



# TANER'S ANCIENT DNA STORY



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SUBMITTED BY:  
ANCESTRAL BREW

SUBMITTED TO:  
TANER

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# INTRODUCTION

Taner, this report has been custom generated using your DNA. The method of analysis used in this report involves interpreting your DNA using an algorithm called Global25 co-ordinates (G25)

This type of ancestry modelling allows for very precise and granular determination of ancestry. G25 ancestry modelling is currently the most effective way to perform a free-form discovery of potential ancestry.

## YOUR UNIQUE G25 CO-ORDINATES

Taner\_scaled,0.087644,-0.075149,0.042238,0.006137,-0.012002,-0.001394,0.014806,0.010846,-0.006545,-0.006196,-0.004222,0.003147,-0.007136,-0.001376,0.002714,0.000398,0.017863,0.00038,0.007668,0.007629,-0.011854,-0.002226,-0.003451,0.004338,-0.00455

Taner,0.0077,-0.0074,0.0112,0.0019,-0.0039,-0.0005,0.0063,0.0047,-0.0032,-0.0034,-0.0026,0.0021,-0.0048,-0.001,0.002,0.0003,0.0137,0.0003,0.0061,0.0061,-0.0095,-0.0018,-0.0028,0.0036,-0.0038

# DEFINITIONS

## What is "Ancestry Breakdown"?

This section is designed to provide "fine structure" ancestry analysis via pre designed ancestry models specific to various regions of the world.

## What is "Fit"?

The "fit" value shows the accuracy of the model.

## What is "Closest Populations"?

This section shows your genetically closest (up to 50) modern populations and ancient samples estimated using Euclidean distances method. Genetic Distance/Distance values show how closely a given population/sample resembles your autosomal genetic profile. However, this does not necessarily prove you are related or inherited from a population/sample on your list.

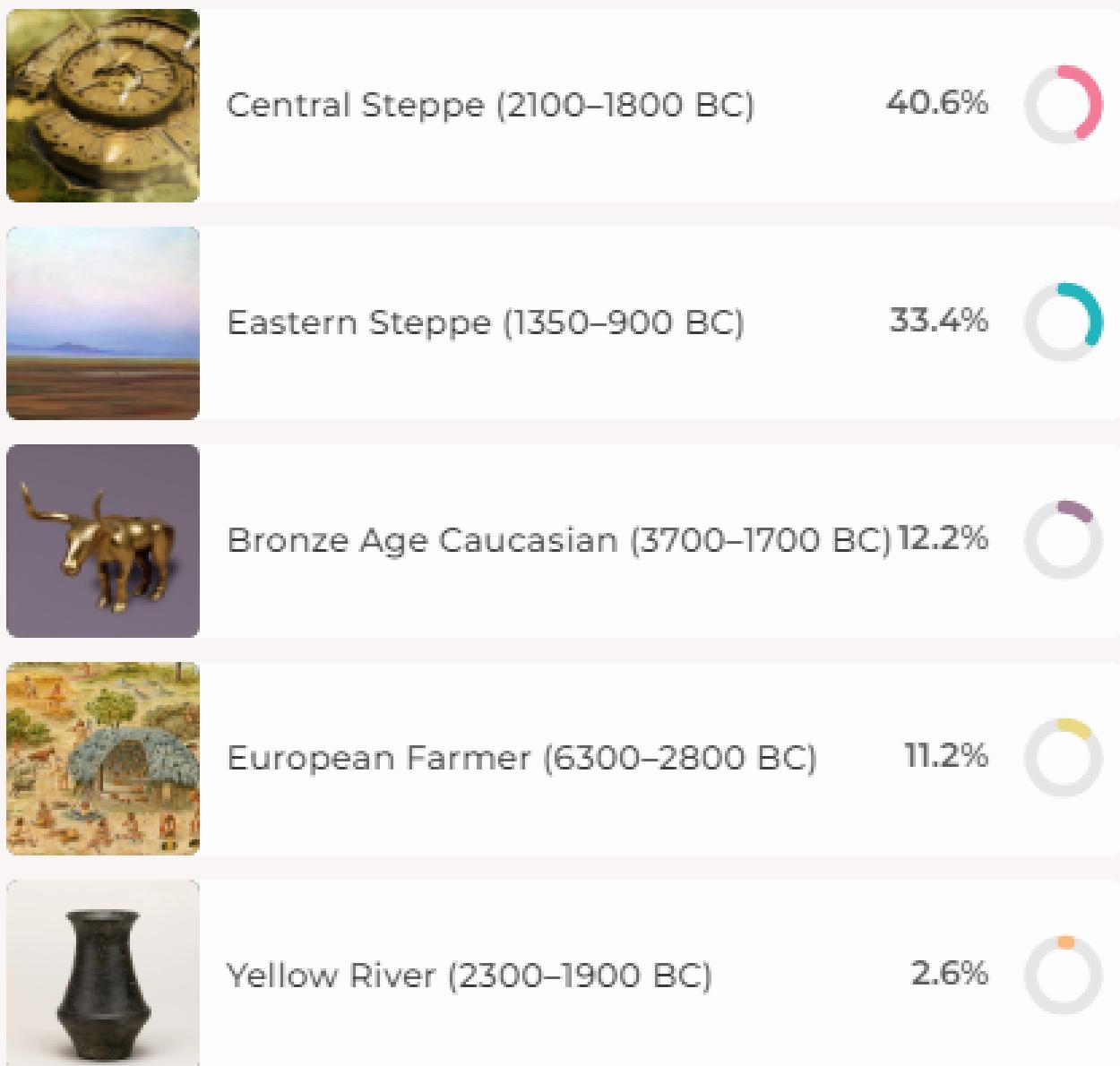
## What is "PCA Plot"?

Drift sensitive PCA (Principal Component Analysis) models are designed to provide most meaningful and in depth clusters based on your ethno-geographical background.

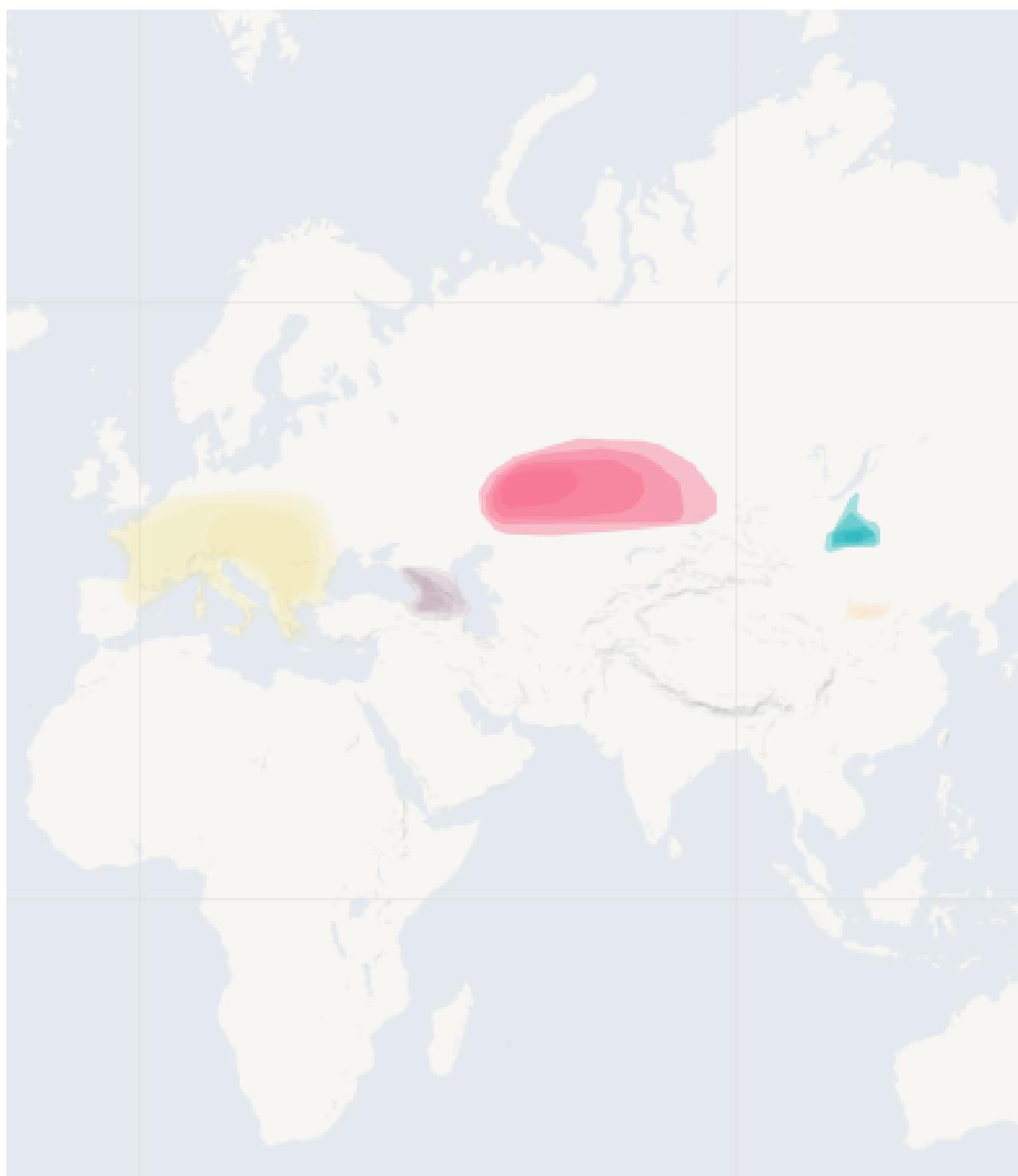
## What is "Mixed Mode"?

Mixed Mode module is an unsupervised way of modelling your genetic profile with two and three best fitting ancient and modern samples. You can browse up to 50 different models (possibilities) and decide which one makes sense the most.

# YOUR BRONZE AGE DNA BREAKDOWN



# YOUR BRONZE AGE DNA BREAKDOWN



# CENTRAL STEPPE (2100–1800 BC)

## DESCRIPTION



Narasimhan 2019 analyzed the remains of several members of the Sintashta culture. mtDNA was extracted from two females buried at the Petrovka settlement. They were found to be carrying subclades of U2 and U5. The remains of fifty individuals from the fortified Sintashta settlement of Kamennyi Ambar was analyzed. The Y-DNA from thirty males was extracted. Eighteen carried R1a and various subclades of it (particularly subclades of R1a1a1), five carried subclades of R1b (particularly subclades of R1b1a1a), two carried Q1a and a subclade of it, one carried I2a1a1a, and four carried unspecified R1 clades. The majority of mtDNA samples belonged to various subclades of U, while W, J, T, H, and K also occurred. A Sintashta male buried at Samara was found to be carrying R1b1a1a2 and J1c1b1a. The authors of the study found the Sintashta people to be closely genetically related to the people of the Corded Ware culture, the Srubnaya culture, the Potapovka culture, and the Andronovo culture. These were found to harbor mixed ancestry from the Yamnaya culture and peoples of the Central European Middle Neolithic. Sintashta people were deemed genetically almost indistinguishable from samples taken from the northwestern areas constituting the core of the Andronovo culture, which were genetically largely homogeneous. The genetic data suggested that the Sintashta culture was ultimately derived of a remigration of Central European peoples with steppe ancestry back into the steppe.

40.6% of your Ancient DNA is Central Steppe. This genetic component is thought to have originated from the people who lived in the steppe region during the Bronze and Iron Ages. It has been found to be particularly common among pastoralist groups such as the Yamnaya, Afanasievo, and Catacomb cultures.

