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Guido Brandt

Wolfgang Haak


Christina J. Adler

Christina Roth

Anna Szécsényi-Nagy

See next page for additional authors

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Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity

Abstract

The processes that shaped modern European mitochondrial DNA (mtDNA) variation remain unclear. The initial peopling by Palaeolithic hunter-gatherers ~42,000 years ago and the immigration of Neolithic farmers into Europe ~8000 years ago appear to have played important roles but do not explain present-day mtDNA diversity. We generated mtDNA profiles of 364 individuals from prehistoric cultures in Central Europe to perform a chronological study, spanning the Early Neolithic to the Early Bronze Age (5500 to 1550 calibrated years before the common era). We used this transect through time to identify four marked shifts in genetic composition during the Neolithic period, revealing a key role for Late Neolithic cultures in shaping modern Central European genetic diversity.

Keywords

Palaeolithic, Neolithic, mitochondrial DNA, Central European, genetic diversity

Disciplines

Anthropology | Genetics and Genomics | Life Sciences | Social and Behavioral Sciences

Comments

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Author(s)

Guido Brandt, Wolfgang Haak, Christina J. Adler, Christina Roth, Anna Szécsényi-Nagy, Sarah Karimnia, Sabine Möller-Rieker, Harald Meller, Robert Ganslmeier, Susanne Friederich, Veit Dresely, Nicole Nicklisch, Joseph K. Pickrell, Frank Sirocko, David Reich, Alan Cooper, Kurt W. Alt, and Genographic Consortium

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Ancient DNA reveals key stages in the formation of Central European mitochondrial genetic diversity

Guido Brandt^{1,*,\dagger}, Wolfgang Haak^{2,*,\dagger}, Christina J. Adler³, Christina Roth¹, Anna Szécsényi-Nagy¹, Sarah Karimnia¹, Sabine Möller-Rieker¹, Harald Meller⁴, Robert Ganslmeier⁴, Susanne Friederich⁴, Veit Dresely⁴, Nicole Nicklisch¹, Joseph K. Pickrell⁵, Frank Sirocko⁶, David Reich⁵, Alan Cooper^{2,\ddagger}, Kurt W. Alt^{1,\ddagger}, and The Genographic Consortium⁷

¹Institute of Anthropology, Johannes Gutenberg University of Mainz, Colonel-Kleinmann-Weg 2, D-55128 Mainz, Germany

²The Australian Centre for Ancient DNA, University of Adelaide, Adelaide, South Australia 5005, Australia

³Institute of Dental Research, Faculty of Dentistry, University of Sydney, Sydney, New South Wales 5006, Australia

⁴State Office for Heritage Management and Archaeology Saxony-Anhalt and Heritage Museum, Richard-Wagner-Straße 9, D-06114 Halle (Saale), Germany

⁵Department of Genetics, Harvard Medical School, Boston, Massachusetts, MA 02115, USA

⁶Institute of Geosciences, Johannes Gutenberg University of Mainz, Johann-Joachim-Becher-Weg 21, D-55128 Mainz, Germany

Abstract

The processes which shaped modern European mitochondrial DNA (mtDNA) variation remain unclear. The initial peopling by Palaeolithic hunter-gatherers ~42kyrs ago and the immigration of Neolithic farmers into Europe ~8kyrs ago appear to have played important roles, but do not explain present-day mtDNA diversity. We generated mtDNA profiles of 364 individuals from prehistoric cultures in Central Europe to perform a chronological study, spanning the Early Neolithic to the Early Bronze Age (5,500–1,550 cal BC). We use this transect through time to identify four marked shifts in genetic composition during the Neolithic period, revealing a key role for Late Neolithic cultures in shaping modern Central European genetic diversity.

*Correspondence to: brandtg@uni-mainz.de, wolfgang.haak@adelaide.edu.au.

[†]These authors contributed equally to this work

[‡]These authors are equal senior authors

⁷Consortium members are listed in the Supplementary Materials

Supplementary Materials

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Materials and Methods

Figs. S1 to S10

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Tables S1 to S17

Movie S1

Main Text: The Central European Neolithic and the subsequent Early Bronze Age (EBA), reflect periods of momentous cultural changes (1–4). However, the extent to which such prehistoric cultural changes were accompanied by differences in the underlying genetics of local populations (1–5) and how such population shifts contributed to the present-day genetic diversity of Central Europe (6–9) are yet to be understood. Ancient DNA studies have revealed genetic discontinuities between indigenous hunter-gatherers and early farmers, and between the latter and present-day Europeans (10–11). While this confirms the importance of genetic shifts after the arrival of farming, the number and sequence of events and their potential origins and contributions to the genetic composition of modern-day Central Europe remain unclear (5–6, 12).

