Your Ancestral Journey

The origin of our species lies in Africa: It's where we first evolved and where we've spent the majority of our time on Earth. We have since migrated to every corner of the globe, a journey that is written in our DNA.

With the DNA sample you sent us, we ran a comprehensive analysis to identify thousands of genetic markers—breadcrumbs—in your DNA, which are passed down from generation to generation. By looking at the order in which these markers occurred over time, we can trace the journey of your ancestors out of Africa. Furthermore, with these markers we have created a human family tree. Everyone alive today falls on a particular branch of this family tree. We have examined your markers to determine which branch you belong to. The results of our analysis—your personal journey—are outlined below.

Help Me Understand My Results

Your Hominin Ancestry (60,000 Years Ago & Older)

1 of 705,343

PARTICIPANTS

Share Your Journey With Friends

Download a personal infographic and let your friends know what you've been up to for the last 140,000 years.

Download





Family Tree DNA Analysis

Explore more about your DNA with our partner FTDNA.













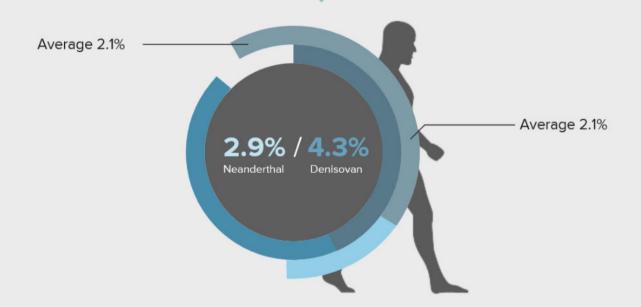






Your Hominin Ancestry

(60,000 Years Ago & Older)



As our modern human ancestors migrated through Eurasia, they met other hominin species and interbred. These "cousin" species, Neanderthal and Denisovan, are now extinct, but the genetic makeup of nearly everyone born outside of Africa today includes 1 to 4 percent **DNA** from these other hominins, living relics of ancient encounters.

Family Tree DNA Analysis

Explore more about your DNA with our partner FTDNA.

Transfer Your Results >



Print Your Results

You can print your results to read and share with others.

Print >















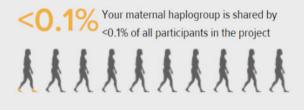






(1,000 Years - 100,000 Years Ago)









Modern humans started to leave Africa between 60,000 and 70,000 years ago. They traveled in groups, taking different paths and arriving at different destinations. These journeys can be traced through DNA "markers" that form the human genetic tree. Based on these personal markers, each person alive today can be assigned to a specific haplogroup, which identifies their branch on the tree.

Our Story

Read about other Genographic Project participants who share your migratory journey-and contribute your own story.

Contribute Your Story >



FAQs

Have a question? Explore common questions about the Genographic Project.

Read the FAQ >



















Your Regional Ancestry

(5,000 Years - 10,000 Years Ago)

48%
Northern European

Breaking the Code

Part 1: Genographic Project Director Spencer Wells takes you through the process of breaking down your DNA markers.

Watch the Video >



The Keys To Discovery

Part 2: Dr Spencer Wells explains how genetic markers can be used to build a family tree for everyone alive today.















Based on their different destinations, humans migrating out of Africa developed regional affiliations over time. These affiliations are present as patterns of DNA and are visible in the variety of physical traits humans possess. Scientists have identified typical individuals, genetically speaking, from different parts of the globe and defined them as "reference populations." Genographic participants are assigned to the reference population they most resemble genetically. The significant mixing of peoples over time, however, means that a reference population may only provide a rough estimate of an individual's ancestral diversity.

Explore Your Results

Help Us Contribute to The Science

If you have already contributed your results to our research efforts—thank you! Your participation has helped scientists learn more about the migratory history of the human race out of Africa—truly one of the greatest journeys of all time. If you haven't contributed your results you find out what it means to contribute

The Keys To Discovery

Part 2: Dr Spencer Wells explains how genetic markers can be used to build a family tree for everyone alive today.

Watch the Video >



The Journey Of Your Past

Part 3: Dr Spencer Wells explains how we use genetic markers to assign every participant to a branch on the human family tree.

Watch the Video >

















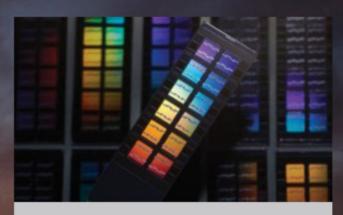
A Guide to Exploring Your Journey

Your Results Explained

- 1. Overview
- 2. Hominin Ancestry Explained
- 3. Deep Ancestry Explained
- 4. Regional Ancestry Explained
- 5. Our Story

1. Overview (All Genographic kits)

Your results were inferred about you from a very small sample of your DNA. The DNA sample you gave us is unique to you, coming from a mixture of the DNA from your two parents. Your parents inherited their DNA from your four grandparents, and their DNA came from your eight great-grandparents, and so forth and so on. In a way, you are the product of a chemical combination of all those people that came before you, and all of them are your ancestors.



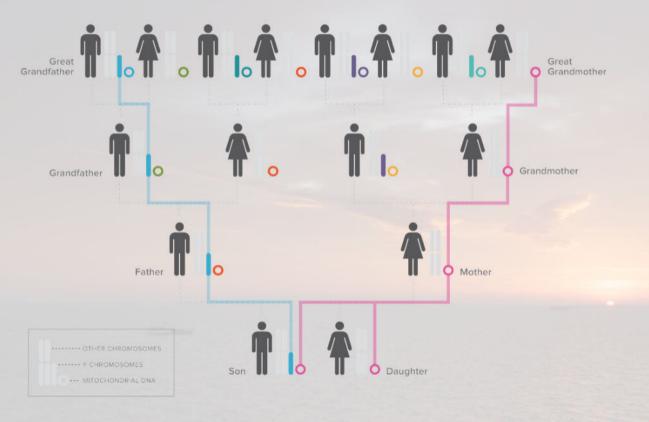
Behind the Science

Learn More >



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Learn More >



Questions?

Click Here For a List of FAQs >

--- MITOCHONDRIAL DNA

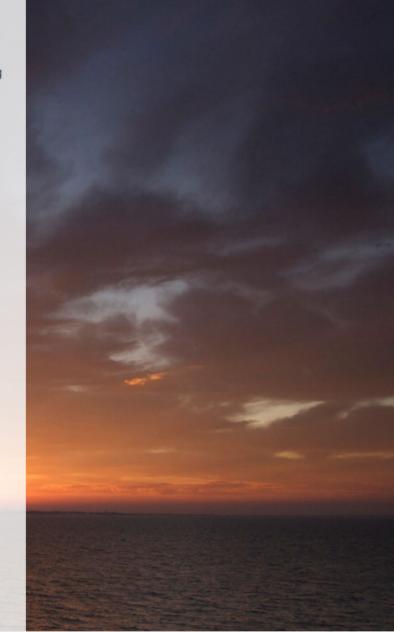
In recent years, scientists have discovered that different parts of your DNA can tell us about historical and prehistorical events in your ancestral story. We can estimate when or where these events happened by looking for small variations between your DNA and that of other people around you. These small variations are called mutations. Mutations are usually rare and, in nearly all cases, occurred only once in the past. Therefore, any two people who share a rare mutation must have inherited it from a shared common ancestor. By counting your rare mutations and comparing them to those of thousands of other people, we can begin to construct your personal story.

Why do results about deep and regional ancestry differ (Geno 2.0)?

Deep ancestry is based on either your mitochondrial DNA or your Y-chromosome DNA, and it shows only a single line of descent (either your direct maternal or paternal line). For men it shows both lines of descent, while for women it shows only the maternal, since women do not have a Y chromosome. In contrast, your regional ancestry is based on the mutations across all of your DNA and therefore shows the contribution from every one of your hundreds of ancestors.

2. Your Hominin Ancestry Explained (Geno 2.0)

In recent years, scientists have determined that modern humans are not the only ancestors represented in our DNA. During your ancestors' journey from our original African homeland, they might have mixed with ancient hominins who lived tens and even hundreds of thousands of years ago—our human cousins like the Neanderthals in Europe and the Middle East and the Denisovans in Asia. Their distinct genetic markers are still with us today. This means that you may find you have a small percentage (between 0 to 8 percent) of Neanderthal or Denisovan ancestry, even though those ancient species have long since gone extinct.



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Why am I Neanderthal?

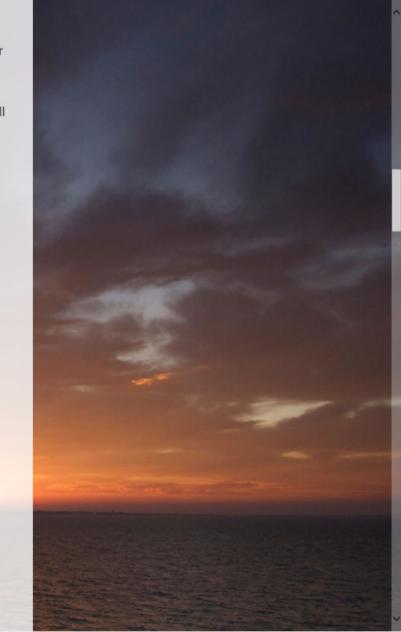
Why am I Denisovan?