# EASTERN STEPPE (1350–900 BC)

## DESCRIPTION



In contrast to the MLBA and EIA cultures of the Altai and northern Mongolia, different burial traditions are found in the eastern and southern regions of Mongolia (Honeychurch, 2015), notably the LBA Ulaanzuukh (1450–1150 BCE) and EIA Slab Grave (1000–300 BCE) cultures. In contrast to other contemporaneous Eastern Steppe populations, individuals associated with these burial types show a clear northeastern Asian (ANA-related) genetic profile lacking both ANE and WSH admixture.

33.4% of your Ancient DNA is Eastern Steppe related. This component peaks in populations from the Eastern Steppes region, specifically in ancient Kazakhstan, Mongolia, and parts of Russia. It is attributed to the interactions many civilizations had with the people of the Eastern Steppe, as well as the expansion of nomadic groups like the Scythians and the Xiongnu during the Bronze Age. This component is also found in lower frequencies in other parts of Asia and Europe, likely due to the spread of these ancient cultures and their interactions with other groups.

# BRONZE AGE CAUCASIAN (3700–1700 BC)

## DESCRIPTION



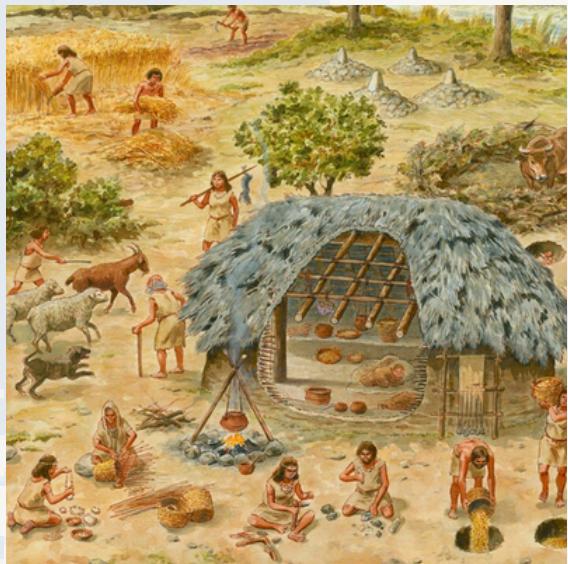
When the Caucasus Hunter-Gatherer ancestry is taken as a local baseline and the oldest Eneolithic Caucasus individuals as a proxy for the local Late Neolithic ancestry, a substantial increase in ancestry related to Anatolian Neolithic Farmers can be noticed in the Bronze Age.

Maykop individuals from the North Caucasian piedmont zone are genetically similar to South Caucasian Kura-Araxes individuals. After the Bronze Age, North Caucasian populations must have received additional gene flow from steppe populations that now separates them from Georgians, who largely retained the Bronze Age ancestry profile.

12.2% of your Ancient DNA is Bronze Age Caucasian-related. The Bronze Age Caucasian DNA component is highest in people of the Caucasus region and Central Asia, specifically in the region of Bronze Age Caucasian-speaking people. It is also found in lower frequencies in other parts of Asia and some non-Asian populations.

# EUROPEAN FARMER (6300–2800 BC)

## DESCRIPTION



Recent genetic studies have shown that in Europe, farming was introduced by an expansion of early farmers from Anatolia who were closely related to those from Barçın. These farmers replaced Western hunter-gatherers (WHG) to a large extent, ultimately becoming the main genetic contribution to current European populations, especially those of the Mediterranean. Haak et al. 2015 found that the amount of WHG ancestry among EEFs had significantly increased during the Middle Neolithic, documenting a WHG resurgence.

11.2% of your Ancient DNA is European Farmer related. this genetic component is present at the highest levels in populations of the Mediterranean, especially in southern Europe, as well as in central and western Europe. It is also present at lower levels in populations of northern Europe, with the lowest levels being observed in populations of the far north and in Eastern Europe.

# YELLOW RIVER (2300–1900 BC)

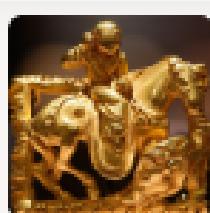
## DESCRIPTION



The Longshan Culture was a late Neolithic culture in northern China's middle and lower Yellow River valley areas from about 3000 to 1900 BCE. The culture is named after the nearby modern town of Longshan in Zhangqiu, Shandong. The culture was noted for its highly polished black pottery. The population expanded dramatically during the 3rd millennium BCE, with many settlements having rammed earth walls. It decreased in most areas around 2000 BCE until the central area evolved into the Bronze Age Erlitou culture. The Longshan culture has been linked to the early Sinitic (of the Sino-Tibetan languages). The Longshan individuals overlap with present-day Han populations in the PCA.

2.6% of your Ancient DNA is Yellow River related. This component peaks in populations living near the Yellow River, specifically in the regions of ancient China. It is attributed to the interactions many civilizations had with the people living along the Yellow River and the expansion of ancient Chinese groups like the Xia, Shang, and Zhou dynasties during the Bronze Age. This component is also found in lower frequencies in other parts of Asia, likely due to the spread of these ancient cultures and their interactions with other populations.

# YOUR IRON AGE DNA BREAKDOWN



Xiongnu (150–1 BC)

31.2%



Balto-Slavic (900–350 BC)

20.8%



Saka (540–50 BC)

18.6%



Thracian (1100–200 BC)

15.2%



Anatolian (780–30 BC)

5.8%



Sinitic (1230–130 BC)

4.4%

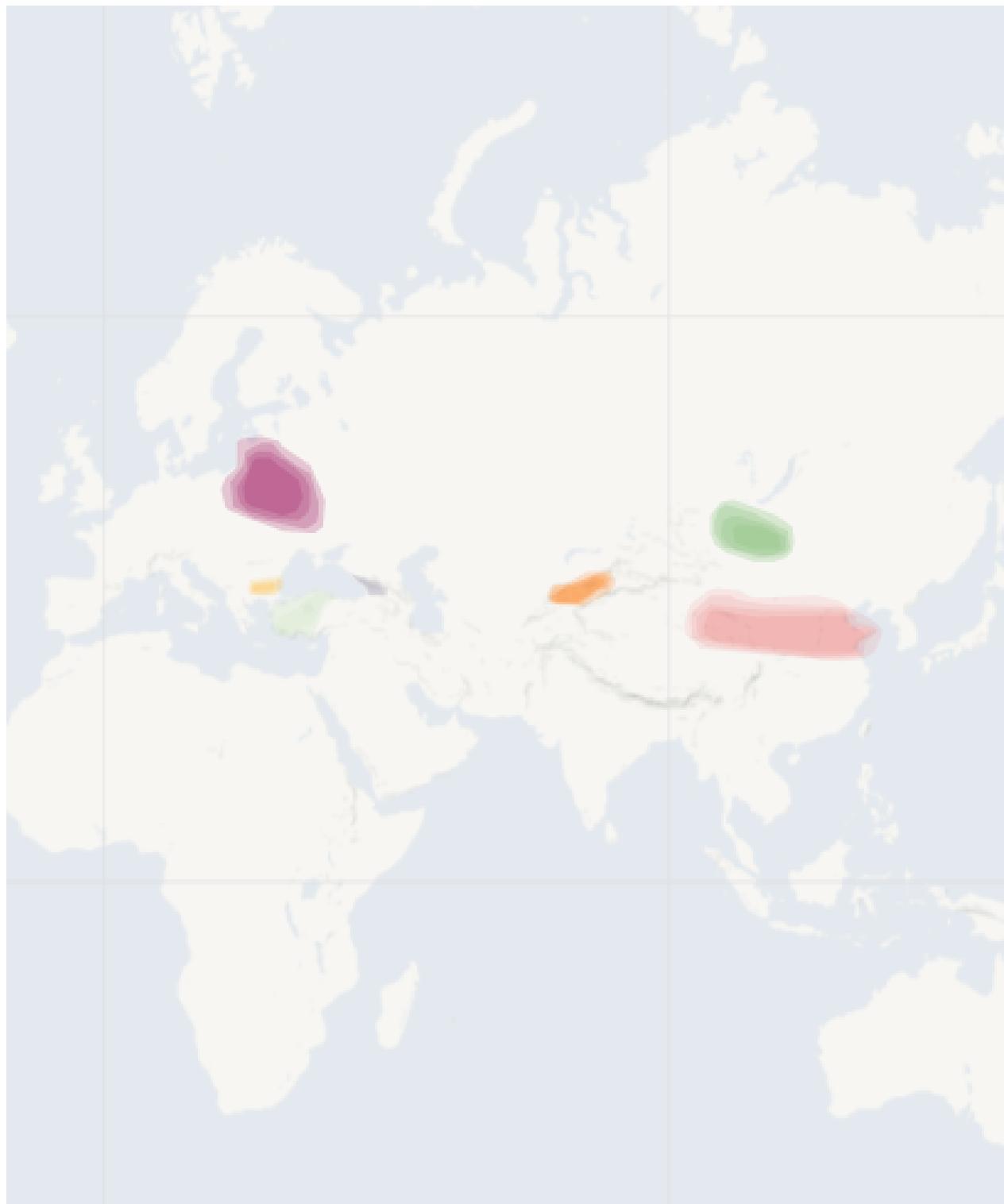


Colchian (780–30 BC)

4.0%



# YOUR IRON AGE DNA BREAKDOWN



# XIONGNU (150–1 BC)



## DESCRIPTION

Arising from the prehistoric populations of the Eastern Steppe, large-scale polities began to develop during the late first millennium BCE. The Xiongnu was the first historically-documented empire founded by pastoralists, and its establishment is considered a watershed event in the sociopolitical history of the Eastern Steppe. The Xiongnu held political dominance in East and Central Asia from the third century BCE through the first century CE.

This cluster is represented by the Late Xiongnu individuals who are mostly of East Eurasian ancestry.

31.2% of your Ancient DNA is Xiongnu related. This component peaks in populations from the Xiongnu region, specifically in the regions of ancient Mongolia and parts of China. It is attributed to the interactions many civilizations had with the people of the Xiongnu, as well as the expansion of Xiongnu during the Bronze Age. This component is also found in lower frequencies in other parts of Asia and Europe, likely due to the spread of these ancient cultures and their interactions with other groups.

# BALTO-SLAVIC (900–350 BC)

## DESCRIPTION



Balto-Slavic speakers comprise around one-third of present-day Europeans and occupy nearly a half of the European subcontinent. There is a near consensus among linguists that the Baltic and Slavic languages stem from a common root, Proto-Balto-Slavic, which separated from other Indo-European languages.

Modern Eastern Baltic populations cluster with Baltic BA on the PCA plot and exhibit among all modern populations the highest shared genetic drift with ancient Baltic populations, but show substantial differences to samples from the Bronze Age. The statistic  $D(\text{Lithuanian}, \text{Baltic BA}; X, \text{Mbuti})$  reveals significantly positive results for many modern Near Eastern and Southern European populations. Limited gene-flow from more south-western neighbouring regions after the Bronze Age is sufficient to explain this pattern, as nearly all modern populations besides Estonians, especially for Central and Western Europe, have a higher amount of farmer ancestry than Lithuanians.

20.8% of your Ancient DNA is Balto-Slavic related. The Balto-Slavic DNA component peaks in Eastern and Central Europe, with particularly high concentrations in Poland, the Czech Republic, Slovakia, and the Baltic countries such as Latvia and Lithuania. It also has a strong presence in Russia, Belarus, and Ukraine, as well as parts of Germany, Austria, and Hungary.

