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Ramos Madrigal, Jazmín, Runge, Anne Kathrine Wiborg, Bouby, Laurent et al. (14 more authors) (2019) Palaeogenomic insights into the origins of French grapevine diversity. Nature Plants. ISSN: 2055-026X

https://doi.org/10.1038/s41477-019-0437-5

Palaeogenomic insights into the origins of French grapevine diversity

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The Eurasian grapevine (*Vitis vinifera*) has long been important for wine production and a food source. Despite being clonally propagated, modern cultivars exhibit great morphological and genetic diversity, with thousands of varieties described in historic and contemporaneous records. Through historical accounts, some varieties can be traced to the Middle Ages, but the genetic relationships between ancient and modern vines remain unknown. We present target-enriched genome-wide sequencing data from 28 archaeological grape seeds dating to the Iron Age, Roman era, and medieval period. When compared to domesticated and wild accessions, we found the archaeological samples were closely related to Western European cultivars used for winemaking today. We identified seeds with identical genetic signatures present at different Roman sites, as well as seeds sharing parent-offspring relationships with varieties grown today. Furthermore, we discovered one seed dated to ~1100 CE was a genetic match to 'Savagnin Blanc', providing evidence for 900 years of uninterrupted vegetative propagation.

Since its domestication in Southwestern Asia more than 6000 years ago [1–3], the Eurasian grapevine (*Vitis vinifera* L.) has become one of the world's most widely produced and economically valuable fruit crops. Although grapevine products are widely consumed as table grapes, dried raisins, fruit preserves, and cooked leaves, both archaeological and historical evidence indicates that wine has been

its primary use [4,5]. A key unresolved question in ancient viniculture is the origin and proliferation of vegetative propagation [6]. Like many other fruit crops, grapevine is grown almost exclusively as clonal lineages, wherein favored varieties are maintained through horticultural techniques like grafting, layering, and planting of shoots [7,8]. These methods take advantage of its natural ability to reproduce asexually under certain conditions, and ultimately enable the establishment of genetic clones of valuable cultivars. With vegetative propagation, viniculturists can consistently harvest berries with a desired flavor profile, and with relatively limited effort, have the potential to expand cultivars to new vineyards and distant regions. The alternative approach of sowing seeds is unreliable because grapevine genomes are highly heterozygous and individuals grown from seed are highly diverse in quality, yield, phenotype, and phenology [8]. Moreover, winemakers have to wait from three to five years until vines reach maturity [9], before it is possible to assess berry quality and yield. Thus, clonal lineages of high-quality vines have become indispensable in modern viniculture. Discovering the antiquity of vegetative propagation technologies and the unique histories of individual grapevine varieties will mark a major advancement in our understanding of ancient viniculture, provide a means to investigate longstanding local agricultural traditions, and generate pertinent information for future development of breeding schemes (*e.g.* through better understanding why some varieties have been more successful than others, or adding historical value to present-day cultivars).

The history of winemaking in France provides a useful model to explore how vegetative propagation helped establish ancient vineyards, and how those

actions ultimately shaped the economy and landscape of one of the world's most esteemed winegrowing countries. Written sources and archaeological records indicate vineyards were first planted at the Greek colony of *Massalia*, present day Marseille, during the 6th century BCE [10,11]. Winemaking subsequently spread along the Mediterranean coast [12], but it was not until end of the first century BCE that Romans greatly increased wine production across southern France [10]. Roman authors, including Pliny the Elder in the first century CE ([13]: Book XIV), discussed grafting and grapevine varieties, thereby demonstrating their proficiency in vegetative propagation techniques. While Pliny describes 91 varieties, it is currently impossible to link Roman names to modern grapevines; however, it is frequently speculated that some living varieties were grown by the Romans, and that those genetic clones have been maintained for two millennia [9]. After the fall of the Roman Empire, winemaking traditions continued in France, and by the Middle Ages, contemporary variety names appear in written records [14]. Even though historic names are still used today, it remains unknown whether the same genetic clone has been maintained, or if names have been assigned to other lineages.

Archaeobotanical remains, in particular seeds, have the potential to shed new light on the legacy of French grapevine varieties, and more generally on the history of viniculture. Using morphometric analyses of seed shape, researchers have shown seeds from most domesticated grapevines (*V. vinifera* subsp. *vinifera*) can be distinguished from those produced by wild vines (*V. vinifera* subsp. *sylvestris*) [15,16]. With this approach, Bouby *et al.* [10] determined that early Roman sites in Southern France (50 BCE–225 CE) contained greater numbers of

morphologically wild seeds than the following period (225–600 CE), raising the question of whether Romans collected and cultivated wild berries for winemaking. Through this time series, seed shapes tended toward domesticated morphotypes, a finding the authors hypothesize represents a combination of continued selective pressures with a sporadic incorporation of native varieties through sexual reproduction. While these interpretations are thought provoking, the authors also recognize critiques that some wild and domesticated vines produce morphologically indistinguishable seeds.

One of the most promising avenues of research for ancient viniculture is palaeogenomic (or ancient DNA, aDNA) analysis of well-preserved archaeological pips [17–19]. For example, Wales *et al*. [20] demonstrated that many waterlogged grape seeds contain high proportions of endogenous DNA that could be interrogated with state-of-the-art, high-throughput aDNA sequencing. With the establishment of genomic databases for hundreds of modern cultivars and wild grapevines [21], we sought to examine how DNA recovered from archaeological samples could sidestep some of the challenges of conventional archaeobotanical methods and reveal relationships between ancient samples and modern varieties, thereby providing otherwise unachievable insights on past implementation of vegetative propagation and the antiquity of some of the world's most produced grapevine varieties.

Results and discussion

Successful enrichment of SNP loci in archaeological pips

We performed targeted enrichment and shotgun sequencing of 10,000 SNP loci in 28 archaeological grape seeds. The pips were recently excavated from waterlogged features (wells, latrines, ditches, and pits) at 9 French sites (Supplementary Fig. 1), and based on archaeological context, date as early as the Iron Age (510–475 BCE) and as late as the medieval period (1050–1200 CE) (Table 1). SNP loci were selected from the GrapeReSeq panel, a DNA microarray that was developed to authenticate varieties for breeding and germplasm management [21]. This reference panel provides data for 783 domesticated varieties (*V. vinifera* subsp. *vinifera*), 112 wild (*V. vinifera* subsp. *sylvestris*) accessions collected from Eurasia and North Africa, and 11 other *Vitis* species. We obtained a 4- to 400-fold enrichment at the targeted SNP sites, leading to an on-target depth of coverage of 1–25.7× (Supplementary Table 1 and Supplementary Fig. 2). Nucleotide misincorporation patterns observed in the sequencing data and read length distributions were consistent with those expected for degraded DNA [22] (Supplementary Figs. 3, 4 and 5a) .