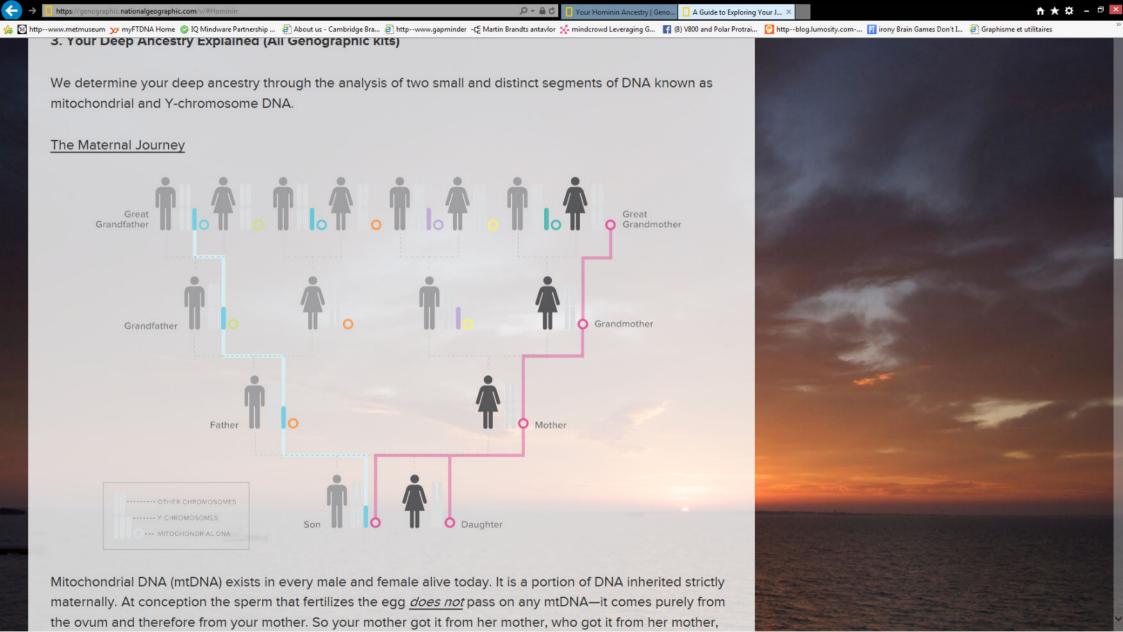
3. Your Deep Ancestry Explained (All Genographic kits)

We determine your deep ancestry through the analysis of two small and distinct segments of DNA known as mitochondrial and Y-chromosome DNA.

The Maternal Journey

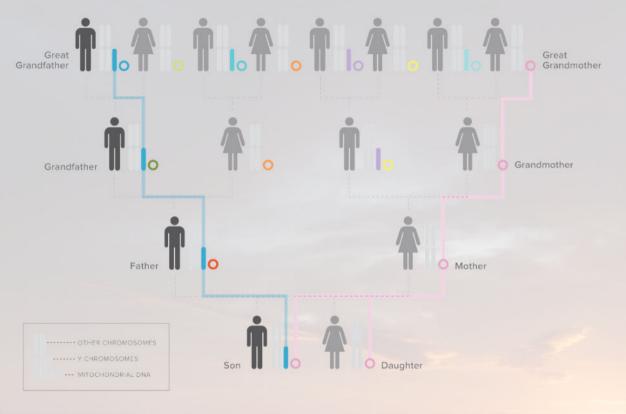




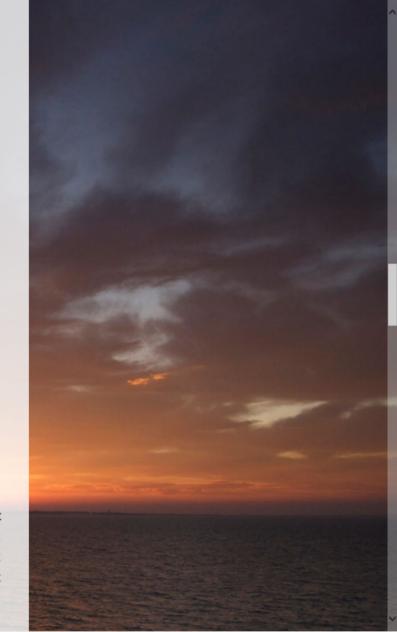


haplogroup for every Genographic participant.

The Paternal Journey



The Y chromosome, on the other hand, only exists in males: Each man inherited his Y chromosome from his father, who got it from his father, and so forth, forming another deep branch of direct ancestry. However, since Y-chromosome DNA (Y-DNA) only exists in males, we are currently unable to identify a paternal haplogroup from a female's DNA sample. Female participants eager to learn about the paternal part of their ancestry will need their father, paternal uncle, or a full male sibling to participate, in order to obtain that part of the story.



part of the story.

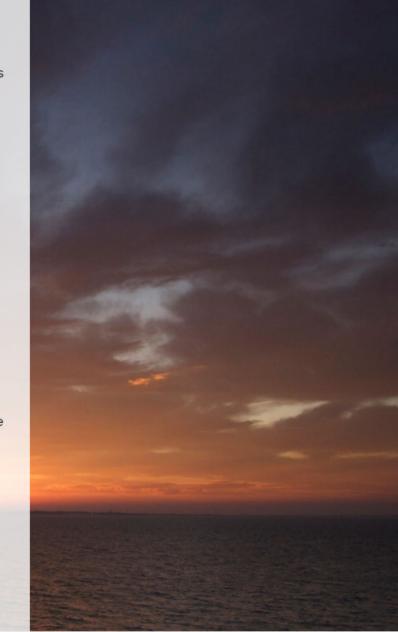
When you click on Deep Ancestry, you're taken to a map showing the route that either your maternal or paternal ancestors followed from Africa to the end point of their journey several hundred to thousands of years ago. This journey through time and space begins with the marker for your oldest ancestor and moves forward through time, showing at each step the possible route taken by the ancestor living at that point. Each successive step on the map represents the migratory path of a group descendent from the previous group, eventually forming the complete path taken by your **haplogroup**, or your deep ancestral branch of the tree. Each haplogroup has a name expressed by alternating letters and numbers—like Q2, J1c, R1b1a, and so forth—or by a letter followed by your terminal mutation, like R-M222. Your terminal mutation is the most recently occurring mutation in your ancestral journey. Y chromosome haplogroups are often identified by their terminal mutation.

In the Deep Ancestry section we have highlighted major migratory movements or events along the way. For some of these movements or events, we provide more information about that part of the journey, including approximately when and where it happened—and our best understanding of how.

The last step in the journey is illustrated by a heat map showing through shaded plots the percentage distribution of your haplogroup in more recent times (time ranges vary from hundreds to a few thousand years ago for different groups). This information, gathered from participants in the Genographic Project as well as from the scientific literature, helps build a more detailed picture of where migratory groups settled during more modern history, helping to bridge the knowledge gap between our regional and our deep ancestries.

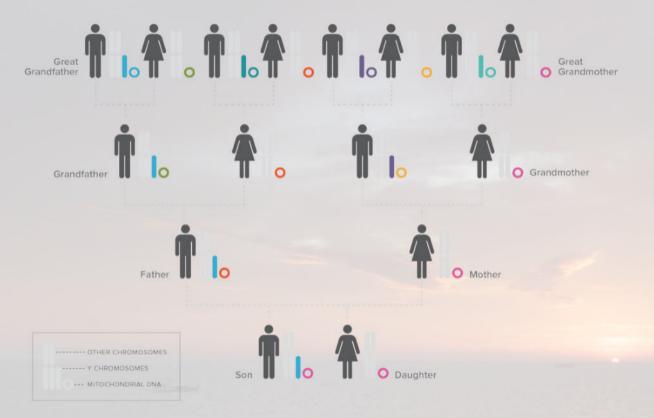
4. Your Regional Ancestry Explained (Geno 2.0)

We determine your recent ancestry by analyzing small bits of DNA scattered across your entire genome. This portion of your ancestry comes equally from both parents, all four grandparents, all eight great-grandparents, and so forth. Unlike **mtDNA** and **Y-DNA** (see Your Deep Ancestry Explained), this portion of your DNA gets scrambled every successive generation, so what we can learn from it is not so much your deep history, but

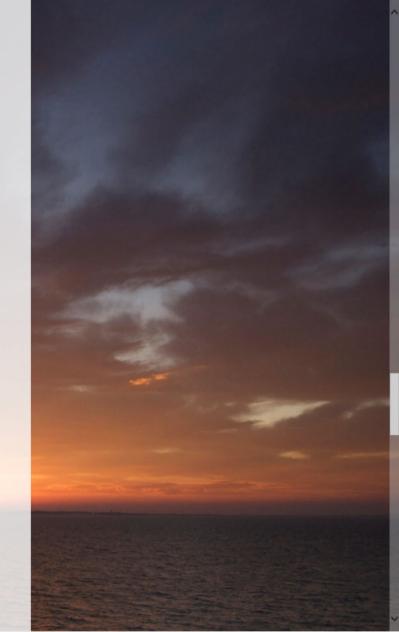


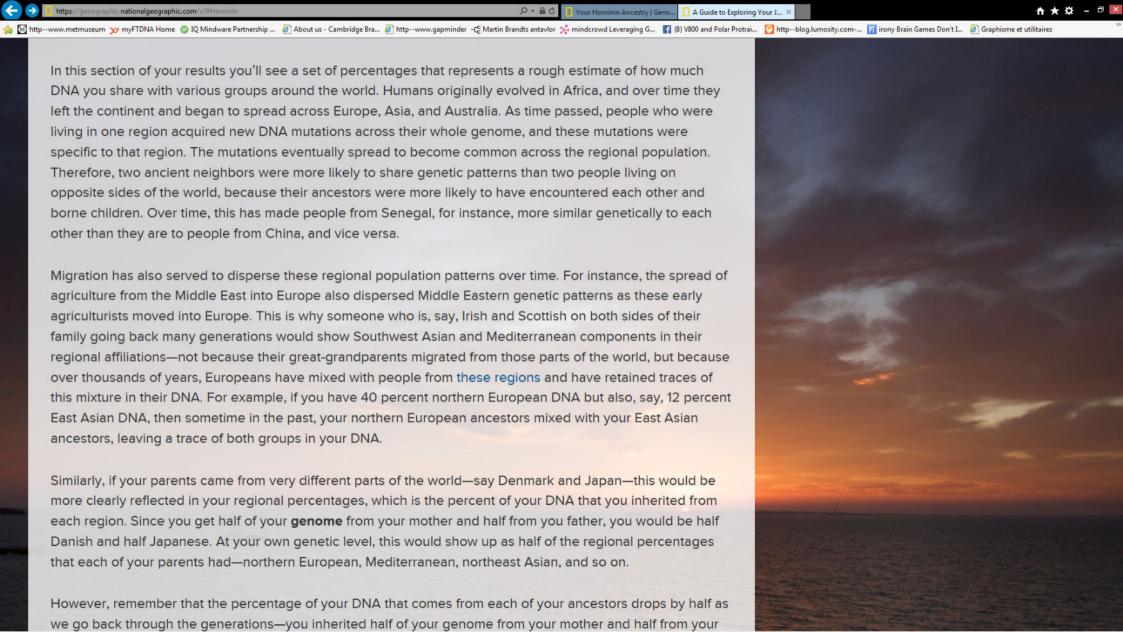
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In this section of your results you'll see a set of percentages that represents a rough estimate of how much DNA you share with various groups around the world. Humans originally evolved in Africa, and over time they left the continent and began to spread across Europe, Asia, and Australia. As time passed, people who were