We collected samples from 25 sites of the Mittelbe-Saale region in Saxony-Anhalt, Germany, attributed to nine archaeological cultures of the Early, Middle, and Late Neolithic period and the EBA, spanning ~4,000 years (Figs. 1A, S1-S2, Table S1) (13). Mittelbe-Saale played a key role in human prehistory in Central Europe (4, 13), and the continuous settlement activity from the Palaeolithic until today provides a detailed record of Neolithic cultures, including those with expansive European importance such as the *Linear Pottery* (LBK), *Funnel Beaker* (FBC), *Corded Ware* (CWC), and *Bell-Beaker* (BBC) (Fig. S2) (1–4, 13). We genotyped the hyper-variable segment I and II of the control region and 22 single-nucleotide coding region polymorphisms from 364 individuals (Tables S2-S3) (13), allowing unambiguous haplogroup assignment, in order to characterise changes in the mtDNA variability of the Mittelbe-Saale cultures. To examine genetic affinities of the investigated cultures to prehistoric and modern-day populations, we used 198 mtDNA data from published Mesolithic, Neolithic and Bronze Age specimens across western Eurasia (Fig. 1B, Table S4) (13) and a database of 67,996 sequences from present-day Eurasian populations (13). We animated our results to illustrate the observed changes in space and time (Movie S1).

In order to detect patterns of continuity or discontinuity among and between the archaeological cultures we conducted cluster analysis (Fig. 2A, Table S5) based on haplogroup frequencies and used sequence data to perform genetic distance analysis (F_{st}) (Fig. 2B-C, Table S6), and analyses of molecular variance (AMOVA) (Table S7) (13). We performed a Mantel-test to examine whether the genetic distances correlate with the temporal distance between the ancient cultures, as expected from genetic drift affecting small populations. However, the Mantel-test shows no strong correlation with time (Pearson's coefficient $r=0.3923$, $p=0.0591$), suggesting more sudden and marked fluctuations in genetic composition. We also developed a test for population continuity (TPC) (Figs. 2D, Table S8) to further evaluate whether changes in haplogroup frequencies and composition could be explained by genetic drift, or are likely due to other factors such as introgression via migration (introducing new haplogroups) or replacement (13). Our detailed transect through time reveals a complex pattern of both genetic continuity and discontinuity (Figs 2A-D, Tables S5-S8), based on the assumption that haplogroups are monophyletic and neutral, i.e. not evolving into new haplogroups via mutations from an existing haplogroup or due to selection. Indigenous Central European hunter-gatherers (HGC) (10, 14) are clearly set apart from the Neolithic Mittelbe-Saale cultures on the basis

of both cluster analysis (Fig. 2A), and significantly different F_{st} -values ($F_{st}=0.0845-0.21358$, $p=0.00000-0.03292$) (Fig. 2B), due to mutually exclusive haplogroup compositions (Fig. S3, Movie S1). The results of the TPC show that the transition from hunter-gatherers to the LBK farmers cannot be explained by genetic drift alone ($p=0.000001$) (Fig. 2D), consistent with previous findings (10–11).

The Mittelbe-Saale cultures themselves can be further differentiated into distinct Early/Middle Neolithic and Late Neolithic/EBA clusters (Fig. 2A), as shown by significantly higher F_{st} -values ($F_{st}=0.02776-0.05605$, $p=0.00000-0.016616$) (Fig. 2B-C). The two groupings are also strongly supported in AMOVA tests, where 289 different combinations of the ancient cultures were examined. We found the highest among group variance, and low variation within the groups, when the Mittelbe-Saale cultures were separated into two groups of Early/Middle Neolithic and Late Neolithic/EBA cultures (among groups: $F_{st}=0.03061$, $p=0.00683$; within groups: $F_{st}=0.00468$, $p=0.18891$) (Table S7). Similarly, TPC also indicates that changes in the mtDNA profiles between most of the Early/Middle Neolithic cultures and the Late Neolithic/EBA ($p=0.000007-0.049428$) as well as between the BBC and EBA ($p=0.000803$) (Fig. 2D) cannot be explained by drift alone. These results suggest multiple population genetic shifts: the first during the introduction of farming, followed by further changes during the later Neolithic.

