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# MtDNA ANALYSIS OF EARLY-MEDIEVAL HUMAN REMAINS FROM THE CEMETERY IN GRODOWICE (PL)

The genetic composition of the medieval populations of Central Europe, Poland in particular, has been poorly investigated to date. Although a few DNA datasets from Poland have been published recently, no large-scale ancient DNA study on medieval populations has hitherto been reported. This paper reports the study of mitochondrial DNA (mtDNA) and presents the first population-level human DNA study from Lesser Poland by establishing mitochondrial DNA profiles for 13 samples from the Grodowice cemetery dated to the Medieval Period (11$^{th}$ to mid-13$^{th}$ century). The medieval sequences encompass almost the entire range of Western Eurasian macro-haplogroups: H, J, U. Interestingly, there is one sample which belongs to the Asian haplogroup G. aDNA sequences were compared with a dataset of 35,203 present-day sequences of the HVR I region of mtDNA including European, Near Eastern, and Asian populations, as well as 775 ancient sequences. Analyses of population genetics were performed, including genetic distances ($F_{ST}$), multidimensional scaling (MDS), principal component analysis (PCA) and shared haplotype analysis (SHA). The shared haplotype analysis (SHA) showed that the medieval population from Grodowice shares the majority of haplotypes with the medieval populations from the contact-zones of today's Slovakia and Croatia (53.85%) as well as with Hungarian conquerors (46.15%).

KEY WORDS: ancient DNA, mitochondrial DNA, medieval period, Lesser Poland

## INTRODUCTION

There has been a remarkable increase in the number of ancient human DNA studies in recent years. As a result, a substantial record of mitochondrial sequences from many prehistoric sites – including medieval ones from across Western Eurasia – is now available ((Brandt *et al.* 2013, Bollognino *et al.* 2013; Juras *et al*. 2014; Kozłowski *et al.* 2014; Płoszaj *et al.* 2016; Płoszaj *et al.* 2017; Rudbeck *et al.* 2005; Stolarek *et al*. 2018). Although ancient human DNA datasets regarding Europe are numerous, those for modern-day Poland (medieval Lesser Poland, in particular) remain uninvestigated. To reconstruct the ethnic history of different peoples, modern molecular genetic approaches are widely used. The most appropriate tool which allows for the characterization of gene pools and for tracking maternal gene flow seems to be analysis of maternally inherited mitochondrial DNA (mtDNA).

Over the centuries the populations of Western Eurasia were undoubtedly subject to various episodes of expansion, population replacement, admixtures between divergent groups, as well as the formations of new medieval states and ethnicities

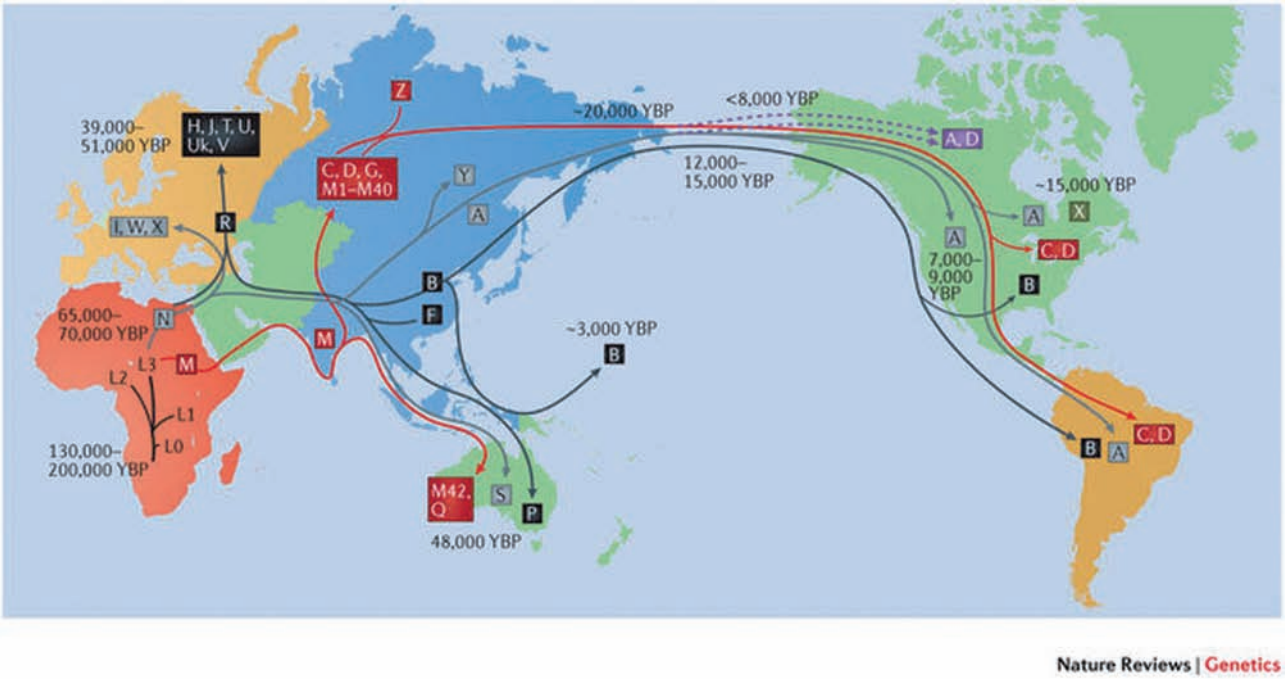


Fig. 1. Migration of human populations based on major mitochondrial haplogroups (Stewart & Chinnery 2015)

– and this is visible in present-day human genomes. Recent DNA studies suggest that most medieval populations were heterogeneous and shared common Western Eurasian mtDNA haplogroups, self-contained in their geographical locations and origin (Csákyova *et al.* 2016; Lazaridis *et al.* 2014; Meyer *et al.* 2012).

At present, the vast territories of East-Central and South-Eastern Europe are inhabited by Slavic populations. One should mention, however, that no large-scale ancient DNA study on the alleged ancestral populations of modern-day Slavs has been carried out to date. However, there are a few DNA datasets from Poland (Bogdanowicz, Grzybowski, Buś 2015; 2016; Juras *et al*. 2014; Juras *et al.* 2016; Kozłowski *et al.* 2014; Płoszaj *et al.* 2016; Płoszaj *et al.* 2017) and the regions geographically adjacent to present-day Poland: medieval Slovakia (Csákyová *et al.* 2015; 2016; Nagy *et al.* 2012; 2016), modern Czechia (Malyarchuk *et al.* 2006), Russia (Grzybowski *et al.* 2007), and 10th century Hungary (Tömöry *et al*. 2007; Csősz *et al*. 2016).

Mitochondrial DNA is often used in archaeogenetic research due to its smaller size compared to nuclear DNA, the lack of repetitive sequences, compact structure, and higher resistance to physical damage affecting it over the centuries. Mitochondrial genomes are located in the energy-generating organelles called mitochondria that are in each eukaryotic cell, where their amount per cell (about 8000 copies) depend on the type of organism and type of cells (Brown and Brown 2011). Human mtDNA is a double-stranded closed circular molecule of 16.6 kb in length consisting of a coding and non-coding region. The non-coding region (control region) of 1.1 kb in length contains two hypervariable regions (HVR I and HVR II). These regions are characterized by mutation rates ten times higher than for the coding region (Howel *et al.* 2007). Sequence variation of mtDNA has been generated by the sequential accumulation of new mutations along maternal lineages. Accordingly, human mtDNA contains a molecular recording of genealogical history and of the migrations of women who transmitted mitochondria through the generations (Torroni *et al.* 2006). Based on these mutations we can determine haplogroups, as was mentioned above, whose place of origin and extension path are already known (Fig. 1). Accordingly, there are Sub-Saharan (African) haplogroups: L0, L1, L2, L3, L4, L5, L6, L7, Western Eurasian haplogroups: H, T, U, V, X, K, I, J, W, Eastern Eurasian haplogroups: A, B, C, D, E, F, G, haplogroups of Native Americans: A, B, C, D, X, and the haplogroups of the South Pacific: P, Q, S (van Oven and Kayser 2009).

The universal standard for mtDNA nomenclature is derived from the first published complete mtDNA sequence "Cambridge Reference

Sequence" (CRS) (Anderson *et al.* 1981). A modified version of the CRS, in which 11 sequencing errors were corrected, was renamed "revised Cambridge Reference Sequence" (rCRS) and published in 1999 (Andrews *et al.* 1999). Nowadays, another reference sequence is used too – namely, the RSRS (Revised Sapience Reference Sequence) which contains a completely revised version of the rCRS (Behar *et al.* 2012).

The aim of this study is to determine matrilineal genetic structure and to present the first population-level human DNA study from Lesser Poland by establishing mitochondrial DNA profiles for 13 samples from the Grodowice cemetery dated to the Medieval Period (11th to mid-13th century)[1].

## MATERIALS AND METHODS

### Sample information, ancient DNA extraction, and amplification

The human skeletal remains (bones and teeth) used in this study were provided by the Institute of Archaeology, Jagiellonian University in Kraków (Poland). Thirteen bone specimens were collected from the Grodowice cemetery (Poland). Two bone fragments – one tooth and one compact bone fragment of a femur – were collected from each individual (see Table S1[2]). All stages of the work were performed under sterile conditions in a dedicated ancient DNA (aDNA) laboratory (Laboratory of Archaeogenetics at the Institute of Archaeology, Research Centre for the Humanities, Hungarian Academy of Sciences) following well-established aDNA workflow protocols.

The specimens were prepared following the protocols described by Kalmár *et al.* 2000; Shapiro and Hofreiter 2012. The bone and tooth samples were irradiated with UV-C light (1.0 J/cm$^2$, 25 min). The surfaces of tooth samples were cleaned by sandblasting (Bego, EasyBlast), while the surfaces of bone samples were removed with a fresh drilling bit at slow speed, followed by UV exposure for 20 min on each side. Bone and tooth fragments were mechanically ground into fine powder in a sterile mixer mill (Retsch MM301). Standard DNA extraction methods were used as described by Csákyová *et al.* (2016). First the samples (250 mg of bone powder) were washed with 8 ml EDTA (0.5 M, pH = 7.5) overnight at room temperature with continuous vertical rotation. After centrifugation, the supernatant was discarded and the remaining samples were suspended in 1.6 ml digestion mix (0.1 MEDTA, 20% N-lauryl sarcosine and 20 mg/ml proteinase K) and incubated overnight at 37°C with continuous vertical rotation. On the next day the samples were centrifuged at 13,000 rpm for 10 min, 350 µl supernatant was transferred to a fresh tube, 350 µl NH4-acetate (4 M) and 700 µl absolute ethanol were added, and samples were incubated overnight at −20°C. The DNeasy Tissue Kit (Qiagen) was used for further purification of the aDNA extract following the manufacturer's instructions: the mixture was transferred into a DNeasy Mini spin column and centrifuged at 6500 rpm for 1 min. The column was washed twice, DNA was eluted in a final volume of 70 µl and subsequently stored in the pre-PCR lab at −20°C. Several fragments of mtDNA hypervariable region I (HVR I) and the coding region were amplified in a total volume of 40 µl reaction mix, containing 6 µl of DNA extract, 20.4 µl $H_2O$, 1 × AmpliTaq Gold buffer, 0.8 mM dNTP mix, 0.9 mM MgCl2, 0.16 mg/ml BSA, 0.625 µM primers and 1.5 U AmpliTaq Gold DNA polymerase. The HVR I region of mtDNA was amplified in two overlapping fragments with two sets of primers, and an additional four primer pairs were used to amplify haplogroup diagnostic nucleotide positions in the coding region (see Table S2). The PCR reactions were performed in 38 amplification cycles consisting of three steps (denaturation at 94°C for 30 s, annealing at 55°C for 1 min and extension at 72°C for 30 s) with an initial denaturing step at 95°C for 10 min and final elongation at 72°C for 5 min. PCR products were checked on 8% native polyacrylamide gel. The purification of PCR products was performed using a QIAquick1PCR Purification Kit (Qiagen) following the manufacturer's protocol. Sequencing reactions were performed using the ABI PRISM BigDye1Terminator v3.1 Cycle Sequencing Ready Reaction Kit (Applied Biosystems) and sequencing products were purified

[1] Interdisciplinary research programme of materials from Grodowice was financed by the Ministry of Science and Higher Education in Poland (the *Diamond Grant*, project nr 0053/DIA/2012/41).

[2] All tables are included on the CD attached to this volume of *Przegląd Archeologiczny*.

by ethanol precipitation. The sequences were determined on an ABI PRISM 3100 (PE Applied Biosystems) in cooperation with BIOMI (Budapest, Hungary). The sequences were evaluated with Chromas Lite 2.4.1 and GeneDoc (Nicholas *et al.* 1996). The sequence polymorphisms in mtDNA (the range of HVR I is nucleotide positions (np) 16053–16420) were compared with the revised Cambridge Reference Sequence (rCRS) (Andrews *et al.* 1999) as well as the Reconstructed Sapiens Reference Sequence (RSRS, www.mtdnacommunity.org) (Behar *et al.* 2012). Haplogroup determination was carried out according to the mtDNA phylogeny of PhyloTree build 17, accessed on 18 February 2016 (www.phylotree.org) considering polymorphic positions of HVR I and four haplogroup- diagnostic position of the coding region (van Oven, Kayser 2009).