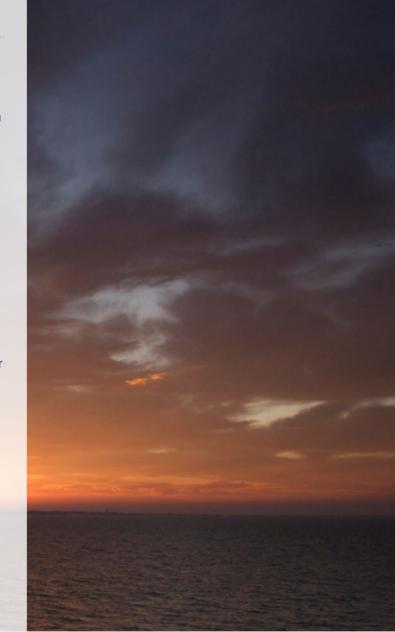
However, remember that the percentage of your DNA that comes from each of your ancestors drops by half as we go back through the generations—you inherited half of your genome from your mother and half from your father but only a quarter from each of your grandparents. Because of this, our ability to see your regional ancestry decreases with each preceding generation. If, say, your great-grandmother (three generations removed) was 100 percent Native American, that would show up as roughly 12 percent of your DNA. Our rough limit is six generations, or 64 ancestors, each of whose contribution is roughly 2 percent of your DNA. Beyond that, we can't be certain that the percentages are significant. For this reason, we don't identify regional percentages that are less than 2 percent in your results, even when they *do* exist.

People with recent ancestry from different populations can have a mix of regions in their DNA that's not typically seen in indigenous populations. Hispanics, for instance, will often have typical European as well as Native American and/or African components—a result of the mix of cultures and peoples that has occurred in the Americas over the past 500 years.

Modern-day populations around the world carry particular blends of regional affiliations. After calculating your regional percentages, we compared your DNA results to the averages from each of 42 reference populations we currently have in our database, and we estimated which of these populations were most similar to you in terms of the genetic markers you carry.

Notice some unusual populations listed for you? This doesn't mean that you belong to these groups, only that these were the groups in our limited number of reference populations that were closest to you. As we expand our set of reference populations, you may find that you are closer to another group. This simply reflects the ongoing scientific refinement of the Genographic reference dataset, as well as improvements in our methodology for assessing your closest populations. Remember, the regional blends that show up in your regional ancestry were determined over thousands of years, so you may see surprising regional percentages reflected in these populations.

Read more about the ancestral regions



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Read more about the ancestral regions

Read more about the reference populations composed of ancestral regions

Dr. Spencer Wells analyzes several participants' results in the following case studies

5. Our Story Explained (Geno 2.0)

The visualization shown under Our Story is not only a data map of your own genotype, but also that of other participants in the Genographic Project with whom you share genetic markers. The goal of this experience is to allow you to read the recent genealogical stories of other participants and in doing so perhaps learn about the ancestry of those with whom you share a migratory journey. The stories told here also help scientists and researchers learn more about the recent migratory movements of certain specific lineages or haplogroups.

Participants within your mtDNA and Y-DNA haplogroups are displayed within the circle, and their proximity to you is based on their level of "relation" to you, defined in this experience as how recently you share a common genetic marker. Those more recently related to you (in time) are displayed near the center of the circle, and those more distantly related to you are displayed on the outer edges. If a user has shared their story with the community, the dot identifying them displays as a larger circle. Clicking on the dots will reveal their story. You can share your own story with the community by typing it into the box below, checking "Show My Story" and then clicking "Save."







Tweet 11 8+1 38







Your Deep Ancestry

(1,000 Years - 100,000 Years Ago)



Introduction to Your Story

305 M42 M168 P143 M89 M578 P128 M526 M45 M207 P231 M417 M17

Introduction to Your Story

INTRO

We will now take you back through the stories of your distant ancestors and show how the movements of their descendants gave rise to your lineage.

Each segment on the map above represents the migratory path of successive groups that eventually coalesced to form your branch of the tree. We start with the marker for your oldest ancestor, and walk forward to more recent times, showing at each step the line of your ancestors who lived up to that point.

What is a marker? Each of us carries DNA that is a combination of genes passed from both our mother and father, giving us traits that range from eye color and height to athleticism and disease susceptibility. As part of this process, the Y-chromosome is passed directly from father to son, unchanged, from generation to generation down a purely male line. Mitochondrial DNA, on the other hand, is passed from mothers to their children, but only their daughters pass it on to the next generation. It traces a purely maternal line.

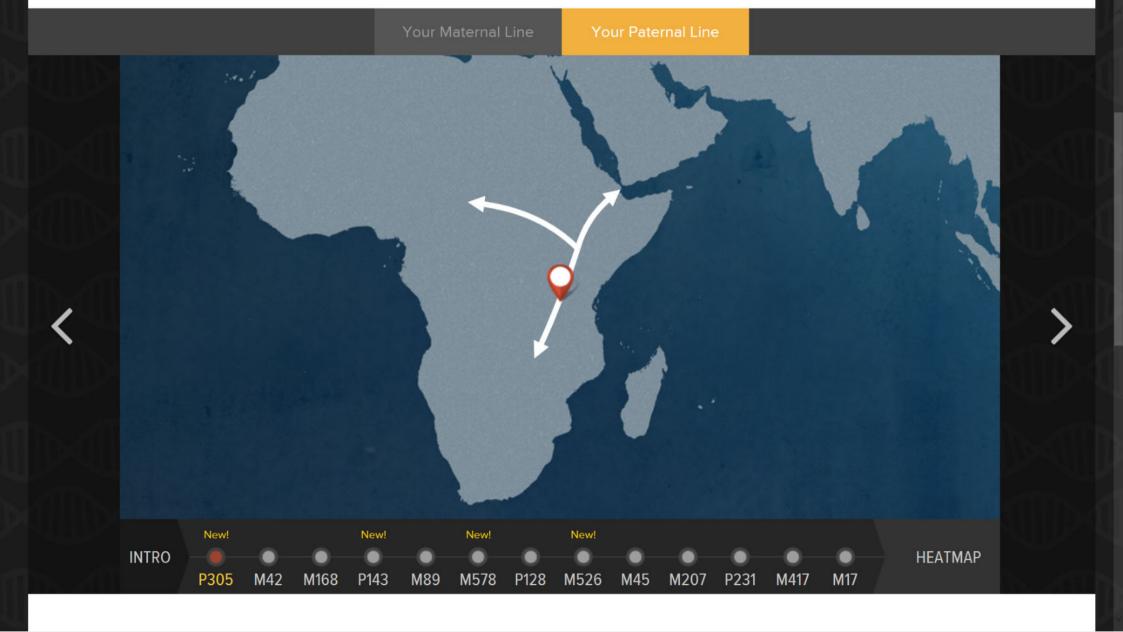
The DNA is passed on unchanged, unless a mutation—a random, naturally occurring, usually harmless change—occurs. The mutation, known as a marker, acts as a beacon; it can be mapped through generations because it will be passed down for thousands of years.

When geneticists identify such a marker, they try to figure out when it first occurred, and in which geographic region of the world. Each marker is essentially the beginning of a new lineage on the family tree of the human race. Tracking the lineages provides a picture of how small tribes of modern humans in Africa tens of thousands of years ago diversified and spread to populate the world.

By looking at the markers you carry, we can trace your lineage, ancestor by ancestor, to reveal the path they traveled as they moved out of Africa. Our story begins with your earliest ancestor. Who were they, where did they live, and what is their story? Click "Next" to begin.

IOUS STEP

HEATMAP



Branch: P305

Age: More than 100,000 years old

Location of Origin: Africa

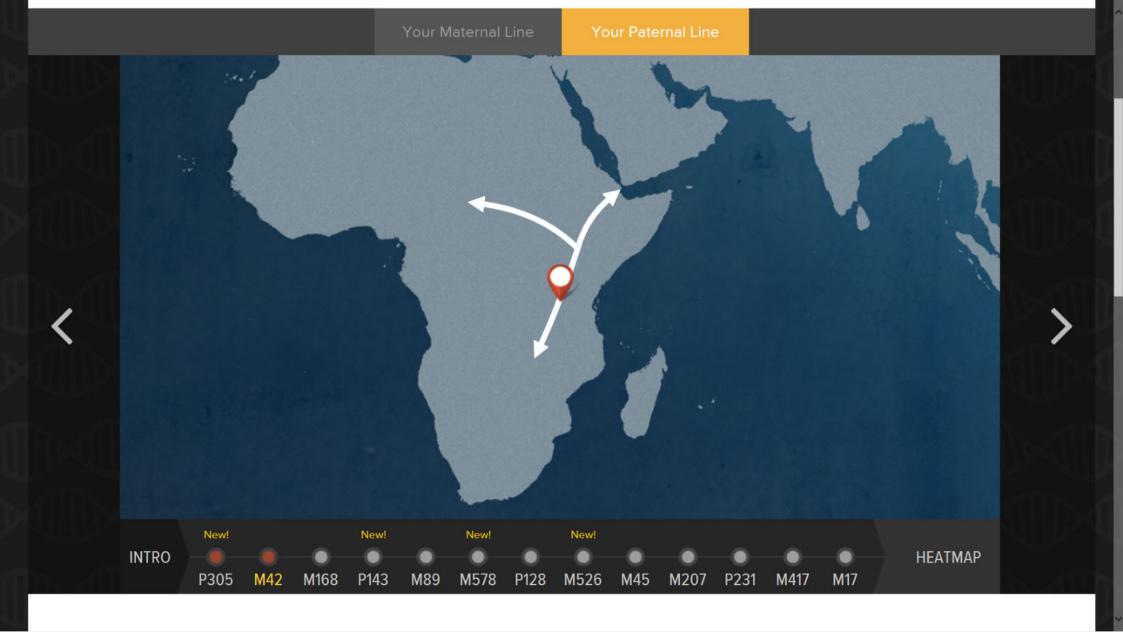
The common direct paternal ancestor of all men alive today was born in Africa between 300,000 and 150,000 years ago. Dubbed "Y-chromosome Adam" by the popular press, he was neither the first human male nor the only man alive in his time. He was, though, the only male whose Y-chromosome lineage is still around today. All men, including your direct paternal ancestors, trace their ancestry to one of this man's descendants. The oldest Y-chromosome lineages in existence, belonging to the A00 branch of the tree, are found only in African populations.