# Saka (540–50 BC)

## DESCRIPTION



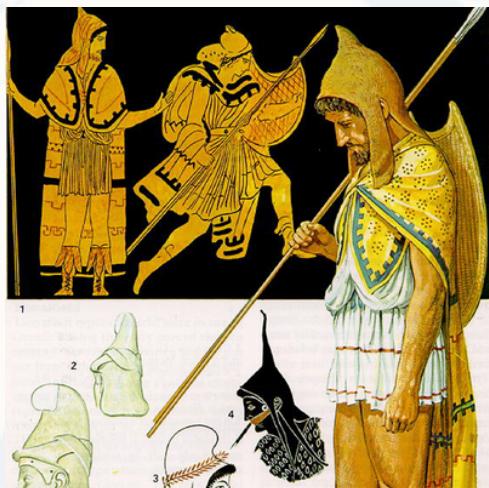
In the 8th century BCE, a warlike nomadic people burst forth from Central Asia whom the Persians, who had frequent and often violent contact with them, called the Saka. Famed for their prowess with the bow and arrow, especially from horseback, the Saka were also master goldsmiths and left behind magnificent and intricate work of jewelry, as well as weapons and armor wrought from this precious metal.

18.6% of your Ancient DNA is Saka related. The Saka DNA component is highest in people of Central Asia, specifically Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan. It is also found in lower frequencies in other parts of Asia and in some non-Asian populations.

Arabian  
Sea

# THRACIAN (990–200 BC)

## DESCRIPTION



The Thracians were a group of Indo-European tribes inhabiting a large area in Southeast Europe. The first historical record of the Thracians is found in the Iliad, where they are described as allies of the Trojans in the Trojan War against the Ancient Greeks.

By the 5th century BC, the Thracian population was large enough that Herodotus called them the second most numerous people in the part of the world known by him, and potentially the most powerful, if not for their lack of unity.

15.2% of your Ancient DNA is Thracian related. This component is often times found highest in Balkan, Greek, and Italian populations. It may signify distant ancestry from these regions.

# ANATOLIAN (780–30 BC)

## DESCRIPTION



The samples from Gordion, the capital of Ancient Phrygia are made up predominantly of Neolithic Anatolian and CHG-related ancestry. Ancient Phrygia was successively incorporated into Lydia, the Persian Empire, and the Hellenistic Empire following the campaigns of Alexander the Great. The samples are centuries apart within this sequence of historical events. Importantly, they are rather homogeneous in terms of their ancestry, so they represent the local “Phrygian” population whatever its origins may have been. The Phrygians were Indo-European speakers thought to have migrated from the Balkans. Importantly, though, the samples from Gordion have only small amounts of EHG ancestry, suggesting that either migration from steppe-enriched Balkan populations was minimal, or that it originated from Balkan populations with little steppe ancestry.

5.8% of your Ancient DNA is Anatolian related. This component peaks in populations from the Anatolian region, specifically in the regions of ancient Anatolia which is now located in modern-day Turkey. It is attributed to the interactions many civilizations had with the people of Anatolia, as well as the expansion of Anatolian groups like the Hittites and the Luwians during the Bronze Age. This component is also found in lower frequencies in other parts of Europe and Asia, likely due to the spread of these ancient cultures and their interactions with other groups.

# SINITIC (1230–130 BC)

## DESCRIPTION



Known as the cradle of the Chinese civilization, the Yellow River was the birthplace of the prosperous Chinese civilizations in early Chinese history.

4.4% of your Ancient DNA is Sinitic related. This component peaks in Han Chinese populations, specifically those along the Yellow River, but it is also detectable across a variety of East Asian people. According to historical documents, the generally accepted view is that the Han Chinese can trace their origins to the Huaxia ethnic group, which formed during the Shang and Zhou dynasties (21st–8th centuries BC) in the Central Plain region of China (Yong-Bin Zhao 2015).

# COLCHIAN (780–30 BC)

## DESCRIPTION



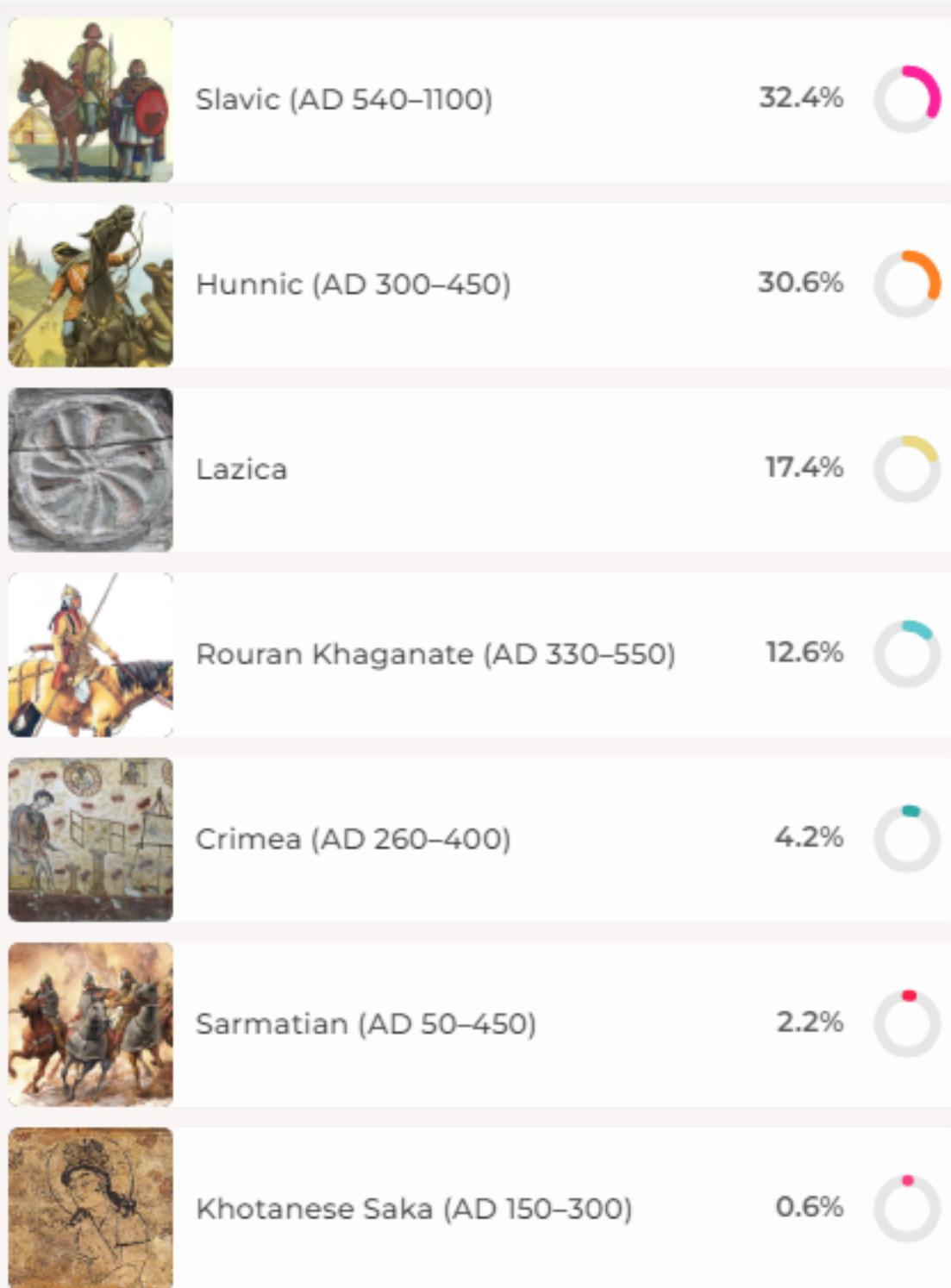
Colchis, which existed from the c. 13th to the 1st centuries BCE, is regarded as an early South Caucasian-speaking polity; the name of the Colchians was used as the collective term for early South Caucasian-speaking tribes which populated the eastern coast of the Black Sea in Greco-Roman ethnography.

4.0% of your Ancient DNA is Colchian related. This component peaks in populations from the Colchian region, specifically in the regions of ancient Colchis which is now located in western Georgia. It is attributed to the interactions many civilizations had with the people of Colchis, as well as the expansion of Colchian groups during the Bronze Age. This component is also found in lower frequencies in other parts of Europe and Asia, likely due to the spread of these ancient cultures and their interactions with other groups.

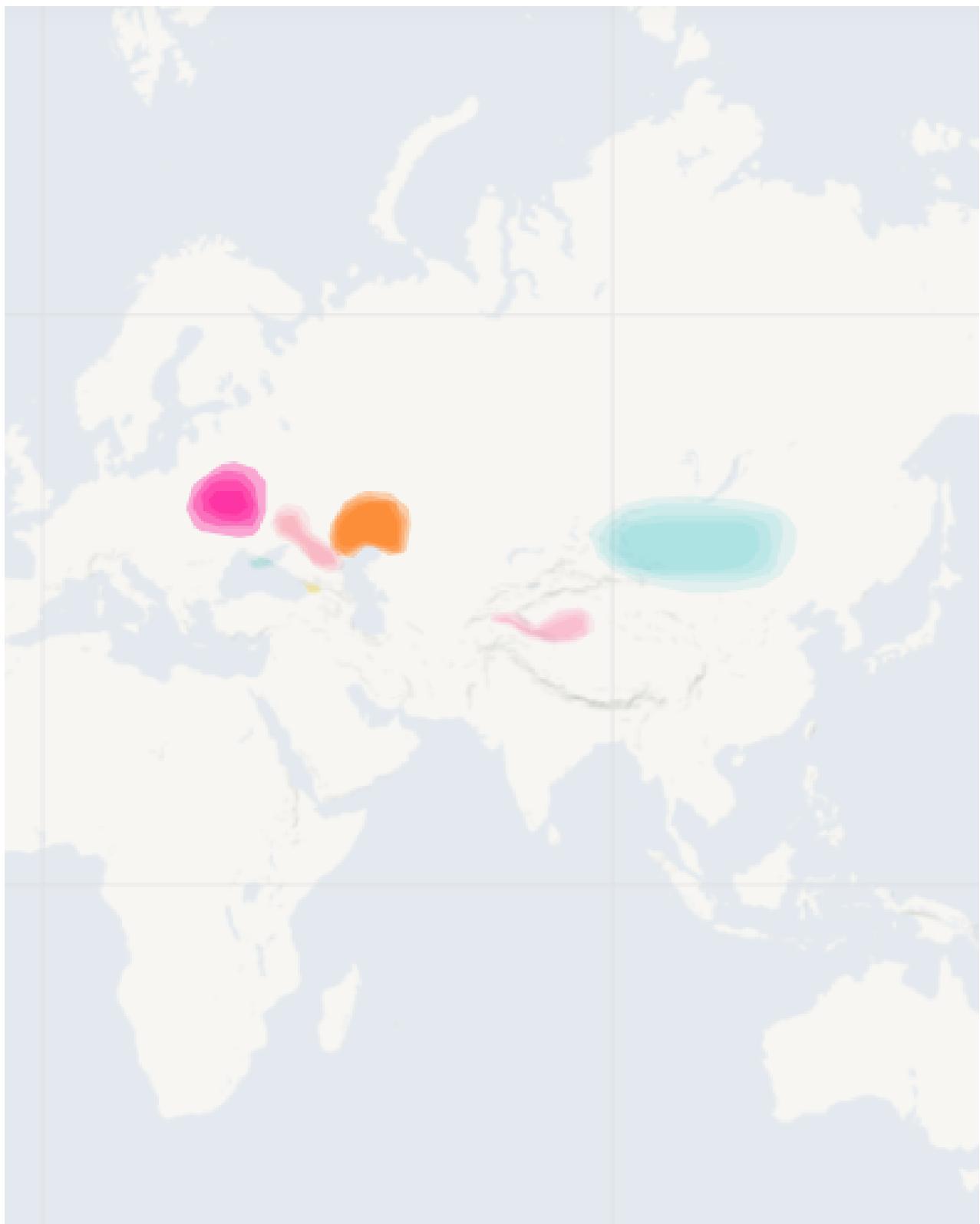
Arabian  
Sea

# YOUR MIGRATION

## PERIOD DNA BREAKDOWN



# YOUR MIGRATION PERIOD DNA BREAKDOWN



# SLAVIC (AD 540–1100)

## DESCRIPTION

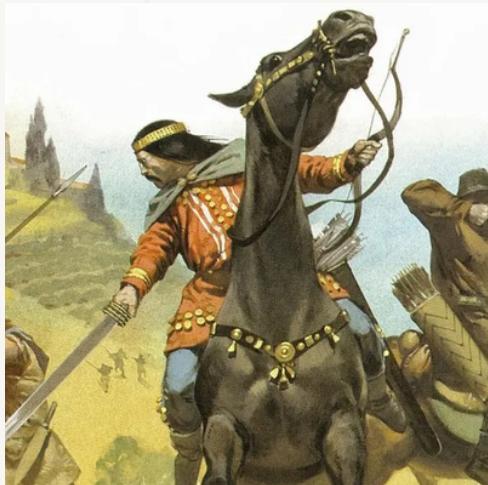


The Slavs emerged from obscurity when the Huns left many regions devastated and caused the westward movement of Germanic peoples. Early in the Middle Age, the Slavs occupied a large region, which encouraged the emergence of several independent Slavic states. From the 10th century CE onwards, the Slavs underwent a process of gradual cultural divergence that produced a set of closely related but mutually unintelligible languages classified as part of the Slavic branch of the Indo-European language family.