To further explore these patterns we used principal component analysis (PCA) and cluster analysis (Fig. 1C-D, Table S9) to describe the characteristic haplogroups of each culture and to identify genetic affinities to other prehistoric populations (13). We then examined affinities to present-day Eurasian populations to inform on potential geographic origins of the different cultures. We performed multidimensional scaling (MDS) (Fig. S4A-I, Table S10) based on continuous sequence data, which is sensitive to shared haplotypes between populations (13). In parallel, we also used PCA (S5A-I, Table S11), Procrustes and cluster analyses (Figs. S6A-I, Table 12), and genetic distance mapping (Figs. 7A-I, Table 13) based on discrete haplogroup frequencies (13).

Detailed investigation of the mtDNA composition of each culture reveals a series of haplogroup frequency changes due to different genetic profiles for hunter-gatherers, the Early/Middle Neolithic group, and individual cultures of the later Neolithic/EBA including the *Bernburg* culture (BEC) and the temporally overlapping BBC, CWC, and EBA (Figs. 3, S3, Movie S1). The latter suggests that this period was heterogeneous, with genetically differentiated cultures resulting in a separation in the PCA (Fig. 1C). These shifts are also visible in the genetic distance maps and Procrustes-projected PCAs, where the Near Eastern affinity of the LBK and its subsequent regional derivatives switches to a clear European affinity in later Neolithic/EBA cultures, with distinct geographic orientations (see below, Movie S1, Figs. S6A-I-7A-I).

We synthesised the different lines of evidence from our comparative genetic analyses to reconstruct a series of four prominent population dynamic events (termed A-D, Fig 3, Movie S1), which we reconcile with known European cultural expansions (1–5). Overall, these analyses reveal a pattern of relative genetic continuity for the first 2,500 years after the

introduction of farming in Central Europe, followed by a series of discontinuities in the later Neolithic.

Event A marks the transition from foraging to farming introduced by the LBK, which reached Central Europe ~5,500 cal BC (Movie S1) (1–3). MtDNA data from Central European hunter-gatherers comprises exclusively U lineages (U, U4, U5, and U8) (10, 14), whereas the LBK is characterised by a distinct haplogroup profile including N1a, T2, K, J, HV, V, W, and X (Figs. 1C) (11). These haplogroups can be denoted as a mitochondrial ‘Neolithic package’, and comprise around 79.4% of the diversity in the LBK, while hunter-gatherer lineages are rare (2.9%) (Fig. 3). This marked shift suggests a rapid transition process, with the comparative analyses indicating a genetic influx from the Near East, Anatolia and the Caucasus (Movie S1, Figs. S4A–S7A) (1–3, 11). The subsequent Early/Middle Neolithic cultures closely resemble the mtDNA haplogroup composition of the LBK (Figs. 1C–D, 2A–D, Table S7) with similar affinities to present-day Near East populations (Figs. S4B–E–S7B–E), suggesting a period of genetic continuity over 2,500 years.

Event B describes a bidirectional interaction along a north-south axis during the Early and Middle Neolithic, which saw the introduction of the ‘Neolithic package’ to southern Scandinavia by Central European cultures (B₁ ~4,100 cal BC), followed by a reflux of hunter-gatherer lineages to Central Europe (B₂ ~3,100 cal BC) (Movie S1). The Neolithic transition of southern Scandinavia was closely linked to the FBC, which replaced local foragers that had retained the Mesolithic lifestyle for ~1,500 years after farming arrived in Central Europe (1–3). FBC individuals from Scandinavia (10, 15–16) have yielded high frequencies of hunter-gatherer haplogroups (30%) alongside a large amount of ‘Neolithic package’ haplogroups (60%) (Table S9), leading to an intermediate position between hunter-gatherers and the Early/Middle Neolithic Mittelbe-Saale cultures in the PCA (Fig. 1C). This suggests that pioneer groups from Central Europe had interacted with local hunter-gatherers who adopted farming (Movie S1) (1–4), a view also supported by ancient genomic data (16). Subsequently, around a millennium later in Mittelbe-Saale, a genetic shift associated with the BEC (Fig. 1A–D, Table S7), a late representative of the FBC in Central Europe (4), saw an increase in hunter-gatherer lineages (29.4%) and decrease in farmer lineages (47.1%) (Fig. 3) resulting in a haplogroup composition similar to the Scandinavian FBC (Fig. 1C) (10, 15). While previous populations show affinities to the Near East, the BEC marks a clear shift towards those in present-day North Europe (Movie S1, Figs. S4F–S7F).