Around 100,000 years ago the mutation named P305 occurred in the Y chromosome of a man in Africa. This is one of the oldest known mutations that is not shared by all men. Therefore, it marks one of the early splits in the human Y-chromosome tree, which itself marks one of the earliest branching points in modern human evolution. The man who first carried this mutation lived in Africa and is the ancestor to more than 99.9% of paternal lineages today. In fact, men who do not carry this mutation are so rare that its importance in human history was discovered only in the past two years.

As P305-bearing populations migrated around the globe, they picked up additional markers on their Y chromosomes. Today, there are no known P305-bearing individuals without these additional markers.

« PREVIOUS STEP

NEXT STEP »





Branch: M42

Age: About 80,000 Years Ago

Location of Origin: East Africa

Photograph by Pere Fernandez, My Shot

Around 80,000 years ago, the BT branch of the Y-chromosome tree was born, defined by many genetic markers, including M42. The common ancestor of most men living today, some of this man's descendants would begin the journey out of Africa to the Middle East and India. Some small groups from this line would eventually reach the Americas, while other groups would settle in Europe, and some would remain near their ancestral homeland in Africa.

Individuals from this line whose ancestors stayed in Africa often practice cultural traditions that resemble those of the distant past. For example, they often live in traditional hunter-gatherer societies. These include the Mbuti and Biaka Pygmies of central Africa, as well as Tanzania's Hadza.

Point of Interest

The M42 branch is shared by almost all men alive today, both in Africa and around the world.

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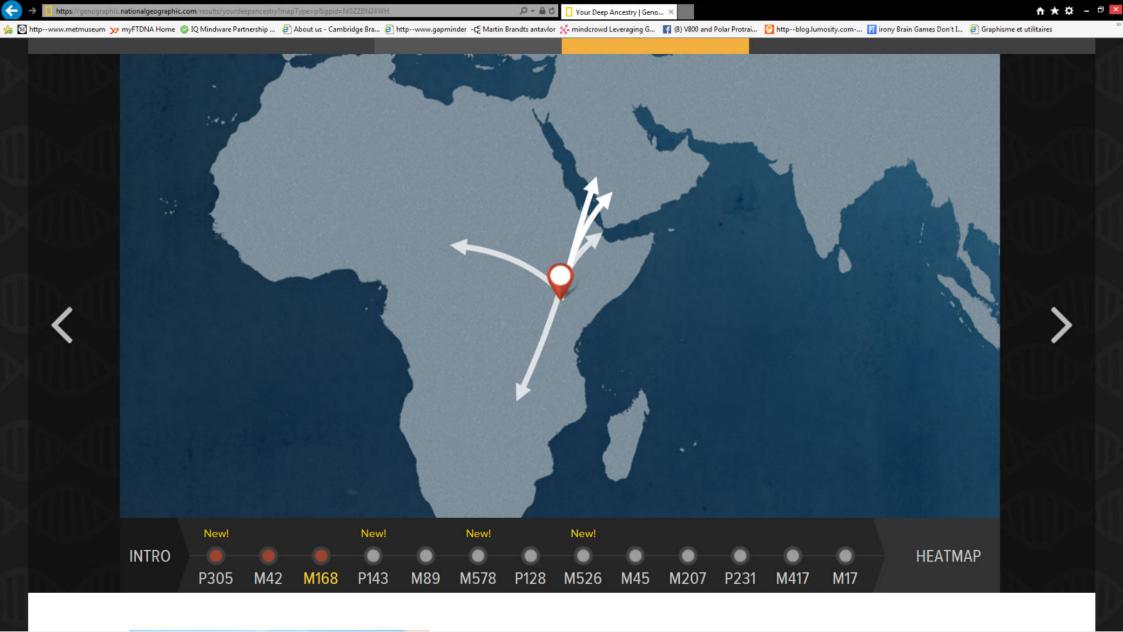
Photos From This Region

People on this branch carry one of Africa's—and the world's—oldest paternal lineages. Many of its members still live near its South African point of origin.

Photograph by Derwei Chan, My Shot



>





Branch: M168

Age: About 70,000 years ago

Location of Origin: East Africa

Photograph by Ali Talan, My Shot

When humans left Africa, they migrated across the globe in a web of paths that spread out like the branches of a tree, each limb of migration identifiable by a marker in our **DNA**. For male lineages, the M168 branch was one of the first to leave the African homeland.

The man who gave rise to the first **genetic marker** in your lineage probably lived in northeast Africa in the region of the Rift Valley, perhaps in present-day Ethiopia, Kenya, or Tanzania. Scientists put the most likely date for when he lived at around 70,000 years ago. His descendants became the only lineage to survive outside of Africa, making him the common ancestor of every non-African man living today.

Your nomadic ancestors would have followed the good weather and the animals they hunted, although the exact route they followed remains to be determined. In addition to a favorable change in climate, around this same time there was a great leap forward in modern humans' intellectual capacity. Many scientists believe that the emergence of language gave us a huge advantage over other early humanlike species. Improved tools and weapons, the ability to plan ahead and cooperate with one another, and an increased capacity to exploit resources in ways we hadn't been able to earlier allowed modern humans to rapidly migrate to new territories, exploit new resources, and replace other hominids such as the Neanderthals.

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Point of Interest

This male branch is one of the first to leave the African homeland.

Photos From This Region

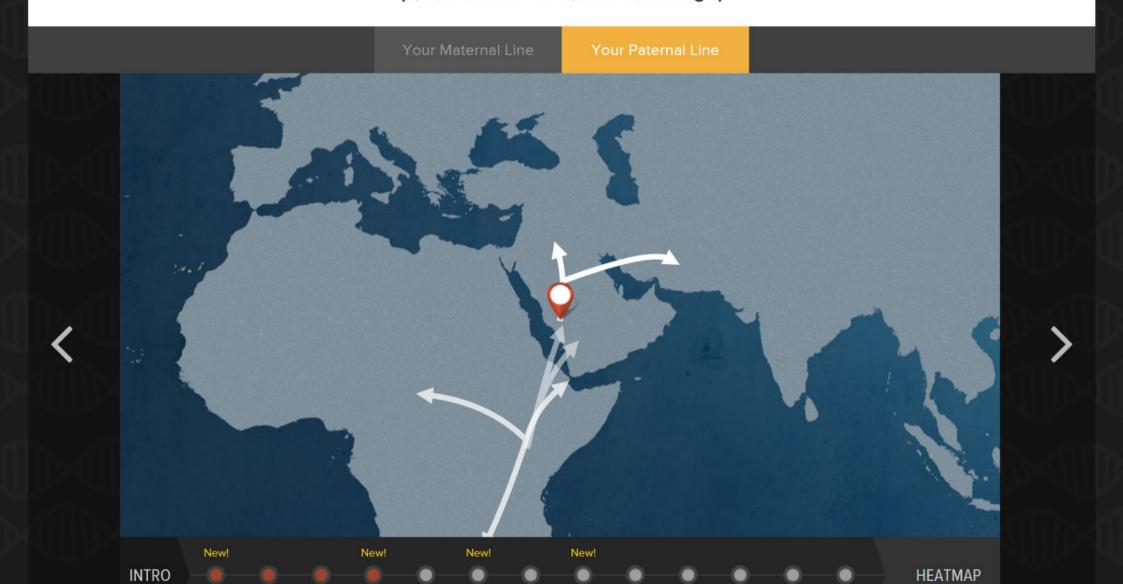
The Serengeti Plain's Maasai people, seen here in dance, still measure wealth and prestige by the cattle and other herds at the foundation of their pastoral society.

Photograph by Blake Ezra Cole, My Shot



rour Deep Aricestry

(1,000 Years - 100,000 Years Ago)



Branch: P143

Age: About 60,000 years old

Location of Origin: Southwest Asia

This mutation is one of the oldest thought to have occurred outside of Africa and therefore marks a pivotal moment in the evolution of modern humans. Moving along the coastline, members of this lineage were some of the earliest settlers in Asia, Southeast Asia, and Australia.

But why would man have first ventured out of the familiar African hunting grounds and into unexplored lands? The first migrants likely ventured across the Bab-al Mandeb strait, a narrow body of water at the southern end of the Red Sea, crossing into the Arabian Peninsula and soon after developing mutation P143—perhaps 60,000 years ago. These beachcombers would make their way rapidly to India and Southeast Asia, following the coastline in a gradual march eastward. By 50,000 years ago, they had reached Australia. These were the ancestors of some of today's Australian Aborigines.