### Reference population data

aDNA sequences were compared with a dataset of 35,203 present-day mtDNA sequences from the HVR I region including European, Near Eastern and Asian populations, as well as 775 ancient sequences. The sequences were collected from published data and are listed in Tables S7-S9. Only those modern mtDNA sequences which were reported for the same sequence range as our ancient HVR I data were included in the comparison.

### Population genetics analysis

Population comparison was calculated using Arlequin 3.5.1 (Excoffier, Lischer 2010). Pairwise genetic distances ($F_{ST}$) were calculated based on HVR I sequences (np 16050–16383) assuming a Tamura & Nei substitution model (Tamura, Nei 1993) with a gamma value of 0.325. Significant variations in $F_{ST}$ values were tested by 10,000 permutations between 52 modern and 23 medieval populations and particularly between the medieval populations alone (Tables S7 and S8).

Multidimensional scaling (MDS) of medieval and modern populations was applied on the matrix of linearized Slatkin $F_{ST}$ values (Slatkin 1995) (Table S7 and S8) and visualized in a two-dimensional space (Fig. 2 and 3) using the metaMDS function based on Euclidean distances implemented in the Vega library of R 3.1.3 (http://www.r-project.org/).

Principal component analysis (PCA) was performed, based on mtDNA haplogroup frequencies of 22 medieval and 53 modern-day populations (Table S5 and S6). In the PCA of medieval populations, we considered 31 mtDNA haplogroups (A, B, C, D, G, F, H, HV, I, J, K, M, N, N1a, N1b, R/R0, T, T1, T2, U, U2, U3, U4, U5a, U5b, U7, U8, V, W, X, YZ), whereas in PCA with modern day populations 36 mtDNA haplogroups (A, B, C, D, G, F, H, HV, HV0, I, J, K, M, N, R/R0, T, T1, T2, U, U1, U2, U3, U4, U5, U5a, U5b, U6, U7, U8, U9, V, W, X, Y, Z, Other – all remaining haplogroups) were considered (Figs. 4-7). All PCA was performed using the prcomp function for categorical PCA, implemented in R 3.1.3 and plotted in a two-dimensional space, displaying the first two or the second and third principal components (PCs), respectively.

Shared haplotype analysis (SHA) was performed in order to detect and compare the mtDNA haplotypes shared between 22 ancient populations. Twelve populations from Europe and ten from Asia were studied, and the absolute and relative shared haplotypes were counted (Table S4).

## RESULTS

We obtained thirteen mtDNA sequences spanning the range of np 16053-16420. The DNA of investigated samples were extracted and amplified at least twice per individual from different elements, the HVR I fragments were reproduced in several PCR products. The results of these replicates along with the negative control results suggest the haplotypes to be authentic.

The medieval sequences encompass almost the entire range of Western Eurasian macro-haplogroups: H, J, U. Interestingly, there is one sample which belongs to an Asian haplogroup G (Table S3). We detected identical haplotypes by individuals G2 and G4 (belonged to haplogroup U5a1), G44 and G51 (haplogroup J2a1a1). Furthermore, there were three individuals with rCRS haplotype (haplogroups H2a2a1).

Pairwise genetic distances were calculated between 23 medieval populations (Table S7) and between the same medieval populations and a set of modern-day populations from Eurasia (Table S8). Following populations of ancient population-pool

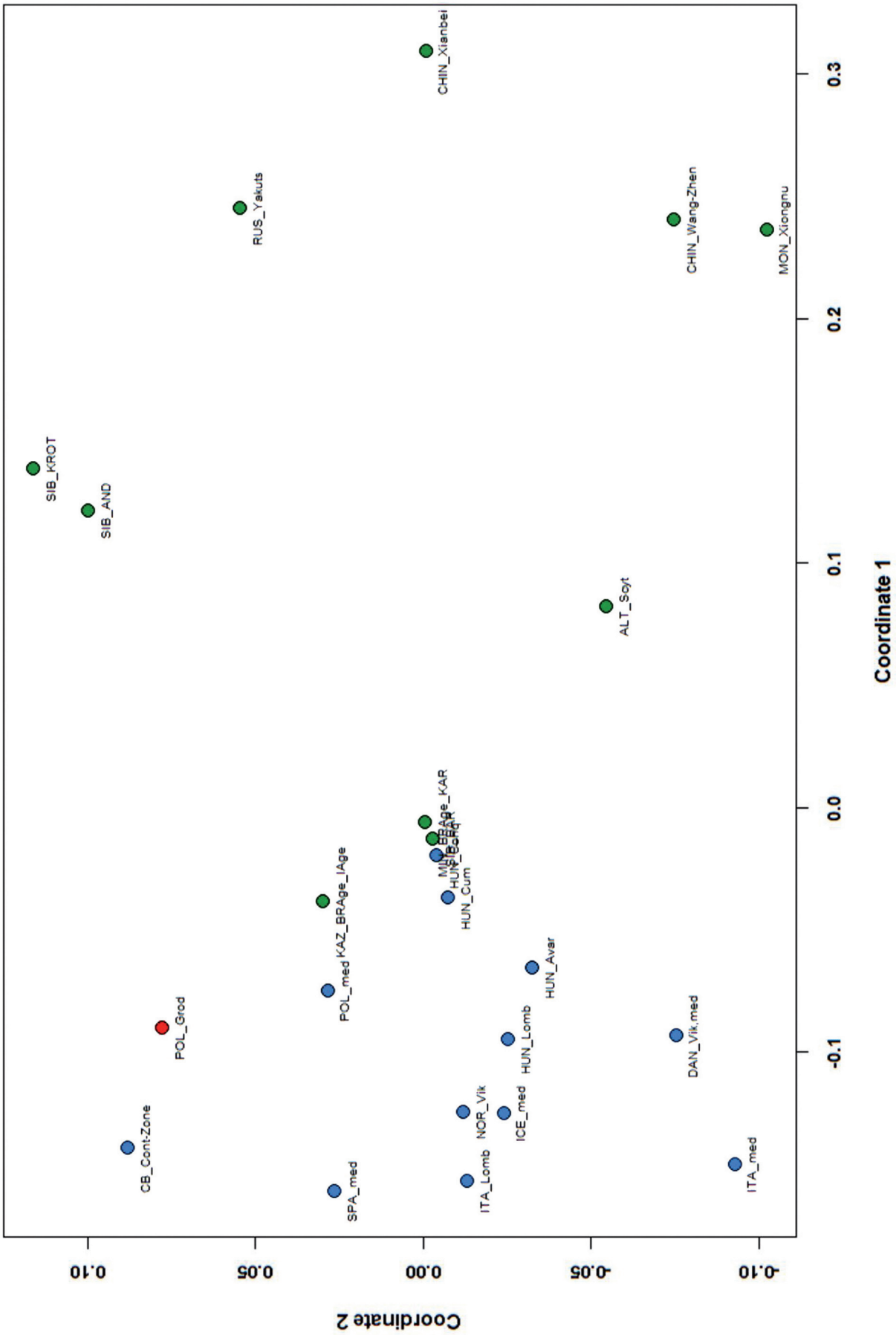


Fig. 2. MDS plot of ancient populations: The MDS plot was performed with linearized $F_{ST}$ values of 13 European populations (blue dots; the medieval population from Grodowice is marked with a red dot) and 10 Asian populations (green dots). (For $F_{ST}$ values, abbreviations and reference see Tables S7 and S9)

showed a non-significant difference from the medieval Grodowice (POL_Grod): medieval population of Conquest period from Hungary (HUN_Conq; $F_{ST}$ = 0.02553 and p = 0.06504±0.0025), medieval population from present-day Slovakia and Croatia (CB_Cont-Zone; $F_{ST}$ = 0.02743 and p = 0.12415±0.0038), medieval Cumanians from Hungary (HUN_Cum; $F_{ST}$ = 0.02904 and p = 0.19018±0.0038), Lombards from Szólád – Hungary (HUN_Lomb; $F_{ST}$ = 0.02398 and p = 0.11543±0.0032), Lombards from Italy (ITA_Lomb; $F_{ST}$ = 0.02488 and p = 0.14117±0.0032), medieval Spaniards (SPA_med; $F_{ST}$ = 0.02600 and p = 0.12444±0.0034), medieval Slavs from Poland (POL_med; $F_{ST}$ = 0.00602 and p = 0.32799±0.0049), Vikings from Norway (NOR_Vik; $F_{ST}$ = 0.00029 and p = 0.41026±0.0055), medieval Danes and Vikings (DAN_Vik,med; $F_{ST}$ = 0.03358 and p = 0.05207±0.0023), early medieval Icelander (ICE_med; $F_{ST}$ = 0.01977 and p = 0.12197±-0.0033), south western Siberian Baraba Late Bronze Age culture (SIB_Bar; $F_{ST}$ = 0.03615 and p = 0.06584±0.0025), Bronze Age population from south central Siberian Minusinsk Hollow (MIN_BRAge_KAR; $F_{ST}$ = 0.02477 and p = 0.12355±0.0034) and Bronze and Iron Age populations in present-day Kazakhstan (KAZ_BRAge_IAge; $F_{ST}$ = 0.02767 and p = 0.08286±0.0029) (Table S6 and Fig. 2). Pairwise $F_{ST}$ values of modern-day populations indicated non-significant difference (p > 0.05) between Grodowice and populations with Slavic languages: Russian (RUS; $F_{ST}$ = 0.02506 and p = 0.06217±0.0024), Poles (POL; $F_{ST}$ = 0.02358 and p = 0.06732±0.0027), Czechs (CZE; $F_{ST}$ = 0.01095 and p = 0.19186±0.0041), Slovaks (SVK; $F_{ST}$ = 0.02273 and p = 0.06772±0.0025), Ukrainians (UKR; $F_{ST}$ = 0.02044 and p = 0.08108±0.0026), Slovenians (SLO; $F_{ST}$ = 0.02622 and p = 0.05891 ±0.0027), Belarusians (BEL; $F_{ST}$ = 0.01802 and p = 0.10850±0.0029), furthermore with Khants (KHAN; $F_{ST}$ = -0.00082 and p = 0.44015±0.0047), Armenians (ARM; $F_{ST}$ = 0.01407 and p = 0.12821±0.0034), Iranians (IRN; $F_{ST}$ = 0.00872 and p = 0.21077±0.0037), Iraqi (IRQ; $F_{ST}$ = 0.01120 and p = 0.17978±0.0040), Turks (TUR; $F_{ST}$ = 0.01322 and p = 0.14454±0.0036), Austrians (AUS; $F_{ST}$ = 0.02566 and p = 0.06267±0.0024), Germans (GER; $F_{ST}$ = 0.02392 and p = 0.06584±0.0024), Hungarians (HUN; $F_{ST}$ = 0.02435 and p = 0.06296±0.0024), Szeklers from Romania (ROM_Sek; $F_{ST}$ = 0.01845 and p = 0.10157±0.0032), Albanians (ALB; $F_{ST}$ = 0.02368 and p = 0.07871±0.0028), Bulgarians (BUL; $F_{ST}$ = 0.02453 and p = 0.05455±0.0022), Greeks (GRE; $F_{ST}$ = 0.02124 and p = 0.06752±0.0024), Estonians (EST; $F_{ST}$ = 0.00683 and p = 0.26393 ±0.0038), Danes (DAN; $F_{ST}$ = 0.01237 and p = 0.17790±0.0037), Norwegians (NOR; $F_{ST}$ = 0.01718 and p = 0.12335±0.0033), Icelanders (ICE; $F_{ST}$ = 0.02318 and p = 0.08870±0.0027) and Lithuanians (LIT; $F_{ST}$ = 0.02670 and p = 0.05386±0.0021) (Table S7 and Fig. 3).

The multi-dimensional scaling (MDS) plot based on linearized Slatkin $F_{ST}$ values of ancient populations (stress value = 0.0945, Fig. 2) contains segregation of west and east Eurasian populations along the coordinate 1. The nearest population to our investigated Grodowice is that of the medieval Contact-Zone population from Slovakia and Croatia.

In order to visualize the genetic distances, the values of linearized Slatkin $F_{ST}$ of 23 ancient and 52 modern populations were displayed on the MDS plot (stress value = 0.0969, Fig. 3). The plot contains aggregation of the European population along the coordinates 1 and 2. The Asian populations are separated along the coordinate 1. Between the European and Asian populations the Near-Eastern are situated. The ancient populations are separated on this European-Asian lineage along coordinate 1, too. The medieval population from Grodowice is between the modern European and Asian populations near to modern Near-Eastern and ancient European populations, but along coordinate 2 it is separated from these European populations as well as the medieval contact zone population from Slovakia and Croatia.

PCAs were calculated based on mtDNA haplogroup frequencies of medieval and modern populations (Tables S5 and S6).