In the Late Neolithic, we identify two independent events (C and D), each associated with major contemporary Pan-European phenomena. Event C (~2,800 cal BC) is marked by the emergence of the CWC (Movie S1), whose subgroups were widespread across Central and Eastern Europe (Fig. S2) (2–4). The CWC is characterised by haplogroups I and U2 (4.6%), which are new maternal elements in Mittelbe-Saale (Fig. 1C, S3), and appear alongside other Late Neolithic/EBA lineages such as T1 (6.8%) and hunter-gatherer haplogroups U4 and U5 (20.5%), while Early/Middle Neolithic haplogroups further decrease (45.5%) (Fig. 3). The binomial probability that we missed I and U2 in 211 individuals of preceding cultures is very low ($p=0.00$). Haplogroup U2 has been reported exclusively from Paleolithic, Mesolithic, and Bronze Age samples from Russia (17–19) and PCA and Cluster

analyses reveal similarities of the CWC to two ancient Kurgan groups of South Siberia (19) and Kazakhstan (20) (Figs. 1C-D), in which haplogroups I, U2, and T1 are frequent (18.2–37.5%) (Table S9). Intriguingly, the Y chromosomal haplogroup R1a1a, frequent in ancient Siberian populations (19), has previously been detected in our CWC dataset (21), suggesting additional paternal genetic links to Kurgan cultures. Together with the affinities of the CWC to present-day populations of Eastern Europe, the Baltics, and the Caucasus (Figs. S4G-S7G), this suggests a genetic influx into Central Europe from the East, likely influenced by Kurgan cultures (Movie S1) (2–3).

Event D (~2,500 cal BC) is defined by the BBC (Movie S1), the western counterpart of the CWC (Fig. S2) (2–4). BBC groups appeared ~300 years later in Mittelbe-Saale and coexisted alongside the CWC for more than 300 years (4). The BBC is distinguished from the CWC by the absence of haplogroup I and U2, and an overwhelmingly dominant genetic signature of haplogroup H (48.3%) (Fig. S3), leading to a separation of the BBC from all other Mittelbe-Saale cultures in PCA and cluster analyses (Figs. 1C-D). H remains the most frequent haplogroup in West European populations today (~40%) (8–9) and was absent in Central European hunter-gatherers (10, 14), but prevalent in ancient populations of the Iberian Peninsula since Mesolithic times (20.7–70.7%) (Table S9) (22–24). As a result, the BBC clusters with these Iberian populations (Figs. 1C-D), whereas the results from Procrustes and MDS were less informative. However, genetic links between the BBC and modern Iberian populations were supported by genetic distance maps accounting for H sub-haplogroups (Fig. S7H) and ancient mitochondrial H genomes (12). These suggest the BBC was associated with a genetic influx from Southwest Europe (Movie S1), which is consistent with the oldest archaeological signs of this culture being found in Portugal ~2,800 cal BC (2–3).

The onset of the EBA in Mittelbe-Saale (~2,200 cal BC) was characterised by socially and economically stratified societies associated with the emerging metallurgies (2–4). All the analyses show close genetic links between the EBA and the CWC (Figs 1C-D, 2A), on the basis of elevated frequencies of Late Neolithic/EBA haplogroups such as I, U2, and T1 (22.3%) (Figs. 1C, 3, S3), and both appear to have similar affinities to modern-day East European populations (Movie S1, Figs. S5I-S8I). TPC (Fig. 2D) indicate a minimal contribution of the BBC to the EBA in Central Europe. Thus, the Late Neolithic/EBA in Mittelbe-Saale appears to have witnessed rapid and dynamic changes in mtDNA composition at the crossroads of distinct Eastern and Western European influences (Movie S1).

