to assess the relative contribution of pollen and seeds in the global gene flow. First, genotyping methods (microsatellites and indels) were developed to screen polymorphisms in nuclear, chloroplast, and mitochondrial genomes, which should show contrasting mutation rates (Wolfe *et al.*, 1987) and could therefore also give complementary information about the impact of demographic processes operating at different historical scales on the species genetic variability and structure. The inheritance of both cytoplasmic organelles was beforehand tested in a few progenies in order to ensure that their polymorphisms can be used to study seed dispersal. A marked genetic differentiation between populations was detected, especially on nuclear data for which a strong IBD was observed confirming a limitation of gene flow, especially for the pollen. The implications of our results for investigating mating strategies in *C. fruticans* were finally briefly discussed.

PDF Proof

MATERIAL AND METHODS

PLANT SAMPLING AND DNA EXTRACTION

Leaves of a total of 196 individuals ('ramets') from 13 French populations and one Spanish population were collected and preserved in silica gel (Table 1). To avoid sampling clones, we collected ramets that were at least 3 m apart. Floral morph and GPS coordinates of individuals (or populations) were also recorded (Table 1; Supporting Information, Table S1). Although style length varies in both morphs (Thompson & Dommée, 2000), the distinction between brevistylous (B) and longistylous (L) individuals has never been ambiguous on open flowers. In addition, 15 herbarium specimens from the Museum National d'Histoire Naturelle de Paris (MNHN-P) were sampled (Supporting Information, Table S2), representing *Chrysojasminum fruticans* populations throughout its range (from Morocco-Portugal in the West to Iran-Turkmenistan in the East). Nine of those specimens were collected more than a century ago.

Those specimens were used as outgroups to our study and also allowed us to test the utility of our markers over the whole distribution area of *C. fruticans*. All populations sampled in this study are assumed to have a natural origin, with the exception of the one from the "plateforme des terrains d'expérience du LabEx CeMEB" ('CEFE', Centre d'Étude Fonctionnelle et Evolutive de Montpellier), known to have an artificial origin since it was planted ca. 35 years ago by John D. Thompson and Bertrand Dommée, with individuals from different localities near Montpellier.

The DNA of each sample was extracted with the BioSprint DNA Plant Kit (QIAGEN). About 20 mg of material was placed in a 2-mL tube with three tungsten beads and frozen at -80°C for one hour before being crushed using TissueLyser II (QIAGEN). Then, after one hour of incubation at 65°C in 500 µL of 2X CTAB buffer, DNA extraction was performed following the supplier's protocol. Finally, the DNA was resuspended in 130 µL of TE buffer and stored at 4°C.

PDF Proof

GENOPYING PROCEDURE

To genetically characterize all the sampled *C. fruticans* individuals, we developed 29 nuclear DNA loci (including 23 microsatellites and six indels) and 15 cytoplasmic loci [five mitochondrial DNA (mtDNA) loci (four indels and one microsatellite) and ten chloroplast DNA (cpDNA) loci (two indels and eight microsatellites)] (Supporting Information, Tables S3 to S5). We used shotgun genome sequencing data (*i.e.* HiSeq data on individual 'Celleneuve L11') to random search and assemble microsatellite or indel regions as described in Salmona *et al.* (2020). All assembled nuclear sequences are deposited in GenBank. In contrast, the cytoplasmic DNA loci were developed from length polymorphisms revealed on plastomes and mitogenomes of individuals collected in France (GenBank no MH559274, and OQ124187 to OQ124196).

The primers used to amplify the 44 loci are given in the Supporting Information (Tables S3 to S5). All primers were defined to have the same annealing temperature (T_m).

Some markers were amplified alone (simplex), while others were amplified in multiplex (either two markers for nuclear loci, or three or four for cytoplasmic loci). The PCR conditions are those reported by Besnard *et al.* (2011). These amplifications were performed in a total volume of 25 µL following the method of Schuelke (2000), which allows the integration of fluorescence on fragments amplified with a dye-labeled M13 primer. Three different fluorochromes were used depending on the markers: 6-FAM, ATTO565 and HEX. The PCR multiplexes and the fluorochrome used for each locus are given in the Supporting Information (Tables S3 to S5). The same PCR program was used for all markers: denaturation of the DNA at 95°C for 2 min followed by 25 cycles with a 30 sec denaturation at 95°C, followed by an annealing at 55°C and then a 90 sec elongation at 72°C. Ten additional cycles with a lowered annealing temperature of 51.5°C allowing integration of the dye-labeled M13 primer into amplified fragments were added and were followed by a final elongation of 20 min at 72°C.

After PCR amplification, the markers were multiplexed (several markers of different sizes were mixed together) in formamide with ROX-500 (Applied Biosystems) used as internal size standard. The amplified fragments at each locus were separated by chromatography on an ABI 3730 capillary sequencer (Applied Biosystems) by GenoScreen (Lille). The chromatograms were then read on GENEIOUS v.9.1.2 (Kearse *et al.*, 2012). To limit reading errors, all loci were read twice independently by AP and GB.

PDF Proof

DEFINING CYTOPLASMIC HAPLOTYPES AND NETWORK RECONSTRUCTION

For chloroplastic and mitochondrial genomes, polymorphisms were revealed at multiple loci (see above). Plastid and mitochondrial DNA profiles (chlorotypes and mitotypes) were defined by the combination of alleles from these loci. Relationships between chlorotypes on one hand, and between mitotypes on the other hand, were established by constructing a reduced-median haplotype network with NETWORK v.10.2 (Bandelt, Forster & Röhl, 1999). All polymorphisms observed were coded as in Gryta *et al.* (2017) [*i.e.* number of repeats for microsatellites, or binary (0/1) for indels].

ON THE INHERITANCE OF ORGANELLES IN *C. FRUTICANS*

As potential for paternal leakage of chloroplasts and mitochondria has been previously reported in several *Jasminum* species (Sodmergen *et al.*, 1998; Zhang, Liu & Sodmergen, 2003), it was necessary to check the inheritance of organelles in *C. fruticans*. As a first source of evidence, we measured the linkage disequilibrium (LD) between chlorotypes and mitotypes. In the case of a strict maternal inheritance, we expect a strong LD (as already shown in beet, *Silene*, and olive; Desplanque *et al.*, 2000; Olson & McCauley, 2000; Besnard *et al.*, 2002). In contrast, the presence of a few paternal leakages may reduce LD between haplotypes of the two organelle genomes. The LD was estimated with Lewontin's normalized *D'* (Lewontin, 1964, 1988), and its significance was tested with Fisher's exact tests using ARLEQUIN (Excoffier & Lischer, 2010). The *D'* index was calculated (i) separately on each sampled population where polymorphism was observed on both organellar genomes, and (ii) on all French individuals considered as a single population. Then, we also verified the inheritance of organelles in a few progenies (*i.e.* seeds resulting from open pollination) for which parents display different cpDNA and/or mtDNA haplotypes. In the 'CEFE' and 'Moulis' populations, we previously identified 36 progenies issued from such crosses (*i.e.* 33 with a different chlorotype, and 32

PDF Proof

with a different mitotype; Supporting Information, Table S6). Genotyping of the chloroplastic and mitochondrial haplotypes in these progenies allowed us to determine from which parent cytoplasmic organelles were inherited.

POPULATION GENETICS ANALYSES

To avoid bias in population genetics analyses due to repetitions of the same individual, clones (genets) needed to be excluded. In a population, plants sampled a few meters apart may correspond to ramets from the same stump, and the probability of finding the same genotype at 29 multi-allelic nuclear loci is theoretically very low (e.g. Baali-Cherif & Besnard, 2005). Thus, when several close individuals shared the same genotype or a very similar genotype (*i.e.* differing by a mutation step on a long allele), we considered them as a clone. In this case, only one ramet was kept for analyses. In order to represent the genetic proximity between all analyzed individuals, Bruvo *et al.* (2004) genetic distances were first calculated on the nuclear microsatellite data between each pair of genotypes with the R package *Poppr* (Kamvar, Tabima & Grünwald, 2014) and a dendrogram was reconstructed according to the unweighted pair group method with arithmetic mean (UPGMA). For further analyses, we only considered populations with at least seven genotypes.

Populations' genetic diversity

Genetic diversity patterns were described for each population. First, observed (H_O) and expected (H_E) heterozygosities under the Hardy-Weinberg ideal population model (*i.e.* population of infinite size, panmictic reproduction, non-overlapping generations), and the Weir & Cockerham Fixation Index (F_{IS}, Weir & Cockerham, 1984) were calculated using the GENETIX software (Belkhir *et al.,* 2004) for each nuclear locus. Allelic richness (A_R) was calculated with the R package HIERFSTAT (Goudet, 2005) to compare the number of alleles between populations. The presence of null alleles was tested for each population with a 95%-

confidence interval using MICRO-CHECKER v.2.2.3 (van Oosterhout *et al.,* 2004). As all loci were successfully amplified, the null allele frequency was estimated according to Brookfield (1996). For cytoplasmic data (cpDNA and mtDNA), haplotypic diversity was calculated from the formula $D = 1 - \Sigma p_i^2$ with p_i the frequency of haplotype i and was multiplied by $n / (n - 1)$ to account for differences in sample sizes, as described in Gryta *et al.* (2017). This parameter was estimated independently for chloroplast and mitochondrial data (D_{cp} and D_{mt}), and for their combination (D_{cp+mt}).

Genetic structure of populations

To measure genetic differentiation between populations, the fixation index F_{ST} of Weir & Cockerham (1984) was calculated between each pair of populations using GENETIX. These calculations were performed separately for nuclear data (bi-paternally transmitted, and thus dispersed by pollen and seed) and cytoplasmic data (assumed to be maternally transmitted, and dispersed by seed). However, for cytoplasmic data, the main mode of transmission of plastids and mitochondria remains uncertain in Jasmineae (Sodmergen *et al.*, 1998; Zhang, Liu & Sodmergen, 2003). Occasional paternal transmission of one or both cytoplasmic genomes could impact on differentiation patterns between populations. Because of this uncertainty, we estimated the F_{ST} of the cytoplasmic data using four different approaches: (i) only on haplotypes of the chloroplast genome, (ii) only on haplotypes of the mitochondrial genome, (iii) considering the chloroplast and mitochondrial genomes as two independent cytoplasmic loci, and (iv) combining cpDNA and mtDNA information to define cytoplasmic haplotypes. Patterns of isolation by distance (IBD) were then compared between each approach. The geographical distribution of cpDNA and mtDNA haplotypes across populations was also mapped using QGIS v.3.0.3 (QGIS Development Team, 2018).

PDF Proof

In order to determine the number of genetic clusters actually present in our sample and to assess the isolation between populations, a Bayesian approach was then used to assign individuals to genetic clusters on the basis of their genotypes. STRUCTURE v.2.3.4 (Pritchard, Stephens & Donnelly, 2000) was used on the nuclear data set. For this analysis, the Spanish population ('La Aliseda') was excluded due to its great distance from all the other studied populations and the absence of intermediate populations between them. The artificial 'CEFE' population was also excluded in order not to bias the analyses (e.g. due to admixture between individuals). This analysis was carried out under the admixture model (mixing of gametes possible at reproduction) for a duration of 200,000 generations after a burn-in period of 50,000 generations. The analysis was performed for a number of clusters (K) ranging from 1 to 14 with ten iterations for each value of K. The most likely number of clusters was determined using the *ad hoc* measure of ΔK performed with STRUCTURE HARVESTER (Earl & vonHoldt, 2012). In order to determine the putative origin of the artificial CEFE population, we then assigned each individual from this location to the ten natural French populations (with at least ten genets) using GENECLASS2 (Piry *et al.*, 2004). The standard criterion described by Rannala & Mountain (1997) was used to compute the probabilities with Bayesian statistics. The population assignment simulation algorithm described by Paetkau *et al.* (2004) was used in order to simulate 10,000 genotypes for each population. An arbitrary threshold probability value of 0.05 or greater was then applied to identify the possible origin of CEFE genotypes among natural populations.

Limitation of gene flow by distance and relative contribution of pollen and seeds

As IBD was expected, Mantel (1967) tests between geographical distances and F_{ST} values between pairs of populations were performed in southern France on the ten natural populations with at least ten genotypes. These tests were done with 999 permutations using the R package *ade4* (Chessel, Dufour & Thioulouse, 2004) for each genomic compartment in order to compare

PDF Proof

patterns according to the origin of the data (nuclear *vs*. cytoplasmic). In addition, the relative contribution of pollen and seeds in the global gene flow (*R*) was investigated following the method of Ennos (1994). This approach allows an indirect estimation of pollen and seed flows from genetic differentiation estimates (F_{ST}) on both bi-parentally inherited nuclear markers (F_{STn}) and maternally inherited cytoplasmic markers (F_{STc}). The *R* estimation is based on a model of island migration (Wright, 1965), and can be used under several assumptions: (i) a very low mutation rate compared to migration rate, (ii) a constant and equal size of populations, and (iii) a constant and equal migration rate between populations, the last two points representing a drift/migration equilibrium. This equilibrium turns out to be rapidly reached in nature (Slatkin, 1993). However, when the species has a long generation time and/or if perturbations are quite recent, it might be necessary to check these assumptions. In addition, the precision of estimates of genetic differentiation used to infer gene flow depends on the sampling of populations (Petit *et al.*, 2005; Besnard *et al.*, 2021). Although the *R* estimate can help comparing the relative contribution of pollen and seeds in global gene flow among taxa (Ennos, 1994; Petit *et al.*, 2005), it thus still needs to be interpreted with caution.

PDF Proof

RESULTS

All loci were successfully amplified in all *Chrysojasminum fruticans* individuals freshly collected in southern France and Spain (whole dataset provided in the Supporting Information, Table S1), and all revealed polymorphisms. A few genets with several ramets were identified in populations 'La Aliseda', 'Amélie-les-Bains', 'Prades-le-Lez', and 'La Turbie'. These genets can cover a relatively large surface (up to about 90 m² for an individual of the Spanish population 'La Aliseda'). Only one ramet per genet was subsequently kept for our analyses (for a total of 186 genets). Among the 179 genets sampled in France, 89 were recorded as

brevistylous and 90 as longistylous (Table 1). In addition, most of our markers yielded amplifications with herbarium samples, pointing out their high potential to analyze genetic variation in old specimens collected more than 100 years ago. Cytoplasmic markers revealed the presence of seven chlorotypes and six mitotypes in French populations, most of them being shared with the few analyzed individuals from the Southern Iberian Peninsula to the Eastern Maghreb (e.g. all mitotypes, and chlorotypes 1, 3, 4 and 7; Supporting Information, Table S1). By combining cpDNA and mtDNA information, 20 cytoplasmic haplotypes were identified in southern France (Table 3), where five of the six mitotypes were associated with more than one chlorotype, and five of the seven chlorotypes were associated with more than one mitotype. Consequently, the LD between haplotypes of the two organellar genomes, measured according to Lewontin (1964), was relatively low ($D' = 0.368$, p-value < 0.001) compared to other plants where such data are available [e.g. $D' > 0.95$ in *Olea europaea* (Besnard *et al.*, 2002), *Silene vulgaris* (Olson & McCauley, 2000), and *Beta vulgaris* (Desplanque *et al.*, 2000)]. However, relatively strong and significant LD between organellar genomes was found at the population scale (*i.e.* 'La Aliseda' and 'CEFE'; $D' > 0.88$, p-value < 0.005; Supporting Information, Table S7). Overall, a non-strict association between haplotypes of both cytoplasmic genomes indicates that organelles are not always inherited together (implying paternal leaks). Yet, analyses of all 36 progenies only revealed a maternal inheritance of the two organellar genomes (Supporting Information, Table S6), suggesting that paternal leaks may be occasional. Consequently, the structure of organellar DNA diversity should be mostly influenced by seed dispersal. In addition, all 36 crosses involved a pair of brevistylous and longistylous individuals (24 B x L and 12 L x B; Supporting Information, Table S6).

PDF Proof

STRUCTURE OF THE NUCLEAR GENETIC DIVERSITY ON THE WHOLE SAMPLE

The genetic proximity between all individuals of *C. fruticans* is represented by a dendrogram (Supporting Information, Fig. S1). All individuals from French populations were clustered together. Individuals from the same population were generally found in the same group suggesting a strong structure of populations in the South of France. Individuals from the Spanish population 'La Aliseda' formed the closest cluster to the French populations. Individuals from the rest of the Mediterranean were more distant from French and Spanish populations, except for individuals from Tunisia and Portugal. This analysis also showed that individuals from Iran and Turkmenistan are very similar to each other and genetically the most distant from all other individuals analyzed.

GENETIC DIVERSITY OF POPULATIONS ANALYSES

Most nuclear loci revealed polymorphism within populations, even the di-allelic indel markers (Supporting Information, Table S8). Nevertheless, a few loci were not variable in some populations, especially in 'Moulis' (eight loci) and 'La Aliseda' (six loci). Among populations, most loci showed no excess of homozygosity or significant deviation from expected heterozygosities at the Hardy-Weinberg equilibrium, suggesting that the species reproduces mainly via outcrossing. For all populations, the global F_{IS} value was thus not significantly different from 0. The MICRO-CHECKER analysis detected probable presence of null allele in only five populations for one locus each (Cf-TA-1 for 'Bages', Cf-ATT2 for 'CEFE', Cf-GAA19 for 'Moulis', Cf-GAA22 for 'St-Maurice-Navacelles', and Cf-GAA4 for 'Puycelsi', with respectively the followings Brookfield estimates of null allele frequencies: 0.019, 0.215, 0.093, 0.079, and 0.154). Considering the multiple tests performed (*i.e.* 29 loci x 12 populations), such observations may be fortuitous and all loci should have a very low frequency of null alleles. Finally, the average expected heterozygosity and allelic richness (calculated for seven diploid

individuals) showed that 'Moulis' ($H_E = 0.35$; $A_R = 2.36$) is genetically impoverished compared to all other populations ($0.41 < H_E < 0.56$; $2.84 < A_R < 3.89$; Table 2). The highest level of nuclear diversity was revealed in 'St-Maurice-Navacelles'.

Most populations showed polymorphisms on both chloroplast and mitochondrial genomes (Fig. 2; Supporting Information, Table S8), with a maximum of five mitotypes in 'St-Maurice-Navacelles' and four chlorotypes in 'CEFE'. The combination of both genomes allowed us to detect from two to eight cytoplasmic haplotypes per population, with a haplotypic diversity (D_{cp+mt}) varying from 0.19 ('Celleneuve') to 0.91 ('St-Maurice-Navacelles'). Conversely to the nuclear genome, the 'Moulis' population did not show a particularly reduced diversity of cytoplasmic haplotypes ($D_{cp+mt} = 0.50$), although its chlorotype diversity was among the lowest ($D_{cp} = 0.11$; Table 2).

POPULATION STRUCTURE

The F_{ST} values calculated from the nuclear data supported a significant genetic differentiation between most pairs of populations (Supporting Information, Table S9). The dendrogram reconstructed from these F_{ST} (Supporting Information, Fig. S2) showed that geographically close populations were also genetically close, except in the case of 'Moulis', which was found here genetically more differentiated from the other French populations than the Spanish population was. Also, the artificial population of 'CEFE' (Montpellier) whose individuals originate from neighboring populations was found to be close to the other populations sampled near Montpellier ('Celleneuve' and 'Prades-le-Lez').

An analysis performed with STRUCTURE on nuclear data from ten natural French populations (with at least ten genotypes) revealed the presence of several genetic clusters. Peaks in the graphical representation of ΔK (Fig. 1A) allowed the identification of population structuring at two levels: $K = 2$ and 10. For $K = 2$, 'Moulis' was distinguished from other

PDF Proof

populations (Fig. 1B), whereas the ten populations defined *a priori* were relatively well supported at K = 10 (Fig. 1C). The assignment of 'CEFE' individuals to these natural populations confirmed the putative origin of this artificial population from collects around Montpellier, since successful assignments (27% of genets) only concerned the three locations collected in Hérault ('St-Maurice-de-Navacelles', 'Celleneuve', and 'Prades-le-Lez'; Supporting Information, Table S10).

Genetic relationships between cytoplasmic haplotypes assessed by reduced-median network analyses (Fig. 2) showed three slightly differentiated lineages of chlorotypes (*i.e.* 1-2, 3-6, and 7) and no clear genetic structure for mitotypes. The geographical distribution of these chlorotypes and mitotypes (Fig. 2) did not show any clear pattern of geographical structuring. However, F_{ST} values calculated from these cytoplasmic data were relatively high and most of them were significantly different from 0 (Supporting Information, Table S8).

PDF Proof

ISOLATION BY DISTANCE AND CONTRIBUTION OF POLLEN AND SEEDS TO GLOBAL GENE FLOW

Strong IBD was observed for the nuclear data (Mantel test, r = 0.528, p-value = 0.004; Fig. 3A). In contrast, the cytoplasmic data did not show any isolation pattern by distance (Fig. 3B), regardless of how the F_{ST} values were calculated (*i.e.* based on cpDNA, mtDNA, or when combining information of both organellar genomes; Supporting Information, Fig. S3). Based on the estimates of global genetic differentiation between populations for nuclear markers (F_{STn}= 0.17, F_{IS} = 0.17) and cytoplasmic genomes (F_{STc} = 0.50), the Ennos's index (R = 3.618) showed that the contribution of the pollen to global gene flow is somewhat greater than that of seeds. However, this index was relatively low compared to many other plants (median R = ca. 17; Petit *et al.*, 2005).

DISCUSSION

This work represents the first population genetics study of *Chrysojasminum fruticans*. We mainly sampled populations in southern France and recorded floral morphs on all individuals. Genetic variation was then detected in the three genome compartments allowing revealing contrasting levels of diversity among populations as well as a strong genetic structure resulting from limited gene flow. It also brought information on the relative contribution of seeds and pollen in the global gene flow. Our results will have various methodological implications when developing genetic studies on this species, especially to study its reproductive and dispersal strategies.

First, our sampling in southern France revealed that both floral morphs have a balanced frequency among all populations (89 B *vs.* 90 L), and the few analyzed progenies (36) also confirmed that crosses should mainly occur between these two morphs (Dommée, Thompson & Cristini, 1992; Gutián, Gutián & Medrano, 1998). These preliminary observations are consistent with a diallelic self-incompatibility system but a wider sampling is still necessary, especially to measure how mating patterns vary among populations and floral morphs (for instance, to test if cross-compatibility or selfing rate vary among morphs in relation with stigma height or any other traits; Thompson & Dommée, 1993, 2000).

