

DISTRIBUTION OF HAPLOGROUP G-P15 OF THE Y-CHROMOSOME AMONG REPRESENTATIVES OF ANCIENT CULTURES AND MODERN POPULATIONS OF NORTHERN EURASIA

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Abstract. The Alans represent a medieval nomadic pastoral people of the North Caucasus, who settled in Europe as a result of the Great Migration of Peoples. The genetic data of the Alans of the early Middle Ages and their relationship with the ancient and modern European populations remain insufficiently studied. It is assumed that the haplogroup G-P15 of the Y-chromosome was introduced in the Alans as a result of admixture with the autochthonous populations of the Caucasus. However, the impact of the Alan gene pool on the Medieval European populations appears to be unlikely, which may also indicate the absence of a significant genetic flow from steppe populations to European populations during the early Middle Ages.

Keywords: Y-chromosome, haplogroup, ancient DNA, human, population genetics.

Introduction

In recent years, a great interest toward the study of the ancient DNA samples has been detected worldwide. This was facilitated by the development of technologies that significantly improve the processes of purification, DNA isolation and bioinformatic analysis of the obtained nucleotide sequences, which almost completely excludes false results, as well as the awarding of the Nobel Prize in Physiology and Medicine in 2022 to Svante Paabo known as the founder of paleogenomics and one of the major evolutionary biologists in the world. This provided in recent decades a significant accumulation of genetic data on the ancient cultures, which have been previously examined exclusively by the methods of anthropology, archeology, and history. Considering the available data on the autosomal genome and mtDNA and Y-chromosome haplogroups in contemporary populations, the study of the continuity of the ancient cultures and nowadays populations inhabiting the same geographical regions, but separated in time period became one of the most challenging directions. The Y-chromosome as a

population-genetic marker used to examine a genetic history has several advantages. Together with the X-chromosome, the Y-chromosome is one of two sex chromosomes in male genome. It is much larger in size than mtDNA and its length is assigned to 60 kb, which indicates the possibility of higher number of polymorphic sites. A decreased level of homology to the X-chromosome is related to a low number of pseudoautosomal telomeric regions, which do not exceed 5%, and the presence of the original non-recombining region (NRY) comprising 95% of the total length. The NRY is the most examined region by population geneticists in phylogenetic studies, since this region is a single linkage group inherited as a single locus and together with mtDNA it represents a uniparental marker, which is paternally transmitted to the male descendants. The Y-chromosome as an object of research by evolutionary geneticists is very promising in the upcoming era of next-generation sequencing of the human genome, and, consequently, a detection of novel markers inside the haplogroups. A geographical distribution of the Y-chromosome is affected

by both genetic and social-demographic factors; in this regard, another prompt of the Y-chromosome markers such as patrilocality should be noted: in 70% of nowadays societies a woman moves to her husband's place of residence (Jobling *et al.*, 2003). This is an important factor that increases genetic subdivision of populations according to the Y-chromosome data. However, it should be noted that global movements are mainly characteristic for men. This is primarily caused by conquest wars, for example, in South America (Bedoya *et al.*, 2006), apparently related to enhanced aggression (Strous *et al.*, 2003) and the search for novel locations observed in men.

The Alans represent an extremely interesting culture, which monuments are still preserved on the territory of the Caucasus. The first mentions of the Alans appear almost simultaneously in the texts of different authors from various regions (Alemany, 2000). A major part of the Alans settled in the Northern Pre-Caucasus in the first century A.D. and eventually developed an early feudal state, which competed with the Khazar Khaganate and Byzantium at various stages of its development. However, there is no generally accepted hypothesis regarding the affiliation of the Alan language (Abu-Ali Ahmed Ben Omar Ibn-Dast, 1869; Miller, 1893; Abayev, 1949; Abu Reyhan Biruni, 1957; Nemet, 1960; Kuznetsov, 1962; Kuznetsov, 1968; Byazyrov, 1981; Kumekov, 1987; Tsutsiev, 1999; Abu-l-Fida, 2002; Kambolov, 2006; Konovalova, 2009; Dobrovits, 2011; Cheng, 2012; Basayev, 2013; Tuallagov, 2014; Tuallagov, 2015a; Tuallagov, 2015b; Tuallagov, 2018; Kambolov, 2021). Currently, a large number of hypotheses on the language affiliation of the Alans exist; however, three main hypotheses that are the most popular among specialists can be selected:

1) The theory of Iranian (Ossetian) language origin of the Alans. To date, a majority of scientists support this hypothesis. This hypothesis is mainly referred to three late written sources: the Theology of John Thats, the Zelenchuk Inscription, and the Yass Glossary (Miller, 1893; Abayev, 1949; Nemet, 1960; Kuznetsov, 1962; Kuznetsov, 1968; Byazyrov, 1981; Kambolov,

2006; Basayev, 2013; Tuallagov, 2014; Tuallagov, 2015a; Tuallagov, 2015b; Tuallagov, 2018; Kambolov, 2021).

2) The theory of Turkic language origin of the Alans. The followers of this hypothesis mainly refer to written Arabic and Chinese sources, and to the Eastern European Turkic runic and onomastics of the Alan names (Abu-Ali Ahmed Ben Omar Ibn-Dast, 1869; Abu Reyhan Biruni, 1957; Abu-l-Fida, 2002; Dobrovits, 2011; Cheng, 2012).

3) The theory of mixed language origin of the Alans has been also discussed before; however, the development of molecular-genetic methods of analysis of the ancient DNA provided an increasing support by the specialists (Damgaard *et al.*, 2018).

To date, the findings on only five samples belonging to this culture have been published (Afanasiev *et al.*, 2014; Damgaard *et al.*, 2018). One of them corresponds to haplogroup G, namely, to G-P15. Haplogroup G is the most common in the Caucasus and had the highest frequencies in North Ossetins (69%) and Megrels (50%) (Kutuev *et al.*, 2011; Yunusbayev *et al.*, 2012). Its frequency decreases up to 5-15% in the Near and Middle East, and in Southern Europe (Rootsi *et al.*, 2012). To date, there is convincing evidence obtained from the study of ancient DNA, which confirms a significant proportion of the haplogroup G of the Y-chromosome in the Neolithic population of Central Europe. In particular, it was detected in four of six archaeological sites located in Spain, France, Italy, and Germany, and the total frequency of haplogroup G was more than 70% (Haak *et al.*, 2008; Haak *et al.*, 2010; Lacan *et al.*, 2011a; Lacan *et al.*, 2011b; Keller *et al.*, 2012; Lee *et al.*, 2012). Obviously, this observation points to the link between the presence of haplogroup G and the distribution of agriculture on the European continent (Seminio *et al.*, 2000a).

Materials and Methods

The study included DNA samples obtained from 29 Northern Eurasian populations, that were collected during 2002 to 2022, including Abazines, Abkhazes, Avars, Adyghes, Andis,

Bagvalals, Balkars, Darginians, Ingushes, Kabdines, Karachays, Lezgis, Megrels, Karanogays, Kuban Nogays, Kumyks, Osetins, Tabasarans, Chamalals, Cherkessians, Chechens, Altaians, Udmurts, Besermyans, Komi, Mari, Mordva, Chuvash, Bashkirs (from Perm Territory, Samara and Saratov region, Abzelilovsky, Sterlibashevsky, Baimaksky district of the Republic of Bashkortostan, Orenburg region), and two subpopulations of Tatars (from Tuymazinsky district of Bashkortostan and Kazan).

Ethnic background, ancestry and relative relationship were assigned using a questionnaire considering the data obtained from up to third generation. All the enrolled individuals were informed about the aim of the research. DNA isolation from the peripheral blood leukocytes was carried out via standard method of chloroform extraction (Mathew *et al.*, 1984). The analysis of Y-chromosome markers was performed using a polymerase chain reaction (PCR) of DNA synthesis with corresponding oligonucleotide primers, restriction fragment length polymorphism (RFLP) and a direct Sanger's sequencing. The haplogroups of the Y-chromosome were assigned according to the updated classification of the Y-Chromosome Consortium (YCC) (YCC, 2002; Karafet, 2008).