The PCA plots showed a marked difference between ancient European and Asian populations. Furthermore, along the PC1 and PC2 components (values of displayed variance: PC1 = 20.4%, PC2 = 11.2%) the plot shows a clustering of populations of the Bronze and Iron Ages from Kazakhstan and Avars and conquerors from Hungary, South European populations from Italy and Spain (Fig. 4). The medieval population from Grodowice is situated between European and Asian populations along the PC1, which could be caused by the presence of Asian haplogroup G; along PC2 it is separated from most of the populations, whilst along the PC3 (10.5% of total variance) this phenomenon is not presented (Fig. 5).

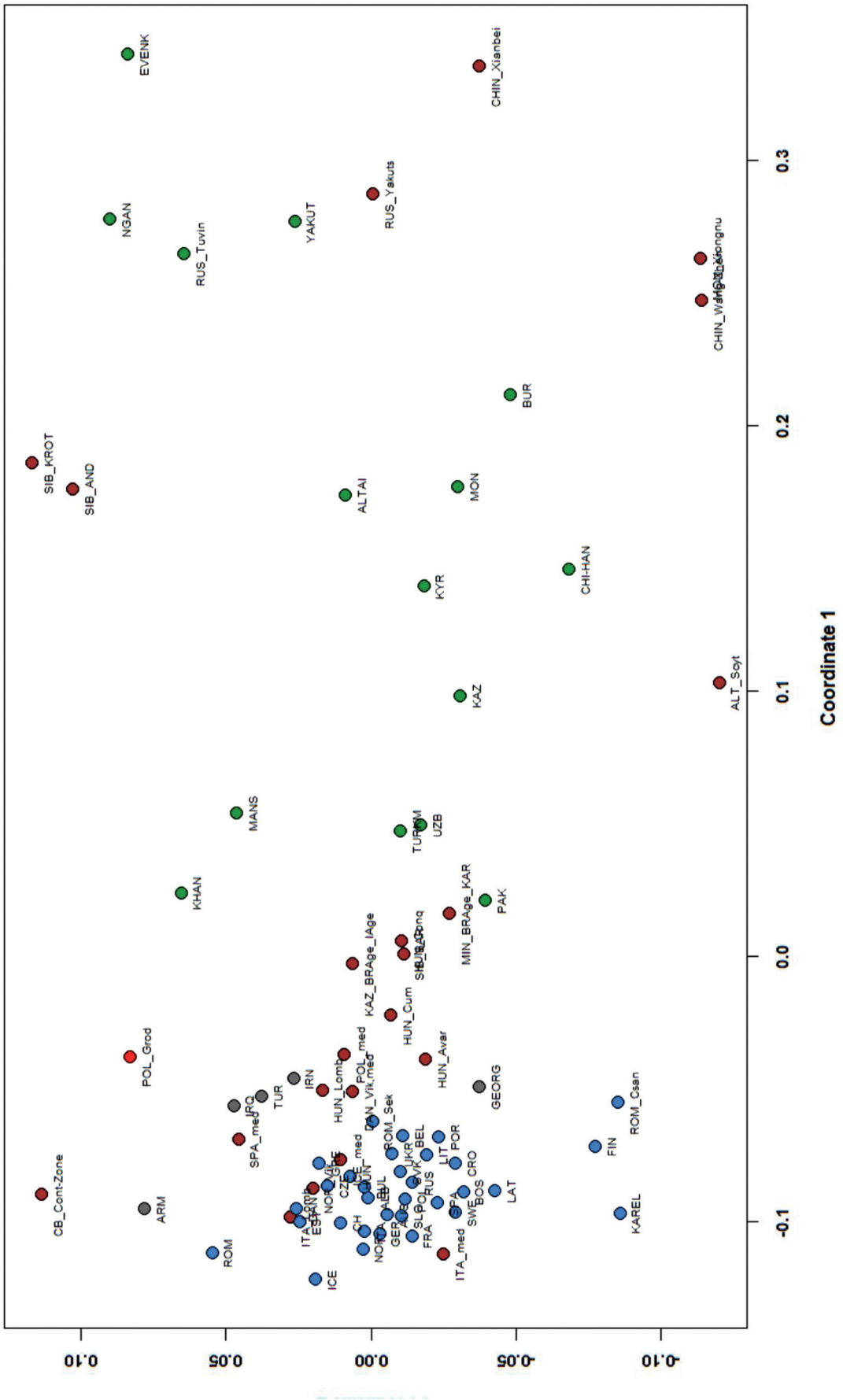


Fig. 3. MDS plot of ancient and modern populations: The MDS plot was performed with linearized $F_{ST}$ values of 52 modern European (blue dots), Near Eastern (grey dots), Asian (green dots) and 23 ancient (brown dots; the medieval population from Grodowice is marked with a red dot) populations. (For $F_{ST}$ values, abbreviations and reference see Tables S8 and S9)

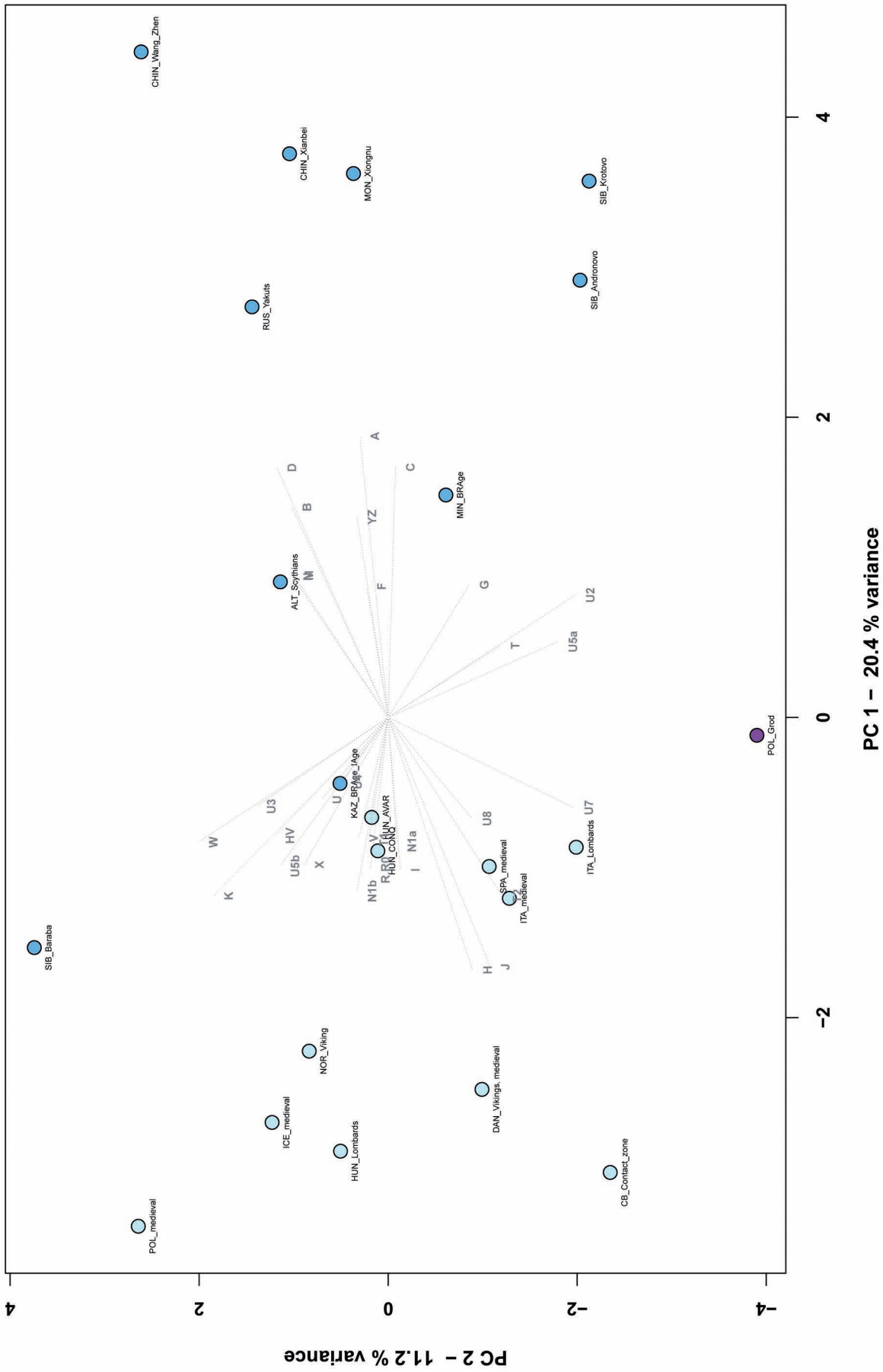


Fig. 4. PCA of ancient populations. The PCA is based on mtDNA haplogroup frequencies of the medieval population from Poland (marked with a violet dot), 11 ancient European (light blue dots) and 10 ancient Asian populations (blue dots), and shows PC1 and PC2. The haplogroup frequencies and the population information are shown in Table S5

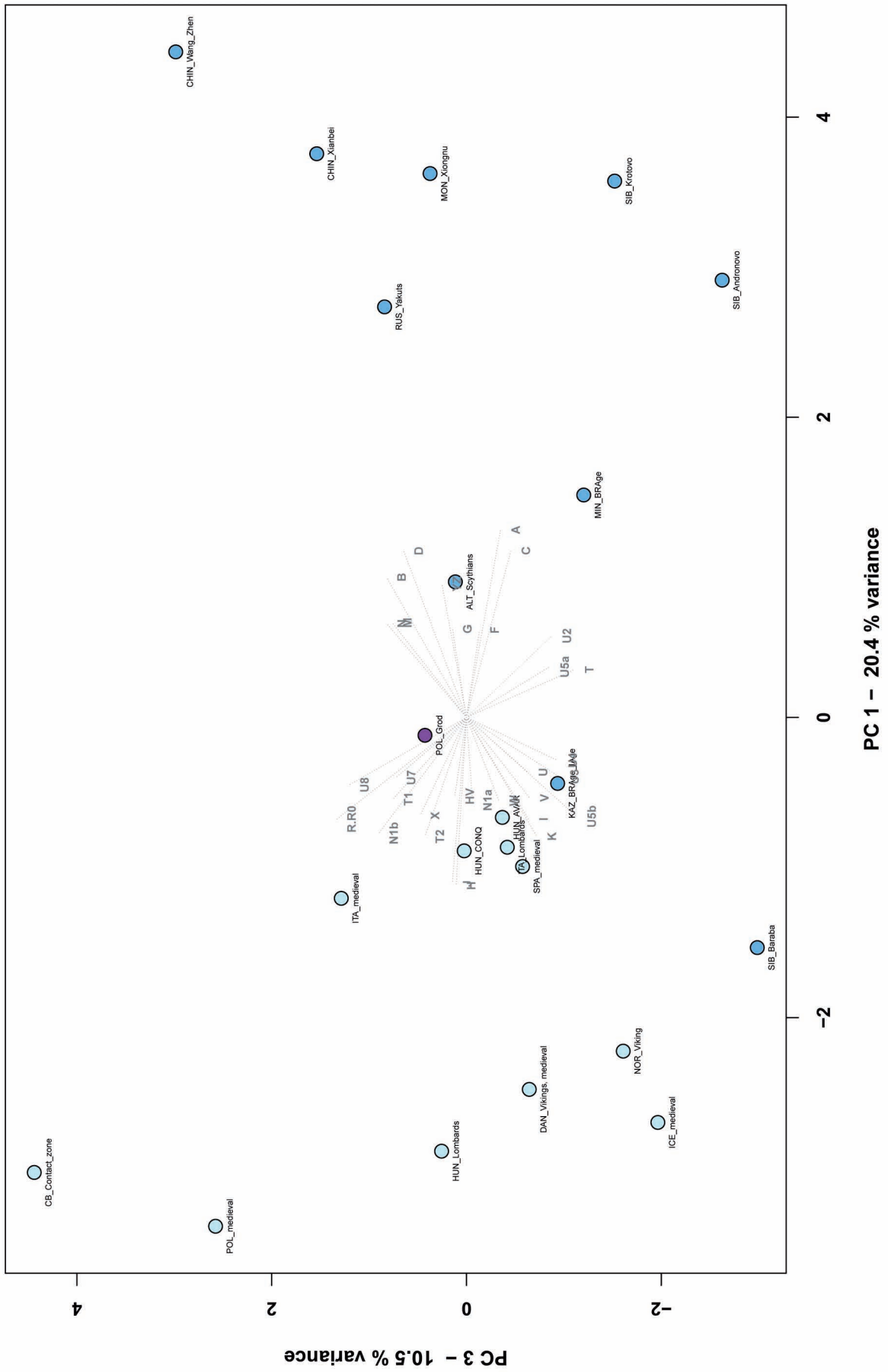


Fig. 5. PCA of ancient populations. The PCA is based on mtDNA haplogroup frequencies of the medieval population from Poland (marked with a violet dot), 11 ancient European (light blue dots) and 10 ancient Asian populations (blue dots), and shows PC1 and PC3. The haplogroup frequencies and the population information are shown in Table S5