Archaeological seeds related to European winemaking lineages

We employed multidimensional scaling (MDS) to investigate whether archaeological samples were more closely related to wild accessions or domesticated varieties. Samples were compared to the GrapeReSeq panel following the random allele sampling strategy described in *bammds* [23], to account for varying depth of coverage in the archaeological samples. Additionally, we expanded our reference dataset with publicly-available whole-genome sequencing data from 27 wild and domesticated grape accessions [24–26] (Supplementary Table 2). The MDS plots showed all 28 archaeological samples

153 fall within the variability of domesticated grapevines, suggesting none of the
154 seeds originated from truly wild vines (Fig. 1a). While it is plausible that samples
155 near the boundary of the domesticated and wild clusters could represent F_1
156 hybrids between domesticated varieties and wild grapevines (*e.g.* specimen R-
157 LLE_09), we find no evidence for large-scale collection of wild berries by Romans
158 or medieval people at these sites. Likewise, the oldest sample, from the Iron Age
159 site of La Cougourlude dating to 510–475 BCE, also falls within the MDS space
160 composed of cultivated grapevines. These findings support Bouby *et al.*'s [10]
161 hypothesis that even though many pips from Roman and medieval sites exhibit
162 wild morphotypes they in fact originate from domesticated varieties.
163
164 Once we determined that archaeological seeds likely originated from
165 domesticated grapevines, we repeated the MDS analysis without wild accessions
166 to achieve a more refined picture of the relationships to regional varieties and
167 types of berries (*i.e.*, predominantly used in winemaking or as table grapes). The
168 majority of the archaeological pips were most closely related to wine cultivars
169 from West and Central Europe (Fig. 1b), although the three Early Roman samples
170 from the Mas de Vignoles XIV site had a closer affinity to wine grapes from the
171 Balkans and the Iberian Peninsula. Overall, this analysis shows that the
172 archaeological seeds are predominantly related to Western European varieties
173 that are used for winemaking, and not grapevines that are today grown further
174 east for wine or table grapes. These data suggest that 2000 years ago cultivated
175 vines in the modern territory of France were distinct from their Near Eastern
176 ancestors and well on their way to founding the germplasm of modern varieties
177 used in Western European winemaking. We also verified that the patterns

observed in the MDS analysis using the GrapeReSeq panel were consistent with those obtained from a whole-genome (WG) reference panel (Supplementary Table 2 and Supplementary Fig. 6).

We further explored the genetic structure of the archaeological seeds with a two-step model-based clustering analysis. First, ADMIXTURE [27] was used to infer the ancestry proportions within the samples in the reference panel, and then FastNGSAdmix [28] was used to estimate the ancestry proportions in the archaeological samples (Fig. 1c and Supplementary Fig. 7). The results were consistent with the MDS analysis, showing that most archaeological seeds were related to wine grapes from Western Europe.

As there is evidence for gene flow with local wild grapevines in Western Europe [1], we explored the wild ancestry components identified through the clustering analysis. Since these proportions are estimated on the GrapeReSeq SNPs they do not necessarily represent whole-genome ancestry proportions. However, this allowed us to: 1) compare the proportions between present-day varieties and the archaeological seeds at these diagnostic sites, and 2) identify the potential source of the wild grape ancestry in the archaeological seeds. Wild grapevines carry four main ancestry components when assuming 8 clusters (Fig. 1c). While American and Asian *Vitis* species (yellow) and Eurasian wild grapes from the Caucasus and Turkey (light blue) separate into individual clusters that do not contribute significant ancestry to any other group, wild grapes from the African and Western European populations display two ancestry components (dark and light green) that are found in some domesticated grapes. All archaeological

samples except for the most recent (M-LM_22) show evidence of genetic contributions from wild grapevines (Fig. 1c and Supplementary Fig. 7), and these wild ancestries are primarily associated with Western and Central European vines. While these data provide the first clues on the timing of genetic introgression from local vines into domesticated lineages, the amount of wild ancestry does not follow a consistent pattern related to sample age. For example, the oldest sample (La Cougourlude, 510–475 BCE) shows some of the highest levels of wild ancestry (~45%), while other early samples from Mas de Vignoles XIV (2nd–1st century BCE) have marginal amounts of wild ancestry (3.5-4.5%), and five samples from La Lesse-Espagnac (175–225 CE) range from ~10–38%. In fact, these proportions of wild ancestry are similar to those observed in modern French varieties, suggesting that the admixture with wild grapevines took place at the earliest stages of viniculture in France, and potentially before other cultivated lineages were introduced to France (*i.e.*, from Greece or the Italian Peninsula). Together, these results suggest that the local wild gene pool played an early role for domesticated varieties, with the gene flow between wild grapevines and domesticated cultivars occurring at least 2500 years ago.

Ancient use of vegetative propagation

The availability of genotype data for hundreds of cultivars in the GrapeReSeq panel, allowed us to explore relationships between archaeological pips excavated from individual sites and across different regions of France. We estimated kinship coefficients among pairs of samples using *KING* [29] and *NgsRelate* [30]. Pairs of samples were classified based on the kinship coefficients and the proportion of sites with 'zero alleles Identical by State' (IBS0)[29], into the following

categories: identical clones, parent-offspring, highly-related/full-siblings or unrelated [21] (Supplementary Table 3). We found six instances of genetically identical pairs or groups of seeds (Fig. 2a). Additionally, we identified first-degree relationships (parent-offspring and highly-related /full-siblings) and unrelated varieties (Fig 2b). However, since grape seeds that have been cross-fertilized contain paternal derived DNA[31] which could affect the relatedness analyses, we explored whether the archaeological seeds contained maternal DNA only (as expected from empty seeds), or both paternal and maternal DNA. To do so, we generated sequencing data from three seeds and a wood sample of the same plant and conducted a simulation study, in an attempt to estimate the parental contribution in the archaeological samples (Supplementary Fig. 8; Supplementary Section 16). We found that data from all archaeological seeds, except R-TDM_06, R-TDM_08, R-HW71_03 and M-MDV12_09, were consistent with a paternal DNA contribution of ≤10% (Supplementary Figs. 8 to 11). Moreover, we studied the dependence of the relatedness analyses on such contribution and found that ≤10% paternal DNA does not significantly affect the results (Supplementary Fig. 12). Therefore, we consider that clonal and parent-offspring relationships are not affected in most samples. On the other hand, full-sibling relationships could derive from multiple scenarios if the samples involved contain paternal DNA (Supplementary Fig. 12c), and thus we classified pairs of samples with this type of relationship as 'highly related'.