To investigate the potential impact of the geographically widespread archaeological cultures and events examined here (Fig. S2) on the demography and genetic variation of present-day Central Europeans we compared the ancient data with a Central European metapopulation (CEM) consisting of 500 randomly selected individuals (13). AMOVA supports a model of continuity from the Late Neolithic/EBA to the CEM with the best inter/intra group variance observed when all Late Neolithic/EBA samples are pooled with the CEM into one group and the Early/Middle Neolithic specimens into another (among groups=2.57%, $F_{st}=0.02572$, $p=0.00891$; within group=0.50%, $F_{st}=0.00511$, $p=0.08089$) (Table S14). TPC analyses also support continuity since the Late Neolithic/EBA ($p=0.134672-0.418949$) (Fig. 2D).

Similarly, Bayesian coalescent-based simulations (13) support a demographic model involving exponential population growth since the Neolithic with a contribution of at least 50% migrants to Mittelbe-Saale during the Early Neolithic. This is followed by a constant ratio of gene flow/admixture between Early/Middle and incoming Late Neolithic/EBA components, and after this fusion, a genetic continuity until the present-day (AIC 99.9%) (Fig. S8, Table S15). The fact that continuity since the Late Neolithic/EBA could not be rejected confirms that the succeeding events B-D, despite their differing geographic affinities, had formed today's mtDNA diversity. Notably, the CEM clusters with the Late Neolithic cultures and individuals of the BBC in particular (Fig 2A), suggesting that the Western European mtDNA variability had a stronger influence than the contemporaneous eastern CWC/EBA complex, implying yet another shift after the EBA.

We evaluated the amount of lineages in the CEM that can be attributed to particular time periods by characteristic haplogroups (13) and found that a total of 53% can currently be assigned to the Palaeolithic/Mesolithic (16%), Early/Middle Neolithic (31.2%) and Late Neolithic periods (5.8%) (Fig. 3). The remaining proportion of lineages (47% - mainly haplogroup H) requires further resolution (12). The presence of all major mtDNA haplogroups by the end of the Neolithic makes it increasingly difficult to discern recent demographic changes, and would require larger population events to have an observable effect and/or full mitochondrial genome sequencing to detect more subtle changes.

The detailed genetic analyses of this transect through Neolithic Central Europe demonstrate the key role of Late Neolithic cultures at the dawn of metallurgy and stratified societies in the formation of modern Central European mtDNA diversity. The four successive genetic shifts highlight the biological cohesiveness of archaeological cultures such as the LBK, FBC, CWC, and BBC cultures, and the importance and dynamics of genetic input from different geographic regions.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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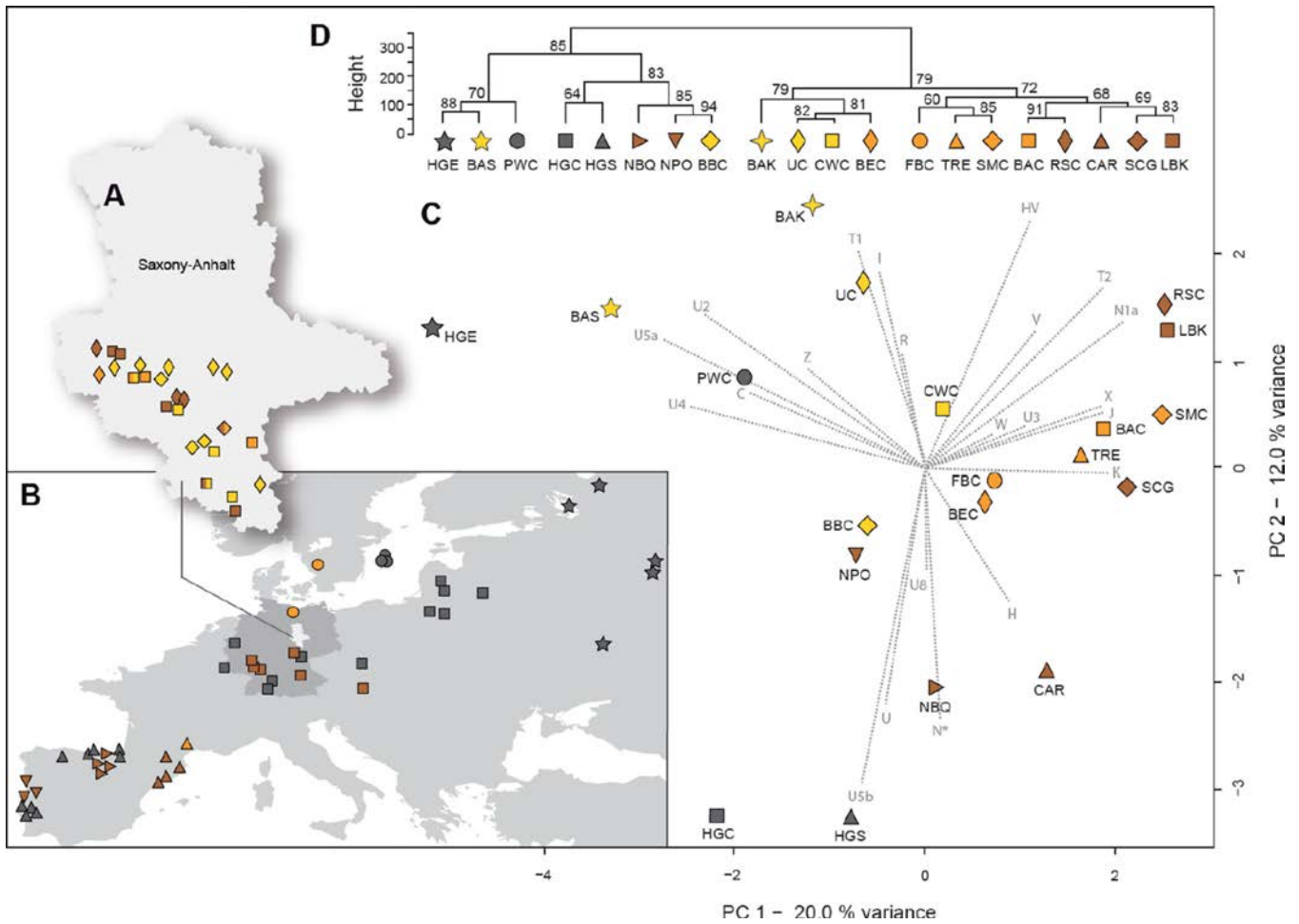