To determine haplogroup G-M201 we used the following primers: F 5'-3' - tatgcatttgtttagtatatgtc; R 5'-3' - gttctgaatgaaagttaacacg, haplogroup G-P15: F 5'-3' - agagagtttctaacaggcg; R 5'-3' - tggaatcaactttgcaact. Detected fragments 326 and 173 bp in length were analyzed using Sanger's sequencing on DNA Analyzer Applied Biosystems 3500 from the forward primer. Obtained chromatograms were examined using Sequenceher 5.1.

Results

The origin of haplogroup G-M201 is linked to a fairly large region, including Eastern Anatolia, Armenia and Western Iran (Rootsi *et al.*, 2012). These regions were characterized by the highest diversity of the basal branches of the haplogroup G-M201 and STR haplotypes (Rootsi *et al.*, 2012).

Haplogroup G-M201 is widespread in the Caucasus, the Near and Middle East, and Southern Europe. The highest frequency exceeding 70% was observed in the Caucasus, in North Ossetia and among the Svans (ethnic and territorial group of Georgians) (Balanovsky *et al.*, 2011; Yunusbayev *et al.*, 2012; Yardumian *et al.*, 2017), while its frequency is diminished up to 13% in Iranians and decreases toward the movement to the East (Regueiro *et al.*, 2006). Haplogroup G-M201 has the frequencies ranging from 5 to 15% in the rest part of the Middle East, Southern Europe (especially in Italy and Greece), while its frequency drops in the Balkans and Northern Europe (Rootsi *et al.*, 2012). However, it was almost absent in India. A subsequent movement toward East, obviously, evidences in the absence of migration of individuals bearing M-201 mutation (Sengupta *et al.*, 2006).

As a result of the present study, we used 2972 DNA samples from the populations of Northern Eurasia (Volga-Ural region and the Caucasus). It was shown that haplogroup G-P15 was more frequent in the populations of the Caucasus and varied from 69.7% in the population of North Osetins up to 0% in the populations of Bagvalals, Tabasarans, Avars, and Armenians (Table 1). In the Volga-Ural region, haplogroup G-P15 occurs with the highest frequencies in the subpopulations of Kazan and Tuymazy Tatars (7.6% and 6%, respectively). Interestingly, in the subpopulations of Bashkirs, which were present in our study as eleven subpopulations from the Republic of Bashkortostan and neighboring regions, haplogroup G-P15 was detected only in three subpopulations such as Gaininsky Bashkirs, Abzelilovsky Bashkirs and Bashkirs from the Orenburg region (Table 1). It is also extremely interesting that this haplogroup is absent in several Volga-Ural populations. In particular, we failed to detect any sample bearing haplogroup G-P15 in populations belonging to the Finno-Ugric linguistic group, which consisted of Udmurts, Komi, Mari, Mordva, and Besermyans in the present study.

Table 1

**Distribution of the frequencies of Y-chromosome haplogroup G-P15
in the examined populations**

Population	N	G2a-P15 (N)	Frequency (%)
Chamalals	27	5	18.52
Andis	49	3	6.12
Lezgis	31	3	9.68
Darginians	67	2	2.98
Adyghehs	154	72	46.75
Abazines	88	36	40.91
Karachays	69	22	31.88
Kumyks	73	10	13.7
Megrels	65	33	50.77
Abkhazes	162	77	47.53
Balkars	135	44	32.59
Cherkessians	126	57	45.24
Osetins N	132	92	69.7
Osetins S	21	10	47.62
Kabardines	140	60	42.86
Chechens	165	2	1.21
Nogays K	87	12	13.79
Karanogays	76	1	1.32
Ingushes	105	5	4.76
Avars	42	0	0
Bagvalals	28	0	0
Tabasarans	43	0	0
Armenians	26	0	0
Kurds	21	0	0
Tats	10	0	0
Bashkirs Sterlibashevsky District	54	0	0
Bashkirs Abzelilovsky District	82	1	1.22
Bashkirs Orenburg region (west)	45	1	2.22
Bashkirs Orenburg region (east)	34	0	0
Bashkirs Samara region	40	0	0
Bashkirs Saratov region	14	0	0
Bashkirs Perm Territory	71	1	1.4
Bashkirs Baimak	76	0	0
Bashkirs Abzelilovsky district of Bashkortostan	70	0	0
Bashkirs Burzyn distinkt of Bashkortostan	140	0	0
Chuvash	43	0	0
Komi	50	0	0
Mari	44	0	0
Mordva	59	0	0
Kazan Tatars	53	4	7.55
Tatars Tuymazinsky district of Bashkortostan	50	3	6
Udmurts	52	0	0
Besermyans	53	0	0