Grape seeds have been found to follow a degradation process of the two tissues that contain paternal DNA, the endosperm and embryo, resulting in empty seeds (*e.g.* in up to 30% of the cases for ‘Chardonnay’ variety [32,33]). Our results suggest that the observed clonal clusters among archaeological samples

represent empty seeds with only maternal tissue, either produced by the same plant, such as might occur at one archaeological site, or by one grapevine variety spread through vegetative propagation (Fig. 2 and Supplementary Table 3). Five of these clonal clusters consist of two or three seeds from a single stratigraphic context: an Early Roman ditch at Mas de Vignoles XIV near Nîmes city (2nd–1st century BCE), a Roman well at Mont Ferrier, Tourbes (1st century CE), a Roman well at La Lesse-Espagnac (ca. 200 CE), a Roman well at Terrasses de Montfau, Magalas (4th century CE), and an early medieval well at Mas de Vignoles XIV (ca. 800 CE). Given that bunches of grapes might have been pressed for juice and discarded *en masse*, these genetically identical specimens may well represent seeds from single plants. The other genetic cluster consists of three seeds from Horbourg-Wihr in Alsace and one seed from La Lesse-Espagnac in Mediterranean France (Fig 2b); while all four samples date to the 2nd century CE, these genetic clones suggest that Romans transported grapevine across long distances (>600 km), most likely as cuttings.

Five archaeological sites in Southern France demonstrated the presence of multiple genotypes within a single temporal stratum, providing genetic evidence that multiple lineages or varieties were maintained at individual vineyards. For example, we identified six different genotypes at Mas de Vignoles XIV near Nîmes, three of which shared first-degree relationships and three of which were unrelated (Fig. 2b). Overall, these relationship data indicate that vegetative propagation, long-distance transportation of varieties, and multivarietal cultivation have been practiced in France since the Roman era, consistent with historic accounts [4].

The antiquity of modern French varieties

We lastly investigated the relatedness between archaeological and modern varieties, by computing kinship coefficients and the proportion of IBS0 sites between pairs of archaeological samples and samples present in the GrapeReSeq panel using *KING* [29] (Fig. 3 and Supplementary Tables 4 and 5). Our results confirm long-held beliefs that Roman and medieval viticulturists maintained ancient lineages using vegetative propagation [13], and that modern French viniculture is in large part a product of these traditions. One archaeological sample from La Madeleine (Orléans), dating to 1050–1200 CE, was an identical clone of 'Savagnin Blanc' (VIVC17636), a variety today cultivated for wine production in Northeastern France and other countries from Central Europe (*kinship coeff*. =0.496; *IBS0*~0.0001; Identity of 99.7% and 99.9% for the GrapeReSeq and WG panels, respectively) (Supplementary Tables 4 and 5). Several researchers previously identified 'Savagnin Blanc', also known as 'Traminer Weiss', as a recurrent parent of many commercially important European varieties [1,34,35], and written accounts document the appellation as early as 1539 CE [36]. Our findings extend the presence of this variety in France by hundreds of years and furthermore, suggest that either 'Savagnin Blanc' or its direct relatives have been cultivated in France since the 1st century CE, since archaeological seeds from Mont Ferrier, Tourbes have a parent-offspring relationship with 'Savagnin Blanc' (Figs. 2b and 3).

Several archaeological seeds were closely related to 'Mondeuse Blanche' (VIVC7919), a French variety characteristic of the Northern French Alps that has

302 been suggested to have acted as a key progenitor [35,37]. We found that four
303 genetically identical 2nd century CE seeds from Horbourg-Wihr and La Lesse-
304 Espagnac have a parent-offspring relationship with 'Mondeuse Blanche',
305 indicating that just one reproductive cycle has taken place in this lineage in the
306 past 1800 years (Fig. 3). This finding presents an exciting consilience of genetic
307 and archaeobotanical data; using morphometric analysis, Terral *et al.* [16] also
308 found evidence for 'Mondeuse Blanche' among 1st–2nd century CE pips from the
309 Rec-de-Ligno site, which lies less than 10 km from La Lesse-Espagnac. We also
310 observed that 'Mondeuse Blanche' is highly related (full-sibling or similar
311 relationship) to an archaeological seed from Colletiere, dating to circa 1000 CE,
312 close to the region where 'Mondeuse Blanche' is still grown today (Savoie, Ain)
313 (Fig. 3). Interestingly, the medieval seed is also highly related to 'Tressot'
314 (12640) (cited since 1396 in France [38]) and 'Servanin' (VIVC11526), both French
315 varieties that are rarely cultivated today.
316
317 In addition to 'Mondeuse Blanche', four other Roman seeds from Southern
318 France provided parent-offspring relationships to modern Alpine varieties: three
319 1st century CE seeds from Mont Ferrier are highly related to 'Arvine'
320 (VIVC664) and 'Amigne' (VIVC425) and one 1st–3rd century CE seed from
321 Roumeges is a first-degree relative to 'Humagne Blanc' (VIVC5450) (Fig. 3).
322 All three are Swiss varieties used for white wine, and the former two are
323 recorded in Switzerland by the 17th century CE [39]. Tradition holds that the
324 Romans brought 'Amigne' to Switzerland as a variety they referred to as
325 '*Aminea*'; however some researchers have suggested the connection is primarily

etymological, with the retained usage of the Latin word *amoenus* for "delicious" [40]. Our findings suggest there indeed is a close genetic link between the varieties grown by the Romans and some modern Swiss cultivars, including 'Amigne'. Moreover, these data suggest that modern Alpine varieties may have been cultivated in a more widespread geographic region during the Roman period, thus posing an important question on their origin and the adaptation of modern grapes. The approaches established here can be applied to other archaeological pip assemblages with the aim of detecting when regional and economically important lineages first appeared and how they were maintained.

Impact of cultural changes in the viniculture of France

Specimens from the Mas de Vignoles XIV site in Nîmes provide one final observation on the changing nature of viniculture in France. This site allowed us to investigate a transect of three time periods: 2nd –1st century BCE in the early Roman period, 417–515 CE in the Late Roman period when viticulture was fully established in the region, and 731–851 CE in the early medieval period. While cultivars from the most recent period were found to share first-degree relationships with modern French varieties, no relationship was found between cultivars from the Roman period and the modern varieties (Fig. 3). Our results from Mas de Vignoles XIV suggest a change in grapevine diversity from Roman to Medieval times. This transition can also be observed in the MDS analyses (Fig. 1b); the three seeds from the early Roman period (R-MDV14_04/07/09) are placed closer to East European and Iberian grape varieties, while Late Roman and early medieval seeds are more similar to West Europe varieties. These results show the relatively high diversity of grapes cultivated in this region

during this period, as well as replacement and incorporation of new varieties through time.