Then, a set of markers was developed for investigating variation of the three genomic compartments in *C. fruticans*. Such tools may have applications in different fields from population genetics and phylogeography to parentage analyses. Here, chloroplast and mitochondrial markers showed great potential for investigating the inheritance of both organellar genomes by either investigating the linkage disequilibrium between chloroplast and mitochondrial haplotypes, or directly by checking their inheritance in progenies. The low linkage disequilibrium on the whole sample supports a non-strict maternal inheritance in

PDF Proof

C. fruticans as already documented in other Jasmineae (Sodmergen *et al.*, 1998; Zhang, Liu & Sodmergen, 2003), but our preliminary progeny analyses indicate that paternal leakage should be rare. Consequently, we used organellar DNA polymorphism for investigating seed dispersal. Furthermore, nuclear microsatellite markers may be useful in assisting the identification of genets in populations and in determining fine population structure to further study demographic processes at a local scale. Here, they revealed shared genotypes by close ramets indicating the presence of clones in the investigated populations due to vegetative growth. The shoots of a single stump can cover up to several tens of m^2 (as already observed in olive trees; Baali-Cherif & Besnard, 2005), indicating *a priori* a long persistence of certain individuals. Based on our observations, avoiding multiple sampling of the same genotype in population genetic studies may therefore require collecting ramets at least ten meters apart.

Once the clones were removed, our population analysis showed a strong structure of the genetic diversity in *C. fruticans* (*i.e.* high differentiation between pairs of populations) on both nuclear and cytoplasmic data. In addition, strong IBD is observed on the nuclear data, but not on the cytoplasmic data (Fig. 3). The presence of a very strong IBD is common in insect-pollinated species with limited pollen and seed dispersal (e.g. Jump *et al.*, 2009). In *C. fruticans*, the pollen is sticky and should be mostly spread by various insects (Thompson, 2001) at the local scale. In contrast, fleshy fruits can be spread by birds (Puech, 1986), and the longest dispersal events may thus occur at a larger distance for seeds than for pollen, especially in a very fragmented landscape (e.g. García-Verdugo *et al.*, 2010; Trapnell *et al.*, 2022). The relative contribution of pollen and seeds to global gene flow reflects this expectation, with an *R* value inferior to 5 as frequently observed in most insect-pollinated and fleshy fruited species (Oddou-Muratorio *et al.*, 2001; Petit *et al.*, 2005). Furthermore, random long-distance dispersal by seeds through the landscape would lead to a patchy structure of organellar lineages in space (Petit *et al.*, 1997), and could explain the absence of IBD on both maternally inherited genomes. In

addition, the plants mainly produced fruits in autumn (Puech, 1986) when migratory birds are travelling southwards, and a latitudinal pattern could thus be expected. It is noticeable that organellar haplotypes observed in southern France are shared with populations from the Southern Iberian Peninsula to the Eastern Maghreb, suggesting that seeds can indeed travel long distances with birds and could have even crossed the Mediterranean Sea, as already shown in another Mediterranean shrub, *Pistacia lentiscus* L. (Martinez-Lopez *et al.*, 2020). Nonetheless, it is possible that cytoplasmic haplotypes identified here have diverged a long time ago, and more variable loci would reveal some differentiation between such distant populations. It is thus presently too speculative to interpret our diversity patterns in the context of Mediterranean micro-refugia (*i.e.* south-eastern Pyrenees, southern Cevennes, Mont Ventoux, eastern Provence, Alpes Maritimes; Médail & Diadema, 2009), and a denser and wider sampling of the studied area would also be required for this purpose.

Finally, in a context of gene flow limitation, small marginal populations are expected to diverge rapidly. In our study, the 'Moulis' population is highly differentiated from the others and is genetically impoverished compared to other populations, supporting the fact that it is highly isolated. This population is relatively large (several hundred thousand individuals over several hundred ha), and its low diversity may be explained by a relatively recent expansion from a few founders. However, the necessity that recent populations were initially founded from at least two compatible individuals could be a constraint, and self-compatible individuals may be temporarily favored on the front of colonization to ensure reproduction (Baker, 1955; Pannell & Barrett, 1998). Although no significant inbreeding index was observed in all populations indicating that the species is mainly out-crossing, preliminary paternity analyses on seeds collected in 'Moulis' from two mother plants in two following years showed a high rate of self-fertilization (ca. 70%) on a brevistylous individual (unpublished data), suggesting that this population is indeed not completely allogamous as similarly reported in some populations of

PDF Proof

Ligustrum vulgare L. (de Cauwer *et al.*, 2021). Thus, effective selfing events could have also contributed to genetic diversity erosion of the 'Moulis' population.

CONCLUSION AND PERSPECTIVES

Our results have several implications for further studies on the variation of mating strategies in *Chrysojasminum fruticans*. Variable levels of genetic diversity among unconnected populations imply contrasting demographic histories with possibly varying loads of deleterious mutations (e.g. Liu *et al.*, 2022). In a distylous species, if the selfing rate is higher in one morph than in the other, questions arise about the allocation of resources and their evolutionary consequences on the reproductive strategies (e.g. possible transition to cryptic dioecy). For this reason, it seems relevant to study mating of the common yellow jasmine in various contexts. One could first compare the rates of self-fertilization (by paternity analysis on seeds) on the two floral morphs in several populations, and in case of marked differences, study the associated inbreeding depression. If one morph is much more self-pollinating in some populations, it would also be very relevant to follow the investment of each morph in reproduction and vegetative growth (Dommée, Thompson & Cristini, 1992).

Finally, the artificial population on the experimental field of the 'CEFE' Montpellier (with approximately 200-300 mature individuals in a hedge of ca. 250 m^2) may also offer some opportunities for studying mating in a semi-natural context. Our genetic data supported that individuals have mostly originated from different localities near Montpellier. Its high accessibility may allow long-term follow up of individuals (e.g. measure of their investment in sexual functions over years). Due to the limitation of gene flow by distance, this population can be considered as strongly isolated from natural stands (at several kilometers). It will be fully characterized with our markers in order to investigate pollen and seed dispersal, as well as

PDF Proof

mating between morphs (Besnard *et al.*, 2020). Microsatellite analyses should allow investigating pollen gene flow via paternity analyses of seeds, while recruitment over last decades could be investigated via reconstructing pedigrees (e.g. Bacles, Lowe & Ennos, 2006; Bittencourt & Sebben, 2007). Finally, cytoplasmic variation in the population could be useful to investigate the inheritance of organelles and estimate the rate of paternal leaks in known crosses.

ACKNOWLEDGEMENTS

We thank Myriam Gaudeul (MNHN-P), Alex Baumel, Elodie Chapuis, Nicolas Juillet, Gérard Largier (CBN-PMP), Elwen Le Bras, Frédéric Médail, James Molina (CBN-Med), and John Thompson, for their help in plant sampling. The 'CEFE' population is managed by the Platform "Terrains d'Expériences" of the LabEx CeMEB (ANR-10-LABX-04-01). We also thank two anonymous referees for their constructive comments.

PDF Proof

FUNDING

This research was funded by the Region Occitanie of France, through the BioDivOc programme (grant RepOl). J.D. and G.B. received support from the H2020 Marie Skłodowska-Curie Actions (grant 842234-FruitFul), and A-L.F., P-O.C. and G.B. from the European Union's Horizon 2020 project Gen4Olive (H2020-SFS-2020-1; G.A. No. 101000427). P.B., L.C., P.J., H.G. and G.B. are members of the EDB laboratory, which is supported by the Laboratoire d'Excellence (LabEx) CEBA (grant ANR-10-LABX-25-01) and LabEx TULIP (grant ANR-10-LABX-0041), both managed by the Agence Nationale de la Recherche in France.

DATA AVAILABILITY

Genotype data generated in this study are provided in the Supporting Information (Table S1). Thirteen herbarium specimens were collected in Amélie-les-Bains, Bages, CEFE, Moulis, Moussoulens, and Puycelsi, and deposited at the Montpellier herbarium (MPU; HG-2023-001 to -005, and GB-2023-001 to -008).

REFERENCES

Baali-Cherif D, Besnard G. 2005. High genetic diversity and clonal growth in relict populations of *Olea europaea* subsp. *laperrinei* (Oleaceae) from Hoggar, Algeria. *Annals of Botany* **96:** 823–830.

Bacles CFE, Lowe AJ, Ennos RA. 2006. Effective seed dispersal across a fragmented landscape. *Science* **311:** 628–628.

Baker HG. 1955. Self-compatibility and establishment after "long-distance" dispersal. *Evolution* **9:** 347–348.

Bandelt HJ, Forster P, Röhl A. 1999. Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution* **16:** 37–48.

Banfi E. 2014. *Chrysojasminum*, a new genus for *Jasminum* sect. *Alternifolia* (Oleaceae, Jasmineae). *Natural History Sciences* **1:** 3–6.

Barrett SCH. 2002. The evolution of plant sexual diversity. *Nature Reviews Genetics* **3:** 274−284.

Belkhir K, Borsa P, Chikhi L, Raufaste N, Bonhomme F. 2004. GENETIX 4.05, logiciel sous Windows TM pour la génétique des populations. Laboratoire Génome, Populations, Interactions, CNRS UMR 5000, Université de Montpellier II, Montpellier (France).

Besnard G, Cheptou PO, Debbaoui M, Lafont P, Hugueny B, Dupin J, Baali-Cherif D. 2020. Paternity tests support a diallelic self-incompatibility system in a wild olive (*Olea europaea* subsp. *laperrinei*, Oleaceae). *Ecology and Evolution* **10:** 1876–1888.

Besnard G, Gorrilliot O, Raimondeau P, Génot B, El Bakkali A, Anthelme F, Baali-Cherif D. 2021. Contrasting genetic footprints among Saharan olive populations: potential causes and conservation implications. *Plants* **10:** 1207.

PDF Proof

Besnard G, Hernández P, Khadari B, Dorado G, Savolainen V. 2011. Genomic profiling of plastid DNA variation in the Mediterranean olive tree. *BMC Plant Biology* **11:** 80.

Besnard G, Khadari B, Baradat P, Bervillé A. 2002. Combination of chloroplast and mitochondrial DNA polymorphisms to study cytoplasm genetic differentiation in the olive complex (*Olea europaea* L.). *Theoretical and Applied Genetics* **105:** 139–144.

Billiard S, Husse L, Lepercq P, Godé C, Bourceaux A, Lepart J, Vernet P, Saumitou-Laprade P. 2015. Selfish male-determining element favors the transition from hermaphroditism to androdioecy. *Evolution* **69:** 683–693.

Bittencourt JVM, Sebben AM. 2007. Patterns of pollen and seed dispersal in a small, fragmented population of the wind pollinated tree *Araucaria angustifolia* in southern Brazil. *Heredity* **99:** 580–591.

Brookfield JFY. 1996. A simple new method for estimating null allele frequency from heterozygote deficiency. *Molecular Ecology* **5:** 453–455.

Bruvo R, Michiels NK, D'Souza TG, Schulenburg H. 2004. A simple method for the calculation of microsatellite genotype distances irrespective of ploidy level. *Molecular Ecology* **13:** 2101–2106.

Busch JW, Joly S, Schoen DJ. 2010. Does mate limitation in self-incompatible species promote the evolution of selfing? The case of *Leavenworthia alabamica*. *Evolution* **64:** 1657–1670.

Charlesworth D. 2006. Evolution of plant breeding systems. *Current Biology* **16:** R726–R735.

Chessel D, Dufour A, Thioulouse J. 2004. The ade4 package - I: One-table methods. *R News* **4:** 5–10.

de Cauwer I, Vernet P, Billiard S, Godé C, Bourceaux A, Ponitzki C, Saumitou-Laprade P. 2021. Widespread coexistence of self-compatible and self-incompatible phenotypes in a diallelic self-incompatibility system in *Ligustrum vulgare* (Oleaceae). *Heredity* **127:** 384–392.

Debussche M, Escarré J, Lepart J. 1982. Ornithochory and plant succession in Mediterranean abndonned orchards. *Vegetatio* **48:** 255–266.

Desplanque B, Viard F, Bernard J, Forcioli D, Saumitou-Laprade P, Cuguen J, Van Dijk H. 2000. The linkage disequilibrium between chloroplast DNA and mitochondrial DNA haplotypes in *Beta vulgaris* ssp. *maritima* (L.): the usefulness of both genomes for population genetic studies. *Molecular Ecology* **9:** 141–154.

PDF Proof

Dommée B, Thompson JD, Cristini F. 1992. Distylie chez *Jasminum fruticans* L. : Hypothèse de la pollinisation optimale basée sur les variations de l'écologie intraflorale. *Bulletin de la Société Botanique de France* **139:** 223–234.

Dupin J, Raimondeau P, Hong-Wa C, Manzi S, Gaudeul M, Besnard G. 2020. Resolving the phylogeny of the olive family (Oleaceae): confronting information from organellar and nuclear genomes. *Genes* **11:** 1508.

Earl DA, vonHoldt BM. 2012. STRUCTURE HARVESTER: A website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* **4:** 359–361.

Ennos RA. 1994. Estimating the relative rates of pollen and seed migration among plant-populations. *Heredity* **72:** 250–259.

Excoffier L, Lischer HEL. 2010. ARLEQUIN suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources* **10:** 564–567.

García-Verdugo C, Forrest AD, Fay MF, Vargas P. 2010. The relevance of gene flow in metapopulation dynamics of an oceanic island endemic, *Olea europaea* subsp. *guanchica*. *Evolution* **64:** 3525–3536.

Goudet J. 2005. HIERFSTAT, a package for R to compute and test hierarchical *F*-statistics. *Molecular Ecology Notes* **5:** 184–186.

Gryta H, Van de Paer C, Manzi S, Holota H, Roy M, Besnard G. 2017. Genome skimming and plastid microsatellite profiling of alder trees (*Alnus* spp., Betulaceae): Phylogenetic and phylogeographical prospects. *Tree Genetics & Genomes* **13:** 118.

Gutián J, Gutián P, Medrano M. 1998. Floral biology of the distylous Mediterranean shrub *Jasminum fruticans* (Oleaceae). *Nordic Journal of Botany* **18:** 195–201.

Jump AS, Rico L, Lloret F, Peñuelas J. 2009. Microspatial population genetic structure of the Mediterranean shrub *Fumana thymifolia*. *Plant Biology* **11:** 152–160.

Kamvar ZN, Tabima JF, Grünwald NJ. 2014. *Poppr*: An R package for genetic analysis of populations with clonal, partially clonal, and/or sexual reproduction. *PeerJ* **2:** e281.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. GENEIOUS Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28:** 1647–1649.

Lewontin RC. 1964. The interaction of selection and linkage. I. General considerations; heterotic models. *Genetics* **49:** 49–67.

PDF Proof

Lewontin RC. 1988. On measures of gametic disequilibrium. *Genetics* **120:** 849–852.

Liu S, Zhang L, Sang Y, Lai Q, Zhang X, Jia C, Long Z, Wu J, Ma T, Mao K, Street NR, Ingvarsson PK, Liu J, Wang J. 2022. Demographic history and natural selection shape patterns of deleterious mutation load and barriers to introgression across *Populus* genome. *Molecular Biology and Evolution* **39:** msac008.

Mantel N. 1967. The detection of disease clustering and a generalized regression approach. *Cancer Research* **27:** 209–220.

Martínez-López V, García C, Zapata V, Robledano F, De la Rúa P. 2020. Intercontinental long-distance seed dispersal across the Mediterranean Basin explains population genetic structure of a bird-dispersed shrub. *Molecular Ecology* **29:** 1408–1420.

Médail F, Diadema K. 2009. Glacial refugia influence plant diversity patterns in the Mediterranean Basin. *Journal of Biogeography* **36:** 1333–1345.

Oddou-Muratorio S, Petit RJ, Le Guerroué B, Guesnet D, Demesure B. 2001. Pollen- versus seed-mediated gene flow in a scattered forest tree species. *Evolution* **55:** 1123–1135.

Olesen JM, Dupont YL, Ehlers BK, Valido A, Hansen DM. 2003. Heterostyly in the Canarian endemic *Jasminum odoratissimum* (Oleaceae). *Nordic Journal of Botany* **23:** 537–539.

Olson MS, McCauley DE. 2000. Linkage disequilibrium and phylogenetic congruence between chloroplast and mitochondrial haplotypes in *Silene vulgaris*. *Proceedings of the Royal Society of London, Series B* **267:** 1801–1808.

Pannell JR, Barrett SCH. 1998. Baker's law revisited: reproductive assurance in a metapopulation. *Evolution* **52:** 657–668.

Paetkau D, Slade R, Burden M, Estoup A. 2004. Genetic assignment methods for the direct, real-time estimation of migration rate: a simulation-based exploration of accuracy and power. *Molecular Ecology* **13:** 55–65.

Petit RJ, Duminil J, Fineschi S, Hampe A, Salvini D, Vendramin GG. 2005. Comparative organization of chloroplast, mitochondrial and nuclear diversity in plant populations. *Molecular Ecology* **14:** 689–701.

Petit RJ, Pineau E, Demesure B, Bacilieri R, Ducousso A, Kremer A. 1997. Chloroplast DNA footprints of postglacial recolonization by oaks. *Proceedings of the National Academy of Sciences of the United States of America* **94:** 9996–10001.

PDF Proof

Piry S, Alapetite A, Cornuet JM, Paetkau D, Baudouin L, Estoup A. 2004. GENECLASS2: A software for genetic assignment and first-generation migrant detection. *Journal of Heredity* **95:** 536–539.

Pritchard JK, Stephens M, Donnelly P. 2000. Inference of population structure using multilocus genotype data. *Genetics* **155:** 945–959.

Puech S. 1986. Production des diaspores et potentialités de germination chez quelques espèces à fruits charnus, ornithochores, dans le sud-est de la France. *Ecologia Mediterranea* **12:** 143–158.

QGIS Development Team. 2018. QGIS Geographic Information System. Open Source Geospatial Foundation Project. https://qgis.org/

Rannala B, Mountain JL. 1997. Detecting immigration by using multilocus genotypes. *Proceedings of the National Academy of Sciences of the United States of America* **94:** 9197–9201.

Salmona J, Olofsson JK, Hong-Wa C, Razanatosa J, Rakotonasolo F, Ralimanana H, Randriamboavonjy T, Suescun U, Vorontsova MS, Besnard G. 2020. Late Miocene origin and recent population collapse of the savanna Malagasy olive (*Noronhia lowryi*). *Biological Journal of the Linnean Society* **129:** 227–243.

Saumitou-Laprade P, Vernet P, Vassiliadis C, Hoareau Y, de Magny G, Dommée B, Lepart J. 2010. A self-incompatibility system explains high male frequencies in an androdioecious plant. *Science* **327:** 1648–1650.

Schuelke M. 2000. An economic method for the fluorescent labeling of PCR fragments. *Nature Biotechnology* **18:** 233–234.

Slatkin M. 1987. Gene flow and the geographic structure of natural populations. *Science* **236:** 787–792.

Slatkin M. 1993. Isolation by distance in equilibrium and non-equilibrium populations. *Evolution* **47:** 264–279.

Sodmergen, Bai HH, He JX, Kuroiwa H, Kawano S, Kuroiwa T. 1998. Potential for biparental cytoplasmic inheritance in *Jasminum officinale* and *Jasminum nudiflorum*. *Sexual Plant Reproduction* **11:** 107–112.

Sork VL. 2016. Gene flow and natural selection shape spatial patterns of genes in tree populations: implications for evolutionary processes and applications. *Evolutionary Applications* **9:** 291–310.

Thompson JD, Dommée B. 1993. Sequential variation in the components of reproductive success in the distylous *Jasminum fruticans* (Oleaceae). *Oecologia* **94:** 480–487.

PDF Proof

Thompson JD, Dommée B. 2000. Morph-specific patterns of variation in stigma height in natural populations of distylous *Jasminum fruticans*. *New Phytologist* **148:** 303–314.

Thompson JD. 2001. How do visitation patterns vary among pollinators in relation to floral display and floral design in a generalist pollination system? *Oecologia* **126:** 386–394.

Trapnell DW, Smallwood PA, Dixon KW, Philipps RD. 2022. Are small populations larger than they seem? Genetic insights into patchily distributed populations of *Drakaea glyptodon* (Orchidaceae). *Botanical Journal of the Linnean Society* **198:** 99–116.

Van Oosterhout C, Hutchinson W, Willis D, Shipley P. 2004. MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes* **4:** 535–538.

Vassiliadis C, Valero M, Saumitou-Laprade P, Godelle B. 2000. A model for the evolution of high frequencies of males in an androdioecious plant based on a cross-compatibility advantage of males. *Heredity* **85:** 413–422.

Vernet P, Lepercq P, Billiard S, Bourceaux A, Lepart J, Dommée B, Saumitou-Laprade P. 2016. Evidence for the long-term maintenance of a rare self-incompatibility system in Oleaceae. *New Phytologist* **210:** 1408–1417.

Wallander E, Albert VA. 2000. Phylogeny and classification of Oleaceae based on *rps16* and *trnL-F* sequence data. *American Journal of Botany* **87:** 1827–1841.

Weir BS, Cockerham CC. 1984. Estimating *F*-statistics for the analysis of population structure. *Evolution* **38:** 1358–1370.

Wolfe KH, LI WH, Sharp PM. 1987. Rates of nucleotide substitution vary greatly among plant mitochondrial, chloroplast, and nuclear DNAs. *Proceedings of the National Academy of Sciences of the United States of America* **84:** 9054–9058.

Wright S. 1965. The interpretation of population structure by *F*-statistics with special regard to systems of mating. *Evolution* **19:** 395–420.

Zhang Q, Liu Y, Sodmergen. 2003. Examination of the cytoplasmic DNA in male reproductive cells to determine the potential for cytoplasmic inheritance in 295 Angiosperm species. *Plant and Cell Physiology* **44:** 941–951.

PDF Proof

Table 1. List of sampled populations, with their location and geographic coordinates. All populations except one ('La Aliseda', Spain) are located in France. Nr and Ng refer to the number of collected 'ramets' and of recorded genotypes (after excluding clones), respectively. For each French locality, the number of brevistylous (B) and longistylous (L) genotypes is given in bracket (for more details see Supporting Information, Table S1). Lat. = Latitude; Long. = Longitude.

