

Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ An indication of 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
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ 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 statistics 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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ 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 d , Pearson's r), indicating how they were calculated
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

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

Data collection BWA v0.6.1, HaploGrep2 v2.1.19, cTools v11/2016, contamMix v1.0-10, ANGSD v0.923, OxCal v4.3.2

Data analysis ADMIXTOOLS v5.1, EIGENSOFT v7.2.1, IBM SPSS Statistics v.25, SYSTAT v.11.5

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The aligned sequences are available through the European Nucleotide Archive under accession number PRJEB32086. Genotype data used in analysis are available at <https://reich.hms.harvard.edu/datasets>.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description	Genetic analyses were performed on DNA data generated from ancient human skeletons. Population genetic statistics, primarily testing historical relationships by measuring allele-sharing patterns across populations, were computed using genome-wide SNP genotypes.
Research sample	Four ancient human individuals buried at Shum Laka in Cameroon; 63 newly reported present-day individuals from five populations in Cameroon (for comparative analyses); ancient African individuals from Gallego Llorente et al. 2015, Schlebusch et al. 2017, and Skoglund et al. 2017; present-day African individuals from Mallick et al. 2016 and Fan et al. 2019.
Sampling strategy	We sampled available bones from six Shum Laka individuals and obtained working data from four. We targeted approximately 1.2 million genome-wide SNPs, which effectively cover almost all independent loci (due to linkage disequilibrium) and provide good power in population history analyses (all remains in this study yielding good coverage).
Data collection	DNA from the ancient remains was extracted, sequenced, and processed into SNP genotype calls (final data overseen by D.R. and S.Mal.).
Timing and spatial scale	Ancient individuals were sampled from the Shum Laka rockshelter in western Cameroon. Newly reported present-day individuals were from western and southwestern Cameroon.
Data exclusions	Two of the sampled skeletons did not yield working data as assessed by pre-established ancient DNA quality criteria.
Reproducibility	All attempts to reproduce were successful.
Randomization	The only subgroup assignments were by date for the ancient individuals and by ethno-linguistic group for the present-day individuals.
Blinding	Analyses were performed either for all four individuals separately, all four grouped together, or for the two temporally separated pairs; other sample-specific features were not relevant to results.
Did the study involve field work?	☐ Yes ☒ No

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants

Methods

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

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Samples were collected at market places or other locations of a similar nature where many individuals of the ethnic group of interest were expected to reside or assemble. Samples were only collected from males who declared themselves to be 18 years of age or older and not the sibling of another donor. The self-declared ethnic identity of the donor was recorded after the sample was taken, but samples were collected without discrimination on the basis of ethnic identity. There was no genotypic
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Recruitment

data on donors available to collectors; subsequently, for analysis, we confirmed that none of the individuals were substantial genetic outliers relative to their ethno-linguistic groups.

Participants were recruited by public announcement at the sampling location with samples taken in the order donors presented themselves. No monetary reward was offered.