32.4% of your Ancient DNA is Slavic related. The Slavic DNA component peaks in Eastern Europe, specifically in countries such as Poland, Ukraine, Belarus, and Russia. It also has a strong presence in the Czech Republic, Slovakia, and Bulgaria. Additionally, it can be found in smaller percentages in countries like Germany, Austria, Hungary, and Romania.

# HUNNIC (AD 300–450)

## DESCRIPTION



The Huns came on the historical scene in Europe during the late 4th century CE when they crossed the Volga River and conquered the Alans, another nomadic people. They became one of the primary contributors to the fall of the Roman Empire, as their invasions of the regions around the empire, which were particularly brutal, encouraged what is known as the Great Migration.

30.6% of your Ancient DNA is Hunnic related. The Hunnic DNA component is highest in people of Central Asia, specifically in regions that were historically inhabited by the Huns. It is also found in lower frequencies in other parts of Asia and in some non-Asian populations.

# LAZICA

## DESCRIPTION



Lazica was the Latin name given to the territory of Colchis during the Roman/Byzantine period, from about the 1st century BCE. By the mid-3rd century CE, Lazica was given partial autonomy within the Roman Empire and developed into kingdom. Throughout much of its existence, it was mainly a Byzantine strategic vassal kingdom that briefly came under Sasanian Persian rule during the Lazic War.

17.4% of your Ancient DNA is Lazica related. This component peaks primarily in the South Caucasus, particularly in Georgia and Azerbaijan, as well as in northern Iran and the North Caucasus. It is also present in smaller frequencies in Anatolia, the Balkans, and Central Asia.

# ROURAN KHAGANATE (AD 330–550)

## DESCRIPTION



The Avars settled the Carpathian Basin in 567/68 CE, establishing an empire lasting over 200 years. Who they were and where they came from is highly debated. Contemporaries have disagreed about whether they were, as they claimed, the direct successors of the Rouran Khaganate that was destroyed by the Turks in ~550 CE. A genetic study published in scientific journal *Current Biology* in May 2022 examined 143 Avar samples from various periods, including elite and commoners. It confirmed their Northeast Asian paternal and maternal origin, with N1a-F4205 being their predominant and characteristic paternal lineage. Autosomes, the Avars preserved very ancient Eastern Steppe pre-Bronze Age genomes, with ca 90% Ancient Northeast Asian ancestry, shared deep ancestry with European Huns. The data are compatible with the Rouran origin of the Avars.

12.6% of your Ancient DNA is Rouran Khaganate related.

# CRIMEA (AD 260–400)

## DESCRIPTION



The Crimean Peninsula was under partial control of the Roman Empire during the period of 47 BCE to c. 340 CE. The territory under Roman control mostly coincided with the Bosporan Kingdom. Rome lost its influence in Taurica in the mid 3rd century CE, when substantial parts of the peninsula fell to the Goths, but at least nominally the kingdom survived until the 340s CE.

4.2% of your Ancient DNA is Cremea related. This component peaks in the most in Ukraine, Russia, and other surrounding countries

# SARMATIAN (360 BC–320 AD)

## DESCRIPTION



The Sarmatians were a nomadic people who gradually moved westward from their original homeland. Like the Scythians to whom they were related, they were highly developed in horsemanship and warfare. Their administrative capability and political astuteness contributed to their gaining widespread influence.

2.2% of your Ancient DNA is Sarmatian related. This component peaks in Central Asian groups like the Tajiks and is also found high amongst many Finno-Ugric and Turkic populations in Russia. It usually signifies additional Steppe related ancestry.

# KHOTANESE SAKA (AD 150–300)

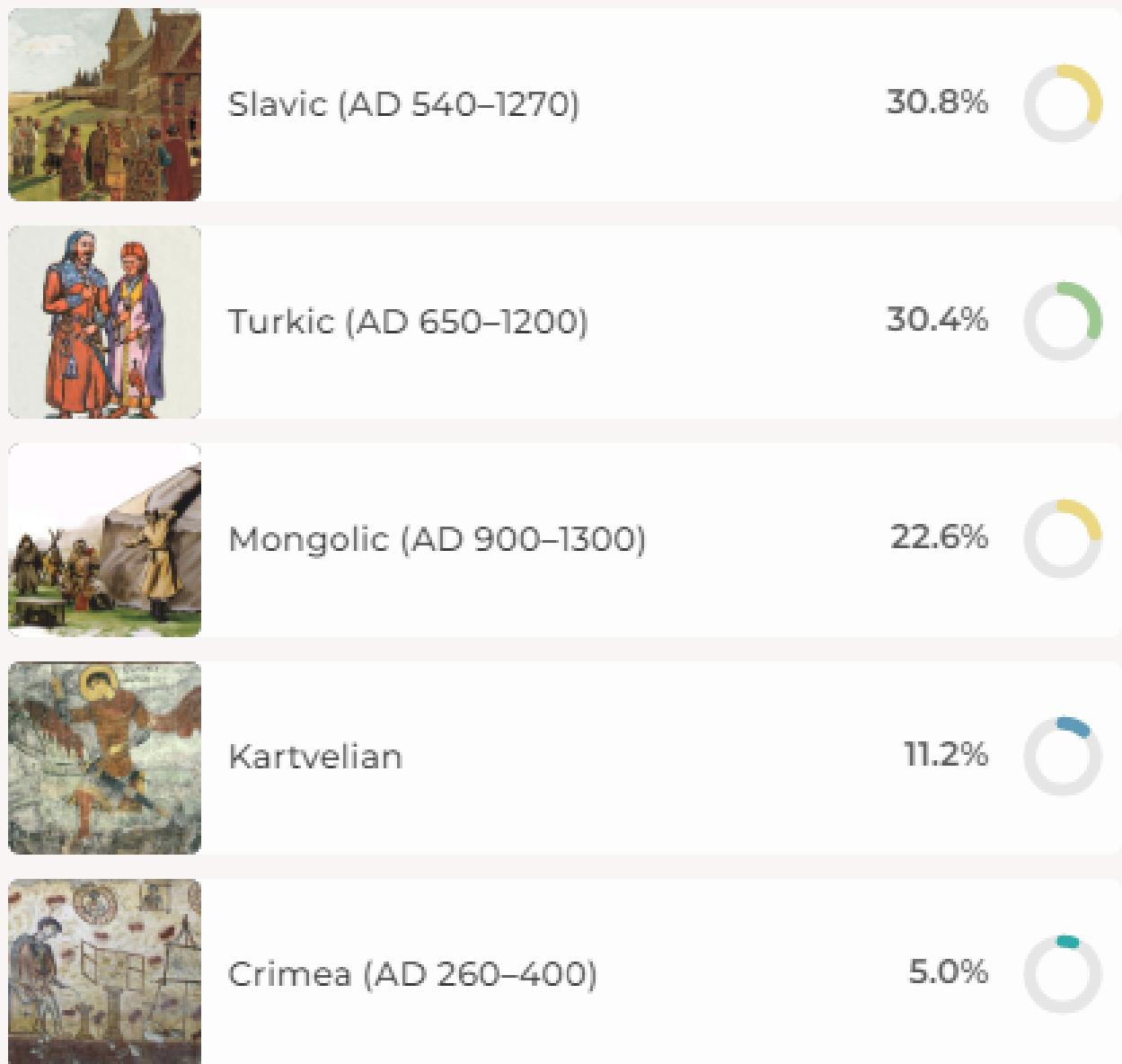
## DESCRIPTION



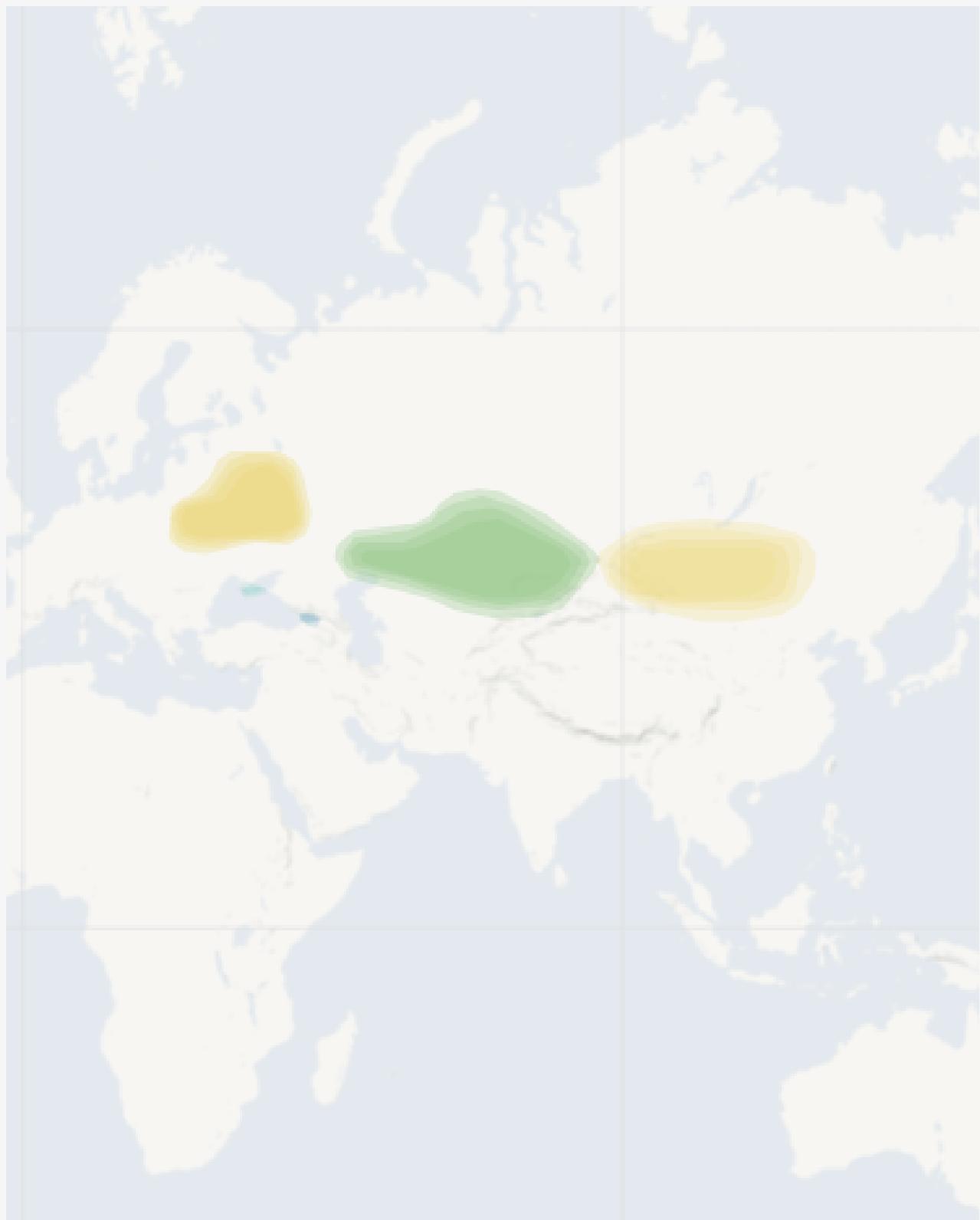
Kumar et al. show an increase of external ancestries appearing in Xinjiang during the Iron Age originating from multiple Central, South, and East Asian sources, demonstrating a broadening of demographic contacts and exchanges between groups from the surrounding areas, with Iron Age nomads, such as the Saka, playing a substantial role. Further, although the spread of languages is not always congruent with population histories, the presence of Saka ancestry in Xinj\_IA populations supports an Iron Age introduction of the Khotanese language, which was spoken by the Saka and later attested to in this region.

