

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	As stated in the Methods and Data Availability statement, reviusly published data were downloaded from original public repositories, included the National Center for Biotechnology Information (project number: PRJNA489970, PRJNA999173, PRJNA393611, PRJNA388292, PRJNA485199, PRJNA490319, PRJNA868429 and PRJNA731597) and the China National Center for Bioinformation (project number: PRJCA009314).
Data analysis	PALEOMIX v1.2.13, Bowtie2 v2.3.4.1, mapDamage2 v2.0.9, PLINK v1.90, SMARTPCA (v1600), ADMIXTURE v1.3.0, NbClust R package v3.0.1, FastME v2.1.6.2, ADMIXTOOLS v7.0.2, READ v2.0.0, R v4.3.2 with tidyverse v.2.0.0, ggplot2 v.4.0.0, rnatuarearth v1.1.0 .

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

As stated in the Data Availability statement, all demultiplexed sequencing data and all alignments against the 12x.2 grape reference genome generated in this study are deposited in the European Nucleotide Archive (ENA) under the following accession code PRJEB94459.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This study is an ancient DNA investigation on 49 archaeological grape pips (<i>Vitis vinifera</i>) aimed at reconstructing grapevine genetic diversity and viticulture practices through time using genome-wide population genetic and relatedness analyses. This work follows a comparative design with individual archaeological grape pips as experimental units structured hierarchically by site and chronological period.
Research sample	The research sample comprises 49 waterlogged archaeological grape pips recovered from 20 sites across France and Ibiza, spanning contexts from the Bronze Age to the Medieval period. These pips are intended to represent the historical grapevine populations associated with their respective spatial and chronological contexts. Sex and individual age are not applicable. All ancient and modern genomic datasets used in this study are cited and described in the Methods and the Data Availability statement.
Sampling strategy	Sampling was dependent upon the availability of ancient waterlogged grape pips.
Data collection	The pips were recovered and documented during archaeological excavations conducted by professional archaeologists from Inrap, CNRS, and partner institutions, who recorded, on paper, contextual information (site, stratigraphy, chronology) as part of standard excavation procedures (cf Supplementary Information and Author contributions statement). Samples were processed in dedicated clean laboratory facilities at the Centre for Anthropobiology and Genomics of Toulouse (CAGT, University of Toulouse, France), using standard molecular biology equipment (see Methods for detailed procedures).
Timing and spatial scale	Temporal coverage: 2200 BCE to 1400 CE. Chronological information derives from AMS radiocarbon measurements, stratigraphic association and artefactual typology. Spatial coverage: 20 sites across southern/northern France and Ibiza (Spain). (Full provenience and dating of samples as well as excavation informations in Supplementary information).
Data exclusions	All data were included.

Reproducibility	All methods and data are described in Methods section with explicit reference to underlying parameters, and made available for future replication.
Randomization	Samples groups were defined to reflect archaeological populations based on genetic profiles.
Blinding	NA

Did the study involve field work? ☐ Yes ☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☐	☒ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Palaeontology and Archaeology

Specimen provenance	49 ancient grape pips (<i>Vitis vinifera</i>) were recovered from securely dated archaeological contexts preserved under anoxic conditions at 20 sites across France and Ibiza. Excavations were conducted between 1977 and 2021 (detailed information on excavation years, excavation teams, site locations, and cultural contexts is provided in the Supplementary Information) with all required legal authorizations issued by the French Ministry of Culture and the Consell Insular d'Eivissa, the regional authority responsible for archaeological heritage in Ibiza.
Specimen deposition	All DNA extracts are stored in freezers at the CAGT (Toulouse), a dedicated ancient DNA laboratory and are available upon direct contact to the corresponding authors.
Dating methods	Chronologies were established through stratigraphic association and artefactual typology. Additional radiocarbon dating of individual grape pips was obtained for several of the sites included in this study. All AMS radiocarbon measurements were performed at the Poznan Radiocarbon Laboratory (POLAND) using standard quality protocol. Radiocarbon data were calibrated with the IntCal20 curve (Reimer et al. 2020) and the OxCal (v4.4.2) software (Bronk Ramsey 2009).
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	As stated in the methods in the 'Ethics and sample' section, all samples were collected and analyzed with the appropriate permits from the relevant authorities (the French Ministry of Culture and the Consell Insular d'Eivissa). All samples are connected to an archaeologist or archaeobotanist co-author of the paper, who has been responsible for their study since the excavation and can vouch for their origin. We confirm that this research respects all ethical standards applicable to archaeology and archaeogenetics as reviewed and approved by the scientific committees of the MICA and Viniculture projects.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	Non relevant for archaeological materials.
Novel plant genotypes	None generated. No transgenic, edited, mutagenized, or hybrid lines were produced; analyses relied on sequencing of archaeological material only.
Authentication	Ancient DNA authenticity and data quality were assessed via: (i) characteristic aDNA damage profiles, (ii) endogenous DNA quantification, and (iii) downstream filters to limit impacts from postmortem DNA damages.