Concluding remarks

Palaeogenomic analysis of archaeobotanical remains has helped reveal the evolutionary histories of annual crops like barley [41] and maize [42,43], but this project represents the first nuclear aDNA study of a vegetatively propagated fruit crop. Our results highlight the utility of state-of-the-art palaeogenomic methods in the study of ancient viniculture through space and time. While previous studies on ancient chloroplast DNA [20], microsatellites [18,19,44], and proteins [18] have provided insights into the history of grapevine cultivation, their resolution is limited. With the availability of a nuclear DNA diversity panel, we interrogated genome-wide data from archaeological grape seeds, identified relationships between ancient pips and modern varieties, observed connections between distant sites, and traced the history of vegetative propagation in France. Future palaeogenomic research on archaeological grape seeds holds great potential in identifying the links between past and present grape varieties, and especially for refining our knowledge of the pace of domestication and improvement under vegetative propagation [45].

Materials and methods

Archaeological sample description

375 Grape seeds were collected from nine archaeological sites in France during
376 excavations of wells, latrines, pits, and ditches (Supplementary Fig. 1; see
377 Supplementary Section 1 for a description of the archaeological sites). Sediment
378 samples were systematically collected and immediately isolated to prevent
379 contamination and stored in cool conditions (4° C). The sediment samples were
380 processed at the Institut des Sciences de l'Evolution (ISEM) in Montpellier,
381 France. To prevent contamination with modern material, seeds were isolated in
382 a clean room separate from the archaeobotanical laboratory. Additionally,
383 surfaces and tools were cleaned with bleach prior to handling. Most of the
384 samples included in this study were photographed inside the clean room, with
385 specific equipment in order to carry out morphological analyses. Archaeological
386 samples were dated either by association with archaeological artifacts found in
387 the same stratigraphic units, dendrochronology, or radiocarbon dating. The age
388 of the samples ranged from the Iron Age (510–475 BCE) to the medieval period
389 (1050–1200 CE) (Supplementary Fig. 1 and Table 1).
390
391 **Archaeological samples processing**
392 Archaeological samples were processed in dedicated aDNA facilities at the
393 University of Copenhagen following standard measures to prevent
394 contamination. Individual seeds were decontaminated with 10% bleach, rinsed
395 with molecular biology grade water, and pulverized. DNA was extracted from the
396 resulting powder following standard protocols standardized for
397 archaeobotanical remains [46]. DNA extracts were converted into double-stranded
398 Illumina libraries using the NEBnext DNA Library Prep Mast Mix Set 2 (E6070L,
399 New England BioLabs) with modifications described in Wales *et al*. [47] (see

Supplementary Section 4 for a description of the protocol). Resulting Illumina libraries were enriched for a set of genomic loci present in the GrapeReSeq reference panel [21] (Supplementary Section 5). This panel covers genomic sites known to be informative for identification of grape cultivars. Libraries were captured following the MYbaits protocol as described in Supplementary Section 6. Finally, pre- and post-capture libraries were sequenced on an Illumina 2500 HiSeq platform in SR100 mode. Sequencing reads obtained from the pre-captured libraries were used to assess the capture efficiency only.

Sequencing data processing

AdapterRemoval2.0 [48] was used to remove Illumina adapter sequences, low quality stretches and ambiguous bases from the read ends. Resulting reads ≥30 base pairs were mapped to the grape nuclear reference genome 12X.2 [49], chloroplast [50] and mitochondrial [51] genomes using *bwa aln* (0.7.5a) [52]; seeding was disabled (-l was set to 1000) to improve the mapping sensitivity of aDNA reads [53]. Reads with mapping quality below 30 or ambiguously mapping were discarded, PCR duplicates were removed using *MarkDuplicates* (http://picard.sourceforge.net), reads were realigned around indels using *GATK* [54] and the MD-tag was recalculated using *samtools* 1.2 [55]. Finally, we excluded 5 bases from the 5' and 3' ends of each read from subsequent analyses to reduce the proportion of bases with aDNA damage. Genotype calling was performed in the resulting alignments using a combination of the *HaplotypeCaller* and *UnifiedGenotyper* algorithms from *GATK* [54] on sites with a minimum coverage of 10× as described in Supplementary Section 12. To evaluate the genotyping pipeline, we generated sequencing data for two modern grape cultivars using the

SNP capture protocol. These two varieties are present in the GrapeReSeq panel, thus provide a direct comparison between our method and the GrapeReSeq microarray. We found a concordance of 99.4% and 99.3%, between the called genotypes and their corresponding genotypes in the GrapeReSeq panel.

Ancient DNA authentication

The authenticity of the aDNA data was assessed on the basis of the length distribution and the nucleotide misincorporation patterns observed in the sequencing data. We used *bamdamage* [23] to estimate per base nucleotide substitutions in the mapped reads. Reads with mapping quality lower than 30 and base quality lower than 20 were discarded. Archaeological samples displayed increased C-to-T and G-to-A substitutions as well as short reads (Supplementary Figs. 3 and 4), consistent with aDNA data [22].

Reference datasets

We used two reference datasets to compare the archaeological grape seeds to present-day grape varieties (see Supplementary Section 11 for a detailed description of the reference panels used). 1) The GrapeReSeq panel consists of 783 modern grape cultivars (*V. vinifera* subsp. *vinifera*) and 112 wild grape individuals (*V. vinifera* subsp. *sylvestris*) representative of the genetic diversity found in Europe (81 accessions), as well as from North Africa (18 accessions) and the Caucasus (13 accessions) genotyped for 10,000 diagnostic SNPs [21]. 2) We assembled a whole-genome (WG) reference panel incorporating sequencing data from 27 publicly available wild and domesticated grape accessions [24–26]. Raw reads were obtained from the NCBI SRA, mapped and processed using similar

parameters as the archaeological samples. To avoid ambiguities due to synonymy the VIVC number [56] is assigned to cultivars as indicated in Supplementary Table 4.

Genetic structure analyses

We explored the genetic relationships between the archaeological grape seeds and the samples in the two assembled reference panels using multidimensional scaling as implemented in *bammds* [23] (Figs. 1a and 1b, and Supplementary Fig. 6). Samples with an on-target depth of coverage ≥3× were included to the reference panel by sampling a random allele from the called genotypes; while the six low coverage samples were incorporated from a majority count consensus sequence (Supplementary Table 1). After filtering low-quality SNPs, the final datasets consisted of 9,896 and 3,076,549 sites for the GrapeReSeq and WG panels, respectively. Note that, for analyses using the GrapeReSeq panel we did not exclude transition sites. However, data from the genotype calls and majority count consensus sequences obtained for the archaeological samples showed error rates comparable to those of modern grape samples (Supplementary Fig. 5), suggesting that the aDNA derived error is unlikely to have a substantial effect in the analyses.