0.6% of your Ancient DNA is Khotanese Saka related. The Khotanese Saka DNA component is highest in people of Central Asia, specifically in the Tarim Basin area where the ancient Khotanese Saka Kingdom existed, now in the modern Xinjiang, China. It is also found in lower frequencies in other parts of Asia and in some non-Asian populations.

# YOUR MIDDLE AGES DNA BREAKDOWN



# YOUR MIDDLE AGES DNA BREAKDOWN



# SLAVIC (AD 540–1270)

## DESCRIPTION



The Slavs emerged from obscurity when the Huns left many regions devastated and caused the westward movement of Germanic peoples. Early in the Middle Age, the Slavs occupied a large region, which encouraged the emergence of several independent Slavic states. From the 10th century CE onwards, the Slavs underwent a process of gradual cultural divergence that produced a set of closely related but mutually unintelligible languages classified as part of the Slavic branch of the Indo-European language family.

30.8% of your Ancient DNA is Slavic related. The Slavic DNA component peaks in Eastern Europe, specifically in countries such as Poland, Ukraine, Belarus, and Russia. It also has a strong presence in the Czech Republic, Slovakia, and Bulgaria. Additionally, it can be found in smaller percentages in countries like Germany, Austria, Hungary, and Romania.

# TURKIC (AD 650–1200)

## DESCRIPTION



The first people to use the ethnonym Turk to refer to themselves entered the political scenery of Central Asia in the early 6th century CE, although the first attested Turkic-speaking peoples appeared in written historical sources before that time, namely when Oghur-speaking tribes appeared in the Pontic steppe in the 5th century CE. The fall of the Western Khaganate in the 7th century CE created a power vacuum, leading to the fragmentation of Turkic peoples in Central Asia.

Medieval Turkic populations from the Central Steppe and Tian Shan can be modeled as a mixture between ancient West Eurasian and East Eurasian populations..

30.4% of your Ancient DNA is Turkic related. The Turkic DNA component is highest in people of Central Asia, specifically in the region of Turkic-speaking people. It is also found in lower frequencies in other parts of Asia and in some non-Asian populations.

# MONGOLIC (AD 900–1300)

## DESCRIPTION



At its greatest extent, the Mongol Empire (1206-1368 CE) spanned nearly two thirds of the Eurasian continent. It was the world's largest contiguous land empire, and the cosmopolitan entity comprised diverse populations that flowed into the steppe heartland. The genetic structure established during the Mongol Empire continues to characterize present-day Mongolic-speaking populations living in both Mongolia and Russia.

22.6% of your Ancient DNA is Mongolic related. This component peaks in the most in Mongolia, Russia, China and other surrounding countries

# KARTVELIAN

## DESCRIPTION



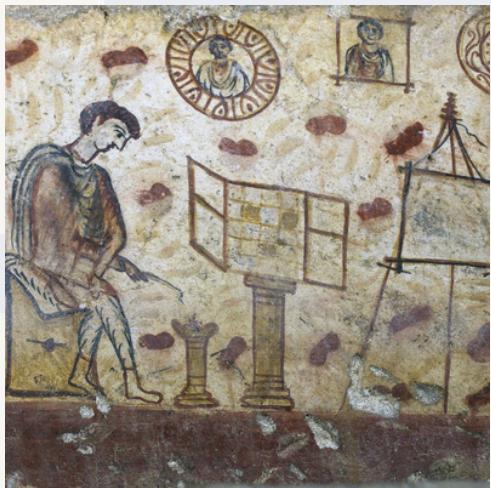
This genetic group is represented by modern Georgians due to lack of medieval samples.

11.2% of your DNA is Kartvelian related. The Kartvelian DNA component peaks in the Caucasus region, specifically in Georgia, Armenia, and Azerbaijan. It also appears in smaller amounts in neighboring countries such as Russia, Turkey, and Iran. This genetic marker is associated with the indigenous population of the Caucasus, and has been found in high frequencies among various ethnic groups in the region, including Georgians, Armenians, and Azerbaijani.

Arabian  
Sea

# CRIMEA (AD 260–400)

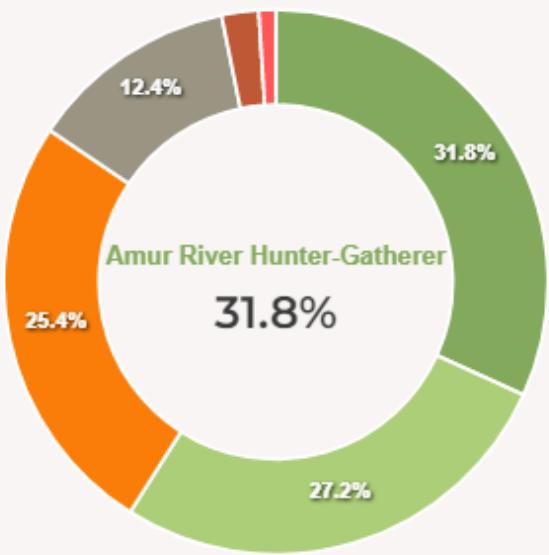
## DESCRIPTION



The Crimean Peninsula was under partial control of the Roman Empire during the period of 47 BCE to c. 340 CE. The territory under Roman control mostly coincided with the Bosporan Kingdom. Rome lost its influence in Taurica in the mid 3rd century CE, when substantial parts of the peninsula fell to the Goths, but at least nominally the kingdom survived until the 340s CE.

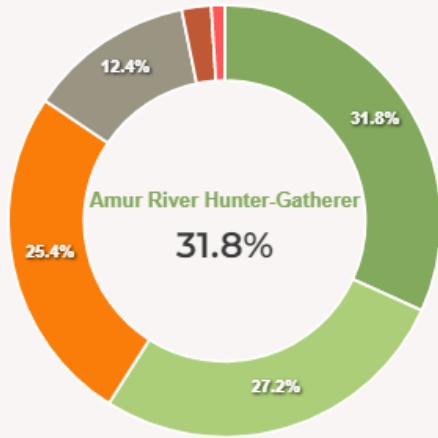
5.0% of your Ancient DNA is Cremea related. This component peaks in the most in Ukraine, Russia, and other surrounding countries

# HUNTER GATHERER VS. FARMER



Amur River Hunter-Gatherer	31.8%	▼
Anatolian Neolithic Farmer	27.2%	▼
European Hunter-Gatherer	25.4%	▼
Caucasus Hunter-Gatherer	12.4%	▼
Southeast Asian Neolithic Farmer	2.2%	▼
Zagrosian Neolithic Farmer	1.0%	▼

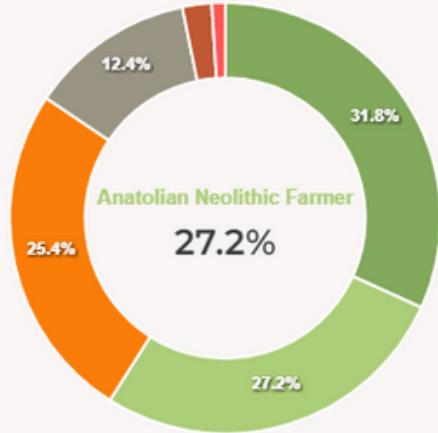
# AMUR RIVER HUNTER-GATHERER



When compared against all populations on record, ancient or modern, the ancient Devil's Gate individuals were found to be genetically closest to the contemporary Ulchi, speakers of a Tungusic language from the lower Amur Basin.

This component forms the primary Neolithic DNA of many Siberian groups including the Nivkh, Oroqen and Ulchi. It is also found high within many Mongolian and Eastern Turkic populations. The presence of this ancestry usually indicates Tungistic, Mongolian or Turkic ancestry

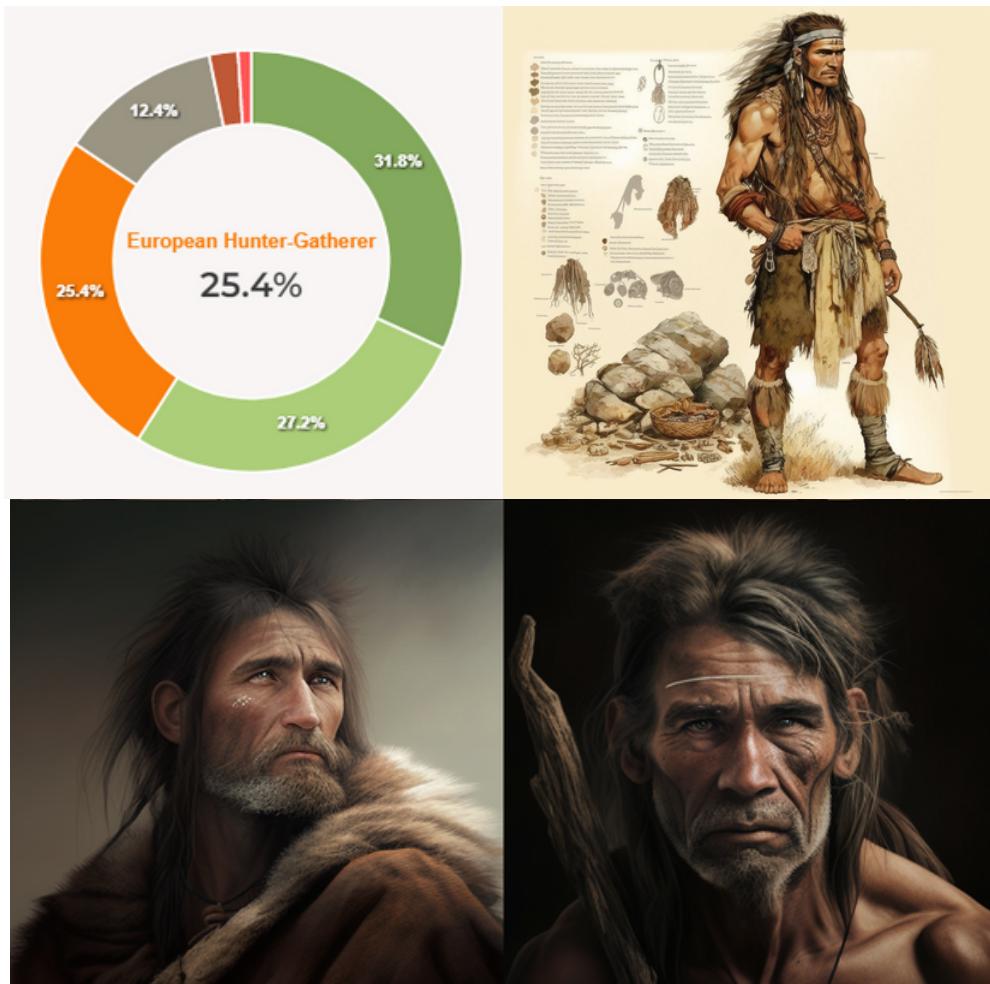
# ANATOLIAN NEOLITHIC FARMER



Recent genetic studies have shown that in Europe, farming was introduced by an expansion of early farmers from Anatolia who were closely related to those from Barçın. These farmers replaced Western hunter-gatherers (WHG) to a large extent, ultimately becoming the main genetic contribution to current European populations, especially those of the Mediterranean.