Locality	**Department (or province)**	**Lat., Long.**	**Nr**	**Ng (B/L)**
La Aliseda	Jaén	38.335, -3.569	10	7
Amélie-les-Bains	Pyrénées Orientales	42.478, 2.666	9	5 (3/2)
Bages	Aude	43.132, 2.985	12	12 (8/4)
Bidon	Ardèche	44.370, 4.532	10	10 (5/5)
CEFE (Montpellier)	Hérault	43.638, 3.862	15	15 (6/9)
Celleneuve	Hérault	43.611, 3.821	21	21 (10/11)
Eguilles	Bouches du Rhône	43.601, 5.2669	10	10 (5/5)
Moulis	Ariège	42.979, 1.084	37	37 (18/19)
Moussoulens	Aude	43.286, 2.249	15	15 (8/7)
Prades-le-Lez	Hérault	43.693, 3.861	11	10 (5/5)
Puycelsi	Tarn	44.015, 1.676	14	14 (8/6)
Sainte-Baume	Bouches du Rhône	43.327, 5.657	10	10 (4/6)
St-Maurice-Navacelles	Hérault	43.891, 3.510	17	17 (8/9)
La Turbie	Alpes Maritimes	43.747, 7.411	5	3 (1/2)

PDF Proof

Table 2. Summary of genetic diversity parameters estimated within populations with at least seven individuals. Expected and observed heterozygosities were calculated using GENETIX (Belkhir *et al.,* 2004), the allelic richness (A_R) with the R package HIERFSTAT (Goudet, 2005), and the haplotypic diversities (D) according to Gryta *et al.* (2017). Parameters estimated per locus are given in the Supporting Information (Table S8). A_R = Allelic richness, H_E = Expected heterozygosity under Hardy-Weinberg, H_O = Observed heterozygosity, D_{cp} = Chloroplast haplotype diversity, D_{mt} = Mitochondrial haplotype diversity, D_{cp+mt} = Cytoplasmic haplotype diversity.

Population	**Nuclear DNA**			**Cytoplasmic DNA**		
	A_R	H_E	H_O	D_{cp}	D_{mt}	D_{cp+mt}
La Aliseda	3.17	0.42	0.45	0.76	0.76	0.76
Bages	3.38	0.50	0.49	0.53	0.44	0.65
Celleneuve	3.32	0.47	0.47	0.10	0.10	0.19
CEFE	3.78	0.55	0.57	0.70	0.53	0.70
Prades-le-Lez	3.21	0.47	0.51	0.69	0.00	0.69
St-Maurice-de-Navacelles	3.89	0.56	0.58	0.63	0.76	0.91
Moussoulens	3.32	0.50	0.54	0.75	0.75	0.83
Puycelsi	3.36	0.50	0.46	0.44	0.54	0.74
Bidon	3.29	0.49	0.58	0.36	0.00	0.36
Sainte-Baume	2.84	0.41	0.46	0.20	0.20	0.20
Eguilles	3.19	0.47	0.52	0.38	0.20	0.38
Moulis	2.36	0.35	0.37	0.11	0.47	0.50

PDF Proof

Table 3. Association between mitotypes and chlorotypes on all *C. fruticans* individuals collected in southern France (179 individuals). Occurrence number of each chlorotype-mitotype combination is reported. Based on these data, the LD between haplotypes of the two organellar genomes, measured according to Lewontin (1964), was relatively low, but still highly significant ($D' = 0.368$, p-value < 0.001).

Mitotype no	**Chlorotype no**							***Total***
	1	**2**	**3**	**4**	**5**	**6**	**7**	
1	36		26	3	1	8		*74*
2	6		1	3				*10*
3	2		4	3			1	*10*
4	37	12	10	15			2	*76*
5				1				*1*
6				5		3		*8*
Total	*81*	*12*	*41*	*30*	*1*	*11*	*3*	*179*

PDF Proof

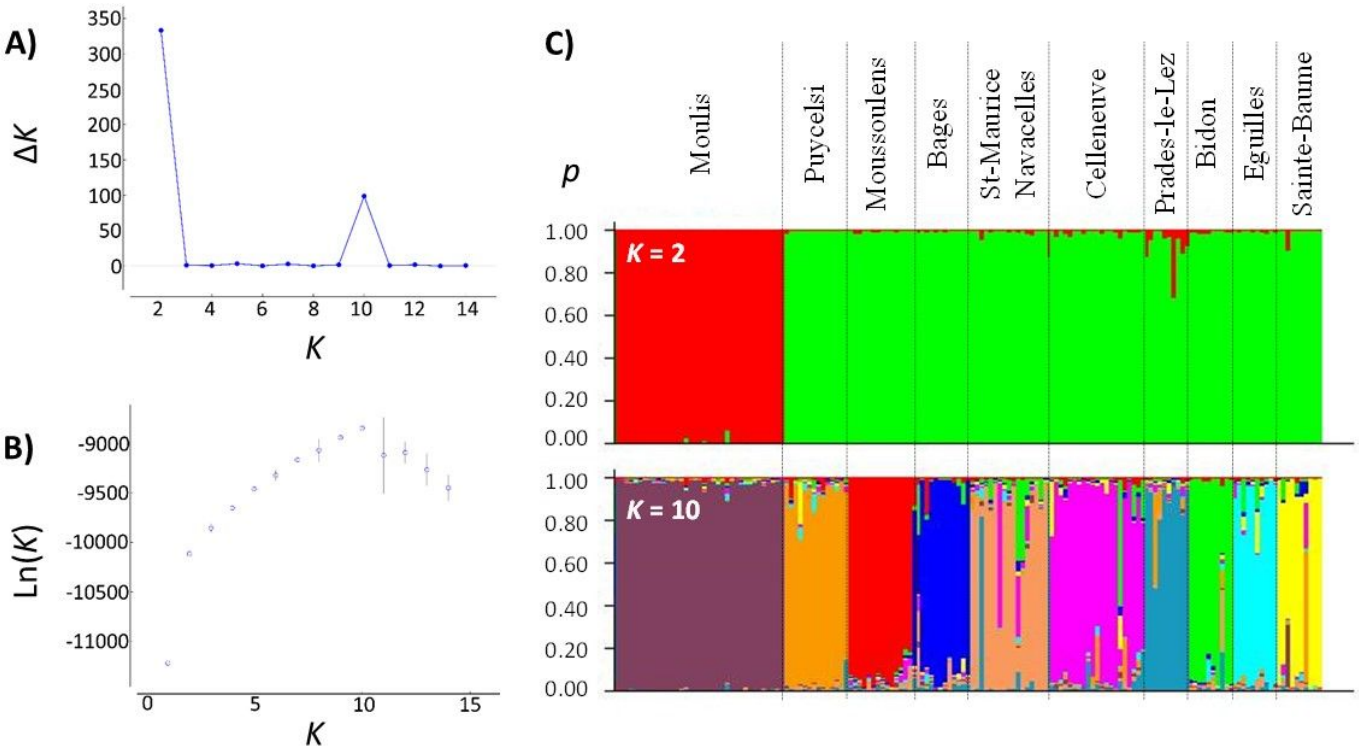

Figure 1. Results of the STRUCTURE analysis on ten French populations. A Bayesian approach was used to assign individuals to populations on the basis of their genotypes with STRUCTURE v.2.3.4 (Pritchard, Stephens & Donnelly, 2000). The analysis was performed for a number of clusters (*K*) ranging from 1 to 14 with ten iterations for each value of *K*. The most likely numbers of clusters were determined using the *ad hoc* measure of Δ*K* performed with STRUCTURE HARVESTER (Earl & vonHoldt, 2012). **(A)** Absolute values of the second-order rate of change of the likelihood distribution divided by the s.d. of the likelihoods (Δ*K*); **(B)** Mean log likelihood [Ln(*K*) +/- s.d.] averaged over the ten iterations for each *K* value; **(C)** Barplots of the population structure for *K* = 2 and 10. Each genetic cluster is represented by a color. Each vertical bar corresponds to an individual with their percentage assignment (*p*) to the clusters. For *K* = 2, the population of 'Moulis' (in red) differs from the nine others (in green). At *K* = 10, the clusters correspond fairly well to the populations defined *a priori*.

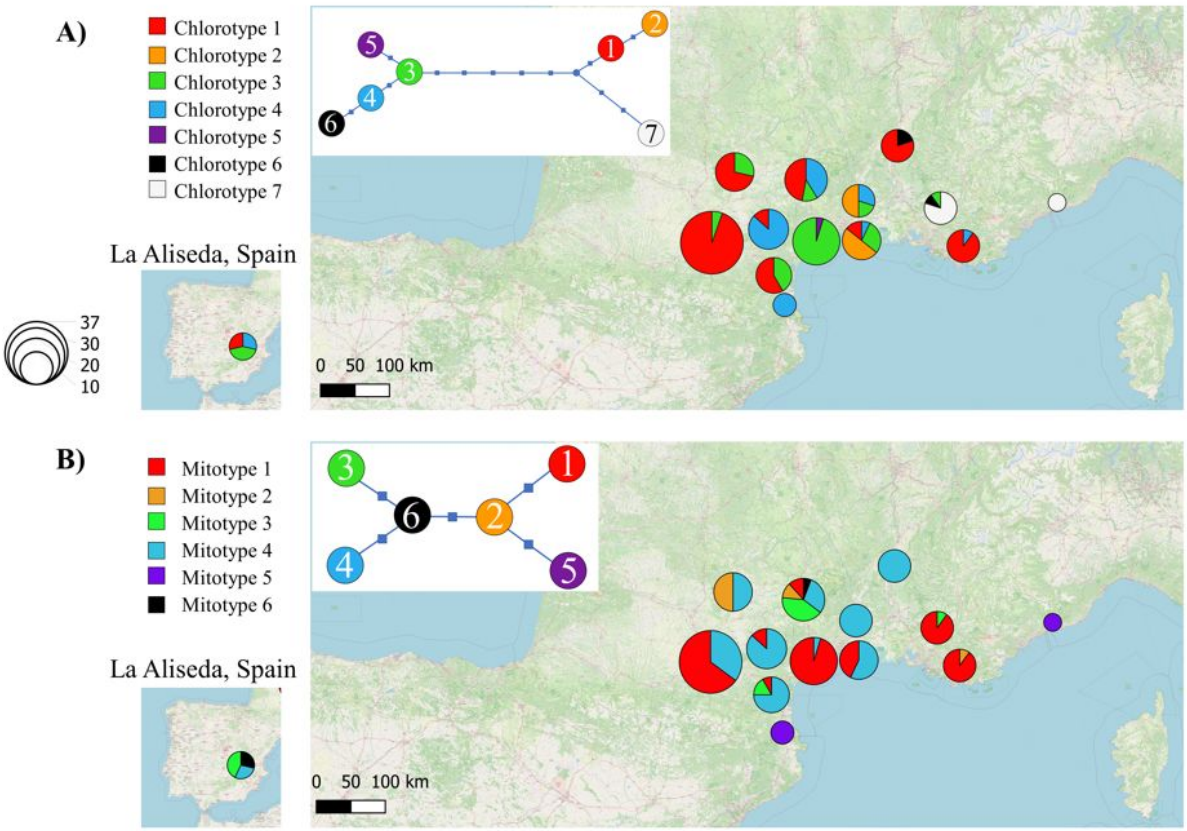

Figure 2. Distribution of **(A)** chloroplastic and **(B)** mitochondrial haplotypes in southwestern France. The haplotypes found in a Spanish population ('La Aliseda', Jaén Province) are also indicated. In the left-hand, top corner of each map, the reduced-median haplotype network (reconstructed with NETWORK v.10.2; Bandelt, Forster & Röhl, 1999) is given for each organellar genome.

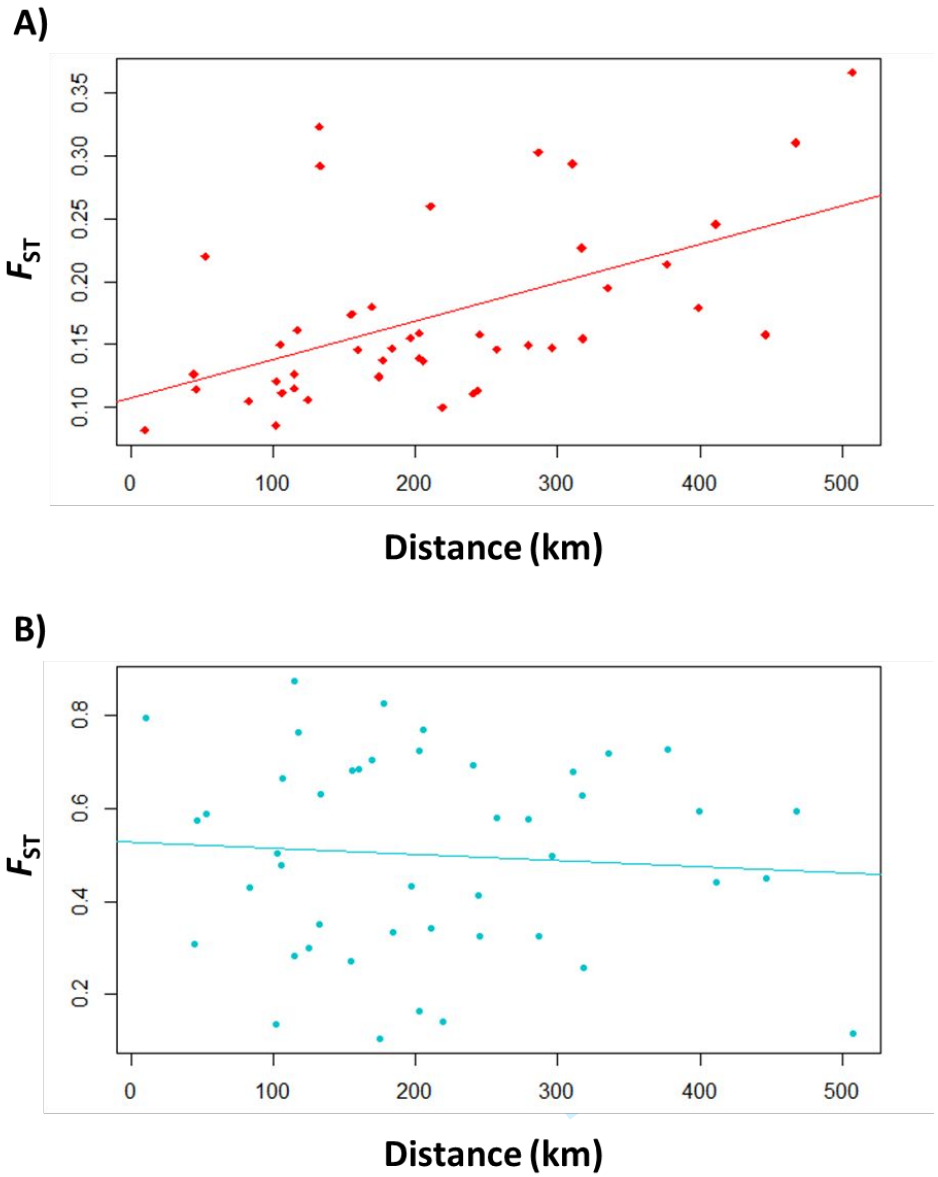

Figure 3. Genetic differentiation between populations as a function of geographical distance for **(A)** nuclear and **(B)** cytoplasmic data. Tests of Mantel (1967) were done with 999 permutations using the R package *ade4* (Chessel, Dufour & Thioulouse, 2004). Genetic distances (F_{ST}) and geographical distances between population pairs show a significant relationship (Mantel test, r = 0.528, *p*-value = 0.003) for nuclear data, but not for cytoplasmic data (r = -0.052, *p*-value > 0.05).

Supporting information

Limitation of gene flow by distance in the common yellow jasmine (*Chrysojasminum fruticans*, Oleaceae): implications for the study of its mating strategies

Aurore Puyoou *et al.*

SI Appendix includes:

Table S1. Plant sampling and complete genotyping dataset - **(see excel file)**

Table S2. List of herbarium specimens of the MNHN-P included in our study

Table S3. Characteristics of the 23 nuclear microsatellite loci developed in the present study

Table S4. Characteristics of the six nuclear indel loci developed in the present study

Table S5. Characteristics of chloroplastic and mitochondrial loci developed in the present study

Table S6. Genotyping of 36 progenies issued from parents with distinct chloroplast and/or mitochondrial DNA haplotypes in the 'CEFE' and 'Moulis' populations

Table S7. Measure of the LD between organellar genomes at the population scale

Table S8. Genetic diversity parameters estimated on both nuclear and cytoplasmic loci within populations with at least seven individuals

Table S9. F_{ST} values calculated between each pair of populations

Table S10. Results of the assignment test comparing nuclear SSR genotypes of individuals of the CEFE collection to nuclear SSR genotypes of natural populations

Figure S1. Dendrogram representing genetic similarity between all individuals based on genetic distances of Bruvo *et al.* (2004) and reconstructed with the unweighted average linkage clustering criterion.

Figure S2. Dendrogram representing genetic similarity between populations based on pairwise F_{ST} estimated from nuclear data and reconstructed on the unweighted average linkage clustering criterion

Figure S3. Cytoplasmic genetic differentiation between populations as a function of geographical distance according to different F_{ST} estimation methods

References

PDF proof

Table S2. List of herbarium specimens of the MNHN-P (Muséum National d'Histoire Naturelle de Paris) included in our study. For each specimen, the collector name (with a collector number when available) and the herbarium inventory number (in brackets) are given. Samples can be viewed at the MNHN website. The geographic origin (locality and country) and date of collection are also indicated ("00" means that day or month are not indicated on the label).

MNHN-P specimen	Locality, country	Date of collection
J. Lewalle 9060 (P03426484)	Oued Cherrad, Morocco	1979-05-01
J.M. Losa Quintana 17304 (P03883854)	Granada, Spain	1994-05-29
E. Bourgeau (P04074654)	Algarve, Portugal	1853-05-30
E. Reverchon 1182 (P04074663)	Granada, Spain	1900-06-00
A. Faure (P01194578)	Oran, Algeria	1940-03-17
A. Letourneux (P03426428)	Ghardimaou, Tunisia	1884-03-31
J. Bourcart (P04074655)	Pishkupije, Albania	1923-06-00
V. Stribrny (P04074662)	Philippopolin, Bulgaria	1893-06-00
B. Balansa (P03869118)	Smyrne, Turkey	1854-05-05
A.H. Brotherus 787 (P03869098)	Gori, Georgia	1881-07-00
R. Gombault 4458 (P03869122)	Zahlé, Lebanon	1930-06-09
A. Callier 252 (P03869093)	Soudak, Crimea	1896-00-00
R. Gombault 4456 (P03869103)	Radjou, Syria	1934-04-15
G. Remaudière 202 (P04254353)	South Sari, Iran	1966-00-00
P. Sintenis 1838 (P03869104)	Kisil-Arwat, Turkmenistan	1901-05-25

Table S3. Characteristics of the 23 nuclear microsatellite (SSR) loci developed in the present study. Name, putative homolog in olive [with SSR gene location: coding sequence (cds), intron, or untranscribed region (UTR)], GenBank accession nos, SSR motif (number of repeats based on the sequenced allele in *C. fruticans*), forward and reverse primers, fluorochrome used (Flu), PCR multiplex (Mx; locus amplified in simplex when no indication), allele size range, and number of alleles revealed (Na). * a M13 tail (TGTAAAACGACGGCCAGT) was added on the 5' extremity of each forward primer. ** Two loci are amplified with GAA20 primers (allele intensity of locus B is lower; allele size range indicates they may occasionally overlap).

Locus ID	Putative homolog in olive (encoded protein) – marker location in gene	GenBank no	SSR Motif	Forward primer*	Reverse primer	Flu	Mx	Allele size	Na
Cf-ATT-1	LOC111367380 (Kinesin prot.) – 3' UTR	OQ124178	$(ATT)_{9-10}$	TGTGGACTCATTTTATTCCTC	TACACTCCTTAGACGGTGGA	HEX	-	130-158	7
Cf-ATT-2	No gene homology	OQ124179	$(AAT)_{9}$	TGTGTCACGCTGGTTTTTC	CCCGATGTGTTTTTGGATACA	HEX	-	188-203	5
Cf-ATT-3	LOC111367396 (F-box prot.) – 3' UTR	OQ127180	$(AAT)_{11-12}$	CCCACATTTGACTCCTCATC	GAATACGATTATAGAACTGTGTTC	HEX	-	143-160	8
Cf-GAA-1	LOC111372306 (Translation initiation factor) – cds	OU230738	$(GAA)_{15}$	TTGGGTTTGACAAAGGATGCT	CAGATGGATTAAACATATTTCCAC	FAM	Dx-I	154-193	7
Cf-GAA-2	LOC111405212 (Unknown prot.) – 3' UTR	OU230739	$(GAA)_{9-10}$	GAACTGAGACAATCAGACACC	CCTCAATGACTTGCCTTTGGT	AT550		204-213	4
Cf-GAA-3	No gene homology	OU230740	$(GAA)_{13-14}$	TCAGTAGTATGTGCTAATTGATG	AAGGTTCTACCCAATGGTATCT	FAM	Dx-II	205-232	9
Cf-GAA-4	No gene homology	OQ124164	$(GAA)_{13-15}$	CGGTGAAAGGGTAGCAGATA	ATAGGAATGCTCGAAGTATCCT	FAM	Dx-II	247-307	19
Cf-GAA-5	LOC111387121 (Beta-1,3-galactosyl transferase) – 5' UTR	OQ124165	$(GAA)_{6}$	CACCAAGTCGACCAACTGT	GCCTGTCTTCTACTCTTCTC	HEX	Dx-III	161-170	6
Cf-GAA-6	No gene homology	OQ124166	$(GAA)_{7-17}$	GCTTCCTCRAACCCAATCATG	GAACAYTGATGTTCGCCTTGG	AT565	-	104-161	11
Cf-GAA-7	LOC111411240 (ATP-dependent 6-phosphofructo kinase) – 5' UTR	OQ124167	$(GAA)_{13-14}$	ACCTCAGTTTCAGTTGAAAGCT	CTTTTCCGAATTTGAAATTGGTAG	HEX	Dx-III	235-250	5
Cf-GAA-9	LOC111395981 (Unknown prot.) - intron	OQ124168	$(GAA)_{17-18}(GAT)_{6}$ $GAA(GAT)_{7}$	ATTTGGTATGGTCTCTGTTG	TTTCTCAAAATCAGCCATTTTCGA	FAM	-	250-289	13
Cf-GAA-11	LOC111378787 (Fasciclin arabino galactan prot.) – cds?	OQ124169	$(AAG)_{11}$	TGTGCTTGGAAACAGCTCCT	AATGCCATGGATTTCCAGATCT	FAM	Dx-I	117-132	6
Cf-GAA-14	No gene homology	OQ124170	$(GAA)_{25-26}$	AATAACGACCAACACCGATCAA	GGAGTTTTTCACCTATTCTCCT	FAM	-	101-182	23
Cf-GAA-16	No gene homology	OQ124112	$(AAG)_{18-20}$	AAGCCCCAATCCATTATCTAAC	AAGCTAATATCCACAATTCAAAGC	FAM	-	162-243	23
Cf-GAA-17	LOC111374342 (60S ribosomal prot.) – 5' UTR	OQ124172	$(GAA)_{18-23}$	CACATGCTTGAGTTTGACAAG	CTGGGAGCACAATTGTTTCC	FAM	-	206-257	14
Cf-GAA-18	LOC111402076 (Histone acetyl transferase) – cds	OQ124173	$(GAA)_{21-23}$	AAGACGGACACCAATGCACT	AGCTTTGCGGCAAGTAAGGA	AT565	-	154-214	16
Cf-GAA-19	No gene homology	OQ124174	$(TAA)_{12-13}(GAA)_{27-30}$	ATAAGATGCATATGCATCTACCTA	ATCGCTAAAAGGTCTTCTTCCT	AT565	-	191-284	25
Cf-GAA-20	No gene homology	OQ124175	$(GAA)_{24-25}$	GACCTGAGATTCCAGATCGA	GACAAAGTCTGGAAAGCTTCG	HEX	-	112-151	15
- (B)**	-	-	-	-	-	HEX	-	94-115	8
Cf-GAA-21	No gene homology	OQ124176	$(GAA)_{11-26}(TAA)_{8-9}$	TTCTTTCGTTGATGCAACAAATC	AACCAAGAAACTTGTGTGGACT	HEX	-	204-357	36
Cf-GAA-22	No gene homology	OQ124177	$(GAA)_{26-32}$	TGCTCTCTAGAGCTATAGTTG	AAGCAAGATATTGAGGAATTCAAG	AT565	-	131-230	32
Cf-ATA-1	No gene homology	OQ808969	$(ATA)_{12-13}$	CTTGTGGTTACGACAGTGCT	TAACTTCTAACCAAACTCCATAGT	FAM	-	223-241	7
Cf-TA-1	LOC111402738 (Transcription factor) – 5' UTR	OQ808968	$(TA)_{11-12}$	GGACTTCTTTCTTTTAGTTGTATG	AAACCAAGATGGAATATTACCTCA	AT565	-	213-223	3

Table S4. Characteristics of the six nuclear indel loci developed in the present study. Name, putative homolog in olive [with indel gene location: coding sequence (cds), intron, or untranscribed region (UTR)], GenBank accession nos, polymorphic motif, forward and reverse primers, fluorochrome used (Flu), PCR multiplex (Mx; locus amplified in simplex when no indication), allele size range, and number of alleles revealed (Na). * a M13 tail (TGTAAAACGACGGCCAGT) was added on the 5' extremity of each forward primer.