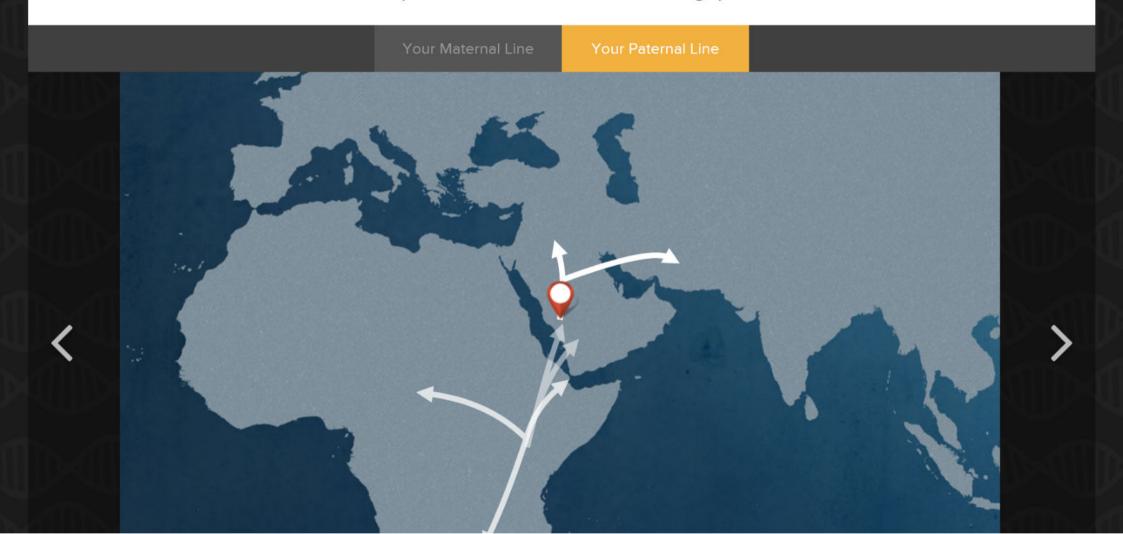
It is also likely that a fluctuation in climate may have contributed to your ancestors' exodus out of Africa. The African ice age was characterized by drought rather than by cold. Around 50,000 years ago, though, the ice sheets of the Northern Hemisphere began to melt, introducing a short period of warmer temperatures and moister climate in Africa and the Middle East. Parts of the inhospitable Sahara briefly became habitable. As the drought-ridden desert changed to a savanna, the animals hunted by your ancestors expanded their range and began moving through the newly emerging green corridor of grasslands.

« PREVIOUS STEP

NEXT STEP »

Your Deep Ancestry

(1,000 Years - 100,000 Years Ago)





Branch: M89

Age: About 55,000 Years Old

Location of Origin: Southwest Asia

Photograph by Ciaran Clancy, My Shot

The next male ancestor in your ancestral lineage is the man who gave rise to M89, a marker found in 90 to 95 percent of all non-Africans. This man was likely born around 55,000 years ago in Middle East.

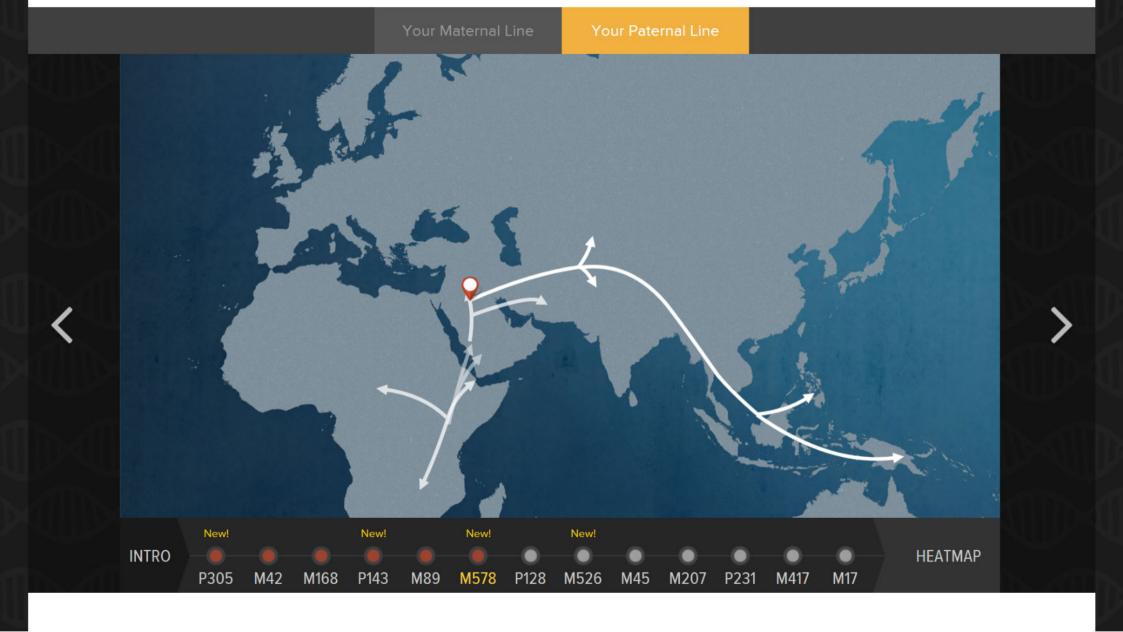
While many of the descendants of M89 remained in the Middle East, others continued to follow the great herds of wild game through what is now modern-day Iran, then north to the Caucasus and the steppes of Central Asia. These semiarid, grass-covered plains would eventually form an ancient "superhighway" stretching from France to Korea. A smaller group continued moving north from the Middle East to Anatolia and the Balkans, trading familiar grasslands for forests and high country.

Photos From This Region

Indian children celebrate Holi, a Hindu celebration. Colored powders and liquids mimic flames—and herald the coming of spring.









Branch: M578

Age: About 50,000 Years Old

Location of Origin: Southwest Asia

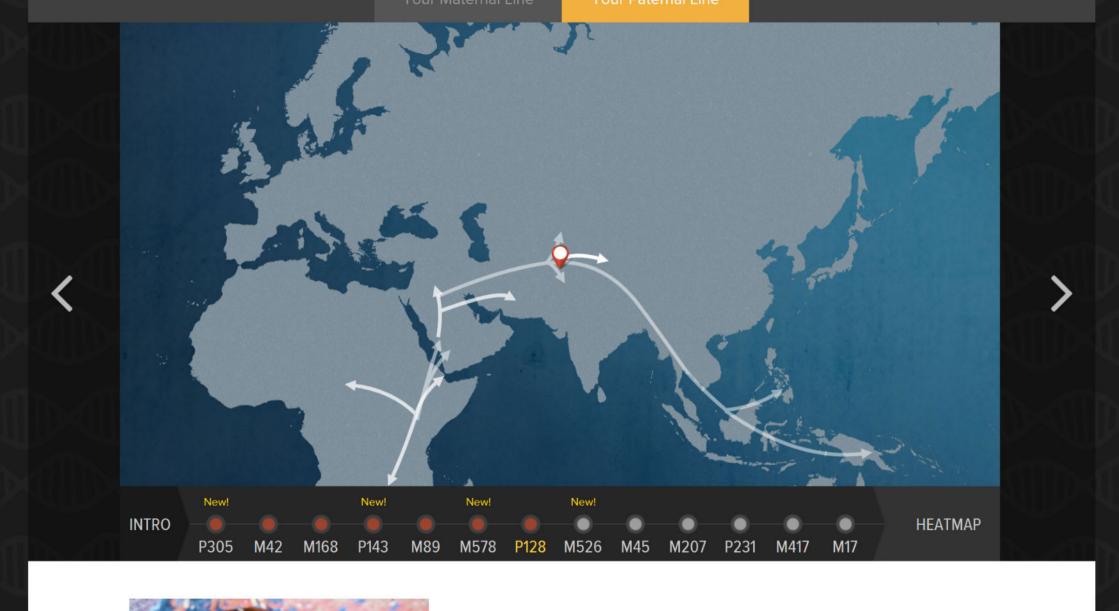
After settling in Southwest Asia for several millennia, humans began to expand in various directions, including east and south around the Indian Ocean, but also north toward Anatolia and the Black and Caspian Seas. The first man to acquire mutation M578 was among those that stayed in Southwest Asia before moving on.

Fast-forwarding to about 40,000 years ago, the climate shifted once again and became colder and more arid. Drought hit Africa and the Middle East and the grasslands reverted to desert, and for the next 20,000 years, the Saharan Gateway was effectively closed. With the desert impassable, your ancestors had two options: remain in the Middle East, or move on. Retreat back to the home continent was not an option.

« PREVIOUS STEP

NEXT STEP »

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Photograph by Georgii Chechin, My Shot

Branch: P128

Age: About 45,000 years ago

Location of Origin: South Asia

The next male ancestor in your ancestral lineage is the man who gave rise to P128, a marker found in more than half of all non-Africans alive today. This man was born around 45,000 years ago in south Central Asia and was likely part of the second wave of migrants to move east from Southwest Asia.

Some of the descendants of P128 migrated to the southeast and northeast, picking up additional markers on their Y chromosomes. This lineage is the parent of several major branches on the Y-chromosome tree: O, the most common lineage in East Asia; R, the major European and Central Asian Y-chromosome lineage; and Q, the major Y-chromosome lineage in the Americas. These descendant branches went on to settle the rest of Asia, the Americas, and Europe. Still many others traveled to Southeast Asia, and some descendants of P128 individuals moved across the waters south and east and are most commonly seen in Oceanian and Australian Aboriginal populations.

Photos From This Region

This Miao village is in Guizhou, China. In China the term "Miao" denotes four ethnic groups not closely related to one another: the



Photograph by Georgii Chechin, My Shot

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Some of the descendants of P128 migrated to the southeast and northeast, picking up additional markers on their Y chromosomes. This lineage is the parent of several major branches on the Y-chromosome tree: O, the most common lineage in East Asia; R, the major European and Central Asian Y-chromosome lineage; and Q, the major Y-chromosome lineage in the Americas. These descendant branches went on to settle the rest of Asia, the Americas, and Europe. Still many others traveled to Southeast Asia, and some descendants of P128 individuals moved across the waters south and east and are most commonly seen in Oceanian and Australian Aboriginal populations.