Discussion

The analyzed haplogroup G-P15, which has been previously detected in the Alans, is quite widely represented in both nowadays populations (Table 1) and certain samples of Neolithic archaeological cultures of Europe (Table 2). To be more precise, it was observed in Treilles culture, which refers to the Neolithic cultures that developed at the territory of nowadays France in the period from 2600 B.C. to 1700 B.C. Chronologically, this culture is

divided into three stages: early (2600–2300 BC), late (2300–2000 BC), and final (2000–1700 BC). The features of the funeral rite of Treilles culture were affected by the environment and are mainly present by dolmens and mounds (Balsan, 1972; Herrscher *et al.*, 2013). The samples for the genetic analysis were obtained from the Treilles cave I at Saint-Jean-et-Saint-Paul (Fig. 1). The haplogroup G-P15 was detected in 20 of 22 examined male samples (Lacan *et al.*, 2011).

Table 2
Y-chromosome haplogroup G-P15 in the ancient archaeological cultures

Culture Grouping	Country	Dating	N	P15 (N)	Reference
Anatolian_Aceramic	Turkey	8300-7800 BC	1	1	Feldman <i>et al.</i> , 2019
Sicily	Italy	7000-1100 BC	16	3	Fernandes <i>et al.</i> , 2020; Van de Loosdrecht <i>et al.</i> , 2020
Anatolia_Neolithic	Turkey	6424-6251 BC 8212-7952 BCE		12	Kilinc <i>et al.</i> , 2016; Mathieson <i>et al.</i> , 2015
Balkans_N Balkans_BA Balkans_LCA Balkans_EBA Balkans_LN Balkans_MP_Neolithic	Balkans	6000-2000 BC	90	30	Lipson <i>et al.</i> , 2017; Mathieson <i>et al.</i> , 2018; Olalde <i>et al.</i> , 2018
Starčevo	Hungary Croatia	5640-5540 BC	19	11	Szécsényi-Nagy <i>et al.</i> , 2015
Anatolia_East_LC Anatolia_Central_LC	Turkey	5592-5472 BP	14	2	Skourtanioti <i>et al.</i> , 2020
ALPc_Szakalhat_MN	Hungary	5300-4900 BC	2	2	Lipson <i>et al.</i> , 2017
Epicardial Culture	Spain	5000 BC	6	5	Lacan <i>et al.</i> , 2011b
Iberia	Spain	5000-500 BC	205	24	Olalde <i>et al.</i> , 2019; Villalba-Mouco <i>et al.</i> , 2019
Linear Pottery culture (LBK)	France Hungary Germany Austria	~5000 BC	54	23	Brunel <i>et al.</i> , 2020; Lipson <i>et al.</i> , 2017; Rivollat <i>et al.</i> , 2020; Nikitin <i>et al.</i> , 2019; Szécsényi-Nagy <i>et al.</i> , 2015; Mathieson <i>et al.</i> , 2018
Epicardial Culture	Spain	5000 BC	6	5	Lacan <i>et al.</i> , 2011b
Tisza Culture	Hungary	5000-4500 BCE	3	1	Lipson <i>et al.</i> , 2017