Locus ID	Putative homolog in olive (encoded protein) - marker location in gene	GenBank no	Polymorphic motif	Forward primer*	Reverse primer	Flu	Mx	Size range	Na
Cf-ind-1	LOC111410094 (Fructose-bisphosphate aldolase) – intron	OQ124181	Indel 25 bp	GACCCTCATTCAAGTATTTCCA	CATTAGGACAGTCGTAACATGT	FAM	Dx-IV	136-161	2
Cf-ind-2	LOC111367381 (Chaperone-like protein) – 5' UTR	OQ124182	$(AT)_{5-6}$ + indel 8 bp	GGAATCTATCATCAAACACTATATC	CTAATCATTTTCTTGATTTGCGGT	HEX	-	274-285	6
Cf-ind-3	LOC111392924 (Trans-resveratrol di-O-methyl transferase) – Intron	OQ124183	Indel 2 bp	CAGGGATCTTCCAAATCCGA	AGCTAGCGTGTCATATCTTAGT	AT565	Dx-V	121-123	2
Cf-ind-4	LOC111406052 (Pollen allergen Ole e 1) – 5'UTR	OQ124184	Indel 7 bp	CTTCCCGAACAACGATACTC	ATTGAGAGACTGGACGAACG	AT565	Dx-V	168-175	2
Cf-ind-5	LOC111367387 (GATA transcription factor) - 3' part	OQ124185	Indel 20 bp	ATGGCATGGGTTTGAGTAGC	CTTTTTAAAGTCTAGCTAGAGAGA	FAM	-	101-121	2
Cf-ind-6	LOC111367389 (Cytochrome P450) – intron	OQ124186	Indels 6+37 bp	AGCTCACTTGTCGTCTCT	AGCTTTCGCAATAGTATTGGAC	FAM	Dx-IV	150-200	3

Table S5. Characteristics of chloroplastic and mitochondrial loci developed in the present study. Name, indel length or microsatellite motif (number of repeats based on the sequenced allele in *C. fruticans*), forward and reverse primers, fluorochrome used (Flu), PCR multiplex (Mx), allele size range, and number of alleles revealed (Na). * a M13 tail (TGTAAAACGACGGCCAGT) was added on the 5' extremity of each forward primer.

Locus ID	GenBank no	Polymorphic motif	Forward primer*	Reverse primer	Flu	Mx	Size range	Na
- Plastome	MH559274							
CP1		$(T)_{13-14}$	cp17-For (olive; Besnard et *al.*, 2011)	CGATCAGGGTTCTTTTTGTATCAC	HEX	cpII	176-177	2
CP2		$(C)_{912}WWW(G)_{7-8}$	GGAGTTTGGCTCTATTAACTAG	ATGATAGTGTTGCGAGTCTATC	HEX	cpI	116-120	3
CP3		$(A)_{8-9}$	GGATTTATCGACATCAAGTTCG	CCGTACAAGGAATTCCGTAG	HEX	cpII	166-167	2
CP4		$(TAATAATA)_{1-2} + (A)_8(TA)_{10}$	CAGATGTATCAGAACTTTTTCGAT	TTGGTCGACTAGATATCGTACA	HEX	cpIII	349-357	2
CP5		$(A)_{8-10}TTC(A)_{8-10}$	GCATGATGACAAGAATTCTATCT	ATAGGAACGAAATAAACTCGAAGA	HEX	cpI	126-129	4
CP6		$(T)_9+(T)_{9-10}$	cp45-For (olive; Besnard et *al.*, 2011)	GTTTTCAAACCGAAGGGCTC	HEX	cpII	136-137	2
CP7		$(A)_{11-12}$	cp46-For (olive; Besnard et *al., 2*011)	cp46-Rev (olive; Besnard et *al.*, 2011)	HEX	cpI	108-109	2
CP8		$(A)_{9-10}$	CTTGAGCCACACCTACATTG	GAATCTATGGAGGGCCAT	HEX	cpIV	90-91	2
CP9		$(T)_{14-15}$	GGAGAAAAAGAGGCATTTACCT	AATCACGTGTCTTTCTCGTAAG	HEX	cpIV	110-111	2
CP10		Indel 8 bp	TTGGAACAAATTACTCTAATGCGT	CGGAGGATGATTCCAAGGA	HEX	cpIV	236-245	2
- Mitogenome	OQ124187-96							
MT1		Indel 8 bp	TGCATAAGGACTGTAAGCT	CGATAGCAGACATCTCCATC	HEX	mtI	301-309	2
MT2		$(A)_{9-10}$	CTACCTGCTTCTACGGAAGA	AGGGAACAAGCAACGGATGA	HEX	mtI	316-317	2
MT3		Indel 8 bp	GTATAGTGGACACGAGCA	TCTGTACACTCCTCTCATGC	HEX	mtI	327-335	2
MT4		Indel 8 bp	GTACTATCCTATTGGTCAAATCA	CGTATACAGGATTTCAGTATTAGA	HEX	mtII	231239	2
MT5		Indel 8 bp	TAGTAATAGGCTCAACTACAAGT	ACCTTCCTATTCGGCCAAGT	HEX	mtII	217-225	2

Table S6. Genotyping of 36 progenies issued from parents with distinct chloroplast and/or mitochondrial DNA haplotypes in the 'CEFE' and 'Moulis' populations. In these two locations, a dense sampling was performed to characterize the genotype of most putative parents in the population (data available under request). Floral morph (L = Longistylous; B = Brevistylous) of each parent is also recorded. Father of each progeny was identified from nuclear microsatellite data with CERVUS (Marshall *et al.*, 1998). Mitochondrial and chloroplast haplotypes were characterized on all parents and progenies, and highlighted in colour when different between both parents. A maternal contribution was systematically revealed in all progenies for both genomes. MD = Missing data.All crosses were between L and B (12), or B and L (24).

	Individual	Floral morphe	GAA20_B	GAA20	GAA21	GAA18	GAA22	GAA19	GAA16	GAA17	GAA1	GAA11	GAA3	GAA4	GAA2	GAA9	GAA5	GAA7	GAA14	ATT3	GAA6	ATT1	indel1	indel6	TA-1	ATA-1	MT1	MT2	MT3	MT4	MT5	mtDNA haplotype		CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	CP9	CP10	cpDNA haplotype	
Mother	CEFE_L1B	L	106:106	121:139	210:285	175:190	170:230	212:227	162:162	236:236	169:169	123:126	214:220	253:283	204:204	277:277	163:170	241:244	134:149	151:157	104:143	156:156	136:136	150:150	221:221	226:232	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_7	B	106:106	115:145	225:255	190:199	173:179	212:221	162:162	239:239	169:172	126:126	214:217	268:307	204:204	274:277	163:170	241:241	119:155	151:151	104:104	136:136	MD	150:150	213:213	229:229	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_L1Bs4A**		**106:106**	**115:121**	**MD**	**190:199**	**MD**	**212:212**	**162:162**	**236:239**	**169:169**	**MD**	**214:220**	**253:307**	**204:204**	**274:277**	**163:163**	**241:241**	**119:149**	**151:151**	**MD**	**136:156**	**MD**	**MD**	**MD**	**226:229**	**301**	**317**	**335**	**239**	**225**	**4**	**1**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**1**
Mother	CEFE_L2	L	106:106	115:136	210:210	196:196	161:191	233:239	162:198	251:251	169:169	126:126	211:214	262:268	204:204	274:274	163:163	235:241	137:137	151:157	104:143	136:136	161:161	150:150	213:221	229:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Father	CEFE_S6	B	106:106	118:136	210:291	199:202	179:203	221:236	162:162	236:251	169:169	126:126	214:214	253:253	204:204	277:280	170:170	241:244	134:152	151:151	104:104	156:156	136:161	150:194	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Progeny (2021)	**CEFE_L2s3**		**106:106**	**118:136**	**MD**	**196:202**	**191:203**	**236:239**	**162:162**	**251:251**	**169:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**163:170**	**241:241**	**134:137**	**151:151**	**MD**	**136:156**	**MD**	**MD**	**MD**	**229:229**	**309**	**316**	**327**	**239**	**225**	**1**	**2**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	**2**
Progeny (2021)	**CEFE_L2s7**		**106:106**	**115:136**	**MD**	**196:202**	**MD**	**221:239**	**162:162**	**236:251**	**169:169**	**MD**	**MD**	**MD**	**204:204**	**MD**	**163:170**	**241:244**	**134:137**	**151:151**	**MD**	**136:156**	**MD**	**MD**	**MD**	**229:229**	**309**	**316**	**327**	**239**	**225**	**1**	**3**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	**3**
Mother	CEFE_L2	L	106:106	115:136	210:210	196:196	161:191	233:239	162:198	251:251	169:169	126:126	211:214	262:268	204:204	274:274	163:163	235:241	137:137	151:157	104:143	136:136	161:161	150:150	213:221	229:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Father	CEFE_83	B	106:106	115:142	210:255	193:193	176:188	206:287	162:162	239:251	163:172	126:126	214:220	253:268	204:204	259:277	163:163	235:241	119:137	151:157	104:143	136:156	MD	150:150	213:221	232:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_L2s9**		**106:106**	**115:115**	**MD**	**193:196**	**MD**	**239:287**	**162:198**	**251:251**	**163:169**	**MD**	**MD**	**MD**	**204:204**	**MD**	**163:163**	**235:241**	**119:137**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:232**	**309**	**316**	**327**	**239**	**225**	**1**		**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	**4**
Mother	CEFE_L2	L	106:106	115:136	210:210	196:196	161:191	233:239	162:198	251:251	169:169	126:126	211:214	262:268	204:204	274:274	163:163	235:241	137:137	151:157	104:143	136:136	161:161	150:150	213:221	229:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Father	CEFE_S2	B	103:103	118:118	210:210	193:202	182:188	221:239	162:162	236:251	163:169	126:126	211:214	253:268	204:204	259:280	163:170	241:244	119:134	151:157	104:104	156:156	136:136	150:150	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Progeny (2021)	**CEFE_L2s10**		**103:106**	**118:136**	**MD**	**196:202**	**MD**	**221:233**	**162:162**	**236:251**	**163:169**	**MD**	**MD**	**268:268**	**204:204**	**274:280**	**163:163**	**235:244**	**134:137**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:229**	**309**	**316**	**327**	**239**	**225**	**1**	**4**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	**5**
Mother	CEFE_L5	L	106:106	115:142	204:294	190:199	188:227	218:257	198:198	215:239	166:169	126:126	211:214	268:280	204:204	265:277	163:170	235:241	140:140	154:157	104:104	136:136	161:161	150:194	213:221	229:229	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Father	CEFE_S6	B	106:106	118:136	210:291	199:202	179:203	221:236	162:162	236:251	169:169	126:126	214:214	253:253	204:204	277:280	170:170	241:244	134:152	151:151	104:104	156:156	136:161	150:194	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Progeny (2021)	**CFEE_L5s1A**		**106:106**	**115:118**	**MD**	**190:199**	**MD**	**221:257**	**162:198**	**215:251**	**169:169**	**MD**	**MD**	**MD**	**204:204**	**MD**	**MD**	**235:244**	**134:140**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:235**	**309**	**316**	**327**	**239**	**225**	**1**	**5**	**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	**6**
Mother	CEFE_L5	L	106:106	115:142	204:294	190:199	188:227	218:257	198:198	215:239	166:169	126:126	211:214	268:280	204:204	265:277	163:170	235:241	140:140	154:157	104:104	136:136	161:161	150:194	213:221	229:229	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Father	CEFE_131	B	106:106	118:121	210:288	190:202	173:182	221:236	162:201	236:251	169:169	126:126	214:214	253:301	204:204	259:274	163:170	235:241	134:134	151:157	104:143	156:156	MD	150:150	213:221	232:232	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Progeny (2021)	**CFEE_L5s2**		**106:106**	**115:118**	**MD**	**190:199**	**MD**	**218:236**	**198:201**	**239:251**	**169:169**	**MD**	**MD**	**MD**	**204:204**	**MD**	**MD**	**235:241**	**134:140**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:232**	**309**	**316**	**327**	**239**	**225**	**1**	**6**	**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	**7**
Progeny (2021)	**CEFE_L5s3**		**MD**	**121:142**	**MD**	**199:202**	**MD**	**218:221**	**162:198**	**215:251**	**166:169**	**MD**	**MD**	**MD**	**204:204**	**MD**	**MD**	**241:241**	**134:140**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:232**	**309**	**316**	**327**	**239**	**225**	**1**	**7**	**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	**8**
Mother	CEFE_149	L	106:106	115:142	288:288	190:199	173:206	215:236	162:162	251:254	169:172	126:126	220:220	253:268	204:204	274:277	163:163	241:241	134:152	151:157	104:104	156:156	MD	150:150	221:221	232:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Father	CEFE_52	B	106:106	115:115	210:222	190:196	161:182	233:257	198:207	242:251	169:169	126:126	214:214	262:262	204:204	256:274	163:163	235:235	137:149	154:157	104:104	136:156	MD	150:194	213:213	232:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**CEFE_L6B(149)s2**		**MD**	**112:115**	**222:288**	**196:199**	**MD**	**215:233**	**162:198**	**242:251**	**169:172**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**235:241**	**134:137**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**309**	**316**	**327**	**239**	**225**	**1**		**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	**9**
Mother	CEFE_S2	B	103:103	118:118	210:210	193:202	182:188	221:239	162:162	236:251	163:169	126:126	211:214	253:268	204:204	259:280	163:170	241:244	119:134	151:157	104:104	156:156	136:136	150:150	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_L2	L	106:106	115:136	210:210	196:196	161:191	233:239	162:198	251:251	169:169	126:126	211:214	262:268	204:204	274:274	163:163	235:241	137:137	151:157	104:143	136:136	161:161	150:150	213:221	229:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**CEFE_S2s1B**		**103:106**	**115:118**	**MD**	**193:196**	**188:191**	**233:239**	**162:162**	**251:251**	**163:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**163:170**	**235:241**	**119:137**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**8**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**10**
Mother	CEFE_S2	B	103:103	118:118	210:210	193:202	182:188	221:239	162:162	236:251	163:169	126:126	211:214	253:268	204:204	259:280	163:170	241:244	119:134	151:157	104:104	156:156	136:136	150:150	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_112	L	103:106	115:136	210:282	175:202	164:212	236:245	162:162	236:239	169:172	126:126	211:214	268:295	204:204	277:277	163:170	235:238	149:152	151:157	104:104	156:156	MD	150:194	221:221	229:232	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S2s3B**		**103:103**	**118:136**	**MD**	**202:202**	**188:212**	**221:245**	**162:162**	**236:236**	**169:172**	**MD**	**MD**	**268:268**	**204:204**	**MD**	**163:170**	**238:244**	**134:149**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:232**	**301**	**317**	**335**	**239**	**225**	**4**	**9**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**11**
Progeny (2021)	**CEFE_S2s4A**		**103:106**	**118:136**	**MD**	**202:202**	**164:188**	**239:245**	**162:162**	**236:239**	**169:169**	**MD**	**MD**	**253:268**	**204:204**	**277:280**	**163:170**	**238:241**	**119:149**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:232**	**301**	**317**	**335**	**239**	**225**	**4**	**10**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**12**
Progeny (2021)	**CEFE_S2s4B**		**MD**	**118:136**	**MD**	**175:202**	**188:212**	**MD**	**162:162**	**236:239**	**163:169**	**MD**	**MD**	**253:292**	**204:204**	**MD**	**163:170**	**235:244**	**119:152**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**232:235**	**301**	**317**	**335**	**239**	**225**	**4**	**11**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**13**
Mother	CEFE_S3	B	103:106	115:142	210:216	175:199	176:227	221:251	162:198	236:251	169:169	126:126	211:214	253:268	204:204	259:265	163:163	241:241	152:152	151:157	104:143	156:156	161:161	150:150	213:221	229:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Father	CEFE_25	L	106:106	121:124	210:291	175:184	182:191	233:236	162:168	236:251	169:169	126:126	211:214	301:301	204:204	274:274	163:163	235:235	137:143	151:151	104:104	136:156	MD	150:194	221:221	229:232	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Progeny (2021)	**CEFE_S3s1B**		**103:106**	**115:121**	**MD**	**175:175**	**MD**	**221:233**	**162:198**	**236:251**	**169:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**235:241**	**143:152**	**151:157**	**MD**	**136:156**	**MD**	**MD**	**MD**	**MD**	**309**	**316**	**327**	**239**	**225**	**1**	**12**	**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	**14**
Mother	CEFE_S3	B	103:106	115:142	210:216	175:199	176:227	221:251	162:198	236:251	169:169	126:126	211:214	253:268	204:204	259:265	163:163	241:241	152:152	151:157	104:143	156:156	161:161	150:150	213:221	229:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Father	CEFE_158	L	106:106	136:139	210:303	196:202	182:227	212:215	162:198	236:239	169:172	123:126	214:214	253:283	204:204	277:277	163:170	241:241	140:152	151:151	104:143	156:156	MD	150:194	213:221	229:229	301	317	335	239	225	4		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S3s3**		**MD**	**115:136**	**MD**	**196:199**	**MD**	**212:251**	**162:198**	**236:251**	**169:172**	**MD**	**211:214**	**268:268**	**204:204**	**265:277**	**MD**	**241:241**	**140:152**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:235**	**309**	**316**	**327**	**239**	**225**	**1**	**13**	**176**	**119**	**167**	**349**	**128**	**136**	**108**	**90**	**110**	**245**	**3**	
Mother	CEFE_S4	B	106:106	115:121	210:288	196:202	173:185	212:221	162:168	236:251	169:172	126:126	214:220	253:268	204:204	274:280	163:163	241:244	152:155	151:151	104:104	156:156	161:161	150:194	221:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_135	L	103:106	142:142	210:210	193:193	200:200	221:221	162:162	251:251	169:169	126:126	211:220	268:268	204:204	277:277	163:163	241:241	152:152	151:151	143:143	156:156	MD	150:150	213:213	232:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S4s1B**		**103:106**	**115:142**	**MD**	**193:196**	**MD**	**212:221**	**162:168**	**251:251**	**169:172**	**MD**	**220:220**	**268:268**	**204:204**	**277:280**	**MD**	**241:241**	**152:155**	**151:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**232:235**	**301**	**317**	**335**	**239**	**225**	**4**	**14**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**15**
Mother	CEFE_S4	B	106:106	115:121	210:288	196:202	173:185	212:221	162:168	236:251	169:172	126:126	214:220	253:268	204:204	274:280	163:163	241:244	152:155	151:151	104:104	156:156	161:161	150:194	221:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_57	L	103:103	115:142	291:291	175:184	188:200	191:212	162:168	251:251	169:169	126:126	214:214	268:301	204:204	274:277	163:170	238:241	131:134	151:151	104:104	156:156	MD	150:194	221:221	226:229	301	317	335	239	225	4		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S4s2**		**103:106**	**115:115**	**MD**	**184:196**	**MD**	**191:221**	**168:168**	**236:251**	**169:172**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:244**	**134:152**	**151:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**		**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**16**

Table S6, end.