These people entered Europe around 7000 years ago, and introduced farming into the region. Because of their ability to harness resources more effectively, they contributed substantially to all European populations. Today, this component makes up the primary Neolithic DNA in Southern and Central European populations, Northern Middle Eastern and Levantine populations, as well as Northern North Africans.

# EUROPEAN HUNTER-GATHERER



European hunter-gatherers can be divided into two main groups. The western group (Western Hunter-Gatherers or WHG) inhabited most of Europe, from Iberia to the Carpathians; while the eastern group (Eastern Hunter-Gatherers or EHG) inhabited an area stretching from the Baltic Sea to the Urals and downwards to the Pontic-Caspian steppe. In comparison with WHG, EHG had much higher affinity with the Ancient North Eurasians (ANE).

These were the first people in Europe. Today, only Northern European groups like the Scandinavians and Baltic people have this as their highest component. In most Europeans, this forms the second highest component in their genome. Its presence in non-European populations is usually associated to the expansion of Indo-European people during the Bronze and Iron Age.

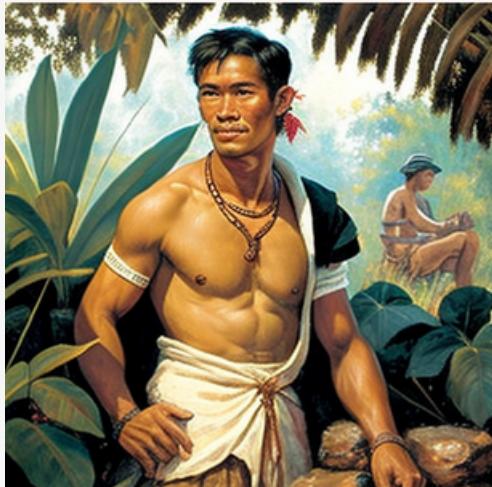
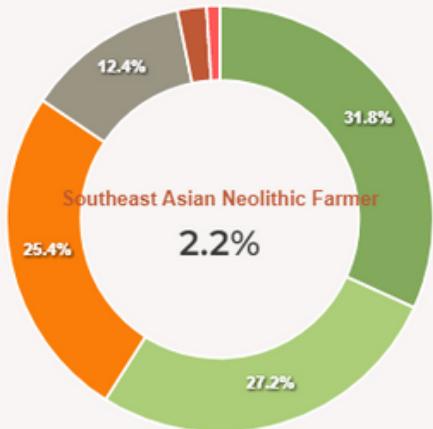
# CAUCASUS HUNTER-GATHERER



Caucasus Hunter-Gatherer (CHG) is an anatomically modern human genetic lineage, first identified in a 2015 study. Eastern Hunter-Gatherers from the Pontic-Caspian steppes have received admixture from CHG, leading to the formation of Western Steppe Herders (WSH). WSH expanded massively throughout Europe during the Late Neolithic and Early Bronze Age.

This genetic component derives from several sources. It is inherent within many European populations because of the expansion of the Indo-European people, but it peaks within Caucasian populations like the Georgians.

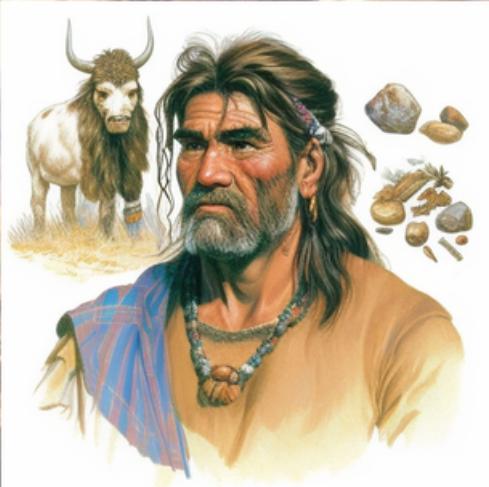
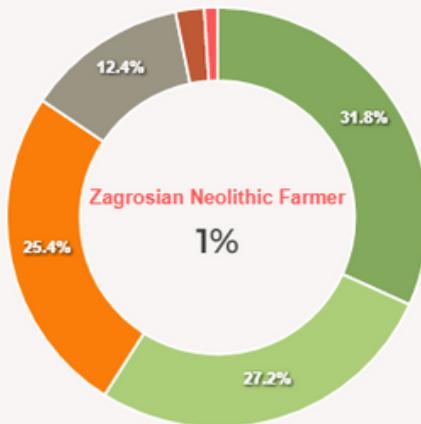
# SOUTHEAST ASIAN NEOLITHIC FARMER



In 2018, researchers successfully extracted low coverage nuclear DNA from the petrous bone of 8 of the individuals from the cemetery at Mán Bạc. The individuals at Mán Bạc appear to be genetically homogenous and resemble present-day Southeast Asians.

Today this genetic component peaks amongst Austronesian groups like the Filipinos, however it is also detected widespread across East and South East Asia. This is because these people existed as far North as China, and were eventually pushed back into South East Asia with the expansion of the Han Chinese. It is also found high amongst Polynesian groups.

# ZAGROSIAN NEOLITHIC FARMER



The Neolithic farmers of western Iran cluster with the likely Mesolithic HotuIIb individual and more remotely with hunter-gatherers from the Caucasus, and share alleles at an equal rate with Anatolian and Levantine early farmers, highlighting the long-term isolation of western Iran. The impact of West Asian farmers extended beyond West Asia. Farmers related to those of Anatolia spread westward into Europe; farmers related to those of the Levant spread southward into East Africa; farmers related to those from the Zagros region spread eastward into the Indian Subcontinent.

Like the Anatolian Neolithic Farmers, the Zagrosian Neolithic farmers were one of the first three groups (the other being Natufian) who discovered farming. Today, this DNA component peaks amongst Iranian groups like the Persians and the Kurds.

# WHICH ANCIENT CIVILISATIONS FIT YOU BEST? (MIXED MODE)

Mixed Mode is a way of modelling your genetic profile with two and three best fitting ancient samples. That is to say, if we had to reconstruct your entire ancestry only based on 2-3 Ancient Civilisations, these are the ones would fit you best. This does not mean you descend from these Civilizations, but rather, your genome could be hypothetically reconstructed from the mixture these groups. It helps to illustrate the components of your genome through an ancient perspective. The lower the number, the more accurate the calculator.

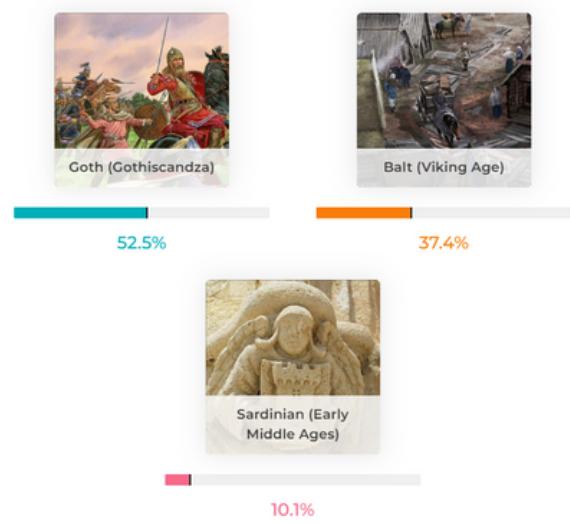
## EXAMPLE:

### 2 Way (Fit: 1.428)



In this scenario we see an English Individual who in the 2 Way model has equal Continental Celtic and Estonian results. This means that their genome is effectively half Central European (Continental Celtic) and half Baltic (Estonian)

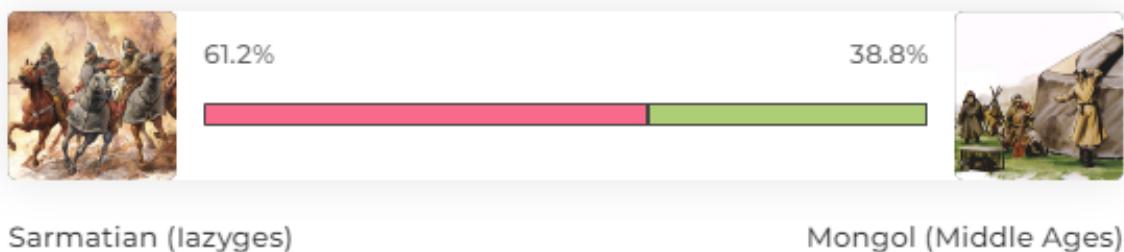
### 3 Way (Fit: 1.192)



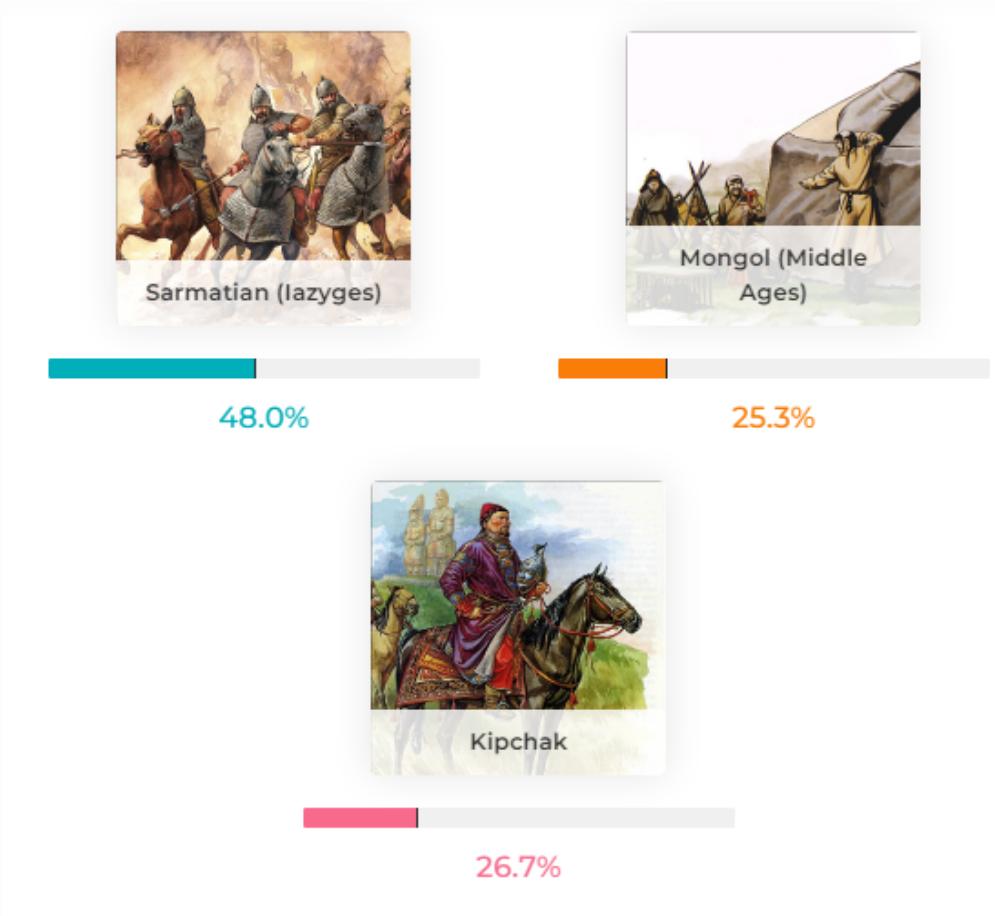
In the 3 way model we see this picture being refined. We see an additional 10.1% Sardinian component. This represents the additional Southern European component that is inherent within their genome. As we can see, the number of the model is lower, which indicates that the calculation is more accurate.