Photos From This Region

This Miao village is in Guizhou, China. In China the term "Miao" denotes four ethnic groups not closely related to one another: the Hmu, Qo Xiong, A-Hmao, and Hmong peoples.

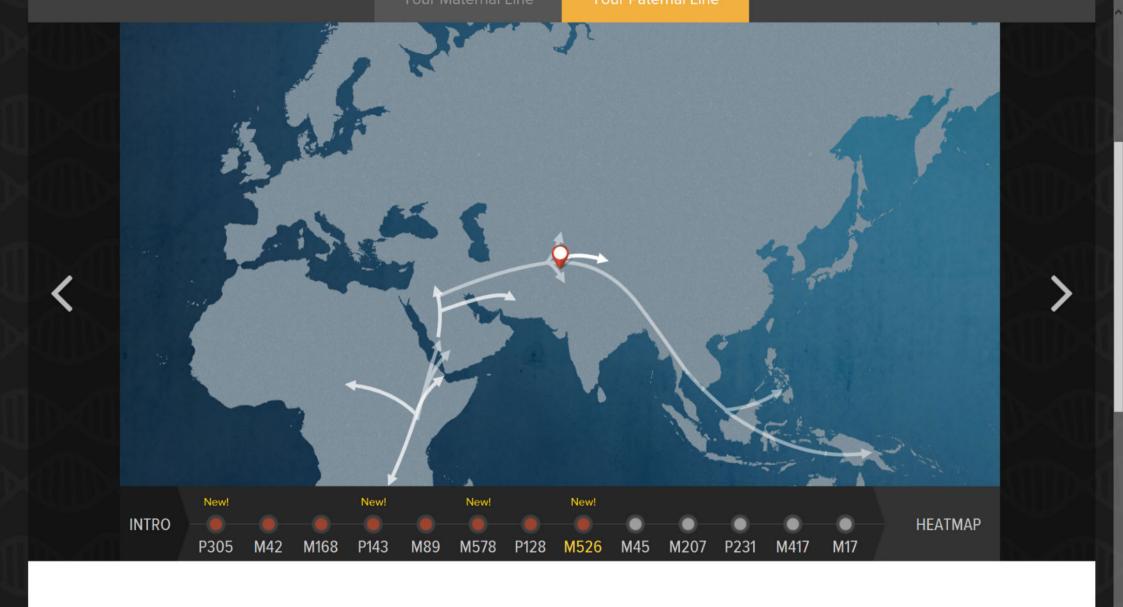
Photograph by Kho Chee Hui, My Shot



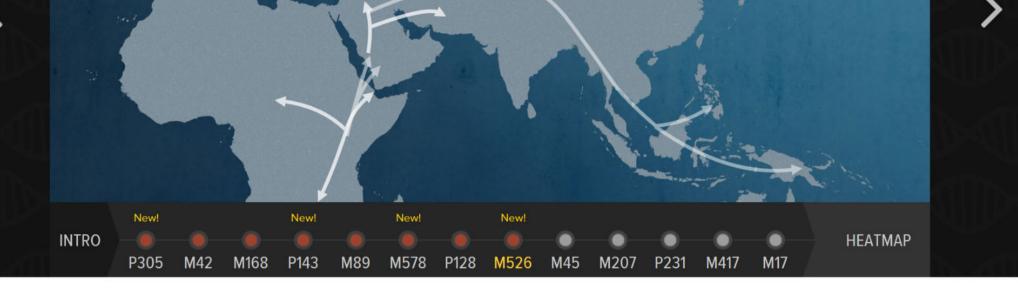
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The Science Behind For Scientists For Educators Press News



Rranch: M526

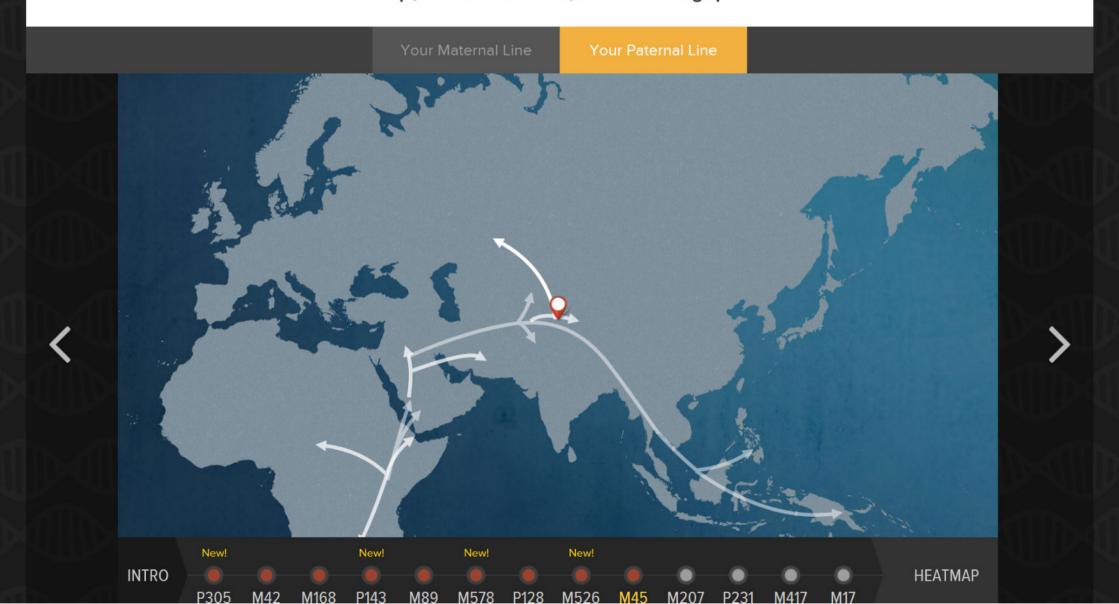


Branch: M526

Age: About 42,000 Years Old

Location of Origin: South or Southeast Asia

The man who first carried mutation M526 was part of the second wave of settlers that migrated around the Indian Ocean and settled in Southeast Asia. This mutation is shared by men from haplogroups M, N, O, P, Q, R, and S; these are groups common in East Asia, Southeast Asia, Oceania, and the Americas.





Photograph by Andrew McConnell, Alamy

Branch: M45

Age: Around 35,000 Years Ago

Location of Origin: Central Asia or South Asia

This paternal ancestor traveled with groups to the open savannas between Central and South Asia during the Paleolithic. These big-game hunters were the parents to two of the most widespread male lineages in modern populations, one that is responsible for the majority of pre-Columbian lineages in the Americas (haplogroup Q)—among others from Asia and Europe—and one that spread farther north and west into Asia and produced the highest frequency lineages in European populations (haplogroup R).

Today, members of this lineage who do not belong to a descendant branch (haplogroups Q or R) are rare, and geneticists have found them most often in India. These populations include such diverse groups as the Saora (23 percent), the Bhumij (13 percent), and Muslims from Manipur (33 percent).

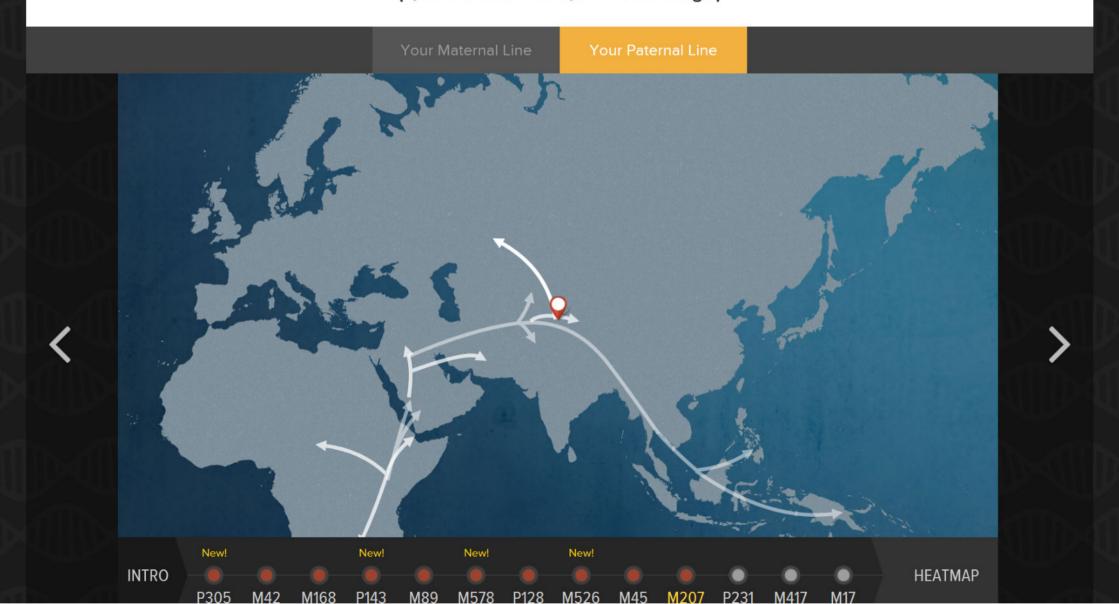
Point of Interest

Known as the Central Asian Clan, this branch gave rise to many distinct lineages that spent the next 30,000 years gradually populating much of the planet.

Photos From This Region

Indian women fish with traditional nets. Today India has the highest population of the M45 lineage, whose later offshoots are found in most Native Americans and Europeans.