	Individual		GAA20_B	GAA20	GAA21	GAA18	GAA22	GAA19	GAA16	GAA17	GAA1	GAA11	GAA3	GAA4	GAA2	GAA9	GAA5	GAA7	GAA14	ATT3	GAA6	ATT1	Indel1	Indel6	TA-1	ATA-1	MT1	MT2	MT3	MT4	MT5	mtDNA haplotype		CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	CP9	CP10	cpDNA haplotype	
Mother	CEFE_S4	B	106:106	115:121	210:288	196:202	173:185	212:221	162:168	236:251	169:172	126:126	214:220	253:268	204:204	274:280	163:163	241:244	152:155	151:151	104:104	156:156	161:161	150:194	221:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_136	L	106:106	118:121	210:210	175:184	170:200	209:215	168:198	236:251	169:169	126:126	211:220	286:301	213:213	274:277	163:170	241:241	134:137	151:157	104:104	156:156	MD	150:150	221:221	226:235	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**CEFE_S4s3A**		**106:106**	**118:121**	**MD**	**175:202**	**MD**	**212:215**	**162:198**	**236:251**	**169:172**	**MD**	**MD**	**268:286**	**204:213**	**MD**	**MD**	**241:241**	**134:152**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**229:235**	**301**	**317**	**335**	**239**	**225**	**4**	**15**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**17**
Progeny (2021)	**CEFE_S4s3B**		**MD**	**115:121**	**MD**	**175:202**	**MD**	**MD**	**162:198**	**251:251**	**169:172**	**MD**	**MD**	**268:286**	**204:213**	**MD**	**MD**	**241:244**	**134:152**	**151:157**	**MD**	**156:156**	**MD**	**MD**	**MD**	**235:235**	**301**	**317**	**335**	**239**	**225**	**4**	**16**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**18**
Progeny (2021)	**CEFE_S4s6**		**MD**	**115:121**	**MD**	**175:196**	**MD**	**MD**	**168:198**	**236:251**	**169:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:241**	**137:155**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**17**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**19**
Progeny (2021)	**CEFE_S4s8**		**106:106**	**121:121**	**MD**	**184:202**	**MD**	**209:212**	**162:168**	**251:251**	**169:172**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:241**	**134:152**	**151:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**18**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**20**
Mother	CEFE_S4	B	106:106	115:121	210:288	196:202	173:185	212:221	162:168	236:251	169:172	126:126	214:220	253:268	204:204	274:280	163:163	241:244	152:155	151:151	104:104	156:156	161:161	150:194	221:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_109	L	103:106	118:121	210:210	175:196	170:200	209:221	168:198	236:236	169:169	126:126	211:214	253:301	204:204	274:277	170:170	241:244	134:152	148:151	104:104	136:156	MD	150:150	221:221	226:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**CEFE_S4s4**		**106:106**	**115:118**	**210:210**	**175:202**	**MD**	**209:221**	**162:198**	**236:251**	**169:172**	**MD**	**MD**	**MD**	**204:204**	**MD**	**MD**	**241:244**	**134:155**	**151:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**232:235**	**301**	**317**	**335**	**239**	**225**	**4**	**19**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**21**
Mother	CEFE_S4	B	106:106	115:121	210:288	196:202	173:185	212:221	162:168	236:251	169:172	126:126	214:220	253:268	204:204	274:280	163:163	241:244	152:155	151:151	104:104	156:156	161:161	150:194	221:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_L6	L	103:109	121:139	288:288	190:202	167:200	221:257	162:207	215:254	163:169	126:126	214:214	253:253	204:204	277:277	163:163	235:241	149:152	148:154	104:143	156:156	136:161	150:150	221:221	226:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S4s5**		**103:106**	**121:121**	**MD**	**190:202**	**MD**	**212:257**	**162:207**	**215:236**	**169:172**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**235:241**	**149:152**	**148:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**20**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**22**
Mother	CEFE_S6	B	106:106	118:136	210:291	199:202	179:203	221:236	162:162	236:251	169:169	126:126	214:214	253:253	204:204	277:280	170:170	241:244	134:152	151:151	104:104	156:156	136:161	150:194	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_L5	L	106:106	115:142	204:294	190:199	188:227	218:257	198:198	215:239	166:169	126:126	211:214	268:280	204:204	265:277	163:170	235:241	140:140	154:157	104:104	136:136	161:161	150:194	213:221	229:229	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S6s1A**		**106:106**	**115:136**	**MD**	**199:199**	**MD**	**MD**	**162:198**	**215:236**	**169:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:244**	**140:152**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**21**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**23**
Progeny (2021)	**CEFE_S6s2**		**MD**	**115:136**	**MD**	**199:199**	**MD**	**218:221**	**162:198**	**215:236**	**166:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:244**	**140:152**	**157:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**22**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**24**
Progeny (2021)	**CEFE_S6s3**		**MD**	**136:142**	**MD**	**199:202**	**MD**	**MD**	**162:198**	**215:236**	**166:166**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**235:241**	**140:152**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**23**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**25**
Progeny (2021)	**CEFE_S6s6**		**106:106**	**136:142**	**MD**	**199:199**	**179:188**	**MD**	**162:198**	**236:239**	**169:169**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:244**	**134:140**	**151:154**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**24**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**26**
Mother	CEFE_S6	B	106:106	118:136	210:291	199:202	179:203	221:236	162:162	236:251	169:169	126:126	214:214	253:253	204:204	277:280	170:170	241:244	134:152	151:151	104:104	156:156	136:161	150:194	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_136	L	106:106	118:121	210:210	175:184	170:200	209:215	168:198	236:251	169:169	126:126	211:220	286:301	213:213	274:277	163:170	241:241	134:137	151:157	104:104	156:156	MD	150:150	221:221	226:235	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**CEFE_S6s7**		**106:106**	**121:136**	**MD**	**175:199**	**170:203**	**209:236**	**162:198**	**236:251**	**169:169**	**MD**	**MD**	**253:301**	**204:213**	**MD**	**MD**	**241:241**	**134:134**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**226:229**	**301**	**317**	**335**	**239**	**225**	**4**	**25**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**27**
Mother	CEFE_S6	B	106:106	118:136	210:291	199:202	179:203	221:236	162:162	236:251	169:169	126:126	214:214	253:253	204:204	277:280	170:170	241:244	134:152	151:151	104:104	156:156	136:161	150:194	213:221	229:235	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_149	L	106:106	115:142	288:288	190:199	173:206	215:236	162:162	251:254	169:172	126:126	220:220	253:268	204:204	274:277	163:163	241:241	134:152	151:157	104:104	156:156	MD	150:150	221:221	232:235	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2021)	**CEFE_S6s1B**		**MD**	**118:142**	**MD**	**199:202**	**MD**	**MD**	**162:162**	**251:254**	**169:172**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:241**	**134:134**	**151:151**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**26**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**28**
Progeny (2021)	**CEFE_S6s8**		**106:106**	**136:142**	**MD**	**199:202**	**173:179**	**MD**	**162:162**	**236:254**	**169:172**	**126:126**	**MD**	**MD**	**MD**	**MD**	**MD**	**241:241**	**134:152**	**151:157**	**MD**	**MD**	**MD**	**MD**	**MD**	**MD**	**301**	**317**	**335**	**239**	**225**	**4**	**27**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**29**
Mother	CEFE_119	B	106:106	121:142	210:288	190:202	179:194	215:236	162:162	236:251	169:172	126:126	211:217	268:268	204:204	259:280	163:170	238:241	152:155	151:151	104:104	136:156	136:161	150:150	213:221	229:232	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_122	L	103:106	115:136	210:264	190:190	164:176	221:221	198:198	239:251	169:169	126:126	211:214	253:253	204:204	274:277	163:163	241:241	137:155	151:151	104:104	156:156	MD	150:150	221:221	229:229	309	316	327	239	225	1		176	119	167	349	128	136	108	90	110	245	3	
Progeny (2022)	**CEFE 119-1A**		**106:106**	**115:142**	**210:288**	**190:190**	**164:194**	**215:221**	**162:198**	**239:251**	**169:172**	**126:126**	**211:214**	**253:268**	**204:204**	**259:277**	**163:170**	**241:241**	**137:152**	**151:151**	**MD**	**136:156**	**136:161**	**150:150**	**221:221**	**229:232**	**301**	**317**	**335**	**239**	**225**	**4**	**28**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**30**
Mother	CEFE_119	B	106:106	121:142	210:288	190:202	179:194	215:236	162:162	236:251	169:172	126:126	211:217	268:268	204:204	259:280	163:170	238:241	152:155	151:151	104:104	136:156	136:161	150:150	213:221	229:232	301	317	335	239	225	4		177	120	166	357	127	137	109	90	110	245	2	
Father	CEFE_109	L	103:106	118:121	210:210	175:196	170:200	209:221	168:198	236:236	169:169	126:126	211:214	253:301	204:204	274:277	170:170	241:244	134:152	148:151	104:104	136:156	MD	150:150	221:221	226:232	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2022)	**CEFE 119-1B**		**103:106**	**121:121**	**210:210**	**196:202**	**179:200**	**221:236**	**162:168**	**236:236**	**169:169**	**126:126**	**211:214**	**253:268**	**204:204**	**274:280**	**163:170**	**238:244**	**134:152**	**148:151**	**MD**	**156:156**	**136:136**	**150:150**	**213:221**	**226:229**	**301**	**317**	**335**	**239**	**225**	**4**	**29**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**31**
Progeny (2022)	**CEFE 119-4**		**106:106**	**118:121**	**210:288**	**175:202**	**170:194**	**221:236**	**162:198**	**236:251**	**169:169**	**126:126**	**211:217**	**253:268**	**204:204**	**259:274**	**163:170**	**238:244**	**134:155**	**148:151**	**MD**	**136:156**	**136:136**	**150:150**	**221:221**	**232:232**	**301**	**317**	**335**	**239**	**225**	**4**	**30**	**177**	**120**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**2**	**32**
Mother	Moulis_8L_9L_13L	L	103:106	136:136	210:216	202:202	146:146	230:230	204:204	251:251	163:169	126:126	214:214	262:268	204:207	259:259	163:163	241:241	137:155	151:151	104:104	133:133	136:136	150:150	213:213	232:235	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Father	Moulis_19S	B	106:106	112:136	210:213	193:202	146:188	230:233	198:204	215:251	163:169	126:126	214:214	262:268	204:207	259:271	163:170	238:238	137:155	151:151	104:104	133:133	136:136	150:150	213:213	235:235	301	317	335	239	225	4		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**Moulis_8s2**		**103:106**	**112:136**	**210:216**	**202:202**	**146:188**	**230:233**	**204:204**	**251:251**	**163:163**	**126:126**	**214:214**	**262:262**	**204:204**	**259:259**	**163:170**	**238:241**	**137:137**	**MD**	**104:104**	**133:133**	**MD**	**MD**	**MD**	**MD**	**309**	**316**	**327**	**239**	**225**	**1**	**31**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	
Mother	Moulis_8L_9L_13L	L	103:106	136:136	210:216	202:202	146:146	230:230	204:204	251:251	163:169	126:126	214:214	262:268	204:207	259:259	163:163	241:241	137:155	151:151	104:104	133:133	136:136	150:150	213:213	232:235	309	316	327	239	225	1		177	119	166	357	127	137	109	90	110	245	1	
Father	Moulis_24S	B	106:109	136:136	210:213	190:202	146:152	221:230	162:198	215:251	163:169	126:126	214:214	262:268	207:207	259:271	170:170	241:241	137:155	151:151	104:143	133:133	136:136	150:150	213:213	232:232	301	317	335	239	225	4		177	119	166	357	127	137	109	90	110	245	1	
Progeny (2021)	**Moulis_9s1A**		**103:109**	**136:136**	**210:213**	**190:202**	**146:152**	**230:230**	**162:204**	**215:251**	**163:169**	**126:126**	**214:214**	**262:268**	**204:207**	**259:259**	**163:170**	**241:241**	**137:155**	**MD**	**104:104**	**133:133**	**MD**	**MD**	**MD**	**MD**	**309**	**316**	**327**	**239**	**225**	**1**	**32**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	
Progeny (2021)	**Moulis_9s1B**		**106:109**	**136:136**	**213:216**	**190:202**	**146:146**	**221:230**	**162:204**	**215:251**	**163:169**	**126:126**	**214:214**	**268:268**	**207:207**	**259:259**	**163:170**	**241:241**	**137:155**	**MD**	**104:143**	**133:133**	**MD**	**MD**	**MD**	**MD**	**309**	**316**	**327**	**239**	**225**	**1**	**33**	**177**	**119**	**166**	**357**	**127**	**137**	**109**	**90**	**110**	**245**	**1**	

Table S7. Measure of the LD (*D'*; Lewontin, 1964) between organellar genomes at the population scale. Significance (*p*-value) of the *D'* estimate was measured with a Fisher's test. This test was only done on populations where polymorphism was observed on both organellar genomes (see Table S1). Ng = Number of genotypes.

Population	**Ng**	***D'***	***p*-value**
La Aliseda	7	1.000	0.005
Bages	12	1.000	0.048
CEFE	15	0.875	<0.001
Celleneuve	21	1.000	1.000
Eguilles	10	1.000	0.212
Moulis	37	1.000	0.118
Moussoulens	12	1.000	1.000
St-Maurice-de-Navacelles	17	0.558	0.181
Puycelsi	15	0.500	0.073
Sainte-Baume	10	1.000	0.109

roof

Table S8. Genetic diversity parameters estimated on both nuclear and cytoplasmic loci within populations with at least seven individuals. The parameters were calculated using GENETIX (Belkhir *et al.,* 2004), except the allelic richness (A_R) that was calculated with the R package HIERFSTAT (Goudet, 2005) and the haplotypic diversities (D) that were estimated according to Grytaet *al.* (2017). N_a = Number of alleles, A_R = Allelic richness, H_E = Expected heterozygosity under Hardy-Weinberg, H_O = Observed heterozygosity, F_{IS} = Fixation index, N_h = Number of haplotypes, D_{cp} = Chlorotypic diversity, D_{mt}= Mitotypic diversity, D_{cp+mt} = cytoplasmic diversity. F_{IS} values significantly different from 0 are indicated in bold (p-value < 0.05 in red, and p-value < 0.01 in green; without considering multiple testing correction). The detection of probable null alleles with MICRO-CHECKER (Van Oosterhout *et al.,* 2004) is indicated by an asterisk.

		Bages (12)					Bidon (10)					CEFE (15)					Celleneuve (21)					Eguilles (10)					Moulis (37)				
Nuclear compartment	**Locus**	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}
- Microsatellite (SSR)	**GAA1**	2	2,00	0,44	0,50	-0,08	4	3,62	0,63	0,50	0,25	4	3,19	0,50	0,40	0,23	2	1,71	0,13	0,14	-0,05	4	3,40	0,59	0,50	0,20	4	3,00	0,54	0,57	-0,03
	GAA2	3	2,98	0,57	0,42	0,31	3	2,92	0,57	0,60	-0,01	3	2,19	0,18	0,20	-0,05	3	2,22	0,25	0,29	-0,12	3	3,00	0,62	0,80	-0,24	2	2,00	0,46	0,57	-0,21
	GAA3	2	1,99	0,33	0,25	0,28	3	2,70	0,40	0,40	0,04	3	2,94	0,50	0,67	-0,30	2	1,82	0,17	0,19	-0,08	1	1,00	0,00	0,00	-	3	2,19	0,51	0,54	-0,05
	GAA4	6	4,94	0,70	0,58	0,21	4	3,68	0,65	0,80	-0,18	8	4,80	0,64	0,67	-0,01	5	3,59	0,65	0,71	-0,08	3	2,68	0,34	0,40	-0,14	3	2,72	0,49	0,51	-0,04
	GAA5	3	2,42	0,23	0,17	0,30	3	2,62	0,27	0,30	-0,08	2	2,00	0,48	0,53	-0,08	2	2,00	0,44	0,38	0,17	2	2,00	0,42	0,60	-0,39	2	1,95	0,29	0,30	-0,01
	GAA6	2	2,00	0,38	0,50	-0,29	2	1,92	0,18	0,20	-0,06	2	2,00	0,39	0,53	-0,33	1	1,00	0,00	0,00	-	3	3,00	0,64	0,80	-0,20	2	1,99	0,37	0,27	0,28
	GAA7	2	1,94	0,22	0,08	0,65	3	2,92	0,51	0,40	0,26	4	3,64	0,58	0,80	**-0,36**	2	2,00	0,44	0,38	0,17	3	2,70	0,45	0,60	-0,30	3	2,96	0,58	0,49	0,18
	GAA9	4	3,41	0,50	0,58	-0,12	5	4,84	0,76	0,80	-0,01	6	5,18	0,75	0,67	0,15	7	5,18	0,76	0,90	-0,17	6	5,10	0,74	0,80	-0,03	4	2,85	0,57	0,59	-0,04
	GAA11	3	2,58	0,43	0,42	0,08	1	1,00	0,00	0,00	-	2	1,86	0,18	0,20	-0,08	3	2,86	0,47	0,38	0,22	2	1,70	0,10	0,10	0,00	2	1,73	0,15	0,16	-0,08
	GAA14	6	4,98	0,74	0,83	-0,08	8	6,92	0,82	0,90	-0,05	8	6,56	0,84	0,80	0,08	9	6,63	0,84	0,90	-0,05	6	5,08	0,72	0,70	0,08	4	3,82	0,69	0,84	**-0,20**
	GAA16	5	4,00	0,64	0,58	0,14	5	4,10	0,60	0,90	**-0,46**	5	4,04	0,58	0,60	0,01	4	2,48	0,26	0,29	-0,10	3	2,70	0,40	0,40	0,04	5	3,27	0,59	0,59	0,01
	GAA17	5	4,36	0,64	0,75	-0,13	3	2,92	0,46	0,60	-0,26	7	5,24	0,73	0,73	0,03	5	3,64	0,64	0,62	0,06	6	5,10	0,75	0,80	-0,01	4	2,92	0,57	0,62	-0,08
	GAA18	7	6,27	0,83	0,83	0,04	5	4,69	0,77	0,90	-0,13	7	6,11	0,83	0,93	-0,09	7	5,09	0,68	0,67	0,04	6	5,32	0,76	0,90	-0,13	6	3,82	0,67	0,78	-0,16
	GAA19	10	7,17	0,79	0,75	0,18	9	7,62	0,85	0,90	-0,01	15	9,42	0,89	1,00	-0,09	13	8,48	0,89	0,86	0,07	8	6,42	0,74	0,70	0,10	9*	5,36	0,76	0,59	**0,23**
	GAA20	7	5,73	0,80	0,83	0,01	7	5,78	0,73	0,70	0,09	7	6,36	0,84	0,87	0,00	7	5,01	0,76	0,81	-0,05	5	4,32	0,66	0,70	-0,01	5	2,70	0,42	0,51	-0,21
	GAA20_B	2	2,00	0,47	0,58	-0,20	1	1,00	0,00	0,00	-	3	2,46	0,41	0,33	0,21	2	2,00	0,41	0,38	0,09	2	2,00	0,32	0,20	0,42	3	2,58	0,53	0,51	0,04
	GAA21	10	6,90	0,74	0,75	0,03	4	3,60	0,48	0,50	0,00	10	6,12	0,72	0,73	0,02	15	8,11	0,85	0,90	-0,04	8	6,42	0,74	0,80	-0,04	4	2,66	0,55	0,65	-0,17
	GAA22	12	8,33	0,84	0,83	0,06	10	8,31	0,86	1,00	-0,11	17	10,31	0,92	1,00	-0,06	18	9,56	0,91	0,95	-0,02	7	5,94	0,76	0,90	-0,13	15	6,49	0,73	0,78	-0,05
	ATT1	4	3,52	0,58	0,67	-0,11	3	2,98	0,61	0,90	-0,45	2	2,00	0,39	0,27	0,35	3	2,71	0,53	0,43	0,21	4	3,62	0,60	0,60	0,04	3	2,11	0,28	0,32	-0,16
	ATT2	2	2,00	0,47	0,42	0,15	2	1,98	0,26	0,30	-0,13	2*	2,00	0,44	0,13	**0,72**	2	2,00	0,41	0,38	0,09	2	2,00	0,46	0,50	-0,05	1	1,00	0,00	0,00	-
	ATT3	2	1,58	0,08	0,08	0,00	2	2,00	0,38	0,50	-0,29	4	3,45	0,58	0,60	0,00	2	1,93	0,24	0,29	-0,14	4	3,32	0,35	0,40	-0,11	1	1,00	0,00	0,00	-
	TA1	3*	3,00	0,64	0,33	**0,51**	3	2,70	0,55	0,40	0,31	2	2,00	0,39	0,53	-0,33	2	2,00	0,47	0,48	0,02	2	1,98	0,26	0,30	-0,13	2	1,47	0,08	0,08	-0,03
	ATA1	4	3,42	0,57	0,50	0,16	2	2,00	0,48	0,60	-0,20	4	3,93	0,73	0,80	-0,07	4	3,12	0,58	0,52	0,12	3	2,70	0,52	0,60	-0,11	2	2,00	0,44	0,38	0,15
- Indel	**indel1**	2	2,00	0,50	0,50	0,04	2	2,00	0,50	0,90	**-0,80**	2	2,00	0,46	0,47	0,03	2	1,99	0,39	0,33	0,16	2	2,00	0,46	0,50	-0,05	1	1,00	0,00	0,00	-
	indel2	2	2,00	0,50	0,50	0,04	3	2,70	0,54	0,90	**-0,65**	2	2,00	0,46	0,47	0,03	2	1,99	0,36	0,29	0,24	2	2,00	0,46	0,50	-0,05	1	1,00	0,00	0,00	-
	indel3	2	1,58	0,08	0,08	0,00	2	1,92	0,18	0,20	-0,06	2	2,00	0,48	0,67	-0,36	2	2,00	0,46	0,62	-0,33	2	1,98	0,26	0,30	-0,13	1	1,00	0,00	0,00	-
	indel4	2	2,00	0,41	0,42	0,04	2	1,92	0,18	0,20	-0,06	2	1,99	0,32	0,40	-0,22	2	1,71	0,13	0,14	-0,05	2	1,92	0,18	0,20	-0,06	1	1,00	0,00	0,00	-
	indel5	1	1,00	0,00	0,00	-	2	2,00	0,50	0,70	-0,37	2	1,99	0,32	0,27	0,20	2	1,33	0,05	0,05	0,00	1	1,00	0,00	0,00	-	1	1,00	0,00	0,00	-
	indel6	2	2,00	0,49	0,50	0,02	2	2,00	0,50	0,90	**-0,80**	2	1,99	0,32	0,27	0,20	2	1,98	0,34	0,33	0,03	2	2,00	0,32	0,40	-0,20	1	1,00	0,00	0,00	-
	Mean	**4,0**	**3,38**	**0,50**	**0,49**	**0,08**	**3,6**	**3,29**	**0,49**	**0,58**	**-0,16**	**4,8**	**3,78**	**0,55**	**0,57**	**-0,01**	**4,6**	**3,32**	**0,47**	**0,47**	**0,01**	**3,6**	**3,19**	**0,47**	**0,52**	**-0,06**	**3,4**	**2,36**	**0,35**	**0,37**	**-0,03**
	- Mean SSR	4,6	3,81	0,55	0,53	0,09	4,0	3,60	0,51	0,57	-0,06	5,5	4,25	0,59	0,61	0,00	5,2	3,70	0,51	0,52	0,01	4,0	3,54	0,52	0,57	-0,05	3,9	2,72	0,49	0,51	-0,03
	- Mean Indel	1,8	1,76	0,33	0,33	0,02	2,2	2,09	0,40	0,63	-0,46	2,0	1,99	0,39	0,42	-0,02	2,0	1,84	0,29	0,29	0,01	1,8	1,82	0,28	0,32	-0,08	1,0	1,00	0,00	0,00	-
Mitochondrial compartment	**Locus**	N_h	D_{mt}				N_h	D_{mt}				N_h	D_{mt}				N_h	D_{mt}				N_h	D_{mt}				N_h	D_{mt}			
	MT1	2					1					2					2					1					2				
	MT2	2					1					2					2					2					2				
	MT3	2					1					2					2					2					2				
	MT4	1					1					1					1					1					1				
	MT5	2					1					1					1					2					1				
	mtDNA haplotype	**3**	**0,44**				**1**	**0,00**				**2**	**0,53**				**2**	**0,10**				**2**	**0,20**				**2**	**0,47**			
Plastid compartment	**Locus**	N_h	D_{cp}				N_h	D_{cp}				N_h	D_{cp}				N_h	D_{cp}				N_h	D_{cp}				N_h	D_{cp}			
	CP1	2					2					2					1					2					2				
	CP2	1					1					2					2					1					1				
	CP3	2					2					2					1					2					2				
	CP4	2					2					2					1					1					2				
	CP5	2					2					3					1					3					2				
	CP6	2					2					2					1					2					2				
	CP7	2					2					2					1					2					2				
	CP8	1					1					1					1					2					1				
	CP9	1					1					1					1					2					1				
	CP10	1					2					1					1					2					1				
	cpDNA haplotype	**2**	**0,53**				**2**	**0,36**				**4**	**0,70**				**2**	**0,10**				**3**	**0,38**				**2**	**0,11**			
Cytolasmic compartment		N_h	D_{cp+mt}				N_h	D_{cp+mt}				N_h	D_{cp+mt}				N_h	D_{cp+mt}				N_h	D_{cp+mt}				N_h	D_{cp+mt}			
	Cytoplasmic haplotype	**4**	**0,65**				**2**	**0,36**				**5**	**0,70**				**3**	**0,19**				**3**	**0,38**				**3**	**0,50**			

Table S8, end.