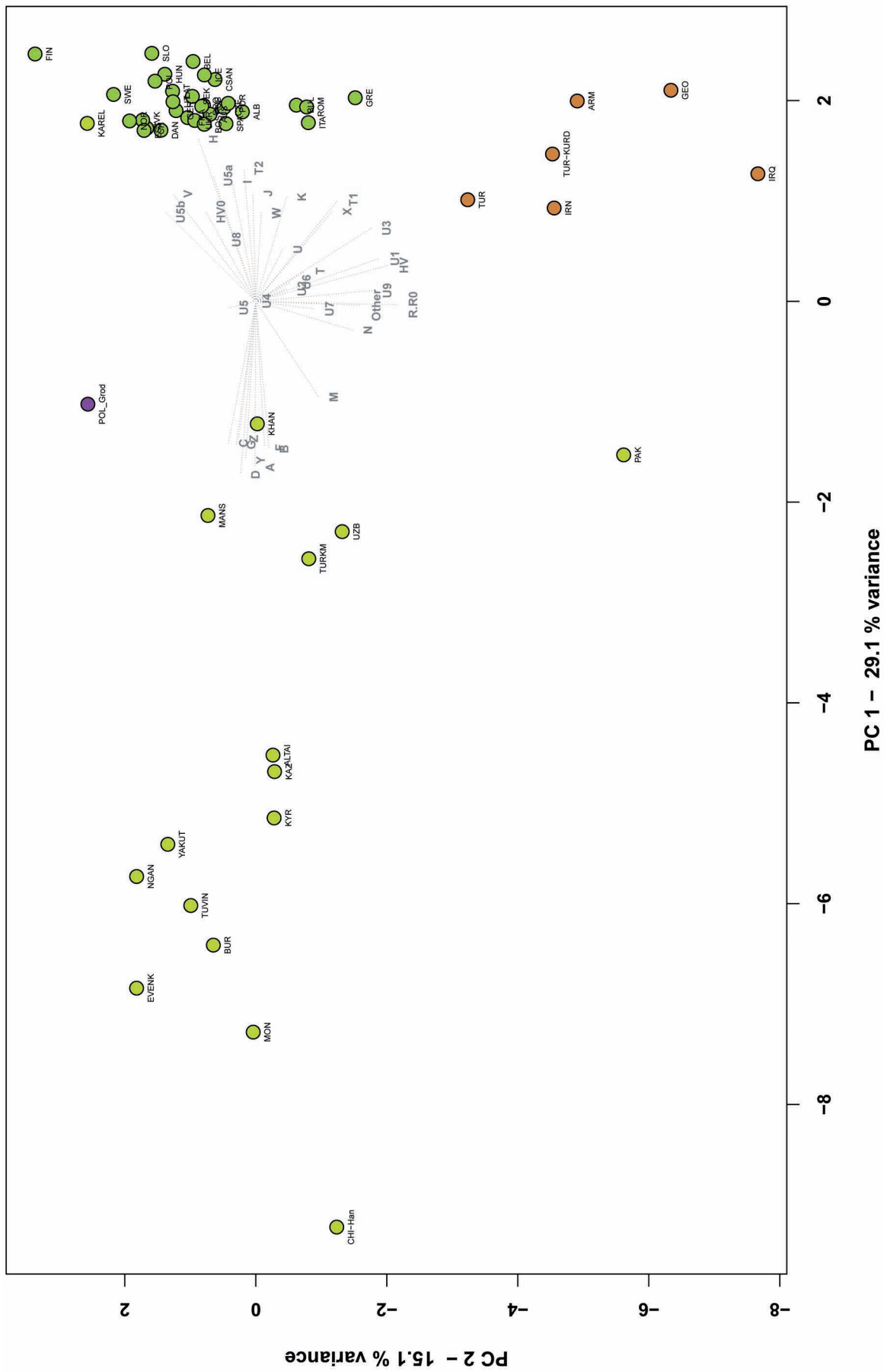


Fig. 6. PCA of the investigated medieval and modern-day populations. The PCA is based on mtDNA haplogroup frequencies of the medieval population from Grodowice (marked with a violet dot) and 53 modern-day populations from Asia (marked with yellow-green dots), Near East (brown dots) and Europe (green dots), and represents PC1 and PC2. For the frequencies and the list of abbreviations see Table S6

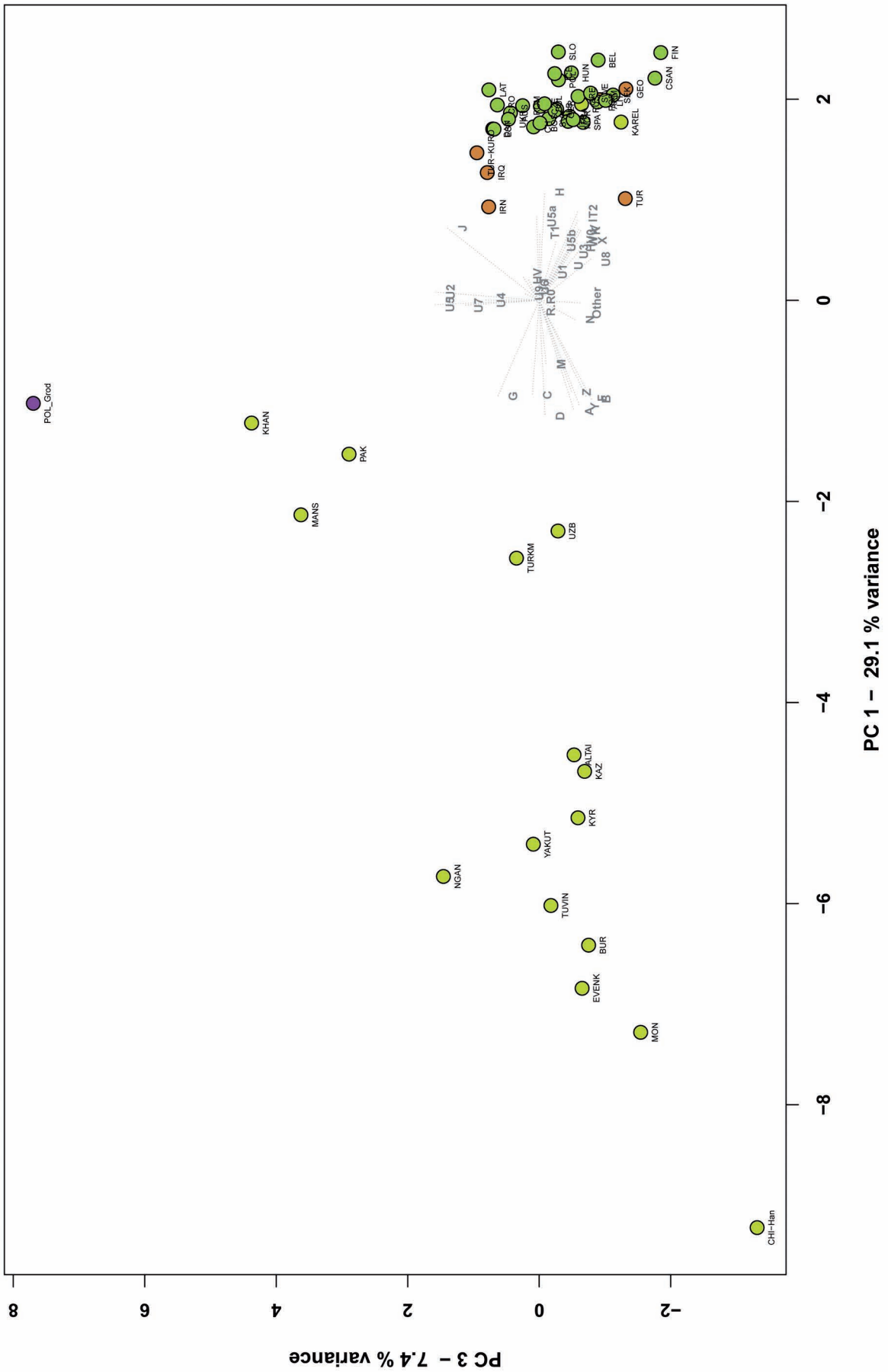


Fig. 7. PCA of the investigated medieval and modern-day populations. The PCA is based on mtDNA haplogroup frequencies of the medieval population from Grodowice (marked with a violet dot) and 53 modern-day populations from Asia (marked with yellow-green dots), Near East (brown dots) and Europe (green dots), and represents PC1 and PC3. For the frequencies and the list of abbreviations see Table S6.

The PCA plots of the modern Eurasian population indicate an alignment of the European populations and separated Asian population on PC1 and PC2 components (variance: PC1 = 29.1%, PC2 = 15.1%). The Near-Eastern populations are clustered together along PC2, but they are closer to the European population along component PC3 (7.4% of total variance). The investigated medieval population is again between the European and Asian populations along these three components (Figs. 6 and 7).

The shared haplotype analysis (SHA) shows that the medieval population from Grodowice shares the majority of haplotypes with medieval populations from Contact-Zones of today´s Slovakia and Croatia (53.85%) as well as with Hungarian conquerors (46.15%) (Table S4).

## DISCUSSION

In this study we investigated a medieval population from the cemetery in Grodowice, Poland. Using well established protocols for aDNA analysis we have obtained the mtDNA dataset of thirteen samples, concerning the genetic variation within the HVR I region and four nucleotide polymorphisms in the coding region of mtDNA. These markers enabled us to assign the mtDNA haplogroup of the samples. The representative haplogroups of the investigated medieval population belong to common modern European (West Eurasian) haplogroups except in the case of 1 sample, namely G26, which belongs to the typical Asian haplogroup G2a5. The age of this haplogroup was estimated by (Behar *et al.* 2012): 1,199.6 ± 1,670.4; CI=95%. The haplogroup G2 is characteristic for east and central Asian population based on the empop haplogroup browser (empop.org) (Röck *et al.* 2013). Relatively high presence of G2a was detected by Buryats from Russia (Derenko *et al.* 2013; 2018), Kazakhs (Comas *et al.* 2004; Gokcumen *et al.* 2008; Irwin *et al.* 2010), Kyrgyz (Comas *et al.* 1998; Irwin *et al.* 2010), populations from China (Yao *et al.* 2000; 2002a; 2002b; 2003; 2004; Qian *et al.* 2001; Oota *et al.* 2002; Kong *et al.* 2003; Wen *et al.* 2004; Li *et al.* 2007; Liu *et al.* 2011), Japanese (Horai *et al.* 1996; Imaizumi *et al.* 2002; Maruyama *et al.* 2003; Tajima *et al.* 2004; Tanaka *et al.* 2004; Mabuchi *et al.* 2007;) , Koreans (Lee *et al.* 2006; Derenko *et al.* 2007; Lee *et al.* 2006), Khants and Mansi (Derbeneva *et al.* 2002; Pimenoff *et al.* 2008) and Yakuts (Derenko *et al.* 2007; Fedorova *et al.* 2003; Pakendorf *et al.* 2003; 2006; Puzyrev 2003). The frequencies of European haplogroups are quite different from present-day populations: the detected frequency of haplogroup H at medieval Grodowice was a little bit lower (38.5%) than it is in European modern-day populations, where this most frequent haplogroup has a frequency of 45.4% (Torroni *et al.* 2006; Brotherton *et al.* 2013). Haplogroup H, the most common haplogroup in Europe, was also detected in all typed individuals in the Late Viking Age cemetery in Bodzia (central Poland) (Bogdanowicz, Grzybowski, Buś 2015; 2016). The most ancient European haplogroup U occurs in higher frequency in the medieval population (30.8%). Haplogroups J (23.1%) occurred nearly two times more frequently than in present-day Europe (Soares *et al.* 2010; Behar *et al.* 2012).

The investigated population from Grodowice evinces a European character based on population genetic analysis, but is situated mostly between Asian and European populations, which is caused by the presence of a haplotype belonging to the haplogroup G. DNA studies for other medieval Polish populations from Cedynia and Lednica indicate that the investigated samples share their more rare haplotypes with East-Central and South-East European populations (Juras *et al.* 2014, 1). Archaeological data suggest that during the Middle Ages, Asian populations, including Altaic tribes (Huns, Avars, and Mongols) were engaged in wars on the European continent (Curta 2001). This could in consequence leave traces in the form of Asian haplotypes in European populations. The existence of a haplotype representing, among other examples, clade G2a in Polish populations could further reflect the influx of Asian haplotypes during medieval wars in which Altaic tribes were engaged (Mielnik-Sikorska *et al.* 2013, 7). The medieval population from the Contact-Zone of Slovakia and Croatia (Csákyová *et al.* 2016; Csősz *et al.* 2016) is relatively near to the investigated population based on haplotype analyses like MDS and SHA (Fig. 2).

## CONCLUSION

It seems that further research of more samples, along with analysis of the whole mitochondrial genome and nuclear DNA markers, are necessary in the investigation of the genetic connections between medieval and modern populations in order to arrive at more concrete conclusions. Further analyses of ancient samples of the region will probably result in a more accurate estimation of the medieval populations' affinity.