Branch: M207

Age: About 30,000 Years Ago

Location of Origin: Central Asia

Photograph by mayat Shan, My Shot

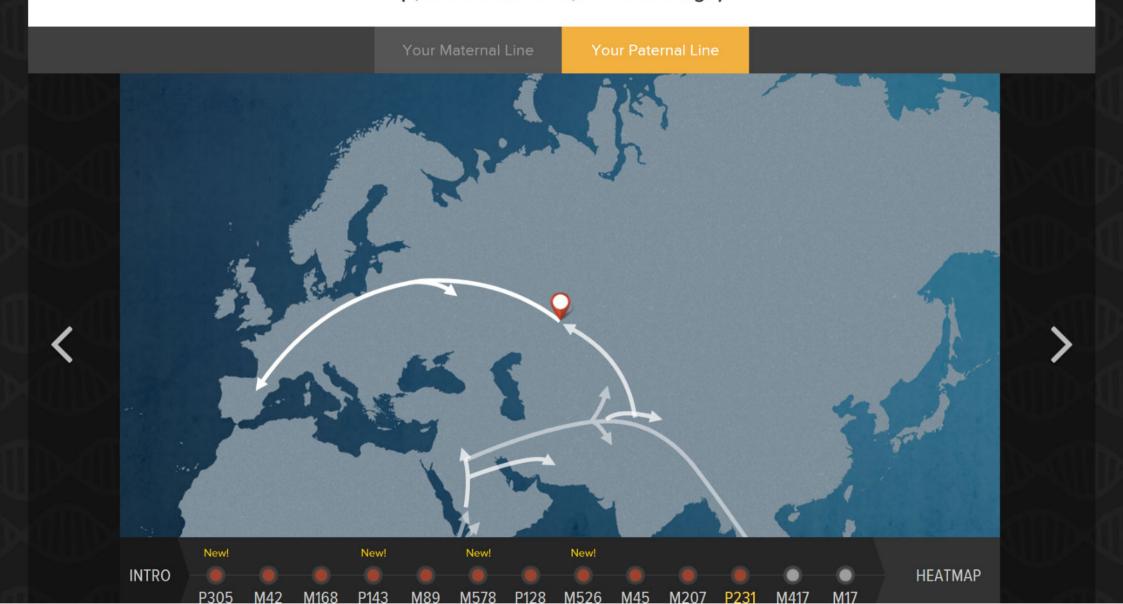
M207 was born in Central Asia around 30,000 years ago. His descendants would go on to settle in Europe, South Asia and the Middle East over the following 20,000 years. Today, most western European men belong to one branch—R-M342—that descended from this lineage. While it appears to have been one of the earliest lineages to settle in Europe more than 25,000 years ago, more recent population expansions associated with the post-glacial repopulation of northern Europe after the end of the last ice age, as well as the spread of agriculture during the Neolithic, also contributed to its high frequency in Ireland, the UK, France and Spain.

One descendant lineage—R-L62—is common in Eastern Europe and India, and was likely spread in part through the migration of Indo-European steppe nomads over the past 5,000 years.

Photos From This Region

A herder poses with his horse in Kazakhstan's Tien Shan Mountains. Mountains like the Tien Shan formed impassible barriers that helped shape genetic patterns in Asia.







Branch: P231

Age: 25,000 – 30,000 Years Ago

Location of Origin: Central Asia

The Paleolithic ancestor who founded this lineage lived a nomadic lifestyle. His descendants include two major descendant branches that today account for most European men and many others from Central Asia, West Asia, and South Asia.

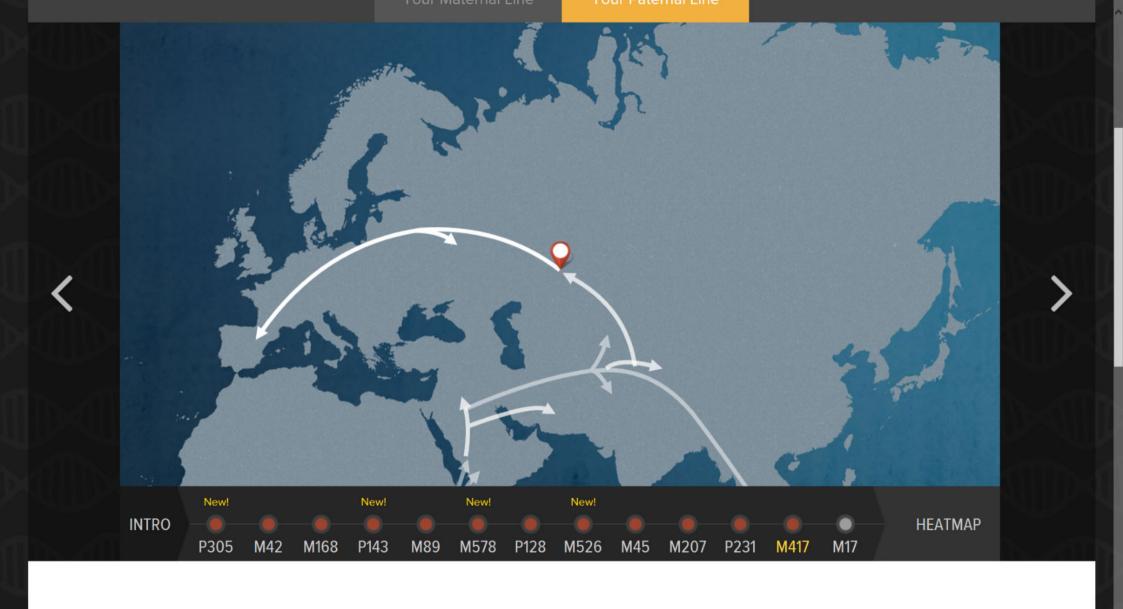
Photos From This Region

A mother and daughter share a moment on a Belarus bench. Belarusians are Slavic peoples closely related to Russians, Poles, and Ukrainians.

Photograph by Mitchell Kanashkevich, Getty Images



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Rranch: M417

Branch: M417

Age: To Be Determined

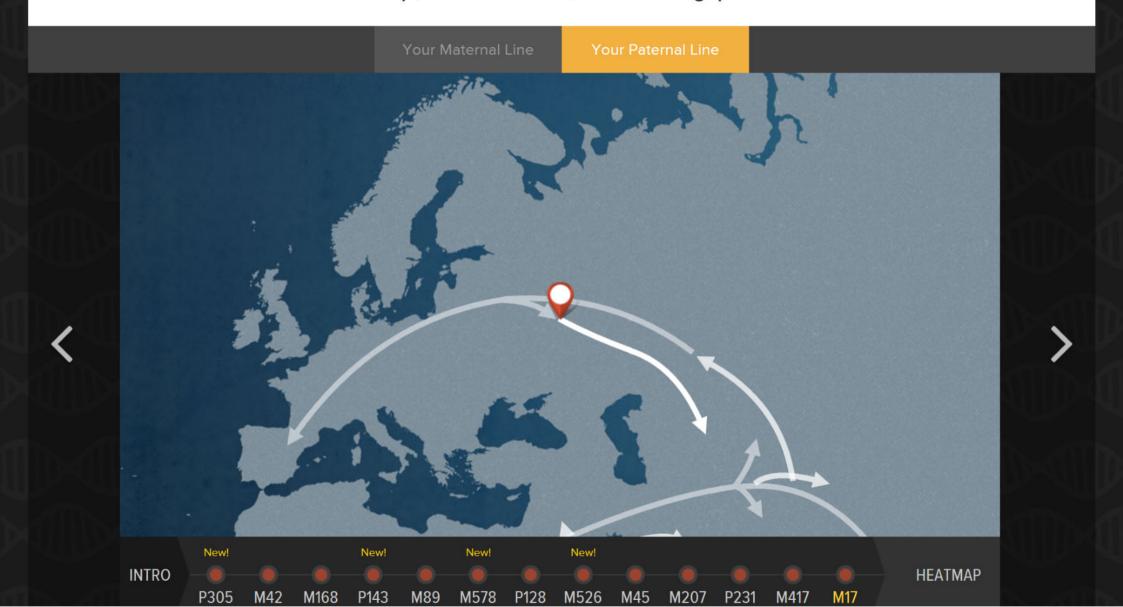
Location of Origin: Central Asia

Today, geneticists have found men from this lineage in Azerbaijan (9 percent), Malta (4 to 5 percent), and Qatar (3 percent). It is present in trace frequencies of less than 1 percent throughout Central and Western Europe.

Note: This branch is not accompanied by a major movement on the map, and research on this branch is continuing.

Point of Interest

This is the ancestral line of the Ashkenazi-Levite founding lineage.





Branch: M17

Age: 12,000 – 19,000 Years Ago

Location of Origin: Central Asia or South Asia

Photograph by Janina Bikova, Your Shot

The earliest members of this lineage lived on the grassy steppes between Central and South Asia, nomadic steppe dwellers. Over time they spread as far west as Western Europe and as far east as East Asia.

Today, geneticists have found it in about 25 percent of the male population in Iceland. It is between 5 and 23 percent of the male population in the Ukraine. It is around 14 percent of the population in Kyrgyzstan. It is around 18 percent of male lineages in Bangladesh.

Point of Interest

Descendants of this lineage may have belonged to the groups responsible for the spread of Indo-European languages, which include English, French, German, Russian, Bengali, and Hindi, among many others.