We used the model-based clustering approaches implemented in *fastNGSadmix* [28] and *ADMIXTURE* [27] to estimate ancestry proportions in the archaeological samples (Fig. 1c and Supplementary Fig. 7). First, ADMIXTURE was run on the GrapeReSeq panel assuming 2-8 populations/clusters (K=2-8). We obtained 1,000 independent replicates for each value of K and kept the one with the best likelihood. Then, we estimated genotype likelihoods for the archaeological

samples using the *samtools* model implemented in *ANGSD* v1.9 [57] at the sites included in the GrapeReSeq panel. Finally, we obtained maximum likelihood estimates of the ancestry proportions for the archaeological samples using the genotype likelihoods and the *ADMIXTURE*-inferred allele frequencies for each value of *K* using *fastNGSadmix.* Figure 1c shows the results for the *K*=8, which resulted among the lowest cross-validation errors (Supplementary Fig. 7b).

Relatedness analyses

To explore the relationships among pairs of archaeological samples and between the archaeological samples and samples in the reference panels, we estimated kinship coefficients using two approaches: the called genotype-based approach implemented in *KING* [29] and the genotype likelihood-based approach implemented in *NgsRelate* [30] (Supplementary Tables 3 to 5).

KING was run assuming non-homogeneous population structure for the two reference panels and using called genotypes for the archaeological samples. Pairs of samples were classified based on the kinship coefficients and the proportion of sites with ‘zero alleles Identical by State’ (IBS0), as suggested in Manichaikul *et al.* [29], in the following categories: identical clones (K≥0.49 and IBS0≤0.001), parent-offspring (0.177<K<0.354 and IBS0≤0.001), highly related/sibling (0.177<K<0.354 and IBS0≤0.25) or unrelated (Supplementary Tables 3 to 5). These values have been shown to be reliable in discerning known first-degree relationships among grape cultivars [21].

NgsRelate was used as a complementary method to validate the results obtained using *KING* and to include low coverage samples for which it was not possible to call genotypes. To run *NgsRelate*, we first estimated genotype likelihoods for the

archaeological samples using the *samtools* model (-gl 1) implemented in *ANGSD* v1.9 [57]. Reads with mapping quality lower than 30 and bases with quality lower than 20 were discarded. We then estimated allele frequencies for the two reference panels using *PLINK 1.9* [58]. These frequencies together with genotype-likelihoods were used to obtain kinship coefficients and the proportion of sites sharing 0, 1 or 2 alleles identical by descent (IBD) between pairs of samples (Supplementary Table 3). These results were evaluated together with the obtained from the genotype-based approach to assign relationships between pairs of archaeological samples.

In Supplementary Section 16, we explore the possibility of paternal DNA present in the archaeological seeds through a simulation study and comparing the archaeological seeds data with that obtained from fresh seeds (Supplementary Figs. 8 to 11 and Supplementary Table 6). While most of the archaeological seeds were found to be consistent with data derived from a single individual, our analyses indicate four seeds contain ≥10% of paternal DNA (Supplementary Fig. 11). Additionally, we evaluate potential effects of paternal DNA in the relatedness analyses and found that: 1) clonal relationships can only be detected from true identical individuals even in the presence of paternal DNA, 2) parent-offspring relationships are only ambiguous when the sample contains >10% paternal DNA, and 3) apparent full-sibling relationships can result from multiple scenarios, thus pairs of samples with this type of relationship were classified as 'Highly related pairs' (Supplementary Fig. 12). Relationships between archaeological seeds and modern grapes were evaluated based on the conclusions from Supplementary Section 16.

We further explored the effect of sequencing depth and panel ascertainment in the robustness of the relatedness inferences (Supplementary Section 17). The results indicate that the metrics used to identify relationships between the samples are reliable for samples with an on-target depth of coverage of ≥2× when using genotypes, and 1× when using genotype likelihoods (Supplementary Table 7). Additionally, we confirmed that samples identified as identical clones display an IBS distance < 0.0001 both in the sites overlapping the GrapeReSeq panel and in off-target sites (Supplementary Fig. 13; Supplementary Section 18).

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Acknowledgments

We thank the Danish National High-throughput Sequencing Centre for assistance in generating the sequencing data. This project was funded by the Danish Council for Independent Research (10-081390) and the Danish National Research Foundation (DNRF94). L.B. and R.B. were supported by the French National Agency of Research (VINICULTURE project - ANR-16-CE27-0013). We would like

to thank the following scientific and technical directors and corresponding institutions for providing the archaeological material used in this project as well as contextual information: P. Blanchard (Inrap, site: La Madeleine), E. Verdel (Isère Patrimoine, site: Colletière), H. Pomarèdes (Inrap, sites: Mas de Vignoles XIV and La Lesse-Espagnac), O. Ginouvez (Inrap, site: Terrasses de Montfau), R. Bourgaut (Communauté d'Agglomération du Bassin de Thau, site: Roumèges), P. Flotte (Archéologie Alsace, site: Horbourg-Wihr), M. Compan (Inrap, site : Mont Ferrier), I. Daveau (Inrap, site: Cougourlude) and C. Tardy (Inrap). We are also grateful to the GrapeReSeq consortium for early access to the genotype data. Finally, we would like to thank J. Víctor Moreno-Mayar, Shyam Gopalakrishnan, Filipe G. Vieira, David Maghradze, and Angela Schlumbaum for their helpful discussion.

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Author contributions

The project was conceived by N.W., M.T.P.G., R.B., and L.B., and headed by N.W. and M.T.P.G.; J.A.S.C., A.K.W.R, R.B. and N.W. designed experimental enrichment methodology with input from J.M.M.Z., R.T. and A.F.A.B.; A.K.W.R. processed ancient DNA with input from N.W.; J.R.M., A.K.W.R., R.B. and N.W. designed analysis strategy; J.R.M. performed bioinformatic analysis with assistance from B.P. and T.S.P. and input from N.W, M.T.P.G. and R.B.; J.R.M., N.W., M.T.P.G., R.B., L.B., T.L. and P.T. interpreted the results; L.B., I.F., C.S. and C.H., curated

archaeological material; J.R.M., N.W. and M.T.P.G. wrote the manuscript with input from R.B., L.B. and T.L. and the other authors. All authors revised, edited and accepted the manuscript. Primary funding acquired by M.T.P.G.

Competing interest

The authors declare no competing interests.

Data availability

Sequencing data produced in this study are available at the NCBI SRA under the reference PRJNA489970. Genotype data are available in the *figshare* repository under the following DOI: 10.6084/m9.figshare.7610987.

Figure legends

Figure 1. Genetic affinities between archaeological grape seeds and modern *Vitis vinifera* accessions. a. Multidimensional scaling plot (MDS) including archaeological samples, wild *V. vinifera subsp. sylvestris* accessions, and domesticated varieties. b. MDS plot restricted to archaeological samples and domesticated varieties. Colors correspond to the main ancestry clusters identified in Laucou *et al.* [21]. *Archaeological samples that were incorporated to the dataset by sampling a random allele from a majority count consensus sequence instead of called genotypes c. Model-based clustering analysis of the GrapeReSeq panel assuming K=8 clusters. Vertical bars represent individual accessions, colors represent the inferred ancestry components, and the fraction of each color corresponds to the estimated ancestry proportion. Archaeological

samples are sorted by age, and by sample identification within a stratigraphic context. Samples that were identified as identical clones are grouped with black lines and capital letters (A-F) at the bottom.