		Moussoulens (15)					St Maurice Navacelles (17)					Prades-Le-Lez (10)					Puycelsi (14)					Sainte-Baume (10)					La Aliseda (7)				
Nuclear compartment	**Locus**	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}	N_a	A_R	H_E	H_O	F_{IS}
- Microsatellite (SSR)	**GAA1**	3	2,72	0,48	0,67	-0,36	4	3,07	0,57	0,47	0,20	2	1,92	0,18	0,20	-0,06	4	3,39	0,60	0,43	0,32	3	2,70	0,45	0,60	-0,30	2	2,00	0,49	0,86	-0,71
	GAA2	2	2,00	0,46	0,47	0,03	3	2,71	0,35	0,35	0,02	3	2,68	0,34	0,40	-0,14	2	2,00	0,44	0,21	0,54	3	2,92	0,54	0,60	-0,06	1	1,00	0,00	0,00	-
	GAA3	3	2,85	0,46	0,47	0,02	4	3,04	0,42	0,53	-0,22	2	2,00	0,42	0,20	0,56	2	1,50	0,07	0,07	0,00	1	1,00	0,00	0,00	-	2	2,00	0,13	0,14	0,00
	GAA4	3	2,83	0,42	0,53	-0,22	8	6,09	0,75	0,76	0,01	4	3,82	0,54	0,40	0,30	5*	4,28	0,69	0,43	**0,41**	4	3,70	0,69	0,60	0,18	4	4,00	0,69	0,71	0,05
	GAA5	3	2,97	0,62	0,60	0,07	3	2,98	0,59	0,53	0,13	2	2,00	0,50	0,80	-0,57	3	2,26	0,20	0,21	-0,05	2	1,98	0,26	0,30	-0,13	1	1,00	0,00	0,00	-
	GAA6	1	1,00	0,00	0,00	-	4	2,88	0,31	0,35	-0,11	1	1,00	0,00	0,00	-	1	1,00	0,00	0,00	-	2	1,92	0,18	0,20	-0,06	1	1,00	0,00	0,00	-
	GAA7	2	1,99	0,32	0,40	-0,22	3	2,89	0,53	0,65	-0,18	2	2,00	0,32	0,40	-0,20	2	2,00	0,41	0,57	-0,37	2	2,00	0,42	0,40	0,10	1	1,00	0,00	0,00	-
	GAA9	7	5,73	0,81	0,80	0,04	6	4,41	0,61	0,59	0,06	5	4,60	0,68	0,80	-0,13	4	3,39	0,56	0,64	-0,12	5	4,02	0,42	0,50	-0,14	5	5,00	0,78	0,57	0,33
	GAA11	4	3,46	0,66	0,60	0,12	3	2,41	0,43	0,59	-0,34	3	2,70	0,40	0,50	-0,22	3	2,99	0,62	0,64	0,00	2	1,70	0,10	0,10	0,00	2	2,00	0,41	0,57	-0,33
	GAA14	6	4,64	0,72	0,73	0,02	11	6,01	0,63	0,71	-0,09	8	6,20	0,74	0,80	-0,04	7	5,72	0,76	0,79	0,01	6	4,72	0,49	0,50	0,03	7	7,00	0,80	0,71	0,18
	GAA16	5	4,38	0,60	0,73	-0,19	5	3,97	0,67	0,82	-0,21	4	3,70	0,67	0,60	0,15	5	3,89	0,65	0,64	0,05	3	2,70	0,49	0,70	-0,40	4	4,00	0,68	0,86	-0,18
	GAA17	5	3,93	0,68	0,73	-0,04	7	5,35	0,78	0,76	0,05	5	4,24	0,49	0,50	0,02	6	4,24	0,55	0,64	-0,14	4	3,92	0,70	0,80	-0,09	5	5,00	0,71	0,57	0,27
	GAA18	9	5,99	0,76	0,80	-0,02	8	5,48	0,77	0,65	0,19	5	4,66	0,73	0,90	-0,18	8	5,76	0,72	0,86	-0,15	4	4,00	0,75	0,90	-0,16	8	8,00	0,77	0,86	-0,04
	GAA19	7	6,08	0,79	0,67	0,19	13	7,92	0,85	0,88	-0,01	8	7,30	0,85	0,80	0,11	14	8,80	0,85	0,86	0,03	3	2,98	0,59	0,70	-0,15	5	5,00	0,73	0,86	-0,09
	GAA20	6	4,87	0,70	0,73	-0,01	8	6,40	0,83	0,88	-0,03	6	5,59	0,79	0,90	-0,09	9	7,26	0,85	0,93	-0,05	5	4,38	0,68	0,70	0,02	6	6,00	0,76	0,71	0,13
	GAA20_B	4	3,45	0,64	0,73	-0,12	3	2,41	0,43	0,35	0,21	2	2,00	0,46	0,70	-0,50	2	1,89	0,19	0,21	-0,08	3	2,70	0,45	0,40	0,15	3	3,00	0,62	0,71	-0,07
	GAA21	7	4,71	0,53	0,60	-0,09	15	8,39	0,84	0,88	-0,03	8	6,56	0,71	0,80	-0,08	5	3,52	0,37	0,43	-0,12	6	4,50	0,43	0,40	0,11	6	6,00	0,79	0,86	-0,01
	GAA22	8	6,73	0,84	0,87	0,01	17*	10,04	0,92	0,76	**0,20**	9	7,34	0,81	0,90	-0,07	12	8,06	0,83	0,79	0,09	8	6,64	0,79	1,00	-0,22	8	8,00	0,85	0,86	0,07
	ATT1	4	3,72	0,69	0,73	-0,03	4	3,38	0,65	0,76	-0,14	2	2,00	0,48	0,20	0,62	4	3,15	0,36	0,36	0,06	3	2,70	0,45	0,60	-0,30	1	1,00	0,00	0,00	-
	ATT2	2	2,00	0,39	0,53	-0,33	2	2,00	0,39	0,29	0,27	2	1,98	0,26	0,30	-0,13	2	2,00	0,48	0,21	0,58	2	2,00	0,46	0,50	-0,05	2	2,00	0,24	0,00	1,00
	ATT3	2	1,47	0,06	0,07	0,00	3	2,94	0,61	0,71	-0,13	2	2,00	0,38	0,50	-0,29	3	2,39	0,25	0,29	-0,10	3	2,70	0,45	0,40	0,15	3	3,00	0,52	0,71	-0,30
	TA1	3	3,18	0,39	0,50	-0,25	3	2,41	0,52	0,41	0,23	2	1,98	0,26	0,10	0,64	3	2,50	0,48	0,50	0,00	3	2,62	0,27	0,30	-0,08	2	2,00	0,46	0,71	-0,50
	ATA1	2	1,47	0,06	0,07	0,00	5	3,81	0,67	0,88	-0,28	3	2,98	0,56	0,70	-0,21	4	3,49	0,64	0,64	0,03	3	2,70	0,45	0,30	0,37	3	3,00	0,62	0,29	**0,59**
- Indel	**indel1**	2	2,00	0,39	0,53	-0,33	2	1,99	0,33	0,41	-0,23	2	2,00	0,50	0,50	0,04	2	2,00	0,50	0,21	**0,59**	2	1,70	0,10	0,10	0,00	2	2,00	0,24	0,29	-0,09
	indel2	3	2,80	0,38	0,47	-0,18	2	1,97	0,29	0,35	-0,19	2	2,00	0,50	0,40	0,25	2	2,00	0,50	0,21	**0,59**	2	1,70	0,10	0,10	0,00	2	2,00	0,13	0,14	0,00
	indel3	2	2,71	0,34	0,29	0,19	2	1,81	0,16	0,18	-0,07	2	2,00	0,50	0,70	-0,37	2	2,00	0,50	0,43	0,18	2	2,00	0,42	0,60	-0,39	1	1,00	0,00	0,00	-
	indel4	2	2,72	0,48	0,64	-0,32	2	2,00	0,47	0,41	0,16	2	2,00	0,38	0,50	-0,29	2	2,00	0,41	0,29	0,33	2	2,00	0,48	0,80	-0,64	1	1,00	0,00	0,00	-
	indel5	2	1,99	0,36	0,20	0,47	2	2,00	0,42	0,47	-0,10	2	1,92	0,18	0,20	-0,06	2	2,00	0,50	0,43	0,18	2	1,92	0,18	0,20	-0,06	2	2,00	0,41	0,57	-0,33
	indel6	2	1,99	0,32	0,40	-0,22	2	2,00	0,50	0,47	0,09	2	1,92	0,18	0,20	-0,06	2	2,00	0,46	0,29	0,41	2	1,70	0,10	0,10	0,00	2	2,00	0,46	0,43	0,14
	Mean	**3,8**	**3,32**	**0,50**	**0,54**	**-0,06**	**5,3**	**3,89**	**0,56**	**0,58**	**-0,02**	**3,5**	**3,21**	**0,47**	**0,51**	**-0,03**	**4,2**	**3,36**	**0,50**	**0,46**	**0,11**	**3,2**	**2,84**	**0,41**	**0,46**	**-0,07**	**3,2**	**3,17**	**0,42**	**0,45**	**0,00**
	- Mean SSR	4,3	3,57	0,55	0,59	-0,06	6,2	4,39	0,61	0,63	-0,01	3,9	3,53	0,50	0,54	-0,02	4,8	3,72	0,53	0,52	0,04	3,5	3,10	0,45	0,50	-0,04	3,6	3,57	0,61	0,64	0,02
	- Mean Indel	2,2	2,37	0,38	0,42	-0,07	2,0	1,96	0,36	0,38	-0,06	2,0	1,97	0,37	0,42	-0,08	2,0	2,00	0,48	0,31	0,38	2,0	1,84	0,23	0,32	-0,18	1,7	1,67	0,21	0,24	-0,05
Mitochondrial compartment	**Locus**	N_h		D_{mt}			N_h		D_{mt}			N_h		D_{mt}			N_h		D_{mt}			N_h		D_{mt}			N_h		D_{mt}		
	MT1	2					2					1					2					1					2				
	MT2	2					2					1					2					1					1				
	MT3	2					2					1					1					2					1				
	MT4	1					1					1					1					1					1				
	MT5	1					2					1					1					1					2				
	mtDNA haplotype	**2**		**0,75**			**5**		**0,76**			**1**		**0,00**			**2**		**0,54**			**2**		**0,20**			**3**		**0,76**		
Plastid compartment	**Locus**	N_h		D_{cp}			N_h		D_{cp}			N_h		D_{cp}			N_h		D_{cp}			N_h		D_{cp}			N_h		D_{cp}		
	CP1	2					2					2					2					2					2				
	CP2	1					1					2					1					1					1				
	CP3	2					2					2					2					2					2				
	CP4	2					2					2					2					2					2				
	CP5	2					3					3					2					2					3				
	CP6	2					2					2					2					2					2				
	CP7	2					2					2					2					2					2				
	CP8	1					1					1					1					1					1				
	CP9	1					1					1					1					1					1				
	CP10	1					1					1					1					1					1				
	cpDNA haplotype	**2**		**0,75**			**3**		**0,63**			**3**		**0,69**			**2**		**0,44**			**2**		**0,20**			**3**		**0,76**		
Cytolasmic compartment		N_h		D_{cp+mt}			N_h		D_{cp+mt}			N_h		D_{cp+mt}			N_h		D_{cp+mt}			N_h		D_{cp+mt}			N_h		D_{cp+mt}		
	Cytoplasmic haplotype	**3**		**0,83**			**8**		**0,91**			**3**		**0,69**			**4**		**0,74**			**2**		**0,20**			**3**		**0,76**		

Proof

Table S9. F_{ST} values calculated between each pair of populations. The parameters were calculated using GENETIX (Belkhir *et al.,* 2004). Values above the diagonal correspond to values obtained with nuclear loci, values below to those obtained with cytoplasmic data (considering chloroplast and mitochondrial data as two different loci). ^{ns} Values not significantly different from 0 at the 5% threshold, estimated on a total of 1000 permutations. All other values are significantly different from 0.

Population	Pop. Code	ALB	BAGE	BIDO	CEFE	CELL	EGUI	MOUL	MOUS	SMN	PLL	PUYC	BAUM	TURB	ALIS
Amelie-Les-Bains	ALB		0,220	0,212	0,194	0,244	0,204	0,433	0,265	0,169	0,269	0,230	0,322	0,260	0,318
Bages	BAGE	0,672		0,100	0,078	0,112	0,146	0,260	0,105	0,086	0,115	0,124	0,147	0,208	0,239
Bidon	BIDO	0,880	0,143^{ns}		0,084	0,126	0,161	0,246	0,149	0,106	0,150	0,155	0,180	0,209	0,298
CEFE	CEFE	0,563	0,179	0,384		0,047	0,107	0,258	0,120	0,070	0,071	0,106	0,105	0,149	0,258
Celleneuve	CELL	0,923	0,664	0,874	0,454		0,146	0,294	0,138	0,114	0,082	0,111	0,137	0,194	0,306
Eguilles	EGUI	0,808	0,579	0,764	0,394	0,684		0,311	0,195	0,155	0,174	0,179	0,220	0,238	0,324
Moulis	MOUL	0,763	0,343	0,442	0,387	0,680	0,593		0,292	0,303	0,227	0,323	0,366	0,445	0,419
Moussoulens	MOUS	0,688	0,431	0,576	0,384	0,825	0,718	0,632		0,174	0,147	0,121	0,214	0,292	0,232
St-Maurice-Navacelles	SMN	0,416	0,136	0,299	0,210	0,575	0,434	0,327	0,272		0,126	0,139	0,158	0,108	0,209
Prades-le-Lez	PLL	0,734	0,284	0,478	0,149	0,795	0,680	0,629	0,333	0,307		0,113	0,159	0,255	0,311
Puycelsi	PUYC	0,659	0,106^{ns}	0,259	0,284	0,693	0,593	0,350	0,503	0,165	0,413		0,158	0,223	0,242
Sainte-Baume	BAUM	0,858	0,499	0,705	0,409	0,770	0,589	0,117^{ns}	0,728	0,327	0,724	0,451		0,265	0,341
La Turbie	TURB	1,000	0,628	0,859	0,530	0,916	0,639	0,749	0,795	0,472	0,736	0,619	0,842		0,310
La Aliseda	ALIS	0,497	0,107^{ns}	0,410	0,177	0,612	0,481	0,464	0,383	-0,022^{ns}	0,308	0,207	0,478	0,485	

Table S10. Results of the assignment test comparing nuclear SSR genotypes of individuals of the CEFE collection to nuclear SSR genotypes of natural populations (with at least ten sampled individuals). We first considered the 15 genotypes initially used in our population genetic study, and then, to increase the power of this analysis, we considered 125 genotypes of the CEFE collection (data not shown). The analysis was performed with GENECLASS2 (Piry *et al.,* 2004); in both cases, 27% of individuals (4/15, 34/125) were assigned to at least one putative population (all in Hérault, at maximum 30 km from Montpellier). This result is consistent with our expectations, since the population was initially funded with individuals from different localities around Montpellier, such as Causse-de-la-Selle near St-Maurice-de-Navacelles (J.D. Thompson, pers. com.). An arbitrary threshold probability value of 0.05 or greater was applied to determine the origin of CEFE individuals.

PDF Proof

Population	**Percent of CEFE individuals assigned (15 genets)**	**Percent of CEFE individuals assigned (125 genets)**
Bages	0	0
Bidon	0	0
Celleneuve	13.3	5.6
Eguilles	0	0
Moulis	0	0
Moussoulens	0	0
St-Maurice-de-Navacelles	20.0	24.0
Puycelsi	0	0
Prades-le-Lez	0	2.4
Sainte-Baume	0	0

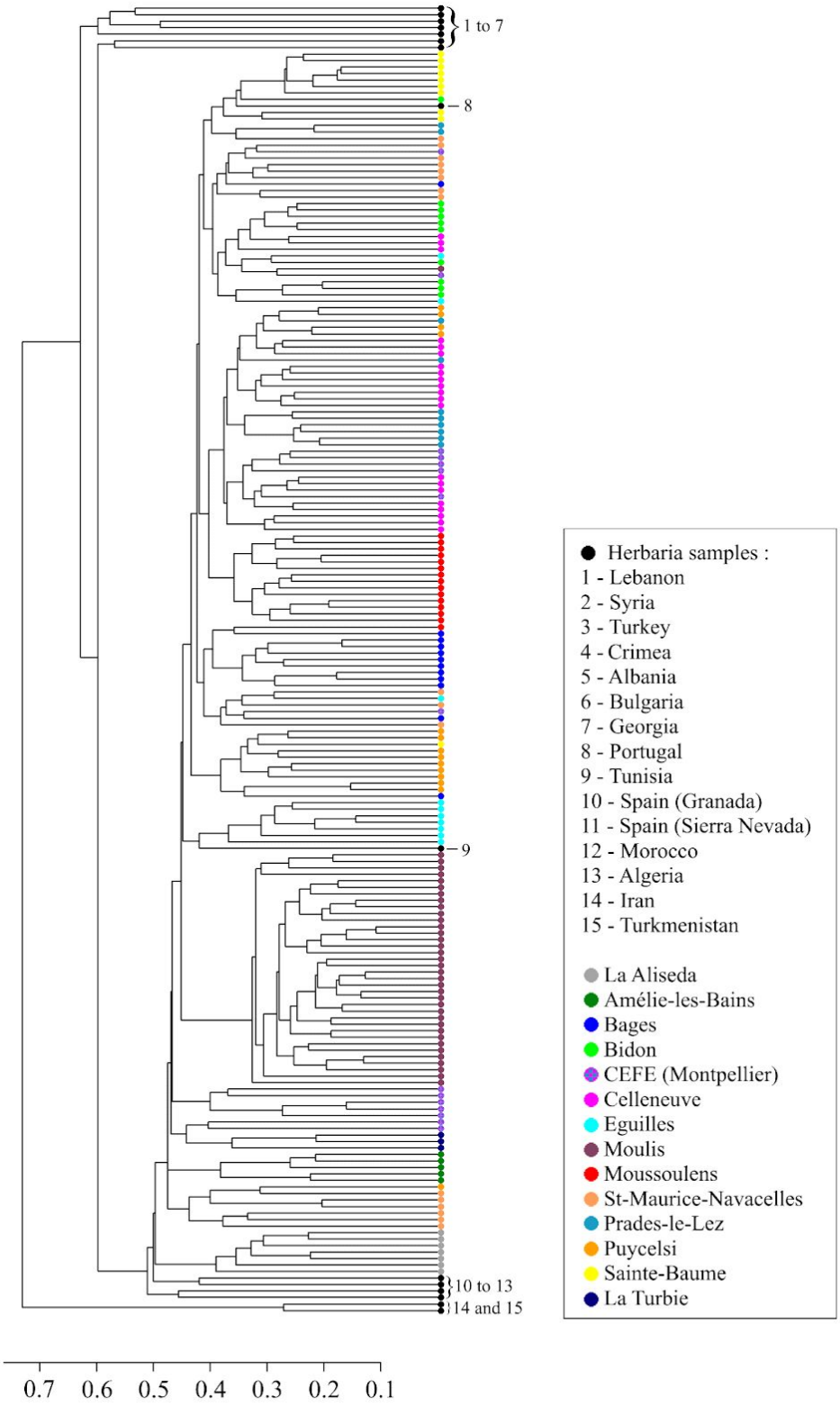

Figure S1. Dendrogram representing genetic similarity between all individuals based on genetic distances of Bruvo *et al.* (2004) and reconstructed with the unweighted pair group method with arithmetic mean (UPGMA) using *Poppr* (Kamvar *et al.*, 2014). French individuals are grouped in the same cluster with the individuals from Tunisia and Portugal. Individuals from the same population also tend to cluster together (e.g. 'Moulis', 'La Aliseda').