Fig. 1. Location of Mittelbe-Saale and prehistoric comparative data, as well as PCA and Ward clustering

Map A show the location of study sites in the Mittelbe-Saale region in Saxony-Anhalt, Germany of the Early Neolithic (LBK=*Linear Pottery* culture, RSC=*Rössen* culture, SCG=*Schöningen* group), Middle Neolithic (BAC=*Baalberge* culture, SMC=*Salzmünde* culture, BEC=*Bernburg* culture), Late Neolithic (CWC=*Corded Ware* culture, BBC=*Bell Beaker* culture), and Early Bronze Age (UC=*Unetice* culture) cultures. Map B display the location of published data from eleven Mesolithic (HGC=*hunter-gatherer Central Europe*, HGS=*hunter-gatherer South Europe*, HGE=*hunter-gatherer East Europe*, PWC=*Pitted Ware* culture), Neolithic (CAR=(Epi)Cardial, NPO=Neolithic Portugal, NBQ=Neolithic Basque Country & Navarre, FBC=*Funnel Beaker* culture, TRE=*Treilles* culture), and Bronze Age (BAS=*Bronze Age Siberia*, BAK=*Bronze Age Kazakhstan* (not shown)) populations. Symbols indicate populations from Central Europe (squares and diamonds), southern Scandinavia (circles), the Iberian Peninsula (triangles), and East Europe/Asia (stars). Colour shading of data points denote to hunter-gatherer (grey), Early Neolithic (brown), Middle Neolithic (orange), and Late Neolithic/EBA (yellow) samples (for further information see 13, Figs. S1-S2, and Table S1-S4). The haplogroup frequencies of these populations (Table S9) were used to perform PCA (C) and Ward clustering (D). The first two principal components of the PCA display 32.8 % of the total genetic variation. We superimposed each

haplogroup as component loading vectors (grey), proportionally to their contribution. P-values of the clusters are given in percent of reproduced clusters based on 10.000 bootstrap replicates.