Taking all of the above data into account, it is relatively difficult to pinpoint any specific region as the place of origin of the examined individuals. The results could be biased due to the small sample size, and genetic drift could also unnoticeably influence our results. It is worth noting that analyses of haplogroup frequencies can be very sensitive to small sample sizes that increase the randomness of the identified genetic affinities. Furthermore, we assessed population interactions and migrations only along the maternal lineages; the paternal side of the medieval population history remained unexamined in this study. Moreover, as has been proved elsewhere, mtDNA analyses of control region sequences alone, do not allow identification of any specific features which would clearly distinguish Slavs from the other European populations. Thus, only large-scale complete mitochondrial genome sequences studies may point out mtDNA lineages, which could have been involved in the formation of Slavs. Nevertheless, the study presented here of the first successful description of medieval mtDNA variability at the Grodowice cemetery contributes an important dataset to help reveal the genetic diversity of medieval Europe.

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# S1: Samples from Grodowice (Poland) used for genetic analysis

| Grave Number | Tooth, Bones | Samples | Sex | Age |
|---|---|---|---|---|
| G2 | T | M3 (Lower, R) | M | Adultus/Maturus |
| | B | Femur R | | |
| G4 | T | M3 (Lower, R) | M | Adultus/Maturus |
| | B | Femur R | | |
| G6 | T | M3 (Upper, L) | M | Adultus |
| | B | Femur R | | |
| G9 | T | M1 (Upper) | F | Adultus |
| | B | Femur L | | |
| G10 | T | M2 (Lower, R) | F | Adultus |
| | B | Femur R | | |
| G20 | T | M1 (Upper, L) | M | Adultus |
| | B | Femur L | | |
| G26 | T | M3 (Lower, L) | M | Maturus |
| | B | Femur | | |
| G44 | T | M1 (Upper, L) | F | Adultus |
| | B | Femur R | | |
| G49 | T | M3 (Lower, R) | M | Adultus |
| | B | Femur R | | |
| G50 | T | M3 (Lower, R) | F | Adultus/Maturus |
| | B | Femur R | | |
| G51 | T | M2 (Lower, L) | F | Adultus |
| | B | Femur L | | |
| G102 | T | M3 (Lower, L) | M | Maturus |
| | B | Femur L | | |
| G104 | T | M1 (Upper, L) | M | Maturus |
| | B | Femur L | | |

## S2: Performed PCRs of 2 overlapped HVI sequences and sequences of coding region contained pointed SNPs and primer pairs used for amplification

| Samples | Tooth, Femur | HVI region | | Coding region | | | |
|---|---|---|---|---|---|---|---|
| | | 16020-16259 | 16182-16401 | 4833 | 7028 | 12308 | 12705 |
| G2 | T | ✓ | ✓ | | | ✓ | |
| | B | ✓ | ✓ | | | | |
| G4 | T | ✓ | ✓ | | | ✓ | |
| | B | ✓ | ✓ | | | | |
| G6 | T | ✓ | ✓ | | ✓ | | |
| | B | ✓ | ✓ | | | | |
| G9 | T | ✓ | ✓ | | | | ✓ |
| | B | ✓ | ✓ | | | | |
| G10 | T | ✓ | ✓ | | ✓ | | |
| | B | ✓ | ✓ | | | | |
| G20 | T | ✓ | ✓ | | ✓ | | |
| | B | ✓ | ✓ | | | | |
| G26 | T | ✓ | ✓ | ✓ | ✓ | ✓ | |
| | B | ✓ | ✓ | ✓ | | | |
| G44 | T | ✓ | ✓ | | | | ✓ |
| | B | ✓ | ✓ | | | | |
| G49 | T | ✓ | ✓ | | | ✓ | |
| | B | ✓ | ✓ | | | | |
| G50 | T | ✓ | ✓ | | | ✓ | |
| | B | ✓ | ✓ | | | | |
| G51 | T | ✓ | ✓ | | | | ✓ |
| | B | ✓ | ✓ | | | | |
| G102 | T | ✓ | ✓ | | ✓ | | ✓ |
| | B | ✓ | ✓ | | | | |
| G104 | T | ✓ | ✓ | | ✓ | | |
| | B | ✓ | ✓ | | | | |

| | Name of primers | Sequences | Reference | Reported as |
|---|---|---|---|---|
| HVR I | L-16020 | 5'-TCT GTT CTT TCA TGG GGA AG-3' | Tömöry et al. 2007 | L16040 |
| | H-16259 | 5'-GTG GCT TTG GAG TTG CAG TT-3' | | H16239 |
| | L-16182 | 5'-AAC CCC CTC CCC ATG CTT AC-3' | Tömöry et al. 2007 | L16201 |
| | H-16401 | 5'-TGA TTT CAC GGA GGA TGG TG-3' | | H16400 |
| SNPs of coding region | L-4833 | 5'-CTATCCTCTTCAACAATATACTCT-3' | Xie et al. 2007 | L4701 |
| | H-4833 | 5'-ATGTGAGAAGAAGCAGGC-3' | | H4848 |
| | 7028-F | 5'-TTT TCA CCG TAG GTG GCC TG-3' | Tömöry et al. 2007 | L6962 |
| | 7028-R | 5'-TGA AAT GGA TTT TGG CGT AGG-3' | | H7126 |
| | 12308m-F | 5'-ACA GAG GCT TAC GAC CCC TTA-3' | Csákyová et al. 2016 | 12308m-F |
| | 12308m-R | 5'-TTT ATT TGG AGT TGC ACC AG-3' | | 12308m-R |
| | 12705-F | 5'-CAT CCC TGT AGC ATT GTT CG-3' | Tömöry et al. 2007 | L12622 |
| | 12705-R | 5'-AAT TCC TAC GCC CTC TCA GC-3' | | H12764 |


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## S3: Obtained mtDNA haplogroups and haplotypes

| Samples | HVI region based on rCRS (1) | HVI region based on RSRS (2) | Coding region | Haplogroup (Phylotree 17 – Haplogrep) | Overall_Rank |
|---|---|---|---|---|---|
| G2 | 16192T 16256T 16270T 16291T 16399G | 16129G 16187C 16189T 16192T 16223C 16230A 16256T 16270T 16278C 16311T 16399G | 12308G | U5a1 | 1.0000 |
| G4 | 16192T 16256T 16270T 16291T 16399G | 16129G 16187C 16189T 16192T 16223C 16230A 16256T 16270T 16278C 16311T 16399G | 12308G | U5a1 | 1.0000 |
| G6 | rCRS | 16129G 16187C 16189T 16223C 16230A 16278C 16311T | 7028C | H2a2a1 | 0.5000 |
| G9 | 16069T 16126C | 16069T 16126C 16129G 16187C 16189T 16223C 16230A 16278C 16311T | 12705C | J | 1.0000 |
| G10 | rCRS | 16129G 16187C 16189T 16223C 16230A 16278C 16311T | 7028C | H2a2a1 | 0.5000 |
| G20 | rCRS | 16129G 16187C 16189T 16223C 16230A 16278C 16311T | 7028C | H2a2a1 | 0.5000 |
| G26 | 16223T 16227G 16234T 16278T 16362C | 16129G 16187C 16189T 16227G 16230A 16234T 16311T 16362C | 4833G 7028T 12308A | G2a5 | 0.8836 |
| G44 | 16069T 16126C 16145A 16231C 16261T | 16069T 16126C 16129G 16145A 16187C 16189T 16223C 16230A 16231C 16261T 16278C 16311T | 12705C | J2a1a1 | 1.0000 |
| G49 | 16129c 16183A 16193.1C 16362C | 16129c 16183A 16187C 16189T 16193.1C 16223C 16230A 16278C 16311T 16362C | 12308G | U2e1h | 1.0000 |
| G50 | 16318T | 16129G 16187C 16189T 16223C 16230A 16278C 16311T 16318T | 12308G | U7 | 0.8607 |
| G51 | 16069T 16126C 16145A 16231C 16261T | 16069T 16126C 16129G 16145A 16187C 16189T 16223C 16230A 16231C 16261T 16278C 16311T | 12705C | J2a1a1 | 1.0000 |
| G102 | 16209C 16261T | 16129G 16187C 16189T 16209C 16223C 16230A 16261T 16278C 16311T | 7028C 12705C | H107 | 1.0000 |
| G104 | 16189C 16288C 16362C | 16129G 16187C 16223C 16230A 16278C 16288C 16311T 16362C | 7028C | H8 | 1.0000 |

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## 14. Shared haplotype analysis with 11 ancient populations

| | | |

## S5: Haplogroup frequencies used for PCA with 22 ancient populations

| PC (Components) | % Variance |
|---|---|
| 1 | 20,435 |
| 2 | 11,166 |
| 3 | 10,496 |