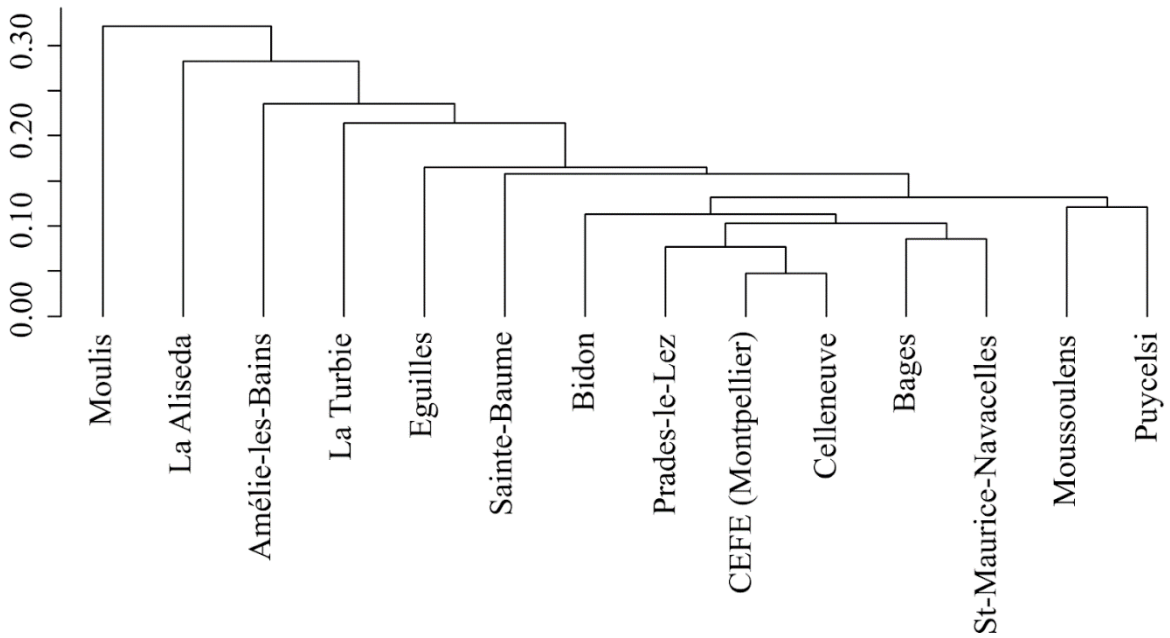

Figure S2. Dendrogram representing genetic similarity between populations based on pairwise F_{ST} estimated from nuclear data and reconstructed on the unweighted pair group method with arithmetic mean (UPGMA) with P*oppr* (Kamvar *et al.*, 2014). With the exception of the 'Moulis' population, geographically close populations tend to cluster together in this dendrogram (e.g. 'Prades-le-Lez', 'CEFE' and 'Celleneuve').

DEFproof

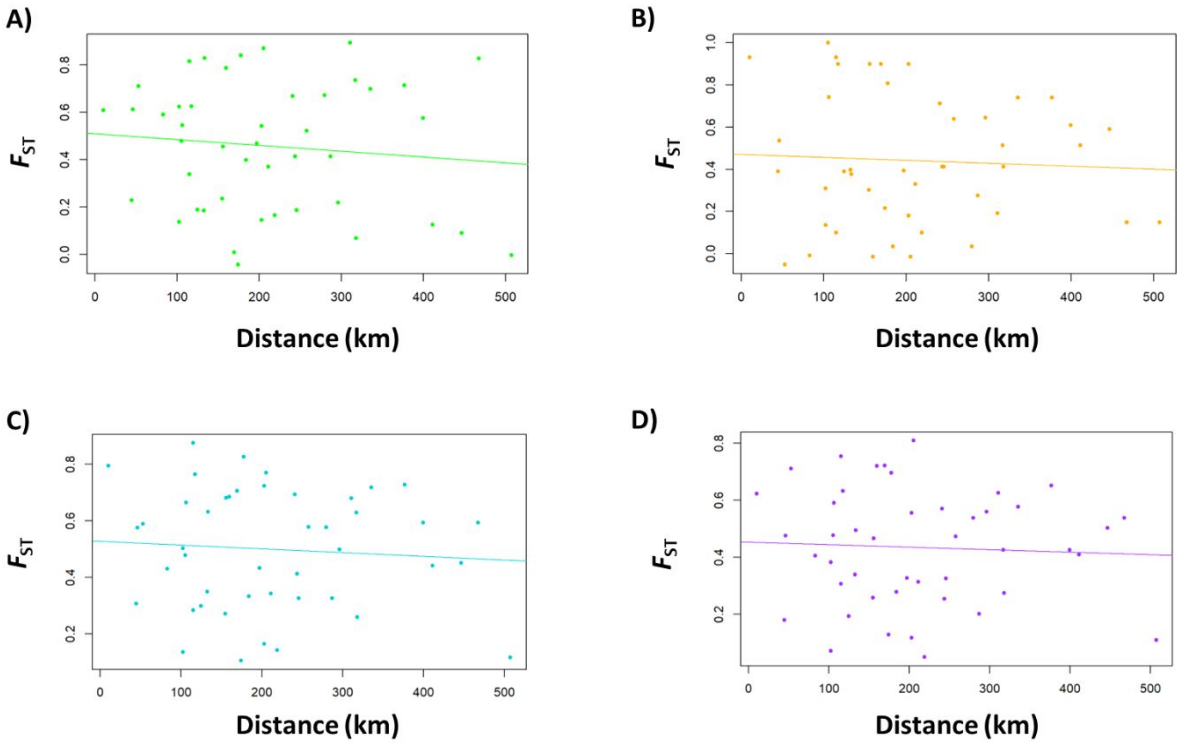

Figure S3. Cytoplasmic genetic differentiation between populations as a function of geographical distance according to different F_{ST} estimation methods: **(A)** with chloroplast data alone, **(B)** with mitochondrial data alone, **(C)** with chloroplast and mitochondrial data considered as two independent cytoplasmic loci, and **(D)** by combining chloroplast and mitochondrial information as a single locus for defining cytoplasmic haplotypes. Tests of Mantel (1967) were done with 999 permutations using the R package *ade4* (Chessel *et al.*, 2004). Genetic and geographical distances between population pairs do not show any significant relationship (Mantel test, r = 0.005, -0.110, -0.009, and -0.064, respectively for A, B, C and D; *p*-value > 0.05) regardless of how the F_{ST} values are estimated.

UF Proof

References

Belkhir K, Borsa P, Chikhi L, Raufaste N, Bonhomme F. 2004. GENETIX 4.05, logiciel sous Windows TM pour la génétique des populations. Laboratoire Génome, Populations, Interactions, CNRS UMR 5000, Université de Montpellier II, Montpellier (France).

Besnard G, Hernández P, Khadari B, Dorado G, Savolainen V. 2011. Genomic profiling of plastid DNA variation in the Mediterranean olive tree. *BMC Plant Biology* **11:** 80.

Bruvo R, Michiels NK, D'souza TG, Schulenburg H. 2004. A simple method for the calculation of microsatellite genotype distances irrespective of ploidy level. *Molecular Ecology* **13:** 2101–2106.

Chessel D, Dufour A, Thioulouse J. 2004. The ade4 package - I: One-table methods. *R News* **4:** 5–10.

Goudet J. 2005. HIERFSTAT, a package for R to compute and test hierarchical *F*-statistics. *Molecular Ecology Notes* **5:** 184–186.

Gryta H, Van de Paer C, Manzi S, Holota H, Roy M, Besnard G. 2017. Genome skimming and plastid microsatellite profiling of alder trees (*Alnus* spp., Betulaceae): Phylogenetic and phylogeographical prospects. *Tree Genetics & Genomes* **13:** 118.

Kamvar ZN, Tabima JF, Grünwald NJ. 2014. *Poppr*: An R package for genetic analysis of populations with clonal, partially clonal, and/or sexual reproduction. *PeerJ* **2:** e281.

Lewontin RC. 1964. The interaction of selection and linkage. I. General considerations; heterotic models. *Genetics* **49:** 49–67.

Mantel N. 1967. The detection of disease clustering and a generalized regression approach. *Cancer Research* **27:** 209–220.

Marshall TC, Slate J, Kruuk LE, Pemberton JM. 1998. Statistical confidence for likelihood-based paternity inference in natural populations. *Molecular Ecology* **7:** 639–655.

Piry S, Alapetite A, Cornuet JM, Paetkau D, Baudouin L, Estoup A. 2004.GENECLASS2: A software for genetic assignment and first-generation migrant detection. *Journal of Heredity* **95:** 536–539.

Van Oosterhout C, Hutchinson W, Willis D, Shipley P. 2004. MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes* **4:** 535–538.

For Proof

Table S1. Plant sampling and complete genotyping dataset. For each sample, we give their code, GPS coordinates (Lat., Long.), date of collect, floral morph (when available), and genetic profiles for 29 nuclear loci, five mitochondrial DNA loci and ten chloroplast DNA loci.
For both mitochondrial and chloroplast genomes, haplotypes were defined (and numbered) by combining the information on their respective loci. Genet duplicates (= identical or nearly identical ramets) are given; ramets that were further excluded for analyses are indicated.

Individual	Lat.	Long.	Date of collect	Floral morph	Clone (excluded ramet)	GAA1	GAA2	GAA3	GAA4
Amelie_les_Bains_1	42.47787	2.66639	9/5/21	Longistyle		166:169	204:207	214:217	250:250
Amelie_les_Bains_2	42.47786	2.66640	27/3/22	Longistyle	= Amélie_les_Bains_1	166:169	204:207	214:217	250:250
Amelie_les_Bains_3	42.47786	2.66636	27/3/22	Brévistyle		166:172	204:207	214:214	250:268
Amelie_les_Bains_4	42.47787	2.66635	27/3/22	Longistyle	= Amélie_les_Bains_1	166:169	204:207	214:217	250:250
Amelie_les_Bains_5	42.47791	2.66599	27/3/22	Brévistyle		166:172	204:207	214:214	250:265
Amelie_les_Bains_6	42.47774	2.66643	27/3/22	Brévistyle		172:172	204:204	214:214	250:268
Amelie_les_Bains_7	42.47787	2.66634	27/3/22	Longistyle	= Amélie_les_Bains_1	166:169	204:207	214:217	250:250
Amelie_les_Bains_8	42.47788	2.66638	27/3/22	Longistyle	= Amélie_les_Bains_1	166:169	204:207	214:217	250:250
Amelie_les_Bains_9	42.47788	2.66628	8/5/22	Longistyle		166:172	204:204	214:217	250:268
Bages_1	43.11844	2.98721	30/03/22	Brévistyle		169:169	204:204	214:214	247:250
Bages_2	43.11845	2.98721	30/03/22	Brévistyle		169:169	204:204	214:214	247:268
Bages_3	43.11876	2.98747	30/03/22	Brévistyle		169:169	204:213	214:214	250:250
Bages_4	43.13280	2.98590	15/04/21	Brévistyle		169:169	204:204	214:217	253:271
Bages_5	43.13362	2.98506	21/04/22	Brévistyle		169:172	204:204	214:214	250:253
Bages_6	43.13357	2.98489	21/04/22	Brévistyle		169:172	204:204	217:217	253:283
Bages_7	43.13332	2.98456	21/04/22	Longistyle		172:172	207:213	214:217	253:253
Bages_8	43.13330	2.98447	21/04/22	Brévistyle		169:172	204:207	214:214	253:268
Bages_9	43.13329	2.98447	21/04/22	Longistyle		169:172	207:207	214:214	253:253
Bages_10	43.13325	2.98431	21/04/22	Brévistyle		169:172	213:213	214:214	253:268
Bages_11	43.13324	2.98432	21/04/22	Longistyle		169:172	204:213	214:214	253:253
Bages_12	43.11874	2.98747	21/04/22	Longistyle		169:169	204:213	214:217	250:250
Bidon_1	44.36565	4.53303	5/14/2021	Longistyle		169:172	204:213	214:217	253:268
Bidon_2	44.36674	4.52774	5/14/2021	Longistyle		169:169	204:204	214:214	268:280
Bidon_3	44.36571	4.53245	11/6/2021	Brévistyle		169:172	204:207	214:214	268:280
Bidon_4	44.36571	4.53242	11/6/2021	Brévistyle		169:169	204:204	214:217	253:268
Bidon_5	44.37116	4.53910	11/6/2021	Brévistyle		166:169	204:207	214:217	253:253
Bidon_6	44.37131	4.53931	11/6/2021	Longistyle		172:172	207:213	214:214	253:253
Bidon_7	44.37131	4.53933	11/6/2021	Longistyle		172:172	207:207	214:214	253:268
Bidon_8	44.37131	4.53937	11/6/2021	Brévistyle		166:172	204:204	214:214	268:298
Bidon_9	44.37134	4.53941	11/6/2021	Longistyle		172:172	204:207	214:214	253:268
Bidon_10	44.36568	4.53187	11/6/2021	Longistyle		163:169	204:207	217:220	253:280
CEFE_L0	46.63855	3.86467	15/04/15	Longistyle		169:169	204:213	214:214	253:268
CEFE_L1	43.63870	3.86174	29/04/21	Longistyle		169:172	204:204	214:220	253:253
CEFE_L1a	43.63871	3.86175	29/04/21	Longistyle		169:169	204:204	214:220	253:283
CEFE_L2	43.63861	3.86179	29/04/21	Longistyle		169:169	204:204	211:214	262:268
CEFE_L3	43.63856	3.86177	29/04/21	Longistyle		169:169	204:207	214:214	268:286
CEFE_L4	43.63847	3.86177	29/04/21	Longistyle		169:169	204:204	214:220	268:307
CEFE_L5	43.63831	3.86177	29/04/21	Longistyle		166:169	204:204	211:214	268:280
CEFE_L6	43.63830	3.86173	29/04/21	Longistyle		163:169	204:204	214:214	253:253
CEFE_S1	43.63866	3.86178	29/04/21	Longistyle		172:172	204:204	214:220	253:253
CEFE_S1B	43.63865	3.86178	29/04/21	Brévistyle		169:172	204:204	211:214	253:298
CEFE_S2	43.63836	3.86178	29/04/21	Brévistyle		163:169	204:204	211:214	253:268
CEFE_S3	43.63832	3.86173	29/04/21	Brévistyle		169:169	204:204	211:214	253:268
CEFE_S4	43.63828	3.86178	29/04/21	Brévistyle		169:172	204:204	214:220	253:268
CEFE_S5	43.63868	3.86174	29/04/21	Brévistyle		172:172	204:213	214:214	253:253
CEFE_S6	43.63831	3.86178	29/04/21	Brévistyle		169:169	204:204	214:214	253:253
Celleneuve_L1	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	211:214	253:292
Celleneuve_L2	*43.61100*	*3.82100*	May-20	Longistyle		169:172	204:204	214:214	268:292
Celleneuve_L3	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	253:268
Celleneuve_L4	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	253:268
Celleneuve_L5	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	253:268
Celleneuve_L6	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	253:292
Celleneuve_L7	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	253:253
Celleneuve_L8	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	211:214	253:292
Celleneuve_L9	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	268:292
Celleneuve_L10	*43.61100*	*3.82100*	May-20	Longistyle		169:169	204:204	214:214	268:268
Celleneuve_L11	*43.61100*	*3.82100*	May-20	Longistyle		169:172	204:213	214:214	253:268
Celleneuve_S1	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:204	214:214	253:253
Celleneuve_S2	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:207	214:214	253:268
Celleneuve_S3	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:207	214:214	268:268
Celleneuve_S4	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:204	214:214	253:268
Celleneuve_S5	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:207	214:214	253:280
Celleneuve_S6	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:204	214:214	253:253
Celleneuve_S7	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:207	214:214	268:292
Celleneuve_S8	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:207	211:214	268:274
Celleneuve_S9	*43.61100*	*3.82100*	May-20	Brévistyle		169:169	204:204	211:214	253:268
Celleneuve_S10	*43.61100*	*3.82100*	May-20	Brévistyle		169:172	204:204	214:214	253:253
Eguilles_1	*43.60052*	*5.26694*	16/05/21	Brévistyle		166:166	204:207	214:214	265:265
Eguilles_2	*43.60052*	*5.26694*	16/05/21	Brévistyle		166:172	204:213	214:214	265:268
Eguilles_3	*43.60052*	*5.26694*	16/05/21	Longistyle		166:169	204:213	214:214	265:268
Eguilles_4	*43.60052*	*5.26694*	16/05/21	Brévistyle		166:172	204:207	214:214	265:268
Eguilles_5	*43.60052*	*5.26694*	16/05/21	Longistyle		172:172	204:207	214:214	265:265
Eguilles_6	*43.60052*	*5.26694*	16/05/21	Brévistyle		172:172	207:207	214:214	265:265
Eguilles_7	*43.60052*	*5.26694*	16/05/21	Longistyle		163:172	204:213	214:214	253:265
Eguilles_8	*43.60052*	*5.26694*	16/05/21	Brévistyle		166:166	204:213	214:214	265:265
Eguilles_9	*43.60052*	*5.26694*	16/05/21	Longistyle		166:172	204:207	214:214	265:265
Eguilles_10	*43.60052*	*5.26694*	16/05/21	Longistyle		166:166	204:204	214:214	265:265
Moulis_AB1S	42.98000	1.08440	02/05/21	Brévistyle		163:169	204:207	211:214	262:268
Moulis_AB2S	42.98001	1.08446	02/05/21	Brévistyle		169:169	204:207	211:211	268:268
Moulis_BA1L	42.98002	1.08447	02/05/21	Longistyle		163:169	204:207	214:214	262:268
Moulis_BA2L	42.98004	1.08446	02/05/21	Longistyle		169:172	204:207	211:214	268:268
Moulis_1A	*42.98046*	*1.08409*	Mar-21	Brévistyle		163:172	204:207	211:214	262:262
Moulis_1B	42.98046	1.08409	02/05/21	Brévistyle		169:169	204:204	211:214	253:268
Moulis_2A	*42.98045*	*1.08403*	Mar-21	Brévistyle		169:169	204:204	211:214	253:268
Moulis_2B	*42.98046*	*1.08402*	Mar-21	Brévistyle		169:169	204:207	214:214	268:268
Moulis_2C	42.98046	1.08402	02/05/21	Brévistyle		154:172	204:207	211:214	262:268
Moulis_3A_3C	42.98050	1.08409	02/05/21	Brévistyle		163:169	204:204	214:214	262:268
Moulis_3B	*42.98051*	*1.08409*	Mar-21	Longistyle		169:169	204:204	211:211	253:268
Moulis_4L	42.97840	1.08206	02/05/21	Longistyle		169:169	204:204	211:214	268:268
Moulis_5L_6L	42.97841	1.08204	02/05/21	Longistyle		169:169	204:207	211:211	268:268
Moulis_7L	42.97843	1.08204	02/05/21	Longistyle		163:169	204:207	214:214	268:268
Moulis_8L_9L_13L_32	42.97842	1.08203	02/05/21	Longistyle		163:169	204:207	214:214	262:268
Moulis_10S_12S	42.97841	1.08202	02/05/21	Brévistyle		163:163	207:207	211:214	262:268