Figure 2. Geographic distribution and relationships between the distinct genetic types of archaeological samples. a. Relatedness among pairs of archaeological samples. Kinship coefficients were estimated using *NgsRelate* between pairs of samples for SNP loci present in the GrapeReSeq panel. Capital letters (A-F) on the left indicate genetically identical clones, *i.e.*, putative ancient and historical varieties. *Archaeological seeds that were found consistent with carrying >10% paternal DNA. b. Map displaying the distribution of genetic types (circles) in each archaeological site. Capital letters (A-F) on the circles indicate clusters of genetically identical seeds represented by more than one seed. Shading of the circles indicates sample age. In red is shown the genetic type that was found in more than one archaeological site. Lines connect pairs of samples that are related as parent-offspring (solid lines) or highly-related/full-sibling (dotted lines). Note that, since in the presence of paternal DNA full-sibling relationships could derive from multiple scenarios, we classified samples consistent with full-sibling relationships as 'highly-related' (see Supplementary Section 16).

Figure 3. Genetic origins of ancient and historic French grapevine varieties. Relationships identified between archaeological samples and modern cultivars included in the GrapeReSeq panel. Solid lines represent parent-offspring relationships and dotted lines represent pairs of highly related (full-sibling or similar) samples. Sibling relationships involving pairs of modern cultivar are not displayed for simplicity. *Archaeological seeds that were found consistent with

764 carrying >10% paternal DNA. The VIVC (http://www.vivc.de) and GrapeReSeq

765 identifiers for the modern cultivars can be found in Supplementary Table 4.

766

767

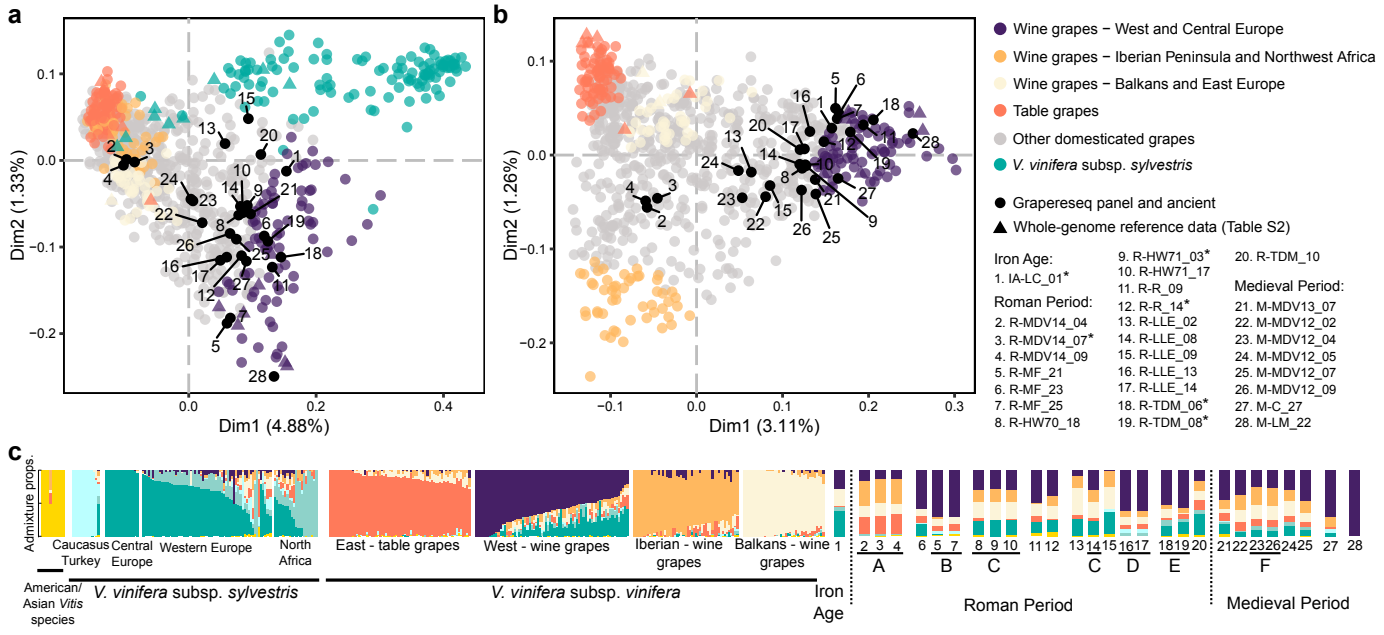
768 **Table 1.** Description of the archaeological grape seeds used in the study.