# YOUR ANCIENT CIVILISATIONS - MIXED MODE

2 Way (Fit: 2.718)



3 Way (Fit: 2.525)





The closest modern populations to this sample:

DISTANCE	MODERN POPULATION
4.684	Balkan Turk (Deliorman)
4.740	Moldovan
5.257	Hungarian
5.395	Romanian
5.403	Bosniak
5.503	Austrian
5.601	Croat
5.648	Serb
5.672	Balkan Turk (Kircaali)
5.701	Slovene

## Sarmatian (lazyges)

The Sarmatians were a nomadic people who gradually moved westward from their original homeland. By the 5th century BCE the Sarmatians held control of the land between the Urals and the Don River. In the 4th century BCE they crossed the Don and replaced the Scythians as the dominant power in the Pontic Steppe. The individuals associated with the Sarmatian culture are highly homogeneous despite being spread over a wide geographic area and time period. Furthermore, Sarmatians show a sharp discontinuity from the other Iron Age steppe groups by forming a cluster shifted toward West Eurasians.



The closest modern populations to this sample:	
DISTANCE	MODERN POPULATION
0.977	Mongol (Mongolia)
2.707	Kalmyk
4.521	Buryat
7.996	Altaian
9.383	Oroqen
10.096	Kyrgyz (China)
10.180	Kyrgyz
10.524	Tibetan (Gangcha)
10.803	Salar (China)
10.831	Mongol (Hulunbuir)

## Mongol (Middle Ages)

At its greatest extent, the Mongol Empire (1206-1368 CE) spanned nearly two thirds of the Eurasian continent. It was the world's largest contiguous land empire, and the cosmopolitan entity comprised diverse populations that flowed into the steppe heartland. Mongol-era individuals almost entirely lack the residual ANE-related ancestry (in the form of Chandman\_IA and Khövsgöl\_LBA) that had been present among the Xiongnu and earlier northern/western MLBA cultures. On average, Mongol individuals have a much higher East Eurasian affinity than previous empires, and this period marks the beginning of the formation of the modern Mongolian gene pool. Mongol era individuals as a group can be modeled with only 15-18% of Western Steppe ancestry, but require 55-64% of Ulaanzuuk\_SlabGrave and 21-27% of Han-related ancestry. Since the fall of the Mongol Empire in 1368 CE, the genetic profile of the Mongolian populations has not substantially changed. The genetic structure established during the Mongol Empire continues to characterize present-day Mongolic-speaking populations living in both Mongolia and Russia.



The closest modern populations to this sample:

DISTANCE	MODERN POPULATION
4.175	Uzbek (Khorezm)
4.383	Nogai (Stavropol)
4.624	Uzbek
4.720	Siberian Tatar (Tomsk)
4.940	Hazara (Afghanistan)
5.092	Uyghur
5.515	Uzbek (Tashkent)
5.607	Siberian Tatar (Ishtyak Toguz)
5.792	Bashkir (Baimaksky)
6.109	Nogai (Astrakhan)

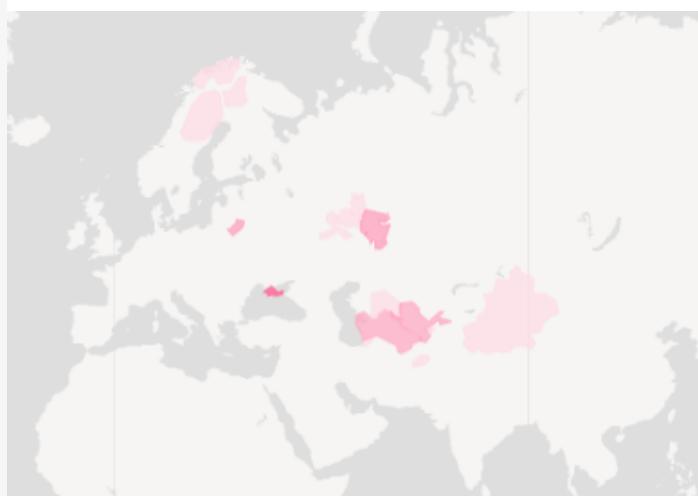
## Kipchak - (AD 1000–1200)

The Kipchaks were a loosely organized Turkic tribal confederation that by the mid-11th century AD occupied a vast, sprawling territory in the Eurasian steppe, stretching from north of the Aral Sea westward to the region north of the Black Sea. The Cumans were the western grouping of the confederation. Following the Mongol invasions, many Kipchaks were sent to Egypt to be sold as slaves, where they would eventually form the Mamluk state. The Kipchak and other medieval Turkic samples from the Central Steppe and Tian Shan can be modeled as a mixture between ancient West Eurasian and East Eurasian populations.

# GENETICALLY CLOSEST MODERN POPULATION

This calculator compares your DNA to thousands of Modern Populations to see how genetically similar you are to populations that do not have mixed ancestry. It does not necessarily mean you descend from these regions, but rather, your ancestry has the highest affinity to the groups below:

#	POPULATION	DISTANCE
1	Crimean Tatar (Steppe)	<b>3.457</b>
2	Uzbek (Khorezm)	<b>5.279</b>
3	Bashkir (Miyakinsky)	<b>6.335</b>
4	Uzbek (Tashkent)	<b>6.388</b>
5	Lipka Tatar	<b>6.784</b>
6	Bashkir	<b>6.939</b>
7	Turkmen (Uzbekistan)	<b>7.087</b>
8	Siberian Tatar (Tomsk)	<b>7.089</b>
9	Siberian Tatar (Yalutorovsky)	<b>7.229</b>
10	Uzbek	<b>7.262</b>

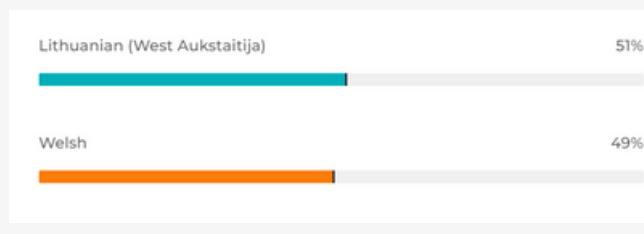


# WHICH MODERN POPULATIONS FIT YOU BEST? (MIXED MODE)

With reference to the previous section, the Modern Mixed Mode module follows the same principle as the Ancient Mixed mode calculation. However, this time, your genetic profile is reconstructed with two and three best fitting modern samples. That is to say, if we had to reconstruct your entire ancestry only based on 2-3 Modern Populations , these are the ones would fit you best. This does not mean you descend from these groups, but rather, your genome could be hypothetically reconstructed from the mixture these groups. It helps to illustrate the components of your genome through an modern perspective. The lower the number, the more accurate the calculator.

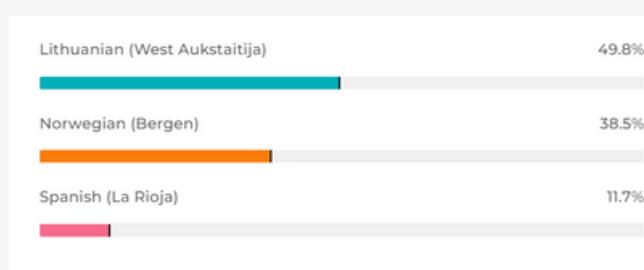
## EXAMPLE:

### 2 Way (Fit: 1.338)



In this scenario we see the same Individual as before who in the 2 Way model has equal parts Lithuanian and Welsh results. This means that their genome is effectively half North Western European Celtic (Welsh) and half Baltic (Lithuanian)

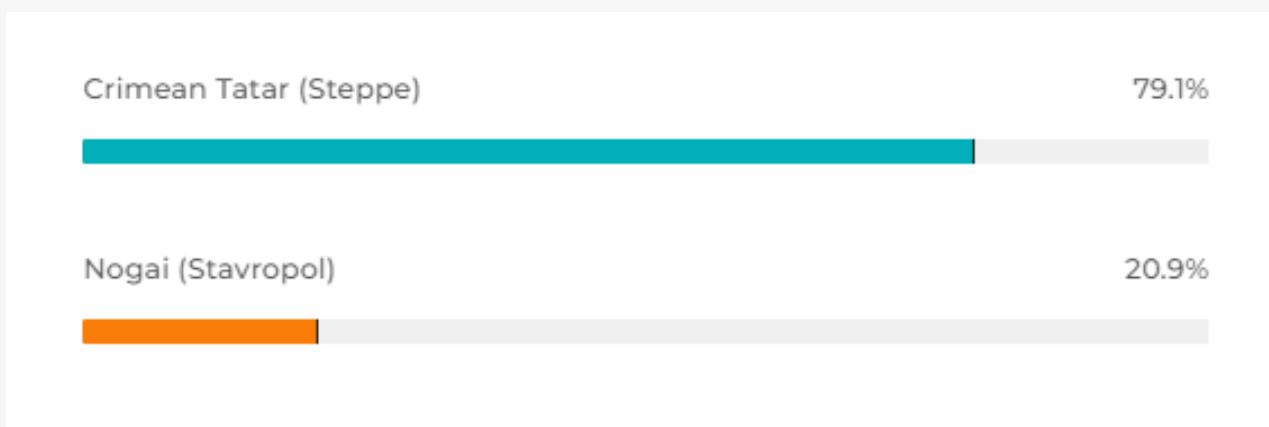
### 3 Way (Fit: 1.268)



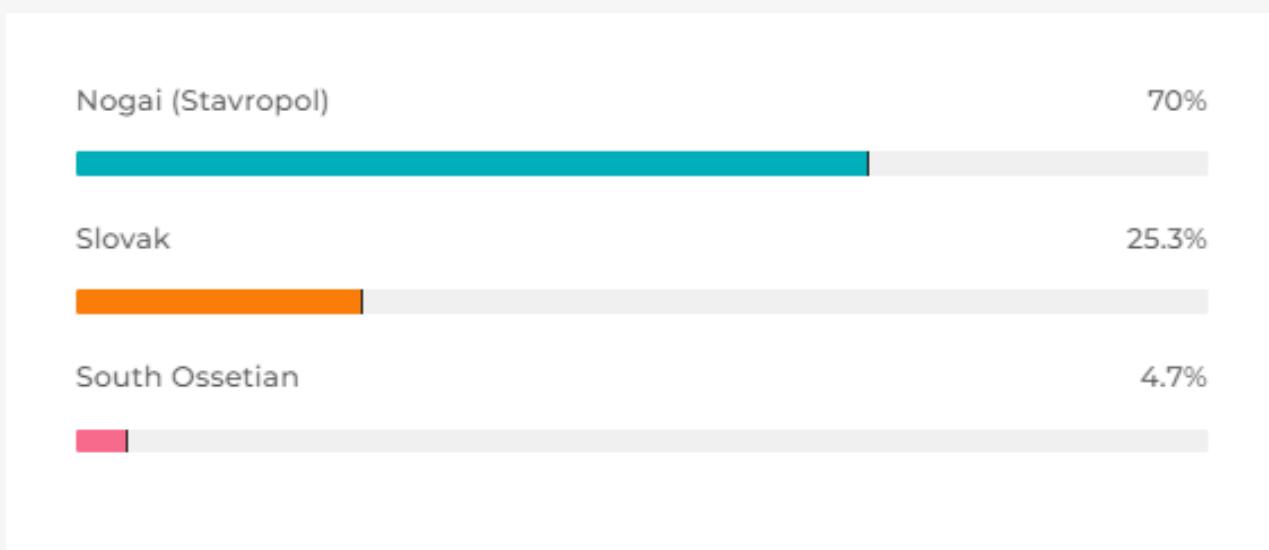
In the 3 way model we see this picture being refined. We see an additional 11.7% Spanish component. This represents the additional Southern European component that is inherent within their genome. As we can see, the number of the model is lower, which indicates that the calculation is more accurate. These results are consistent with the Ancient Mixed Mode modelling.