| Region | Country | Population | Abbreviation | Centuries | Culture/Period | N | Haplogroup frequencies | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | A | B | C | D | G | F | HV | I | J | K | M | N | N1a | N1b | R/R0 | T | T1 | T2 | U | U2 | U3 | U4 | U5a | U5b | U7 | U8 | V | W | X | YZ | |
| | Poland | | | | | 13 | 0 | 0 | 0 | 0 | 7,692307692 | 0 | 38,46153846 | 0 | 0 | 23,07692308 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7,692307692 | 0 | 0 | 15,38461538 | 0 | 7,692307692 | 0 | 0 | 0 | 0 | 0 | Thu study (13) |
| Europe_east | Hungary | medieval populations of Conquest period from Hungary | HUN_CONQ | 10th – 12th AD | medieval | 101 | 6,930693069 | 1,980198022 | 2,97029703 | 5,940594059 | 1,980198022 | 0,990099901 | 21,78217822 | 1,980198022 | 1,980198022 | 4,950495055 | 1,980198022 | 1,980198022 | 0 | 0 | 1,980198022 | 3,96039604 | 1,980198022 | 5,940594059 | 1,980198022 | 1,980198022 | 0 | 4,950495055 | 7,920792079 | 0,990099901 | 0 | 1,980198022 | 1,980198022 | 1,980198022 | 3,96039604 | 0 | Csáky et al. 2016 (75), Tömöry et al. 2007 (26) |
| Europe_east | Hungary | Avars | HUN_AVAR | 6th – 9th AD | medieval | 26 | 0 | 0 | 3,846153846 | 3,846153846 | 0 | 3,846153846 | 38,46153846 | 3,846153846 | 0 | 0 | 0 | 3,846153846 | 3,846153846 | 0 | 0 | 3,846153846 | 3,846153846 | 11,53846154 | 0 | 3,846153846 | 3,846153846 | 3,846153846 | 0 | 0 | 0 | 0 | 0 | 0 | 3,846153846 | 0 | Csáky et al. 2016 (26) |
| Europe_east | Hungary | medieval populations from present-day Slovakia (Nitra-Šindolka, Čakajovce) and Croatia (Zvonimirovo) | CB_Contact_zone | 10th – 11th AD | medieval | 23 | 0 | 0 | 0 | 0 | 0 | 0 | 21,73913043 | 0 | 0 | 17,39130435 | 0 | 0 | 0 | 4,347826087 | 4,347826087 | 0 | 13,04347826 | 13,04347826 | 0 | 0 | 4,347826087 | 8,695652174 | 0 | 4,347826087 | 8,695652174 | 0 | 4,347826087 | 8,695652174 | 0 | „Csáky et al. 2016 (3); Csákyová et al. 2016 (18)" |
| Europe_east | Hungary | Lombards from Hungary: Szolád | HUN_Lombards | 6th AD | Lombard | 28 | 0 | 0 | 0 | 0 | 0 | 0 | 32,14285714 | 7,142857143 | 7,142857143 | 14,28571429 | 7,142857143 | 0 | 3,571428571 | 7,142857143 | 0 | 0 | 0 | 7,142857143 | 3,571428571 | 0 | 0 | 10,71428571 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | Alt et al. 2014 (28) |
| Europe_south | Italy - Piedmont | „Lombards from Italy: Rivoli, Corso Levi (Turin); Rivoli, La Perosa (Turin); Mombello Monferrato (Alessandria); Collegno (Turin); Centallo, San Gervasio (Cuneo)" | ITA_Lombards | 6th – 8th AD | Lombard | 28 | 0 | 0 | 0 | 0 | 0 | 0 | 50 | 0 | 3,571428571 | 17,85714286 | 0 | 0 | 0 | 0 | 3,571428571 | 0 | 7,142857143 | 0 | 3,571428571 | 3,571428571 | 0 | 3,571428571 | 10,71428571 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | Vai et al. 2015 (28) |
| Europe_south | Italy - Tuscany | „medieval Italiane: Firenze, Piazza Signoria; Pisa, Vicopisano; Livorno, Castello Donoratico; Massa Carrara, Fivizzano; Siena, Santa Maria della Scala; Grosseto, San Quirico" | ITA_medieval | 10th – 15th AD | Medieval | 27 | 0 | 0 | 3,703703704 | 0 | 0 | 0 | 66,66666667 | 0 | 0 | 3,703703704 | 3,703703704 | 3,703703704 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3,703703704 | 0 | 0 | 0 | 0 | 0 | Gaimarano et al. 2009 (27) |
| Europe_south | Spain | medieval Spaniards: Basque, Aldasta | SPA_medieval | 6th – 7th AD | Medieval | 56 | 0 | 0 | 0 | 0 | 0 | 0 | 60,71428571 | 0 | 0 | 14,28571429 | 1,785714286 | 0 | 0 | 0 | 0 | 1,785714286 | 0 | 3,571428571 | 5,357142857 | 7,142857143 | 0 | 0 | 0 | 0 | 0 | 1,785714286 | 0 | 0 | 0 | Alnualde et al. 2006 (56) |
| Europe_east | Poland | medieval Slavs from Poland: Cedynia (West Pomerania Province), Ostrów Lednicki (Greater Poland Province) | POL_medieval | 11th – 15th AD | Medieval | 20 | 0 | 0 | 0 | 0 | 0 | 0 | 40 | 10 | 0 | 10 | 10 | 0 | 0 | 5 | 5 | 0 | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 10 | 0 | Juras et al. 2015 (20) |
| Europe_north | Iceland | early medieval Icelander | ICE_medieval | 10th – 12th AD | Medieval | 73 | 0 | 0 | 0 | 0 | 0 | 0 | 32,87671233 | 1,369863014 | 6,849315068 | 15,06849315 | 13,69863014 | 0 | 0 | 0 | 0 | 0 | 0 | 2,739726027 | 0 | 6,849315068 | 0 | 1,369863014 | 4,109589041 | 4,109589041 | 4,109589041 | 0 | 0 | 2,739726027 | 2,739726027 | 1,369863014 | 0 | Helgason et al. 2009 (73) |
| Europe_north | Denmark | medieval Danes with Vikings: Galgedil, Kongemarken, Risby | DAN_Vikings, medieval | 8th – 16th AD | Viking, Medieval | 29 | 0 | 0 | 0 | 0 | 0 | 0 | 34,48275862 | 0 | 13,79310345 | 13,79310345 | 6,896551724 | 0 | 0 | 3,448275862 | 0 | 0 | 0 | 6,896551724 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3,448275862 | Melchior et al. 2010 (29) |
| Europe_north | Norway | Vikings from Norway: Nord-Trøndelag, Nordland, Sør-Trøndelag, Telemark, Troms, Oppland, Hedmark | NOR_Viking | 6th – 11th AD | Viking | 56 | 1,785714286 | 0 | 0 | 0 | 0 | 0 | 39,28571429 | 7,142857143 | 3,571428571 | 17,85714286 | 7,142857143 | 0 | 0 | 0 | 0 | 0 | 0 | 3,571428571 | 0 | 0 | 1,785714286 | 1,785714286 | 7,142857143 | 7,142857143 | 0 | 1,785714286 | 0 | 0 | 0 | Krzewińska et al. 2015 (56) |
| Asia, central | Mongolia | Xiongnu period: Hsiung-nu | MON_Xiongnu | 3rd BC – 2nd AD | Xiongnu | 46 | 17,39130435 | 2,173913043 | 10,86956522 | 43,47826087 | 2,173913043 | 8,695652174 | 0 | 0 | 2,173913043 | 0 | 4,347826087 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4,347826087 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | „Keyser-Tracqui (2003) 43; Kim et al. 2010 (3)" |
| Asia, central | China-Inner Mongolia | Tuoba Xianbei | CHIN_Xianbei | 4th – 5th AD | Xianbei | 16 | 6,25 | 12,5 | 31,25 | 43,75 | 6,25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | Changchun et al. 2006 (16) |
| Asia, central | China-Inner Mongolia | Wanggu, Upper Capital - Zhenzishan | CHIN_Wang_Zhen | 12th – 14th AD | Jin-Yuan period | 33 | 12,12121212 | 6,060606061 | 3,03030303 | 24,24242424 | 0 | 0 | 3,03030303 | 0 | 0 | 0 | 0 | 0 | 27,27272727 | 18,18181818 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6,060606061 | „Fu et al. 2007 (12); Fu et al. 2009 (21)" |
| Asia, north | Russia - Eastern Siberia | Yakuts | RUS_Yakuts | 15th – 19th AD | 15-19th | 57 | 3,508771193 | 5,263157895 | 36,84210526 | 38,59649123 | 0 | 3,508771193 | 1,754385965 | 0 | 0 | 3,508771193 | 1,754385965 | 1,754385965 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1,754385965 | 1,754385965 | Crubézy et al. 2010 (37) |
| Asia, north | Russia | „Sofonovoarmaia: Tataria; Ozat-Abakanets; Bogratskiy; Afontova Gora, south central Siberia" | MIN_BRAge_Karasuk | 14th – 9th BC | Bronze Age | 20 | 5 | 0 | 5 | 5 | 0 | 10 | 10 | 0 | 0 | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 5 | 0 | 5 | 0 | 15 | 20 | 0 | 0 | 0 | 0 | 0 | 5 | „Keyser et al. 2009 (11); Allentoft et al. 2015 (9)" |
| Asia, central | Kazakhstan, Russia | „Ak-Mustafa; Izmaylovka; Ob-Zhaylau III; Vodokhranilische; Zevakinskiy; Birlik; Molaly, Shubarat; Kok-Mardan; Solyanka; Bulanovo; Stepnoe VII; Bol'shekaraganskii; Kapova cave; Tatsbergen II" | KAZ_BRAge_IAge | 23rd – 4th BC | Bronze Age-Iron Age | 34 | 8,823529412 | 0 | 0 | 0 | 2,941176471 | 0 | 20,58823529 | 5,882352941 | 5,882352941 | 8,823529412 | 0 | 8,823529412 | 0 | 0 | 2,941176471 | 0 | 5,882352941 | 5,882352941 | 0 | 8,823529412 | 5,882352941 | 0 | 0 | 2,941176471 | 2,941176471 | 0 | 0 | 0 | 2,941176471 | 0 | „Lalueza-Fox et al. 2004 (27); Allentoft et al. 2015 (8)" |
| Asia, central | Altai Republic, Mongolia | Scytho-Siberian | ALT_Scythians | 5th – 3rd BC | Iron Age | 22 | 4,545454545 | 0 | 9,090909091 | 27,27272727 | 4,545454545 | 4,545454545 | 0 | 13,63636364 | 0 | 4,545454545 | 13,63636364 | 0 | 0 | 0 | 0 | 0 | 0 | 4,545454545 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | „Rikunt et al. 2004 (2); Gonzalez-Ruiz et al. 2012 (16); Allentoft et al. 2015 (1); Pilipenko et al. 2010 (5)" |
| Asia, north | Russia | Early-Late Krotovo | SIB_Krotovo | 23rd – 17th BC | Early Bronze Age | 26 | 15,38461538 | 0 | 34,61538462 | 3,846153846 | 3,846153846 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7,692307692 | 0 | 3,846153846 | 0 | 7,692307692 | 0 | 0 | 19,23076923 | 0 | 0 | 0 | 0 | 0 | 0 | 3,846153846 | Mednikova 2012 (26) |
| Asia, north | Russia | Baraba, Late Bronze Age | SIB_Baraba | 13th – 7th BC | Late Bronze Age | 19 | 5,263157895 | 0 | 10,52631579 | 5,263157895 | 0 | 0 | 10,52631579 | 0 | 0 | 5,263157895 | 15,78947368 | 0 | 0 | 0 | 0 | 0 | 5,263157895 | 0 | 5,263157895 | 0 | 5,263157895 | 15,78947368 | 5,263157895 | 5,263157895 | 0 | 0 | 0 | 5,263157895 | 0 | Mednikova 2012 (19) |
| Asia, north | Russia | Andronovo | SIB_Andronovo | 20th – 13th BC | Middle Bronze Age | 24 | 12,5 | 0 | 41,66666667 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 12,5 | 0 | 0 | 0 | 0 | 8,333333333 | 0 | 8,333333333 | 16,66666667 | 0 | 0 | 0 | 0 | 0 | 0 | Mednikova 2012 (20), Allentoft 2016 (4) |

## S6: Haplogroup frequencies used for PCA with 53 modern and the ancient population of Gioshevice

| G_Georgian | S_Svan |
|---|---|
| C_Chechen | I_Ingush |
| D_Dargin | L_Lezgin |

| Region | Country | Population | Abbreviation | N | Haplogroup frequencies | | |

**S7: FST values, p values and Slatkin FST matrix of 23 ancient populations.**
Np 16050-16383 were considered at the FST computation in Arlequin software. P values are presented in the upper diagonal of the first table.
FST values are presented in the lower diagonal of the first table. Significant Fst values are indicated with p values (<0.05).