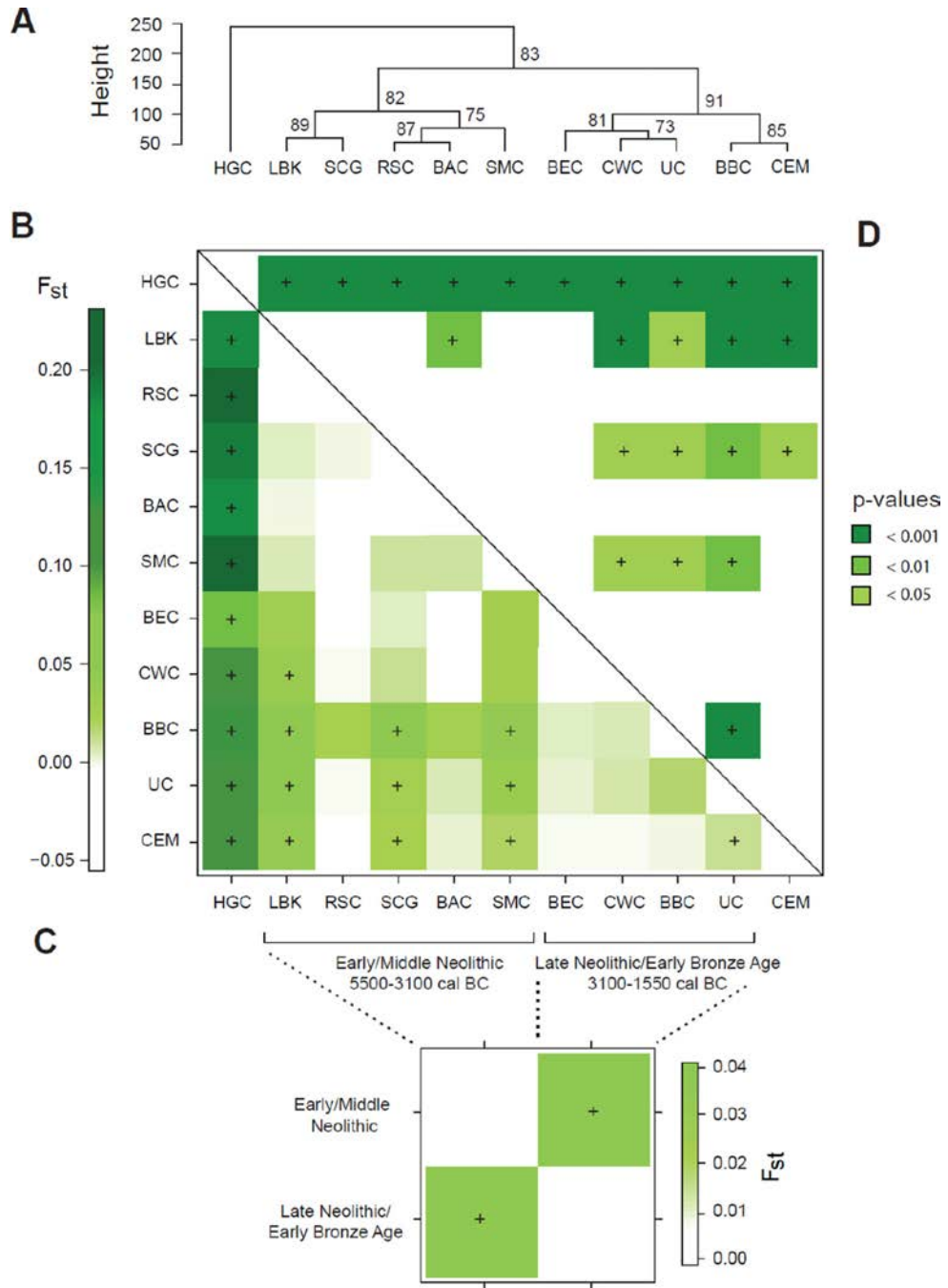


Fig. 2. Ward clustering, genetic distances and test of population continuity

Haplogroup frequencies of Central European hunter-gatherers (HGC), the nine Mittelbe-Saale cultures (see Fig. 1 for abbreviations), and a modern Central European metapopulation (CEM, n=500) (Table S5) were used for hierarchical Ward clustering (A). Cluster significance is given as percent of reproduced clusters on 10,000 bootstrap replicates. We computed genetic distances (F_{st}) (Table S6) based on HVS-I sequences (np 16059–16400) between all cultures (B) and pools of Early/Middle and Late Neolithic/EBA cultures (C). The shading indicates the degree of genetic distance between the cultures ranging from

white (small distances/high similarities) to green (large distance/dissimilarities). Significant differences are indicated by + (after 10,000 permutations and post-hoc Benjamini-Hochberg correction) (Table S6). The upper diagonal (D) summarises the results of the test of population continuity to evaluate possible effects of genetic drift. The p-values (Table S8) describe the probability that changes in haplogroup frequencies between two populations cannot be explained by genetic drift alone (white areas=non significant, green areas=significant (13).