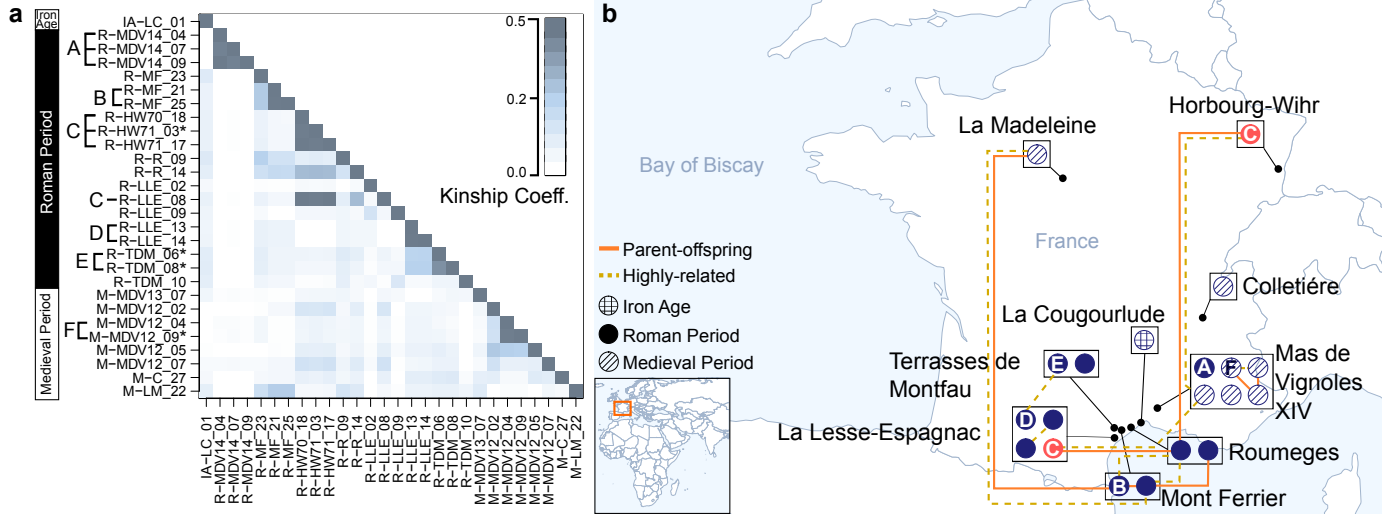
769

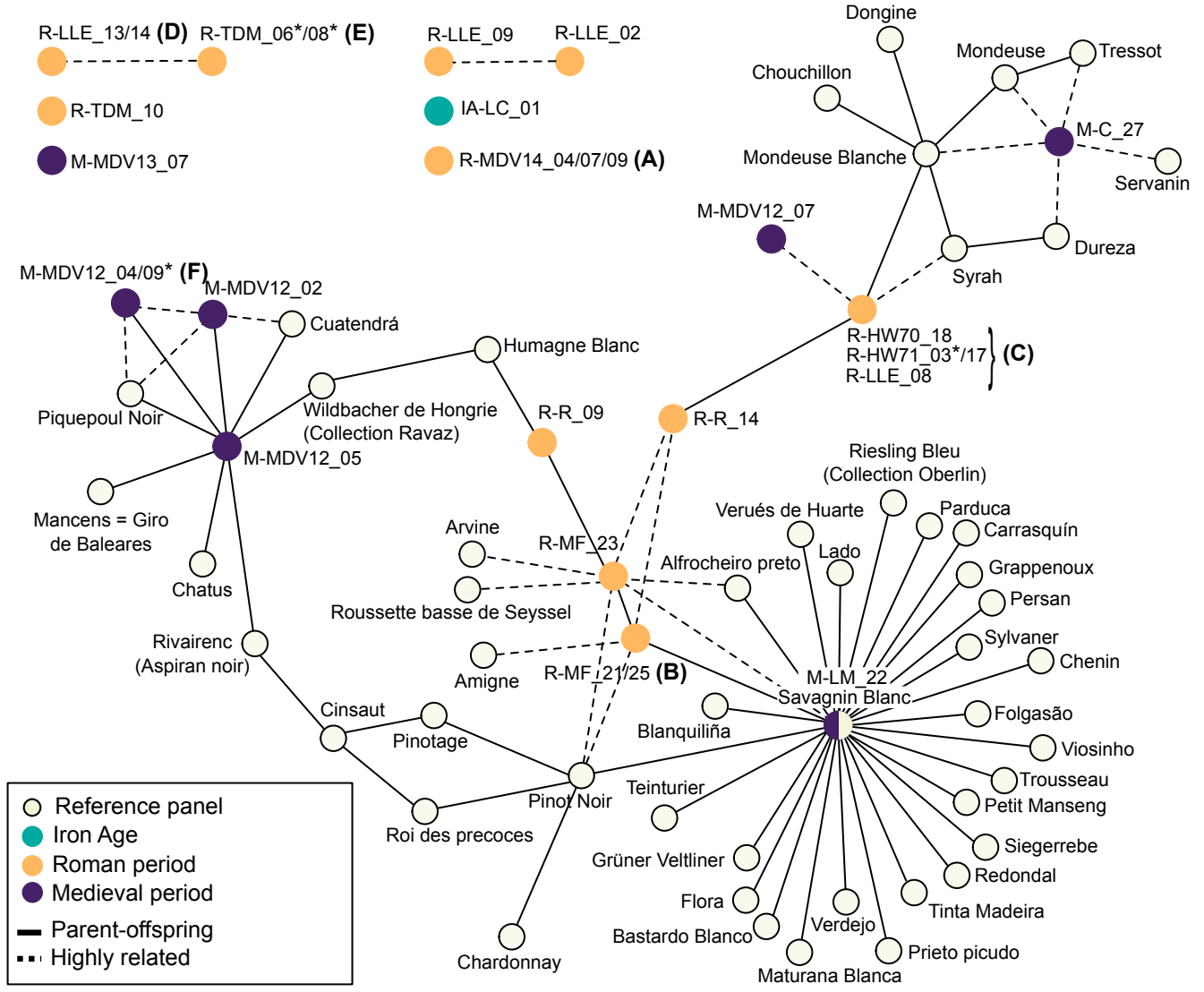
#	Sample ID	Geographic coordinates	Archaeological site	Stratigraphic unit	Structure	Age	Dating method	Period	GC †
1	IA-LC_01	43.573639, 3.914750	La Cougourlude, Lattes	US 31084	Ditch FO 30277	510-475 BCE/2480 ± 30 BP (769-417 cal BCE)	Archaeological artifacts/C14	Iron Age	
2	R-MDV14_04	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 14152	Rural ditch FO 14194	2nd-1st c BCE	Archaeological artifacts	Early Roman	A
3	R-MDV14_07	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 14152	Rural ditch FO 14194	2nd-1st c BCE	Archaeological artifacts	Early Roman	A
4	R-MDV14_09	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 14152	Rural ditch FO 14194	2nd-1st c BCE	Archaeological artifacts	Early Roman	A
5	R-MF_21	43.432556, 3.394222	Mont Ferrier, Tourbes	US 2076	Well PT 2052	1st c CE	Archaeological artifacts	Roman	B
6	R-MF_23	43.432556, 3.394222	Mont Ferrier, Tourbes	US 2076	Well PT 2052	1st c CE	Archaeological artifacts	Roman	
7	R-MF_25	43.432556, 3.394222	Mont Ferrier, Tourbes	US 2076	Well PT 2052	1st c CE	Archaeological artifacts	Roman	B
8	R-HW70_18	48.080500, 7.399194	Horbourg-Wihr	N.D.	Pit ST7054	2nd c CE	Dendrochronology / Archaeological artifacts	Roman	C
9	R-HW71_03	48.080500, 7.399194	Horbourg-Wihr	N.D.	Pit ST7172	2nd c CE	Archaeological artifacts	Roman	C
10	R-HW71_17	48.080500, 7.399194	Horbourg-Wihr	N.D.	Pit ST7172	2nd c CE	Archaeological artifacts	Roman	C
11	R-R_09	43.471306, 3.670139	Roumeges, Poussan	US 5007(12/13)	Well PT 5001	1st-3rd c CE	Archaeological artifacts	Roman	
12	R-R_14	43.471306, 3.670139	Roumeges, Poussan	US 5007(12/13)	Well PT 5001	1st-3rd c CE	Archaeological artifacts	Roman	
13	R-LLE_02	43.300806, 3.239917	La Lesse-Espagnac, Sauvian	US 3019	Well PT 3005	175-225 CE	Archaeological artifacts	Roman	
14	R-LLE_08	43.300806, 3.239917	La Lesse-Espagnac, Sauvian	US 3019	Well PT 3005	175-225 CE	Archaeological artifacts	Roman	C
15	R-LLE_09	43.300806, 3.239917	La Lesse-Espagnac, Sauvian	US 3019	Well PT 3005	175-225 CE	Archaeological artifacts	Roman	
16	R-LLE_13	43.300806, 3.239917	La Lesse-Espagnac, Sauvian	US 3019	Well PT 3005	175-225 CE	Archaeological artifacts	Roman	D
17	R-LLE_14	43.300806, 3.239917	La Lesse-Espagnac, Sauvian	US 3019	Well PT 3005	175-225 CE	Archaeological artifacts	Roman	D
18	R-TDM_06	43.472806, 3.223000	Terrasses de Montfau, Magalas	US 4015	Well PT 4000	4th c CE	Archaeological artifacts	Roman	E
19	R-TDM_08	43.472806, 3.223000	Terrasses de Montfau, Magalas	US 4015	Well PT 4000	4th c CE	Archaeological artifacts	Roman	E
20	R-TDM_10	43.472806, 3.223000	Terrasses de Montfau, Magalas	US 4015	Well PT 4000	4th c CE	Archaeological artifacts	Roman	
21	M-MDV13_07	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 13525	Well PT 13319	1605 ± 35 BP (417-515 CE)	C14	Late Roman/ Medieval	