**pairwise FST values/p values**

| Region | Country | Population | Abbreviation | N | | POL_Grod | HUN_Conq | HUN_Avar | CB_Cont-Zone | HUN_Cum | HUN_Lomb | ITA_Lomb | ITA_med | SPA_med | POL_med | NOR_Vik | DAN_Vik.med | ICE_med | RUS_Yakuts | MON_Xiongnu | CHIN_Wang-Zhen | CHIN_Xianbei | SIB_KROT | SIB_AND | SIB_BAR | MIN_BRAge_KAR | KAZ_BRAge_IAge | ALT_Scyt | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Poland | | POL_Grod | 13 | POL_Grod | * | 0.06504+-0.0025 | 0.03772+-0.0018 | 0.12415+-0.0038 | 0.19018+-0.0038 | 0.11543+-0.0032 | 0.14117+-0.0032 | 0.00564+-0.0007 | 0.12444+-0.0034 | 0.32799+-0.0049 | 0.41026+-0.0055 | 0.05207+-0.0023 | 0.12197+-0.0033 | 0.00010+-0.0001 | 0.00010+-0.0001 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00277+-0.0005 | 0.00960+-0.0010 | 0.06584+-0.0025 | 0.12355+-0.0034 | 0.08286+-0.0029 | 0.01812+-0.0015 | This study (13) |
| Europe, east | Hungary | medieval populations of Conquest period from Hungary | HUN_CONQ | 101 | HUN_Conq | 0.02553 | * | 0.32036+-0.0041 | 0.00347+-0.0006 | 0.63865+-0.0043 | 0.14652+-0.0036 | 0.01297+-0.0012 | 0.01911+-0.0014 | 0.00337+-0.0006 | 0.42748+-0.0048 | 0.00059+-0.0003 | 0.00812+-0.0009 | 0.00109+-0.0003 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00020+-0.0001 | 0.82952+-0.0042 | 0.51302+-0.0046 | 0.53460+-0.0050 | 0.00406+-0.0006 | Csósz et al. 2016 (75), Tömöry et al. 2007 (26) |
| Europe, east | Hungary | Avars | HUN_AVAR | 26 | HUN_Avar | 0.03987 | 0.00233 | * | 0.12108+-0.0032 | 0.41847+-0.0055 | 0.08108+-0.0027 | 0.07851+-0.0032 | 0.57796+-0.0048 | 0.03554+-0.0018 | 0.27354+-0.0045 | 0.05643+-0.0020 | 0.11029+-0.0031 | 0.09851+-0.0032 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00010+-0.0001 | 0.00238+-0.0005 | 0.37947+-0.0044 | 0.58549+-0.0048 | 0.42006+-0.0051 | 0.01287+-0.0011 | Csósz et al. 2016 (26) |
| Europe, east | Slovakia, Croatia | medieval populations from present-day Slovakia (Nitra-Šindolka, Čakajovce) and Croatia (Zvonimirovo) | CB_Contact_zone | 23 | CB_Cont-Zone | 0.02743 | 0.03777 | 0.01634 | * | 0.03158+-0.0018 | 0.01346+-0.0012 | 0.09732+-0.0028 | 0.01544+-0.0015 | 0.00248+-0.0004 | 0.19147+-0.0033 | 0.01158+-0.0010 | 0.01257+-0.0012 | 0.00644+-0.0009 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00020+-0.0001 | 0.01940+-0.0012 | 0.01267+-0.0012 | 0.05891+-0.0020 | 0.00020+-0.0001 | „Csósz et al. 2016 (4); Csákyová et al. 2016 (19)" |
| Europe, east | Hungary | medieval Cumanians | HUN_Cum | 11 | HUN_Cum | 0.02904 | -0.00895 | 0.00030 | 0.05467 | * | 0.33779+-0.0047 | 0.09237+-0.0025 | 0.06069+-0.0021 | 0.33759+-0.0042 | 0.31116+-0.0045 | 0.30908+-0.0046 | 0.09365+-0.0028 | 0.40560+-0.0044 | 0.00277+-0.0006 | 0.00889+-0.0003 | 0.00020+-0.0001 | 0.00020+-0.0001 | 0.01346+-0.0012 | 0.05960+-0.0027 | 0.95426+-0.0020 | 0.68924+-0.0052 | 0.19473+-0.0036 | 0.10771+-0.0031 | Bogácsi-Szabó et al. 2005 (11) |
| Europe, east | Hungary | Lombards from Hungary: Szólád | HUN_Lomb | 28 | HUN_Lomb | 0.02398 | 0.00762 | 0.01676 | 0.04086 | 0.00583 | * | 0.20760+-0.0038 | 0.06603+-0.0023 | 0.02000+-0.0015 | 0.59836+-0.0041 | 0.21226+-0.0039 | 0.22008+-0.0043 | 0.79378+-0.0036 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00010+-0.0001 | 0.00020+-0.0001 | 0.19186+-0.0047 | 0.04267+-0.0019 | 0.07148+-0.0027 | 0.00010+-0.0001 | Alt et al. 2014 (28) |
| Europe, south | Italy - Piedmont | „Lombards from Italy: Rivoli, Corso Levi (Turin); Rivoli, La Perosa (Turin); Mombello Monferrato (Alessandria); Collegno (Turin); Centallo, San Gervasio (Cuneo)" | ITA_Lomb | 28 | ITA_Lomb | 0.02488 | 0.02216 | 0.01893 | 0.02121 | 0.03698 | 0.00863 | * | 0.02327+-0.0014 | 0.02505+-0.0015 | 0.05683+-0.0021 | 0.24602+-0.0044 | 0.06356+-0.0029 | 0.49322+-0.0044 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00010+-0.0001 | 0.06128+-0.0023 | 0.05683+-0.0022 | 0.01525+-0.0012 | 0.00000+-0.0000 | Vai et al. 2015 (28) |
| Europe, south | Italy - Tuscans | „medieval Italians: Firenze, Piazza Signoria; Pisa, Vicopisano; Livorno, Castello Donoratico; Massa Carrara, Fivizzano; Siena, Santa Maria della Scala; Grosseto, San Quirico" | ITA_med | 27 | ITA_med | 0.08406 | 0.02220 | -0.00630 | 0.04787 | 0.05385 | 0.02188 | 0.03746 | * | 0.00475+-0.0007 | 0.02109+-0.0012 | 0.08069+-0.0026 | 0.09851+-0.0028 | 0.12326+-0.0035 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.01238+-0.0011 | 0.01931+-0.0012 | 0.00594+-0.0008 | 0.00020+-0.0001 | Guimaraes et al. 2009 (27) |
| Europe, south | Spain | medieval Spaniards: Basque, Aldaieta | SPA_med | 56 | SPA_med | 0.02600 | 0.01991 | 0.02365 | 0.05358 | 0.00439 | 0.02840 | 0.02833 | 0.04931 | * | 0.06207+-0.0024 | 0.03584+-0.0017 | 0.00406+-0.0006 | 0.03257+-0.0017 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.04089+-0.0019 | 0.02218+-0.0016 | 0.05386+-0.0021 | 0.00000+-0.0000 | Alzualde et al. 2006 (56) |
| Europe, east | Poland | medieval Slavs from Poland: Cedynia (West Pomerania Province), Ostrów Lednicki (Greater Poland Province) | POL_med | 20 | POL_med | 0.00602 | -0.00018 | 0.00642 | 0.01282 | 0.00776 | -0.00592 | 0.02651 | 0.03882 | 0.02353 | * | 0.32729+-0.0042 | 0.09415+-0.0031 | 0.27661+-0.0047 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00050+-0.0002 | 0.00099+-0.0003 | 0.39254+-0.0048 | 0.13870+-0.0031 | 0.39461+-0.0046 | 0.00267+-0.0006 | Juras et al. 2015 (20) |
| Europe, north | Norway | Vikings from Norvay: Nord-Trøndelag, Nordland, Sør-Trøndelag, Telemark, Troms, Oppland, Hedmark | NOR_Vik | 56 | NOR_Vik | 0.00029 | 0.02549 | 0.01653 | 0.03194 | 0.00552 | 0.00587 | 0.00485 | 0.01461 | 0.01473 | 0.00278 | * | 0.06673+-0.0027 | 0.83190+-0.0036 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.03960+-0.0019 | 0.05861+-0.0023 | 0.00822+-0.0010 | 0.00030+-0.0002 | Krzewińska et al. 2015 (56) |
| Europe, north | Denmark | medieval Danes and Vikings: Galgedil, Kongemarken, Risby | DAN_Vik.med | 29 | DAN_Vik.med | 0.03358 | 0.02415 | 0.01475 | 0.03819 | 0.02633 | 0.00761 | 0.01973 | 0.01693 | 0.04019 | 0.01724 | 0.01476 | * | 0.12969+-0.0035 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.01297+-0.0011 | 0.02841+-0.0015 | 0.05108+-0.0023 | 0.00099+-0.0003 | Melchior et al. 2010 (29) |
| Europe, north | Iceland | early medieval Icelander | ICE_med | 73 | ICE_med | 0.01977 | 0.01768 | 0.01245 | 0.03700 | 0.00072 | -0.00764 | -0.00177 | 0.01071 | 0.01375 | 0.00458 | -0.00533 | 0.00959 | * | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.00000+-0.0000 | 0.13038+-0.0033 | 0.03891+-0.0018 | 0.00960+-0.0008 | 0.00000+-0.0000 | Helgason et al. 2009 (73) |
| Asia, north | Russia - Eastern Siberia | Yakuts | RUS_Yakuts | 57 | RUS_Yakuts | 0.16168 | 0.10337 | 0.13531 | 0.18807 | 0.10484 | 0.15236 | 0.19450 | 0.19790 | 0.18479 | 0.12798 | 0.19010 | 0.16460 | 0.18955 | * | 0.00149+-0.0004 | 0.00109+-0.0004 | 0.09989+-0.0030 | 0.00168+-0.0004 | 0.00317+-0.0005 | 0.00030+-0.0002 | 0.00010+-0.0001 | 0.00000+-0.0000 | 0.00010+-0.0001 | Crubézy et al. 2010 (57) |
| Asia, central | Mongolia | Xiongnu period: Hsiung-nu | MON_Xion | 46 | MON_Xiongnu | 0.16426 | 0.09454 | 0.14305 | 0.21200 | 0.11067 | 0.17532 | 0.20933 | 0.22341 | 0.18924 | 0.14496 | 0.19583 | 0.18380 | 0.19580 | 0.04243 | * | 0.05534+-0.0021 | 0.10672+-0.0031 | 0.00000+-0.0000 | 0.00010+-0.0001 | 0.00050+-0.0002 | 0.00030+-0.0002 | 0.00000+-0.0000 | 0.00267+-0.0005 | „Keyser-Tracqui (2003: 4); Kim et al. 2010 (3)" |
| Asia, central | China-Inner Mongolia | Wanggus, Upper Capital - Zhenzishan | CHIN_Wang_Zhen | 33 | CHIN_Wang-Zhen | 0.16614 | 0.08464 | 0.14997 | 0.21978 | 0.13249 | 0.16508 | 0.21776 | 0.24031 | 0.20957 | 0.14690 | 0.18975 | 0.16897 | 0.18806 | 0.04720 | 0.01635 | * | 0.00505+-0.0007 | 0.00000+-0.0000 | 0.00010+-0.0001 | 0.00000+-0.0000 | 0.00020+-0.0001 | 0.00000+-0.0000 | 0.00079+-0.0003 | „Fu et al. 2007 (12); Fu et al. 2009 (21)" |
| Asia, central | China-Inner Mongolia | Tuoba Xianbei | CHIN_Xian | 16 | CHIN_Xianbei | 0.21648 | 0.13933 | 0.18248 | 0.24425 | 0.16935 | 0.22223 | 0.27241 | 0.31859 | 0.29434 | 0.18985 | 0.24674 | 0.21861 | 0.25411 | 0.02274 | 0.02039 | 0.05758 | * | 0.00406+-0.0006 | 0.00634+-0.0007 | 0.00010+-0.0001 | 0.00050+-0.0002 | 0.00000+-0.0000 | 0.00317+-0.0005 | Changchun et al. 2006 (16) |
| Asia, north | Russia | Early-Late Krotovo | SIB_KROT | 26 | SIB_KROT | 0.11010 | 0.06330 | 0.09116 | 0.13509 | 0.08569 | 0.11542 | 0.13901 | 0.16261 | 0.17177 | 0.10027 | 0.11783 | 0.11124 | 0.13188 | 0.06559 | 0.10113 | 0.08109 | 0.08707 | * | 0.99287+-0.0009 | 0.01851+-0.0013 | 0.01881+-0.0014 | 0.00020+-0.0001 | 0.00564+-0.0006 | Molodin 2012 (26) |
| Asia, north | Russia | Andronovo | SIB_AND | 24 | SIB_AND | 0.09514 | 0.05683 | 0.07684 | 0.11530 | 0.05785 | 0.09785 | 0.12014 | 0.14174 | 0.15051 | 0.08519 | 0.10738 | 0.10580 | 0.11923 | 0.05846 | 0.09552 | 0.08514 | 0.07855 | -0.02985 | * | 0.05405+-0.0024 | 0.04366+-0.0019 | 0.00020+-0.0001 | 0.00881+-0.0008 | Molodin 2012 (20), Allentoft 2015 (4) |
| Asia, north | Russia | Baraba, Late-Bronze Age | SIB_BAR | 19 | SIB_BAR | 0.03615 | -0.01003 | 0.00230 | 0.04504 | -0.03374 | 0.01097 | 0.02762 | 0.04762 | 0.02874 | 0.00249 | 0.02447 | 0.03600 | 0.01271 | 0.08864 | 0.08924 | 0.09416 | 0.11973 | 0.05527 | 0.03746 | * | 0.90308+-0.0032 | 0.28839+-0.0046 | 0.13731+-0.0035 | Molodin 2012 (19) |
| Asia, north | Russia | „Solenoozernaia; Tatarka; Oust-Abakansty; Bogratsky; Afontova Gora" | MIN_BRAge | 20 | MIN_BRAge_KAR | 0.02477 | -0.00208 | -0.00544 | 0.04840 | -0.01420 | 0.02491 | 0.02719 | 0.03796 | 0.03413 | 0.01679 | 0.01987 | 0.02883 | 0.02247 | 0.09708 | 0.08777 | 0.08980 | 0.11698 | 0.04882 | 0.03892 | -0.02128 | * | 0.24532+-0.0042 | 0.33630+-0.0045 | „Keyser et al. 2009 (11); Allentoft et al. 2015 (9)" |
| Asia, central | Kazakhstan, Russia | „Ak-Mustafa; Izmaylovka; Oi-Zhaylau-III; Vodokhranilische; Zevakinskiy; Birlik; Molaly, Shubarat; Kok-Mardan; Solyanka; Bulanovo; Stepnoe VII; Bofshekaragankii; Kapova cave; Tanabergen II" | KAZ_BRAge_IAge | 34 | KAZ_BRAge_IAge | 0.02767 | -0.00164 | 0.00014 | 0.02347 | 0.01595 | 0.01661 | 0.03113 | 0.04092 | 0.01715 | 0.00126 | 0.02570 | 0.01871 | 0.02285 | 0.11049 | 0.11870 | 0.10911 | 0.16846 | 0.08099 | 0.07433 | 0.00579 | 0.00757 | * | 0.00228+-0.0005 | „Lalueza-Fox et al. 2004 (26); Allentoft et al. 2015 (8)" |
| Asia, central | Altai Republic, Mongolia | Scytho-Siberian | ALT_Scyt | 22 | ALT_Scyt | 0.06618 | 0.03696 | 0.04427 | 0.11103 | 0.03496 | 0.07947 | 0.09597 | 0.10988 | 0.10984 | 0.06636 | 0.07707 | 0.06983 | 0.07804 | 0.09277 | 0.06195 | 0.07155 | 0.07648 | 0.06760 | 0.06315 | 0.01968 | 0.00463 | 0.05278 | * | „Ricaut et al. 2004 (2); Gonzalez-Ruiz et al. 2012 (16); Allentoft et al. 2015 (1); Pilipenko et al. 2010 (3)" |