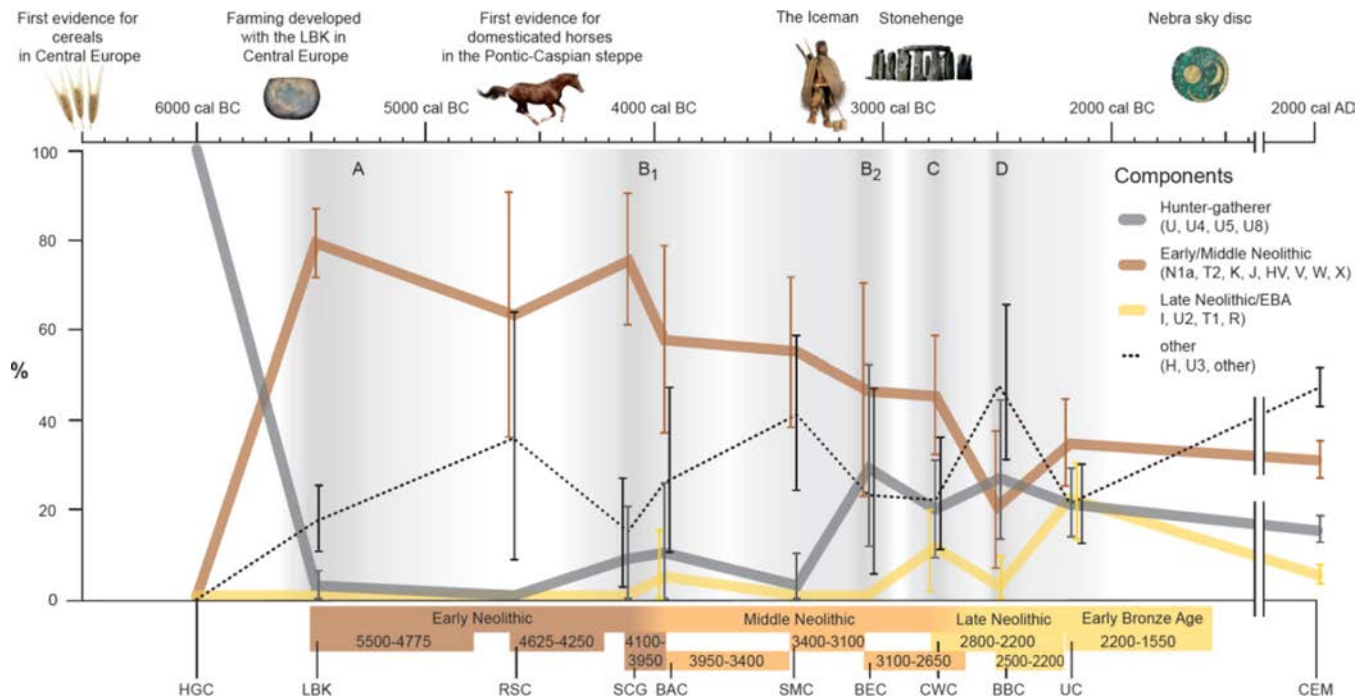


Fig. 3. Development of mtDNA components from the Late Mesolithic to present-day Population data from Central European hunter-gatherers (HGC), the nine Mittelbe-Saale cultures (see Fig. 1. for abbreviations), and a modern Central European metapopulation (CEM, n=500) were placed in chronological order (x-axis) and the amount of lineages ascribed to particular time periods were evaluated in each population. The characterising haplogroups of the hunter-gather (U, U4, U5, U8, grey), Early/Middle Neolithic (N1a, T2, K, J, HV, V, W, X, brown), and Late Neolithic/Early Bronze Age (LN/EBA, I, U2, T1, R, yellow) period were summarised into three respective components (y-axis) (Table S5) accordingly to the differentiation in the PCA (Fig. 1C). Haplogroups that could not be ascertained unambiguously to one of the three components were reported as ‘other’ (H, U3, other African and Asian lineages of the CEM) (13). Error bars of component frequencies indicate the 95% confidence interval of 10,000 bootstrap replicates (Table S5). Horizontal shading denotes the population dynamic events (A, B₁, B₂, C and D) inferred from the synthesis of all population genetic analyses (see main text).