# YOUR MODERN POPULATIONS - MIXED MODE

2 Way (Fit: 2.519)



3 Way (Fit: 2.167)



# YOUR PCA CHART

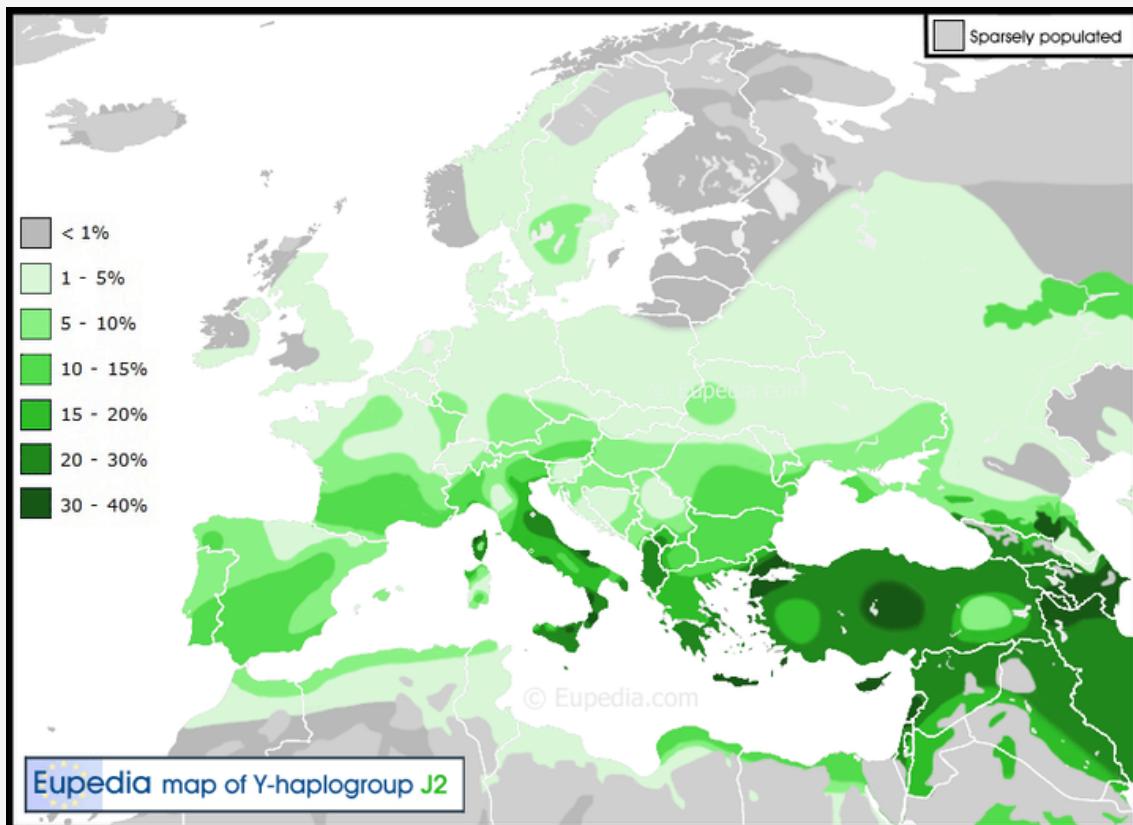
A PCA chart (principle component analysis) plots all the genetic samples we have on a 2D graph. Your location within this graph helps visualise where your ancestry lies compared to thousands of other populations. Each shaded region represents the spread of thousands of other samples. If the shaded region is large, or overlaps, it indicates that individuals from that region are genetically varied and share ancestry with different groups. The closer your dot is to a region, the more your ancestry represents that group.



# YOUR HAPLOGROUP

To gain further insight into your father's lineage, I utilised a tool which extracts the Y-DNA SNPs from your autosomal DNA - allowing us to determine you YDNA Haplogroup. You belong to Haplogroup J-L26 which is a subclade of haplogroup J2

Most specific position on the [YFull YTree](#) is J-L26



Distribution of J2 in Europe and surrounding regions



## Heat map of your specific version of J2



## How J-L26 spread

# DISCUSSION

Taner,

It has been a great pleasure having had the opportunity to compile your Deep Ancestry report. As you may already know, you have an interesting genetic makeup, with significant components of Slavic, Turkic, Crimea, Mongolic, and Kartvelian.

Eastern Europe and the Baltic region have a rich history and diverse population genetics. The Slavic population in Eastern Europe is the largest ethnic group in the area. Slavs have a shared history, culture, and language that has influenced the region for centuries. However, there is still considerable genetic diversity among Slavic people due to historical events such as the Mongol invasion and the expansion of the Austro-Hungarian Empire.

The genetics of the Crimean people reflect a diverse and complex heritage resulting from centuries of historical and cultural interactions in the region. The Crimean Peninsula, situated at the crossroads of Europe and Asia, has been influenced by various populations throughout history. The genetic makeup of the Crimean people demonstrates a mixture of different ancestral components. The indigenous Crimean Tatars, for example, exhibit predominantly Central Asian and Turkic genetic signatures, reflecting their Turkic-speaking heritage. Additionally, the region has seen influences from Greeks, Genoese, Ottomans, Russians, and other neighboring populations. These interactions have contributed to the genetic diversity found among the Crimean population, with various ancestral components from European, Middle Eastern, and Central Asian sources. The unique genetic landscape of the Crimean people serves as a testament to the rich history and cultural fusion that has shaped the region over time.

In modern populations, you are mostly Crimean Tatar (Steppe), Nogai (Stavropol), Slovak, and South Ossetian. These ethnic groups share a common history, as they have been influenced by neighboring cultures throughout centuries. Crimean Tatars and Nogai share Turkic ancestry, with genetic similarities indicating a common origin. Slovaks, a Slavic group, showcase a blend of Slavic heritage with influences from neighboring populations. South Ossetians have genetic connections with other Caucasian groups in the region. While each group has its unique genetic traits, there are also shared genetic affinities resulting from historical interactions and migrations.

Overall, your genetic makeup is complex and multifaceted, reflecting the unique history and ancestry of your family and ancestors. While genetic testing can provide insights into your ancestry and heritage, it is important to remember that genetics is just one piece of the puzzle, and your personal experiences and cultural identity are equally important in defining who you are.

It's worth noting that these are broad generalizations based on genetic markers and can be influenced by many factors such as environment, migration, and cultural exchange. This report is a snapshot of your DNA at one point in time, and it's always possible that further genetic testing could provide more information.

I hope this information helps to give you a better understanding of your ancestry. If you have any questions in relation to any of the findings presented in this report, please do not hesitate to contact me at any time.

## Useful Resources:

G25 Tool: <https://vahaduo.github.io/vahaduo/>

G25 Samples: <https://vahaduo.github.io/g25download/>

Dnur Deep World Calculator:

<https://g25.ancestralwhispers.org/onur.htm>

Other Calculators available here:

<https://www.exploreyourdna.com/calculateurs.aspx>

References Samples & Research Links used in analysis:

### Continental Celtic

- FRA\_Grand\_Est\_IA2
- FRA\_Hauts\_De\_France\_IA2
- FRA\_Occitanie\_IA2
- FRA\_Grand\_Est\_IA1
- CZE\_Hallstatt\_Bylany

1. <https://www.pnas.org/content/117/23/12791>

2. <https://www.nature.com/articles/s41586-018-0094-2>

### Central Amerindian

- USA\_Lovelock\_Cave\_1850BP
- USA\_Lovelock\_Cave\_600BP

1. <https://science.sciencemag.org/content/362/6419/eaav2621>

## South Amerindian

- PER\_Lauricocha\_3500BP
- PER\_Laramate\_900BP
- PER\_RioUncallane\_1800BP
- ARG\_Aconcagua\_500BP

1. [https://www.cell.com/cell/fulltext/S0092-8674\(18\)31380-1](https://www.cell.com/cell/fulltext/S0092-8674(18)31380-1)
2. <https://advances.sciencemag.org/content/4/11/eaau4921>
3. <https://science.sciencemag.org/content/362/6419/eaav2621>

## Insular Celtic

- England\_IA
- England\_Roman
- VK2020\_Scotland\_Orkney\_VA

Note: Some of the reference populations are represented by individual samples

1. <https://www.nature.com/articles/ncomms10408>
2. <https://www.nature.com/articles/ncomms10326>
3. <https://www.nature.com/articles/s41586-020-2688-8>

## Northwest African

- Canary\_Islands\_Guanche

1. [https://www.cell.com/current-biology/fulltext/S0960-9822\(17\)31257-5](https://www.cell.com/current-biology/fulltext/S0960-9822(17)31257-5)

## Iberian

- Iberia\_Northeast\_c.8-12CE
1. <https://www.science.org/doi/abs/10.1126/science.aav4040>

## Aleut

- USA\_AK\_Paleo-Aleut
- USA\_AK\_Neo-Aleut

1. <https://www.nature.com/articles/s41586-019-1251-y>

## Pygmy

- Baka
- Bakola
- Bedzan
- Biaka
- Mbuti

## West African

- Yoruba\_Nigeria
- Kassena\_Ghana
- Akan\_Ghana
- Frafra\_Ghana
- Mossi
- Igbo
- Bambara\_Mali
- Dogon
- Jola\_Gambia
- Malinke\_Mali
- Manjak\_Gambia
- Mende\_Sierra\_Leone
- Mandinka\_Senegal
- Serer\_Gambia
- Wolof\_Gambia
- Mandinka\_Gambia

## Anatolian Neolithic Farmer:

### Reference Samples:

- TUR\_Barcin\_N

### Research Link(s):

1. <https://www.biorxiv.org/content/10.1101/016477v2>

## Anatolian Neolithic Farmer:

### Reference Samples:

- TUR\_Barcin\_N

### Research Link(s):

1. <https://www.biorxiv.org/content/10.1101/016477v2>

## South Amerindian Hunter-Gatherer:

### Reference Samples:

- BRA\_LapaDoSanto\_9600BP

### Research Link(s):

1. [https://www.cell.com/cell/fulltext/S0092-8674\(18\)31380-1](https://www.cell.com/cell/fulltext/S0092-8674(18)31380-1)

## European Hunter-Gatherer:

### Reference Samples:

- RUS\_Sidelkino\_HG
- WHG

### Research Link(s):

1. <https://www.science.org/doi/abs/10.1126/science.aar7711>

2. <https://www.biorxiv.org/content/10.1101/135616v1>

3. <https://www.nature.com/articles/nature17993>

## North Amerindian Hunter-Gatherer:

### Reference Samples:

- CAN\_6000BP

### Research Link(s):

1. <https://www.nature.com/articles/ncomms13175>

## North African Neolithic Farmer:

### Reference Samples:

- MAR\_EN

### Research Link(s):

1. <https://www.biorxiv.org/content/10.1101/191569v1>

## **West African Hunter-Gatherer:**

### Reference Samples:

- CMR\_Shum\_Laka\_3000BP

### Research Link(s):

1. <https://www.nature.com/articles/s41586-020-1929-1>

## **Yellow River Neolithic Farmer:**

### Reference Samples:

- CHN\_Yellow\_River\_LN

### Research Link(s):

1. <https://www.nature.com/articles/s41467-020-16557-2>

## **Caucasus Hunter-Gatherer:**

### Reference Samples:

- GEO\_CHG

### Research Link(s):

1. <https://www.nature.com/articles/ncomms9912>