22	M-MDV12_02	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 12111	Well PT 12024	1220 ± 30 BP (731-851 CE)	C14	Early Medieval	
23	M-MDV12_04	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 12111	Well PT 12024	1220 ± 30 BP (731-851 CE)	C14	Early Medieval	F
24	M-MDV12_05	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 12111	Well PT 12024	1220 ± 30 BP (731-851 CE)	C14	Early Medieval	
25	M-MDV12_07	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 12111	Well PT 12024	1220 ± 30 BP (731-851 CE)	C14	Early Medieval	
26	M-MDV12_09	43.808222, 4.368222	Mas de Vignoles XIV, Nîmes	US 12111	Well PT 12024	1220 ± 30 BP (731-851 CE)	C14	Early Medieval	F
27	M-C_27	45.436417, 5.520306	Colletiere, Charavines	N.D.	Cultural layer, rubbish deposits	1006-1040 CE	Dendrochronology	Medieval	
28	M-LM_22	47.900472, 1.884333	La Madeleine, Orléans	US 15126	Cesspit F 1517	1050-1200 CE	Archaeological artifacts	Medieval	

† Genetic clusters composed of identical clones. The genetic cluster was assigned according to the relatedness analyses described in the results section.


a
b
c
Dim1 (4.88%)
Dim2 (1.33%)
Dim1 (3.11%)
Dim2 (1.26%)
Wine grapes − West and Central Europe
Wine grapes − Iberian Peninsula and Northwest Africa
Wine grapes − Balkans and East Europe
Table grapes
Other domesticated grapes
V. vinifera subsp. sylvestris
Grapereseq panel and ancient
Whole-genome reference data (Table S2)
Iron Age:
1. IA-LC_01*
Roman Period:
2. R-MDV14_04
3. R-MDV14_07*
4. R-MDV14_09
5. R-MF_21
6. R-MF_23
7. R-MF_25
8. R-HW70_18
9. R-HW71_03*
10. R-HW71_17
11. R-R_09
12. R-R_14*
13. R-LLE_02
14. R-LLE_08
15. R-LLE_09
16. R-LLE_13
17. R-LLE_14
18. R-TDM_06*
19. R-TDM_08*
20. R-TDM_10
Medieval Period:
21. M-MDV13_07
22. M-MDV12_02
23. M-MDV12_04
24. M-MDV12_05
25. M-MDV12_07
26. M-MDV12_09
27. M-C_27
28. M-LM_22
Admixture props.
Caucasus Turkey
Central Europe
Western Europe
North Africa
East - table grapes
West - wine grapes
Iberian - wine grapes
Balkans - wine grapes
American/ Asian Vitis species
V. vinifera subsp. sylvestris
V. vinifera subsp. vinifera
Iron Age
Roman Period
Medieval Period


a
Iron Age
Roman Period
Medieval Period
A
B
C
D
E
F
IA-LC_01
R-MDV14_04
R-MDV14_07
R-MDV14_09
R-MF_23
R-MF_21
R-MF_25
R-HW70_18
R-HW71_03*
R-HW71_17
R-R_09
R-R_14
R-LLE_02
R-LLE_08
R-LLE_09
R-LLE_13
R-LLE_14
R-TDM_06*
R-TDM_08*
R-TDM_10
M-MDV13_07
M-MDV12_02
M-MDV12_04
M-MDV12_09*
M-MDV12_05
M-MDV12_07
M-C_27
M-LM_22
0.5
0.2
0.0
Kinship Coeff.
b
Bay of Biscay
France
Parent-offspring
Highly-related
Iron Age
Roman Period
Medieval Period
La Madeleine
Horbourg-Wihr
Colletière
La Cougourlude
Terrasses de Montfau
Mas de Vignoles XIV
La Lesse-Espagnac
Roumeges
Mont Ferrier


R-LLE_13/14 (D)
R-TDM_06*/08* (E)
R-TDM_10
M-MDV13_07
R-LLE_09
R-LLE_02
IA-LC_01
R-MDV14_04/07/09 (A)
Dongine
Mondeuse
Tressot
Chouchillon
M-C_27
Mondeuse Blanche
Servanin
M-MDV12_07
Dureza
Syrah
M-MDV12_04/09* (F)
M-MDV12_02
Cuatendrá
R-HW70_18
R-HW71_03*/17
R-LLE_08
(C)
Humagne Blanc
Piquepoul Noir
Wildbacher de Hongrie
(Collection Ravaz)
R-R_09
R-R_14
M-MDV12_05
Riesling Bleu
(Collection Oberlin)
Mancens = Giro
de Baleares
Verués de Huarte
Parduca
Carrasquín
Arvine
R-MF_23
Lado
Alfrocheiro preto
Grappenoux
Chatus
Roussette basse de Seyssel
Persan
Sylvaner
Rivairenc
(Aspiran noir)
Amigne
R-MF_21/25 (B)
Chenin
M-LM_22
Savagnin Blanc
Cinsaut
Blanquiliña
Folgasão
Pinotage
Viosinho
Trousseau
Teinturier
Pinot Noir
Petit Manseng
Roi des precoces
Siegerrebe
Grüner Veltliner
Redondal
Flora
Tinta Madeira
Verdejo
Bastardo Blanco
Prieto picudo
Chardonnay
Maturana Blanca
Reference panel
Iron Age
Roman period
Medieval period
Parent-offspring
Highly related