Table 2 continued

Culture_Grouping	Country	Dating	N	P15 (N)	Reference
Lengyel Culture	Hungary	4800-4500 BCE	11	3	Szécsényi-Nagy et al., 2015
France_EIA France_EN France_MN France_ENMN France_EBA France_LIA France_EMBA France_LBA France_HG	France	4800-3000BC	123	42	Lacan et al., 2011a; Brunel et al., 2020; Rivollat et al., 2020
Lengyel	Hungary	4800-4500 BC	12	3	Szécsényi-Nagy et al., 2015
Sardinia_Bell_Beaker Sardinia_Neolithic Sardinia_Nuragic_BA Sardinia_Chalcolithic	Italy	4100-1000 BC	26	11	Fernandes et al., 2020
Trypillia Culture	Ukraine	3758-3636 calBCE	9	5	Mathieson et al., 2018; Nikitin et al., 2017
Maykop	Russia	~3500 BC	13	1	Wang et al., 2019; Key et al., 2020
Treilles culture / Final Neolithic	France	3000 BC	22	20	Lacan et al., 2011a
Trentino Chalcolithic Trentino Bronze Age Trentino EBA Polada A Trentino Copper Age I	Italy	3400-2100 calBC	8	3	Graefen et al., 2020
Néolithique	France	3499-3126 calBC	5	4	Brunel et al., 2020
Horgen culture	Switzerland	3323-2581 calBC	32	30	Furtwaengler et al., 2020
SE_Iberia_CA	Spain	2900–2500 BCE	13	5	Olalde et al., 2019
Trentino Chalcolithic	Italy	2891-2702 calBCE	1	1	Graefen et al., 2020
Bell_Beaker	Hungary Germany Italy Great Britain Czech Republic	2800-1900 BC	27	3	Olalde et al., 2018; Fernandes et al., 2020
Unetice_EBA	Czech Republic	2300-1700 BC	7	1	Olalde et al., 2018
Trentino Bronze Age	Italy	2289-2141 calBC	1	1	Graefen et al., 2020
Trentino EBA Polada A	Italy	2284-2136 calBC	2	1	Graefen et al., 2020
Anatolia_MLBA Assyrian IIIc	Turkey	~2000–1750 BC	5	1	Damgaard et al., 2018
Koban Culture	Russia	VIII-VII BC	6	2	BoulyginaJ et al., 2020
Hallstatt Culture – Early «La Tène»	France	800-700 calBC	5	1	Brunel et al., 2020

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End of table 2

Culture_Grouping	Country	Dating	N	P15 (N)	Reference
Early Conqueror Upper Tisza	Hungary	first half of the tenth century CE	14	4	Fóthi <i>et al.</i> , 2020
Imperial Rome	Italy	0-400 CE	24	5	Antonio <i>et al.</i> , 2019
Wielbark culture	Poland	100-300 AD	5	2	Stolarek <i>et al.</i> , 2019
Sardinia_LateAntiquity	Italy	256-403 calCE	2	1	Fernandes <i>et al.</i> , 2020
Alan	Russia	300-400 AD	5	1	Afanasiev <i>et al.</i> , 2014; Damgaard <i>et al.</i> , 2018
Hungary Avar Early	Hungary	VII AD	11	1	Nepáczki <i>et al.</i> , 2019
Late Antiquity Rome	Italy	300-700 CE	16	2	Antonio <i>et al.</i> , 2019
Longobard Kingdom	Italy	580-630 CE	17	1	Amorim <i>et al.</i> , 2018
Alemannic	Germany	580-630 CE	19	2	O`Sullivan <i>et al.</i> , 2018; Veeramah <i>et al.</i> , 2018
Merovingian	Germany	670 CE	6	2	Vanek <i>et al.</i> , 2009
Saltovo-Mayaki	Russia	700-900 CE	11	1	Damgaard <i>et al.</i> , 2018; Afanasiev <i>et al.</i> , 2015; Afanasiev <i>et al.</i> , 2015
Medieval/Early Modern Rome	Italy	1070-1430 calCE	6	3	Antonio <i>et al.</i> , 2019
Late Kushnarenkovo-Karayakupovo	Hungary	X-XI AD	17	1	Csáky <i>et al.</i> , 2020
Viking	Sweden Russia Norway Estonia UK Denmark	700-1100 CE	276	3	Margaryan <i>et al.</i> , 2020; Krzewińska <i>et al.</i> , 2018