Individual	GAA5	GAA6	GAA7	GAA9	GAA11	GAA14	GAA16	GAA17	GAA18	GAA19	GAA20_B	GAA20	GAA21	GAA22	ATT1	ATT2	ATT3	ATA-1	TA-1	indel_1	indel_2	Indel_3
Amelie_les_Bains_1	163:163	104:104	238:241	265:265	126:126	137:137	210:210	248:248	175:181	212:230	106:106	118:127	207:294	137:137	136:136	188:190	154:154	229:229	213:221	136:136	275:279	121:123
Amelie_les_Bains_2	163:163	104:104	238:241	265:265	126:126	137:137	210:210	248:248	175:181	212:230	106:106	118:127	207:297	137:137	136:136	188:190	154:154	229:229	213:221	136:136	275:279	121:123
Amelie_les_Bains_3	163:163	104:104	241:241	265:271	126:126	137:137	201:210	248:251	175:181	212:221	106:106	115:127	207:225	137:152	136:156	188:190	151:154	229:229	221:221	136:161	275:279	121:121
Amelie_les_Bains_4	163:163	104:104	238:241	265:265	126:126	137:137	210:210	248:248	175:181	212:230	106:106	118:127	207:294	137:137	136:136	188:190	154:154	229:229	213:221	136:136	275:279	121:123
Amelie_les_Bains_5	170:170	104:104	241:241	265:274	126:126	137:140	201:201	248:248	181:181	191:191	106:106	127:136	300:303	137:152	156:156	188:188	151:154	229:232	221:221	161:161	275:275	121:121
Amelie_les_Bains_6	170:170	104:104	241:241	274:274	126:126	119:140	201:201	248:257	181:181	212:239	106:106	136:136	306:351	140:152	156:156	188:188	151:151	229:232	221:221	161:161	275:275	121:121
Amelie_les_Bains_7	163:163	104:104	238:241	265:265	126:126	137:137	210:210	248:248	175:181	212:230	106:106	118:127	207:294	137:137	136:136	188:190	154:154	229:229	213:221	136:136	275:279	121:123
Amelie_les_Bains_8	163:163	104:104	238:241	265:265	126:126	137:137	210:210	248:248	175:181	212:230	106:106	118:127	207:300	137:137	136:136	188:190	154:154	229:229	213:221	136:136	275:279	121:123
Amelie_les_Bains_9	163:163	104:104	238:238	265:274	126:126	137:137	189:210	248:248	175:175	224:224	106:106	127:136	294:294	137:251	133:154	188:190	154:154	229:229	221:221	136:161	275:279	123:123
Bages_1	163:163	104:146	241:241	265:274	123:126	137:152	162:198	236:242	175:190	194:248	103:106	115:115	210:210	137:209	154:156	188:190	151:151	229:232	213:221	136:161	279:285	123:123
Bages_2	163:163	104:104	238:241	259:274	126:129	137:137	171:198	236:236	190:199	239:272	103:103	115:127	210:306	170:209	156:156	188:190	151:157	229:232	213:221	136:161	279:285	123:123
Bages_3	163:163	104:146	241:241	265:274	123:123	119:152	162:162	236:251	199:199	194:218	103:106	115:124	213:273	137:212	133:156	188:190	151:151	229:232	221:221	136:161	279:285	123:123
Bages_4	163:163	104:104	238:238	265:274	123:126	137:164	198:210	215:257	193:202	227:227	103:106	124:124	210:210	179:200	133:156	188:188	151:151	229:235	213:213	136:161	279:285	121:123
Bages_5	163:163	104:104	241:241	265:271	126:126	119:164	162:198	236:251	181:199	194:233	106:106	124:136	210:231	137:206	136:156	190:190	151:151	229:232	221:223	161:161	285:285	123:123
Bages_6	165:170	104:104	241:241	265:274	123:126	137:140	162:162	236:236	190:196	239:239	103:106	103:136	210:222	170:191	156:156	190:190	151:151	232:232	221:221	136:136	279:279	123:123
Bages_7	163:170	104:104	241:241	259:265	126:126	119:143	165:198	236:251	175:193	194:194	103:103	124:136	210:237	137:179	136:156	190:190	151:151	229:229	213:213	161:161	285:285	123:123
Bages_8	163:163	104:146	241:241	265:265	126:126	137:164	198:198	236:242	175:181	194:209	103:106	103:136	213:288	137:179	133:156	188:190	151:151	229:229	223:223	136:161	279:285	123:123
Bages_9	163:163	104:146	241:241	265:265	126:126	119:164	162:198	236:242	181:190	194:209	103:106	103:115	213:288	179:179	156:156	190:190	151:151	229:229	223:223	161:161	285:285	123:123
Bages_10	163:163	104:104	241:241	265:265	126:126	119:119	198:198	236:236	193:193	212:239	103:103	103:136	210:210	35(188):2(	133:133	188:188	151:151	229:229	213:223	136:136	279:279	123:123
Bages_11	163:163	104:146	241:241	265:265	126:126	119:137	162:171	236:251	190:199	194:239	103:103	103:139	213:216	188:194	136:156	188:190	151:151	226:226	221:221	136:161	279:285	123:123
Bages_12	163:163	104:146	241:241	265:265	123:126	119:137	162:162	215:251	196:199	194:203	103:106	118:124	210:276	137:137	133:156	190:190	151:151	229:232	221:221	136:136	279:279	123:123
Bidon_1	163:163	104:143	238:241	259:265	126:126	137:146	162:162	236:251	190:193	224:251	106:106	115:133	210:228	152:179	133:156	188:190	151:151	229:229	213:213	136:161	279:285	123:123
Bidon_2	163:163	104:104	238:238	259:259	126:126	134:158	162:198	251:251	193:199	248:251	106:106	115:139	225:228	179:188	133:154	188:190	151:151	229:232	221:221	136:161	279:285	123:123
Bidon_3	163:163	104:104	238:241	265:277	126:126	152:158	162:198	251:251	175:199	230:251	106:106	115:124	210:228	164:179	133:133	190:190	151:157	229:232	213:221	136:161	279:285	123:123
Bidon_4	163:170	104:104	238:238	259:277	126:126	137:161	153:162	236:251	190:199	248:251	106:106	115:142	210:210	152:179	133:156	190:190	151:157	229:229	213:221	136:136	279:279	123:123
Bidon_5	163:170	104:143	235:241	277:280	126:126	137:137	162:198	251:251	190:199	230:254	106:106	115:115	210:210	149:188	154:156	190:190	151:151	229:232	221:223	136:161	275:279	121:123
Bidon_6	163:163	104:104	238:238	265:274	126:126	149:152	162:210	251:254	166:166	245:251	106:106	124:124	210:213	188:191	133:156	190:190	151:157	229:229	221:221	136:161	279:285	121:123
Bidon_7	163:163	104:104	238:238	265:265	126:126	137:146	162:198	251:254	166:193	245:245	106:106	124:127	210:210	170:185	133:156	190:190	151:157	229:232	213:221	136:161	279:285	123:123
Bidon_8	163:165	104:104	241:241	274:280	126:126	152:158	162:201	251:251	190:193	206:236	106:106	118:127	210:210	158:182	133:156	188:190	151:157	229:232	213:213	136:161	279:285	123:123
Bidon_9	163:163	104:104	235:238	265:277	126:126	122:137	162:198	236:251	166:190	245:254	106:106	115:127	210:210	164:170	133:154	190:190	151:151	232:232	213:213	136:161	279:285	123:123
Bidon_10	163:163	104:104	238:238	259:265	126:126	158:161	162:198	236:251	190:193	242:254	106:106	115:115	210:225	152:179	133:156	190:190	151:151	229:232	221:221	136:161	279:285	123:123
CEFE_L0	170:170	104:143	241:244	274:277	126:126	137:152	168:198	248:251	196:202	221:251	103:106	142:142	270:288	143:200	156:156	188:188	151:157	226:235	221:221	161:161	285:285	123:123
CEFE_L1	163:170	104:143	241:244	277:277	126:126	134:149	162:168	236:251	190:196	212:224	106:106	121:136	210:285	170:227	156:156	190:190	148:151	226:232	213:221	136:161	279:285	123:123
CEFE_L1a	163:170	104:143	241:244	277:277	123:126	134:149	162:162	236:236	175:190	212:227	106:106	121:139	210:285	170:230	156:156	190:190	151:157	226:232	221:221	136:136	279:279	121:123
CEFE_L2	163:163	104:143	235:241	274:274	126:126	137:137	162:198	251:251	196:196	233:239	106:106	115:136	210:210	161:191	136:136	190:190	151:157	229:232	213:221	161:161	285:285	121:123
CEFE_L3	163:163	104:104	241:241	265:274	126:126	152:155	162:162	236:236	193:202	215:221	106:106	121:136	210:210	182:212	136:156	190:190	151:151	229:232	213:221	136:161	279:285	121:123
CEFE_L4	163:170	104:143	235:241	259:277	126:126	152:155	162:162	239:254	193:199	236:284	106:106	136:142	255:288	188:200	136:156	190:190	157:157	232:232	221:221	136:161	279:285	121:121
CEFE_L5	163:170	104:104	235:241	265:277	126:126	140:140	198:198	215:239	190:199	218:257	106:106	115:142	204:294	188:227	136:136	188:190	154:157	229:229	213:221	161:161	285:285	123:123
CEFE_L6	163:163	104:143	235:241	277:277	126:126	149:152	162:207	215:254	190:202	221:257	103:109	121:139	288:288	167:200	156:156	188:188	148:154	226:235	221:221	136:161	279:285	121:123
CEFE_S1	163:170	104:104	238:241	259:274	123:126	140:155	162:165	239:251	190:202	215:251	103:106	112:115	210:288	179:200	136:156	190:190	151:157	229:232	221:221	136:161	279:285	121:123
CEFE_S1B	163:170	104:104	238:241	256:265	126:126	137:140	162:207	236:242	181:199	191:245	103:106	112:142	210:222	158:182	136:156	188:188	151:151	229:235	213:221	161:161	285:285	121:123
CEFE_S2	163:170	104:104	241:244	259:280	126:126	119:134	162:162	236:251	193:202	221:239	103:103	118:118	210:210	182:188	156:156	190:190	151:157	229:235	213:221	136:136	279:279	121:123
CEFE_S3	163:163	104:143	241:241	259:265	126:126	152:152	162:198	236:251	175:199	221:251	103:106	115:142	210:216	176:227	156:156	190:190	151:157	229:235	213:221	161:161	285:285	121:123
CEFE_S4	163:163	104:104	241:244	274:280	126:126	152:155	162:168	236:251	196:202	212:221	106:106	115:121	210:288	173:185	156:156	188:190	151:151	229:235	221:221	161:161	285:285	121:123
CEFE_S5	163:170	104:143	241:241	277:277	123:126	131:155	162:198	236:236	175:199	206:212	106:106	115:139	210:285	179:227	156:156	188:188	151:151	232:232	221:221	136:161	279:285	123:123
CEFE_S6	170:170	104:104	241:244	277:280	126:126	134:152	162:162	236:251	199:202	221:236	106:106	118:136	210:291	179:203	156:156	190:190	151:151	229:235	213:221	136:161	279:285	121:123
Celleneuve_L1	163:170	104:104	238:241	265:277	126:126	152:158	162:162	251:251	193:196	203:221	103:106	115:118	210:249	179:188	136:156	190:190	151:151	232:232	221:221	161:161	285:285	121:123
Celleneuve_L2	163:170	104:104	238:241	259:265	126:126	140:158	162:198	251:251	196:202	203:221	106:106	115:136	270:294	137:188	136:136	190:190	151:151	229:232	213:213	161:161	285:285	121:121
Celleneuve_L3	163:170	104:104	241:241	265:274	126:126	137:161	162:198	236:251	190:193	203:212	106:106	139:142	210:252	167:176	136:136	188:190	151:151	229:229	221:221	161:161	285:285	121:123
Celleneuve_L4	163:170	104:104	238:241	265:265	123:129	140:155	162:198	236:251	196:196	221:233	103:103	124:139	210:270	188:191	133:136	188:190	151:151	229:235	221:221	136:161	279:285	121:123
Celleneuve_L5	163:170	104:104	241:241	265:280	126:126	137:155	162:186	239:251	175:196	230:233	106:106	115:136	210:210	173:209	136:136	190:190	151:157	232:235	213:221	161:161	285:285	121:123
Celleneuve_L6	163:170	104:104	238:241	259:265	123:126	155:167	162:162	251:251	196:202	212:221	106:106	142:145	210:273	158:167	136:136	190:190	151:151	229:229	213:221	161:161	285:285	121:121
Celleneuve_L7	163:163	104:104	241:241	265:274	123:129	137:152	162:162	236:251	196:196	218:227	103:106	115:139	210:285	137:158	136:136	188:188	151:151	232:232	221:221	161:161	285:285	121:123
Celleneuve_L8	163:163	104:104	241:241	265:280	126:126	158:158	162:162	236:251	175:202	233:233	106:106	115:142	210:303	176:191	136:156	188:190	151:157	229:232	213:221	136:161	279:285	121:121
Celleneuve_L9	170:170	104:104	241:241	265:274	126:126	152:155	162:162	236:251	196:196	215:227	106:106	115:139	210:294	158:200	156:156	188:190	151:157	226:229	213:221	136:136	279:279	121:121
Celleneuve_L10	163:163	104:104	241:241	265:274	123:126	131:155	162:162	239:251	196:196	227:230	103:106	115:118	267:300	191:203	156:156	188:188	151:157	229:232	221:221	136:161	279:285	121:123
Celleneuve_L11	163:163	104:104	238:241	274:274	126:126	137:158	162:162	239:239	181:196	212:227	103:106	118:118	267:267	137:137	136:156	190:190	151:151	229:229	213:221	136:161	279:285	121:121
Celleneuve_S1	163:170	104:104	238:241	259:265	126:129	131:137	162:162	236:239	196:202	221:230	103:106	139:142	210:267	194:197	136:156	190:190	151:157	229:232	213:221	161:161	285:285	121:123
Celleneuve_S2	170:170	104:104	238:238	265:277	123:129	131:152	162:162	239:251	196:196	221:227	103:103	139:142	249:267	137:188	136:156	188:190	151:151	229:232	221:221	161:161	285:285	121:123
Celleneuve_S3	163:163	104:104	241:241	265:280	126:126	137:158	162:162	239:242	175:190	218:218	106:106	115:142	210:267	173:218	136:136	188:190	151:157	229:232	213:221	161:161	285:285	121:121
Celleneuve_S4	163:163	104:104	241:241	265:283	123:126	155:155	162:162	251:251	196:196	233:233	103:106	142:142	252:285	173:179	136:136	190:190	151:151	229:229	221:221	161:161	285:285	123:123
Celleneuve_S5	163:163	104:104	238:238	259:274	126:126	140:152	162:162	215:251	190:196	230:251	106:106	115:139	288:306	137:161	156:156	190:190	151:151	232:232	213:221	136:161	279:285	121:123
Celleneuve_S6	163:163	104:104	241:241	259:280	123:123	140:149	162:201	251:251	181:196	215:239	103:106	115:142	210:267	158:173	136:156	188:190	151:151	229:229	213:221	136:161	285:285	121:123
Celleneuve_S7	163:170	104:104	238:241	265:280	126:129	140:149	162:162	239:251	202:202	227:251	103:106	139:142	270:285	170:173	136:136	190:190	151:151	232:232	213:213	161:161	285:285	121:121
Celleneuve_S8	170:170	104:104	238:241	274:277	126:126	155:158	162:198	236:251	190:196	203:251	106:106	115:142	210:255	173:176	133:156	190:190	151:151	229:232	221:221	136:161	279:285	121:123
Celleneuve_S9	163:163	104:104	241:241	274:280	126:126	155:158	162:162	236:236	175:196	206:227	106:106	115:115	297:300	167:182	133:156	188:190	151:151	226:229	213:221	136:136	279:279	121:123
Celleneuve_S10	163:163	104:104	238:238	271:274	126:126	137:155	162:162	236:236	190:199	224:260	106:106	115:115	219:294	164:173	136:136	190:190	151:151	229:229	213:213	161:161	285:285	121:123
Eguilles_1	163:170	104:143	241:241	265:274	126:126	137:155	162:162	236:254	196:205	212:212	106:106	136:136	225:297	137:173	136:136	188:188	151:151	232:235	221:221	161:161	285:285	121:121
Eguilles_2	163:170	104:143	241:241	265:289	123:126	137:143	162:162	215:254	181:196	212:212	103:106	127:136	264:297	137:170	139:156	190:190	151:151	232:232	213:221	136:161	279:285	121:121
Eguilles_3	163:163	104:143	235:241	277:289	126:126	134:140	162:198	236:251	181:190	227:254	106:106	115:127	210:210	137:179	156:156	188:190	151:157	229:229	221:221	136:161	279:285	121:123
Eguilles_4	163:170	104:146	235:241	265:265	126:126	134:143	162:162	251:254	196:199	227:254	106:106	127:136	222:297	170:176	133:136	188:190	151:151	229:232	221:221	136:161	279:285	121:121
Eguilles_5	163:170	104:146	235:241	265:289	126:126	134:152	162:198	251:254	190:190	215:254	106:106	136:136	210:300	137:176	136:156	190:190	151:151	229:232	221:221	136:136	279:279	121:123
Eguilles_6	163:163	143:146	238:241	274:274	126:126	137:137	162:198	236:242	181:193	242:245	106:106	127:127	210:210	158:173	136:156	188:190	151:160	232:232	213:221	136:161	279:285	121:123
Eguilles_7	163:163	104:104	241:241	274:289	126:126	137:137	162:162	236:239	181:190	212:212	103:103	136:139	210:216	137:176	156:156	190:190	151:154	232:232	213:221	136:136	279:279	121:121
Eguilles_8	163:170	104:143	235:241	265:286	126:126	137:143	165:198	236:236	190:193	212:260	106:106	115:136	210:225	176:176	133:156	190:190	151:151	229:232	221:221	136:136	279:279	121:121
Eguilles_9	163:170	143:146	235:241	265:289	126:126	134:137	162:162	251:254	190:196	212:254	106:106	127:136	210:297	137:176	136:156	188:190	151:151	229:232	221:221	136:161	279:285	121:121
Eguilles_10	163:163	143:143	241:241	280:289	126:126	134:134	162:162	251:251	190:196	212:236	103:106	127:130	210:213	137:200	156:156	188:190	151:154	229:232	221:221	136:136	279:279	121:121
Moulis_AB1S	163:170	104:104	235:235	259:271	126:126	137:140	198:198	215:251	202:202	233:233	103:106	136:136	210:213	146:155	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_AB2S	163:163	104:104	235:235	259:265	126:126	155:155	198:198	251:251	190:196	233:233	103:103	136:136	210:213	146:194	133:133	190:190	151:151	235:235	213:213	136:136	279:279	123:123
Moulis_BA1L	163:163	104:104	238:241	259:271	126:126	155:155	162:198	215:251	196:202	230:230	106:106	112:136	210:213	146:146	133:133	190:190	151:151	232:235	213:221	136:136	279:279	123:123
Moulis_BA2L	163:163	104:104	238:241	259:259	126:126	140:155	198:204	215:251	196:202	209:230	103:106	136:136	213:213	146:194	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_1A	163:163	104:143	238:241	259:265	126:126	155:155	198:198	251:251	190:202	221:230	103:106	136:136	213:213	200:221	133:156	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_1B	163:163	104:104	238:241	259:271	126:126	137:155	204:219	251:251	190:202	230:230	103:103	136:136	210:210	146:146	133:133	190:190	151:151	235:235	213:213	136:136	279:279	123:123
Moulis_2A	163:163	104:143	241:241	259:271	126:126	137:140	204:204	215:251	202:202	221:236	106:106	136:136	210:213	146:152	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_2B	163:163	104:143	235:241	271:271	126:126	140:143	198:198	251:251	190:202	221:233	103:106	136:136	213:222	146:155	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_2C	163:170	104:104	235:241	259:259	126:126	143:155	162:198	215:251	196:196	230:233	103:106	112:136	210:213	146:200	133:133	190:190	151:151	232:232	213:221	136:136	279:279	123:123
Moulis_3A_3C	163:163	104:143	241:241	259:265	126:126	137:155	198:222	251:251	190:196	221:230	106:106	112:136	210:210	146:152	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_3B	163:163	143:143	238:241	259:259	126:126	137:137	162:198	251:251	196:202	224:248	106:106	112:136	210:210	146:152	133:156	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_4L	163:163	104:104	238:238	271:271	126:126	155:155	162:162	215:215	190:196	230:248	106:109	112:136	213:213	146:155	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_5L_6L	163:170	143:143	241:241	259:271	126:126	140:155	198:204	215:215	196:202	221:221	106:109	112:136	213:213	146:197	133:156	190:190	151:151	232:235	213:213	136:136	279:279	123:123
Moulis_7L	163:170	104:104	238:241	259:271	126:126	140:143	198:198	215:251	190:205	230:230	106:106	112:136	210:213	146:146	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123
Moulis_8L_9L_13L_32	163:163	104:104	241:241	259:259	126:126	137:155	204:204	251:251	202:202	230:230	103:106	136:136	210:216	146:146	133:133	190:190	151:151	232:235	213:213	136:136	279:279	123:123
Moulis_10S_12S	163:163	104:104	235:241	259:268	126:129	137:155	162:198	215:251	196:202	233:236	103:103	136:139	210:213	146:152	133:133	190:190	151:151	232:232	213:213	136:136	279:279	123:123

Individual	Indel_4	indel_5	indel_6	MT1	MT2	MT3	MT4	MT5	Haplotype mtDNA	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	CP9	CP10	Haplotype cpDNA
Amelie_les_Bains_1	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_2	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_3	175:175	101:101	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_4	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_5	175:175	101:101	194:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_6	175:175	101:101	194:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_7	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_8	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Amelie_les_Bains_9	175:175	101:121	150:194	309	316	335	231	225	5	176	119	167	349	129	136	108	90	110	245	4
Bages_1	168:175	121:121	150:194	309	317	335	239	217	3	176	119	167	349	128	136	108	90	110	245	3
Bages_2	168:175	121:121	150:150	309	317	335	239	217	3	176	119	167	349	128	136	108	90	110	245	3
Bages_3	168:175	121:121	150:194	301	317	335	239	225	4	176	119	167	349	128	136	108	90	110	245	3
Bages_4	168:175	121:121	194:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_5	175:175	121:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_6	168:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_7	175:175	121:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_8	175:175	121:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_9	175:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_10	175:175	121:121	194:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bages_11	175:175	121:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Bages_12	168:168	121:121	150:150	301	317	335	239	225	4	176	119	167	349	128	136	108	90	110	245	3
Bidon_1	175:175	101:101	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_2	175:175	101:121	150:194	301	317	335	239	225	4	176	**119**	167	349	**129**	136	**108**	90	110	236	6
Bidon_3	175:175	121:121	150:194	301	317	335	239	225	4	176	**119**	167	349	**129**	136	**108**	90	110	236	6
Bidon_4	168:175	101:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_5	175:175	121:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_6	168:175	101:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_7	175:175	101:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_8	175:175	101:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_9	175:175	101:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Bidon_10	175:175	101:121	150:194	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
CEFE_L0	175:175	101:101	194:194	301	317	335	239	225	4	177	120	166	**357**	127	137	109	90	110	245	2
CEFE_L1	168:175	121:121	150:150	301	317	335	239	225	4	177	120	166	357	127	137	109	90	110	245	2
CEFE_L1a	168:175	121:121	150:150	301	317	335	239	225	4	177	120	166	357	127	137	109	90	110	245	2
CEFE_L2	168:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
CEFE_L3	175:175	121:121	150:150	**301**	**317**	**335**	239	225	4	177	120	166	357	127	137	109	90	110	245	2
CEFE_L4	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
CEFE_L5	168:175	101:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
CEFE_L6	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
CEFE_S1	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
CEFE_S1B	175:175	101:121	150:194	309	316	327	239	225	1	176	119	167	349	129	136	108	90	110	245	4
CEFE_S2	175:175	121:121	150:150	301	317	335	239	225	4	177	120	166	357	127	137	109	90	110	245	2
CEFE_S3	168:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
CEFE_S4	175:175	101:121	150:194	**301**	**317**	**335**	239	225	4	177	120	166	357	127	137	109	90	110	245	2
CEFE_S5	168:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
CEFE_S6	175:175	101:121	150:194	301	317	335	239	225	4	177	120	166	357	127	137	109	90	110	245	2
Celleneuve_L1	168:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L2	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L3	175:175	121:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L4	168:175	121:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L5	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L6	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L7	175:175	121:121	194:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L8	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L9	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L10	175:175	101:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_L11	175:175	121:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S1	175:175	121:121	150:150	309	316	327	239	225	1	176	**119**	167	349	**128**	136	**108**	90	110	245	3
Celleneuve_S2	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S3	175:175	121:121	150:194	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S4	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S5	175:175	121:121	150:194	309	316	327	239	225	1	176	**119**	167	349	**128**	136	**108**	90	110	245	3
Celleneuve_S6	175:175	121:121	150:194	309	316	327	239	225	1	176	**120**	167	349	**128**	136	**108**	90	110	245	5
Celleneuve_S7	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S8	168:175	121:121	150:150	301	317	335	239	225	4	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S9	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Celleneuve_S10	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Eguilles_1	168:175	121:121	150:194	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_2	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_3	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_4	175:175	121:121	150:194	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_5	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_6	175:175	121:121	150:194	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_7	175:175	121:121	150:150	309	317	335	239	217	3	176	119	167	349	129	136	108	90	110	236	6
Eguilles_8	175:175	121:121	150:150	309	316	327	239	225	1	176	119	167	349	128	136	108	90	110	245	3
Eguilles_9	175:175	121:121	150:194	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Eguilles_10	168:175	121:121	150:150	309	316	327	239	225	1	177	119	166	349	127	137	109	91	111	245	7
Moulis_AB1S	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_AB2S	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_BA1L	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_BA2L	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_1A	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_1B	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_2A	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_2B	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_2C	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_3A_3C	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_3B	175:175	121:121	150:150	301	317	335	239	225	4	176	119	167	349	128	136	108	90	110	245	3
Moulis_4L	175:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Moulis_5L_6L	175:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Moulis_7L	175:175	121:121	150:150	301	317	335	239	225	4	177	119	166	357	127	137	109	90	110	245	1
Moulis_8L_9L_13L_32	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1
Moulis_10S_12S	175:175	121:121	150:150	309	316	327	239	225	1	177	119	166	357	127	137	109	90	110	245	1

| | | |

| | | |