**Slatkin FST values**

| Region | Country | Population | Abbreviation | N | | POL_Grod | HUN_Conq | HUN_Avar | CB_Cont-Zone | HUN_Cum | HUN_Lomb | ITA_Lomb | ITA_med | SPA_med | POL_med | NOR_Vik | DAN_Vik.med | ICE_med | RUS_Yakuts | MON_Xiongnu | CHIN_Wang-Zhen | CHIN_Xianbei | SIB_KROT | SIB_AND | SIB_BAR | MIN_BRAge_KAR | KAZ_BRAge_IAge | ALT_Scyt | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Poland | | POL_Grod | 13 | POL_Grod | 0.00000 | 0.02620 | 0.04153 | 0.02821 | 0.02991 | 0.02457 | 0.02552 | 0.09177 | 0.02669 | 0.00605 | 0.00029 | 0.03475 | 0.02017 | 0.19287 | 0.19654 | 0.19924 | 0.27629 | 0.12372 | 0.10514 | 0.03750 | 0.02540 | 0.02846 | 0.07087 | This study (13) |
| Europe, east | Hungary | medieval populations of Conquest period from Hungary | HUN_CONQ | 101 | HUN_Conq | 0.02620 | 0.00000 | 0.00233 | 0.03925 | 0 | 0.00768 | 0.02266 | 0.02271 | 0.02031 | 0 | 0.02615 | 0.02474 | 0.01799 | 0.11529 | 0.10441 | 0.09246 | 0.16189 | 0.06757 | 0.06025 | 0 | 0 | 0 | 0.03838 | Csósz et al. 2016 (75), Tömöry et al. 2007 (26) |
| Europe, east | Hungary | Avars | HUN_AVAR | 26 | HUN_Avar | 0.04153 | 0.00233 | 0.00000 | 0.01661 | 0.00030 | 0.01704 | 0.01930 | 0 | 0.02422 | 0.00647 | 0.01680 | 0.01497 | 0.01261 | 0.15648 | 0.16693 | 0.17642 | 0.22321 | 0.10031 | 0.08323 | 0.00231 | 0 | 0.00014 | 0.04632 | Csósz et al. 2016 (26) |
| Europe, east | Slovakia, Croatia | medieval populations from present-day Slovakia (Nitra-Šindolka, Čakajovce) and Croatia (Zvonimirovo) | CB_Contact_zone | 23 | CB_Cont-Zone | 0.02821 | 0.03925 | 0.01661 | 0.00000 | 0.05784 | 0.04260 | 0.02167 | 0.05028 | 0.05661 | 0.01299 | 0.03300 | 0.03971 | 0.03843 | 0.23164 | 0.26904 | 0.28168 | 0.32318 | 0.15619 | 0.13032 | 0.04717 | 0.05086 | 0.02404 | 0.12490 | „Csósz et al. 2016 (4); Csákyová et al. 2016 (19)" |
| Europe, east | Hungary | medieval Cumanians | HUN_Cum | 11 | HUN_Cum | 0.02991 | 0 | 0.00030 | 0.05784 | 0.00000 | 0.00586 | 0.03840 | 0.05691 | 0.00441 | 0.00782 | 0.00555 | 0.02704 | 0.00072 | 0.11712 | 0.12445 | 0.15272 | 0.20387 | 0.09372 | 0.06140 | 0 | 0 | 0.01621 | 0.03623 | Bogácsi-Szabó et al. 2005 (11) |
| Europe, east | Hungary | Lombards from Hungary: Szólád | HUN_Lomb | 28 | HUN_Lomb | 0.02457 | 0.00768 | 0.01704 | 0.04260 | 0.00586 | 0.00000 | 0.00870 | 0.02237 | 0.02923 | 0 | 0.00591 | 0.00767 | 0 | 0.17975 | 0.21258 | 0.19771 | 0.28572 | 0.13048 | 0.10847 | 0.01110 | 0.02554 | 0.01689 | 0.08633 | Alt et al. 2014 (28) |
| Europe, south | Italy - Piedmont | „Lombards from Italy: Rivoli, Corso Levi (Turin); Rivoli, La Perosa (Turin); Mombello Monferrato (Alessandria); Collegno (Turin); Centallo, San Gervasio (Cuneo)" | ITA_Lomb | 28 | ITA_Lomb | 0.02552 | 0.02266 | 0.01930 | 0.02167 | 0.03840 | 0.00870 | 0.00000 | 0.03892 | 0.02916 | 0.02723 | 0.00487 | 0.02013 | 0 | 0.24147 | 0.26476 | 0.27838 | 0.37441 | 0.16145 | 0.13655 | 0.02840 | 0.02795 | 0.03213 | 0.10615 | Vai et al. 2015 (28) |
| Europe, south | Italy - Tuscans | „medieval Italians: Firenze, Piazza Signoria; Pisa, Vicopisano; Livorno, Castello Donoratico; Massa Carrara, Fivizzano; Siena, Santa Maria della Scala; Grosseto, San Quirico" | ITA_med | 27 | ITA_med | 0.09177 | 0.02271 | 0 | 0.05028 | 0.05691 | 0.02237 | 0.03892 | 0.00000 | 0.05186 | 0.04039 | 0.01482 | 0.01722 | 0.01083 | 0.24673 | 0.28769 | 0.31633 | 0.46755 | 0.19418 | 0.16515 | 0.05000 | 0.03946 | 0.04266 | 0.12344 | Guimaraes et al. 2009 (27) |
| Europe, south | Spain | medieval Spaniards: Basque, Aldaieta | SPA_med | 56 | SPA_med | 0.02669 | 0.02031 | 0.02422 | 0.05661 | 0.00441 | 0.02923 | 0.02916 | 0.05186 | 0.00000 | 0.02410 | 0.01495 | 0.04188 | 0.01394 | 0.22667 | 0.23341 | 0.26514 | 0.41711 | 0.20739 | 0.17718 | 0.02959 | 0.03533 | 0.01745 | 0.12339 | Alzualde et al. 2006 (56) |
| Europe, east | Poland | medieval Slavs from Poland: Cedynia (West Pomerania Province), Ostrów Lednicki (Greater Poland Province) | POL_med | 20 | POL_med | 0.00605 | 0 | 0.00647 | 0.01299 | 0.00782 | 0 | 0.02723 | 0.04039 | 0.02410 | 0.00000 | 0.00279 | 0.01754 | 0.00460 | 0.14676 | 0.16954 | 0.17219 | 0.23434 | 0.11145 | 0.09312 | 0.00250 | 0.01707 | 0.00126 | 0.07108 | Juras et al. 2015 (20) |
| Europe, north | Norway | Vikings from Norvay: Nord-Trøndelag, Nordland, Sør-Trøndelag, Telemark, Troms, Oppland, Hedmark | NOR_Vik | 56 | NOR_Vik | 0.00029 | 0.02615 | 0.01680 | 0.03300 | 0.00555 | 0.00591 | 0.00487 | 0.01482 | 0.01495 | 0.00279 | 0.00000 | 0.01498 | 0 | 0.23472 | 0.24351 | 0.23419 | 0.32756 | 0.13356 | 0.12030 | 0.02509 | 0.02027 | 0.02638 | 0.08351 | Krzewińska et al. 2015 (56) |
| Europe, north | Denmark | medieval Danes and Vikings: Galgedil, Kongemarken, Risby | DAN_Vik.med | 29 | DAN_Vik.med | 0.03475 | 0.02474 | 0.01497 | 0.03971 | 0.02704 | 0.00767 | 0.02013 | 0.01722 | 0.04188 | 0.01754 | 0.01498 | 0.00000 | 0.00968 | 0.19704 | 0.22519 | 0.20332 | 0.27978 | 0.12517 | 0.11832 | 0.03735 | 0.02968 | 0.01906 | 0.07507 | Melchior et al. 2010 (29) |
| Europe, north | Iceland | early medieval Icelander | ICE_med | 73 | ICE_med | 0.02017 | 0.01799 | 0.01261 | 0.03843 | 0.00072 | 0 | 0 | 0.01083 | 0.01394 | 0.00460 | 0 | 0.00968 | 0.00000 | 0.23389 | 0.24348 | 0.23162 | 0.34068 | 0.15191 | 0.13537 | 0.01287 | 0.02298 | 0.02338 | 0.08465 | Helgason et al. 2009 (73) |
| Asia, north | Russia - Eastern Siberia | Yakuts | RUS_Yakuts | 57 | RUS_Yakuts | 0.19287 | 0.11529 | 0.15648 | 0.23164 | 0.11712 | 0.17975 | 0.24147 | 0.24673 | 0.22667 | 0.14676 | 0.23472 | 0.19704 | 0.23389 | 0.00000 | 0.04431 | 0.04954 | 0.02327 | 0.07019 | 0.06209 | 0.09727 | 0.10751 | 0.12421 | 0.10225 | Crubézy et al. 2010 (57) |
| Asia, central | Mongolia | Xiongnu period: Hsiung-nu | MON_Xion | 46 | MON_Xiongnu | 0.19654 | 0.10441 | 0.16693 | 0.26904 | 0.12445 | 0.21258 | 0.26476 | 0.28769 | 0.23341 | 0.16954 | 0.24351 | 0.22519 | 0.24348 | 0.04431 | 0.00000 | 0.01662 | 0.02082 | 0.11251 | 0.10561 | 0.09799 | 0.09621 | 0.13468 | 0.06604 | „Keyser-Tracqui (2003: 4); Kim et al. 2010 (3)" |
| Asia, central | China-Inner Mongolia | Wanggus, Upper Capital - Zhenzishan | CHIN_Wang_Zhen | 33 | CHIN_Wang-Zhen | 0.19924 | 0.09246 | 0.17642 | 0.28168 | 0.15272 | 0.19771 | 0.27838 | 0.31633 | 0.26514 | 0.17219 | 0.23419 | 0.20332 | 0.23162 | 0.04954 | 0.01662 | 0.00000 | 0.06109 | 0.08824 | 0.09307 | 0.10395 | 0.09867 | 0.12247 | 0.07706 | „Fu et al. 2007 (12); Fu et al. 2009 (21)" |
| Asia, central | China-Inner Mongolia | Tuoba Xianbei | CHIN_Xian | 16 | CHIN_Xianbei | 0.27629 | 0.16189 | 0.22321 | 0.32318 | 0.20387 | 0.28572 | 0.37441 | 0.46755 | 0.41711 | 0.23434 | 0.32756 | 0.27978 | 0.34068 | 0.02327 | 0.02082 | 0.06109 | 0.00000 | 0.09538 | 0.08524 | 0.13602 | 0.13248 | 0.20258 | 0.08281 | Changchun et al. 2006 (16) |
| Asia, north | Russia | Early-Late Krotovo | SIB_KROT | 26 | SIB_KROT | 0.12372 | 0.06757 | 0.10031 | 0.15619 | 0.09372 | 0.13048 | 0.16145 | 0.19418 | 0.20739 | 0.11145 | 0.13356 | 0.12517 | 0.15191 | 0.07019 | 0.11251 | 0.08824 | 0.09538 | 0.00000 | 0 | 0.05851 | 0.05133 | 0.08813 | 0.07251 | Molodin 2012 (26) |
| Asia, north | Russia | Andronovo | SIB_AND | 24 | SIB_AND | 0.10514 | 0.06025 | 0.08323 | 0.13032 | 0.06140 | 0.10847 | 0.13655 | 0.16515 | 0.17718 | 0.09312 | 0.12030 | 0.11832 | 0.13537 | 0.06209 | 0.10561 | 0.09307 | 0.08524 | 0 | 0.00000 | 0.03892 | 0.04050 | 0.08030 | 0.06741 | Molodin 2012 (20), Allentoft 2015 (4) |
| Asia, north | Russia | Baraba, Late-Bronze Age | SIB_BAR | 19 | SIB_BAR | 0.03750 | 0 | 0.00231 | 0.04717 | 0 | 0.01110 | 0.02840 | 0.05000 | 0.02959 | 0.00250 | 0.02509 | 0.03735 | 0.01287 | 0.09727 | 0.09799 | 0.10395 | 0.13602 | 0.05851 | 0.03892 | 0.00000 | 0 | 0.00582 | 0.02008 | Molodin 2012 (19) |
| Asia, north | Russia | „Solenoozernaia; Tatarka; Oust-Abakansty; Bogratsky; Afontova Gora" | MIN_BRAge | 20 | MIN_BRAge_KAR | 0.02540 | 0 | 0 | 0.05086 | 0 | 0.02554 | 0.02795 | 0.03946 | 0.03533 | 0.01707 | 0.02027 | 0.02968 | 0.02298 | 0.10751 | 0.09621 | 0.09867 | 0.13248 | 0.05133 | 0.04050 | 0 | 0.00000 | 0.00763 | 0.00465 | „Keyser et al. 2009 (11); Allentoft et al. 2015 (9)" |
| Asia, central | Kazakhstan, Russia | „Ak-Mustafa; Izmaylovka; Oi-Zhaylau-III; Vodokhranilische; Zevakinskiy; Birlik; Molaly, Shubarat; Kok-Mardan; Solyanka; Bulanovo; Stepnoe VII; Bofshekaragankii; Kapova cave; Tanabergen II" | KAZ_BRAge_IAge | 34 | KAZ_BRAge_IAge | 0.02846 | 0 | 0.00014 | 0.02404 | 0.01621 | 0.01689 | 0.03213 | 0.04266 | 0.01745 | 0.00126 | 0.02638 | 0.01906 | 0.02338 | 0.12421 | 0.13468 | 0.12247 | 0.20258 | 0.08813 | 0.08030 | 0.00582 | 0.00763 | 0.00000 | 0.05572 | „Lalueza-Fox et al. 2004 (26); Allentoft et al. 2015 (8)" |
| Asia, central | Altai Republic, Mongolia | Scytho-Siberian | ALT_Scyt | 22 | ALT_Scyt | 0.07087 | 0.03838 | 0.04632 | 0.12490 | 0.03623 | 0.08633 | 0.10615 | 0.12344 | 0.12339 | 0.07108 | 0.08351 | 0.07507 | 0.08465 | 0.10225 | 0.06604 | 0.07706 | 0.08281 | 0.07251 | 0.06741 | 0.02008 | 0.00465 | 0.05572 | 0.00000 | „Ricaut et al. 2004 (2); Gonzalez-Ruiz et al. 2012 (16); Allentoft et al. 2015 (1); Pilipenko et al. 2010 (3)" |

**Mt $F_{ST}$ values at loci and Hudson Fst matrix of 52 modern and 23 ancient populations**

$F_{ST}$ values were calculated between modern and ancient populations, 1000 Genomes non-genomic human SNPs downloaded from ftp.1000genomes.ebi.ac.uk/vol1/ftp/phase3/ and analysed using Arlequin v3.5.1.2. $F_{ST}$ values are presented in the lower diagonal of the table, p-values are listed in the upper diagonal. Significant fst values are indicated with p values (<0.05).

**genome-wide average values**

| Region | Country | Population | Abbreviation | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | References |
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