Another major culture, which samples possessed the Y-chromosome haplogroup G-P15, is the Linear Pottery culture (LBK). This is one of the most examined Neolithic archaeological cultures of Europe (5500–4500 B.C.). It is assumed that agriculture and cattle breeding were widely distributed among the representatives of this culture. The funeral rite included both cre-mation and inhumation (Gimbutas,

1991). According to the radiocarbon analysis, the samples from certain sites were dated to ~ 5000 B.C. The haplogroup G-P15 was observed in 23 of 54 analyzed male samples, which comprises 43% (Haak *et al.*, 2010; Szécsényi-Nagy *et al.*, 2015; Lipson *et al.*, 2017; Mathieson *et al.*, 2018; Rivollat *et al.*, 2020). A specific interest is placed toward the Trypillia Culture representing a Neolithic and

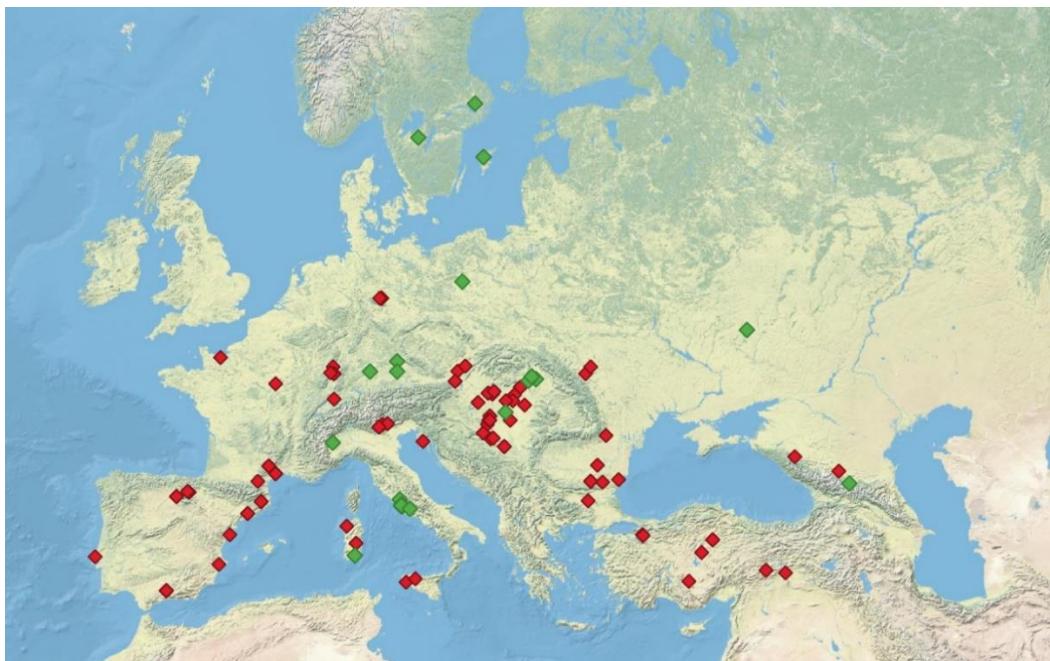


Fig. 1. Location of archaeological sites with detected Y-chromosome haplogroup G-P15

Eneolithic culture (5500–2750 BC), that included the territories from nowadays Moldova, Romania, and Ukraine. The main hypotheses of the decline of this culture are the expansion of the Pit culture (Gimbutas, 1982) and the climate change (Videiko, 2002). The samples for the genetic analysis were obtained from the sites of Verteba Cave, Glăvănești, Mayaki, and Durankulak. A radiocarbon analysis dates the samples to 3900–3000 B.C. (Nikitin *et al.*, 2017; Mathieson *et al.*, 2018). The haplogroup G-P15 was detected in 5 of 9 examined male samples (Nikitin *et al.*, 2017; Mathieson *et al.*, 2018).

Another European culture, which is characterized by a high frequency of haplogroup G-P15, is the Starčevo culture. The Starčevo culture is an archaeological culture from the territory of South-Eastern Europe and dating back to the Neolithic period between 6200 and 4500 B.C. (Chapman, 2000). It is assumed that this culture was formed as a result of migration of Anatolian farmers; the western boundaries of the area of this culture are distributed till the territory of nowadays Croatia (Rajković and Vitezović, 2020). The haplogroup G-P15 was detected in 11 of 19 analyzed male samples (Szécsényi-Nagy *et al.*, 2015).

Therefore, a predominance or high frequency of the Y-chromosome haplogroup G-P15 in representatives of various Neolithic archaeological cultures of Europe with a pronounced decrease or complete absence in the subsequent cultures confirms the hypothesis on Neolithic expansion of Anatolian/Middle Eastern farmers toward Western Europe, which was followed by their displacement by such steppe ancestors as pro-Indo-European steppe nomads.

In this regard, a specific interest belongs to the penetration of the East Eurasian steppe dwellers into the European continent during the early Middle Ages. Nomadic tribes carried out campaigns on the territory of European countries long before the beginning of the Great Migration of Peoples; however, a significant part of them insignificantly affected the culture of the indigenous population of the region. As an exception, we can mention the Alans, who appeared at the eastern border of Europe at the beginning of the New Era.

The earliest mention of the Alans in Western Europe belongs to the first half of the first century A.D. and their mention in Seneca's play. Even in the second half of the first century A.D., Josephus Flavius clarified that the Alans

were a Scythian people and occupied the territories from the Don to the Sea of Azov. Therefore, it may evidence in the penetration of the Alans into Europe. Later, they actively participated in the Great Migration of Peoples and were introduced to Gaul, Spain, and North Africa. In comparison to the previous and subsequent nomads, the Alans significantly contributed to the culture of European peoples. According to different authors, the European military culture owes the occurrence of chivalry to the Scythians and the Alans as their posterities, while the spiritual culture of Catholic Europe accepted the sermons of a number of priests (canonized later) originating from the Alan community. The Alans did not develop their own state on the European continent; however, they were assimilated by the local population by the V-VII centuries A.D. Accordingly, nowadays haplogroup G-P15 in Europe can be both a Neolithic marker and a consequence of medieval migrations.

Since the Alans are potentially Asian migrants, diminished frequencies of the haplogroup G-P15 in nowadays populations of the VUR and its total absence in Finno-Ugric populations may indicate that this haplogroup was obtained by the Alans due to admixture with the autochthonous Caucasian population.

Conclusion

A distribution of haplogroup G is mainly limited to the territory of the Caucasus, the Near

and Middle East, as well as Southern Europe. Its maximal frequency is observed in Svaneti (78%) and North Ossetia (70%), decreases to 13-15% in Iran and is less common in Europe (Al-Zaheri *et al.*, 2003; Luis *et al.*, 2004; Goncalves *et al.*, 2005; Regueiro *et al.*, 2006; Abu-Amero *et al.*, 2007; King *et al.*, 2008; Battaglia *et al.*, 2009; Kutuev *et al.*, 2011; Balanovsky *et al.*, 2011; Roots *et al.*, 2012; Yunusbayev *et al.*, 2012; Khusnutdinova *et al.*, 2012; Yاردumian *et al.*, 2017). Together with the haplogroup J2, representation of this haplogroup is probably related to the spread of agriculture in Europe (Semino *et al.*, 2000a; Roots *et al.*, 2012).

A discovery of the haplogroup G-P15 in the graves belonging to the Alan culture evidence in the active admixture of steppe nomads with the settled autochthonous population of the Caucasus and in the possible further penetration of the Y-chromosomal genetic component from the Caucasus into Europe as a result of migration flows. However, to confirm this hypothesis, a detailed analysis of both the ancient and modern populations of mentioned regions of Western Eurasia is required.

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