Photos From This Region

Men from the steppes of Kazakhstan and Central Asia, a longtime





Location of Origin: Central Asia or South Asia

Photograph by Janina Bikova, Your Shot

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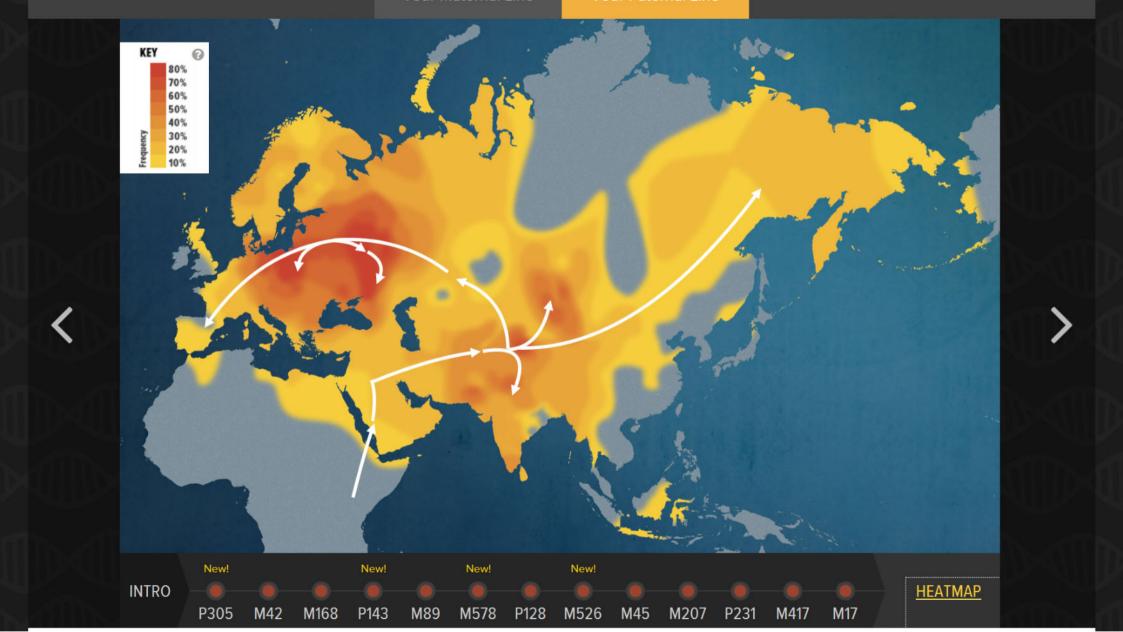
Photos From This Region

Men from the steppes of Kazakhstan and Central Asia, a longtime genetic and cultural crossroads, migrated to both Western Europe and East Asia.

Photograph by Eric Lafforgue, Alamy



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Heatmap for M17

This next step in your journey is a map showing the frequency of your haplogroup (or the closest haplogroup in your path that we have frequency information for) in indigenous populations from around the world, providing a more detailed look at where your more recent ancestors settled in their migratory journey. What do we mean by recent? It's difficult to say, as it could vary from a few hundred years ago to a few thousand years ago depending on how much scientists currently know about your particular haplogroup. As we test more individuals and receive more information worldwide, this information will grow and change.

The colors on the map represent the percentage frequency of your haplogroup in populations from different geographic regions—red indicates high concentrations, and light yellow and grey indicate low concentrations. The geographic region with the highest frequency isn't necessarily the place where the haplogroup originated, although this is sometimes the case.

The map of M17 shows a wide distribution that has spread across Eurasia. Frequency peaks across eastern Europe and south Asia indicate multiple expansions, perhaps (in the case of the eastern European peak) during the post-glacial recolonization of Europe at the end of the last ice age. It is also likely that Indo-European nomads living on the central Asian steppes 3,000-5,000 years ago would have carried this haplogroup during their migrations.

Are you related to people in the areas highlighted on your map? Distantly, yes—we are all connected through our ancient ancestry.

In order for us to learn more ancestry information about where haplogroups settled in more recent times, please choose to contribute your results to science (check the checkbox during Login or from the Account Settings tab of your Profile), and fill out your ancestry information in the Profile section of the site. Also be sure to tell your own story in the Our Story section.

Your Deep Ancestry



HEATMAP



Introduction to Your Story

We will now take you back through the stories of your distant ancestors and show how the movements of their descendants gave rise to your lineage.

Each segment on the map above represents the migratory path of successive groups that eventually coalesced to form your branch of the tree. We start with the marker for your oldest ancestor, and walk forward to more recent times, showing at each step the line of your ancestors who lived up to that point.

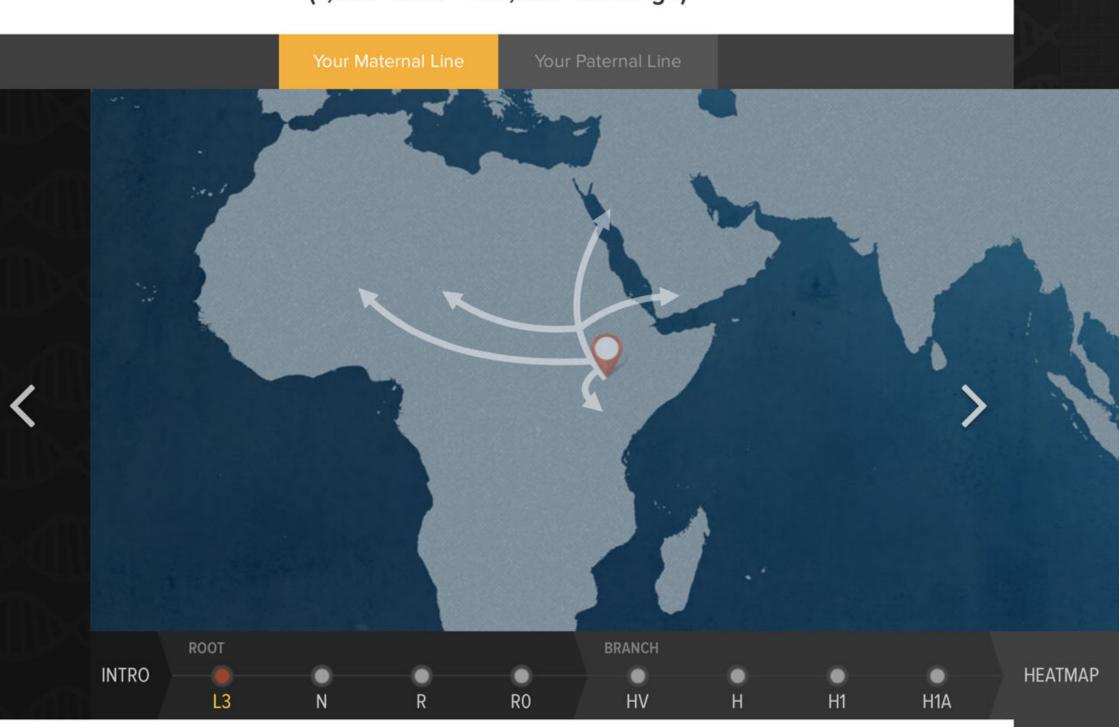
What is a marker? Each of us carries DNA that is a combination of genes passed from both our mother and father, giving us traits that range from eye color and height to athleticism and disease susceptibility. As part of this process, the Y-chromosome is passed directly from father to son, unchanged, from generation to generation down a purely male line. Mitochondrial DNA, on the other hand, is passed from mothers to their children, but only their daughters pass it on to the next generation. It traces a purely maternal line.

The DNA is passed on unchanged, unless a mutation—a random, naturally occurring, usually harmless change —occurs. The mutation, known as a marker, acts as a beacon; it can be mapped through generations because it will be passed down for thousands of years.

When geneticists identify such a marker, they try to figure out when it first occurred, and in which geographic region of the world. Each marker is essentially the beginning of a new lineage on the family tree of the human race. Tracking the lineages provides a picture of how small tribes of modern humans in Africa tens of thousands of years ago diversified and spread to populate the world.

By looking at the markers you carry, we can trace your lineage, ancestor by ancestor, to reveal the path they traveled as they moved out of Africa. Our story begins with your earliest ancestor. Who were they, where did they live, and what is their story? Click "Next" to begin.

tour Deep Ancestry



INTRO

L3 N R R0 HV H H1 H1A



Branch: L3

Age: 67,000 Years Ago

Location of Origin: East Africa

HEATMAP

Photograph by Claudia Wiens, Alamy

This woman's descendants would eventually account for both out-of-Africa maternal lineages, significant population migrations in Africa, and even take part in the Atlantic Slave Trade related dispersals from Africa.

The common direct maternal ancestor to all women alive today was born in East Africa around 180,000 years ago. Dubbed "Mitochondrial Eve" by the popular press, she represents the root of the human family tree. Eve gave rise to two descendant lineages known as L0 and L1'2'3'4'5'6, characterized by a different set of genetic mutations their members carry.

Current genetic data indicates that indigenous people belonging to these groups are found exclusively in Africa. This means that, because all humans have a common female ancestor, and because the genetic data shows that Africans are the oldest groups on the planet, we know our species originated there.

Eventually, L1'2'3'4'5'6 gave rise to L3 in East Africa. It is a similar story: an individual underwent a **mutation** to her mitochondrial **DNA**, which was passed onto her children. The children were successful, and their descendants ultimately broke away from L1'2'3'4'5'6, eventually separating into a new group called L3.

While L3 individuals are found all over Africa, L3 is important for its movements north. Your L3 ancestors were significant because they are the first modern humans to have left Africa, representing the deepest branches of the tree found outside of that continent.

From there, members of this group went in a few different directions. Many stayed on in Africa, dispersing to

■ genographic.nationalgeographic.com

west-central Africa, later dispersing throughout the continent and spreading this L3 lineage from Mail to South Africa. Today, L3 is also found in many African-Americans.

Other L3 individuals, your ancestors, kept moving northward, eventually leaving the African continent completely. These people gave rise to two important macro-haplogroups (M and N) that went on to populate the rest of the world.

Why would humans have first ventured out of the familiar African hunting grounds and into unexplored lands? It is likely that a fluctuation in climate may have provided the impetus for your ancestors' exodus out of Africa.

The African Ice Age was characterized by drought rather than by cold. Around 50,000 years ago the ice sheets of northern Europe began to melt, introducing a period of warmer temperatures and moister climate in Africa. Parts of the inhospitable Sahara briefly became habitable. As the drought-ridden desert changed to savanna, the animals your ancestors hunted expanded their range and began moving through the newly emerging green corridor of grasslands. Your nomadic ancestors followed the good weather and plentiful game northward across this Saharan Gateway, although the exact route they followed remains to be determined.

Point of Interest

The L branch is shared by all women alive today, both in Africa and around the world. The L3 branch is the major maternal branch from which all mitochondrial DNA lineages outside of Africa arose.

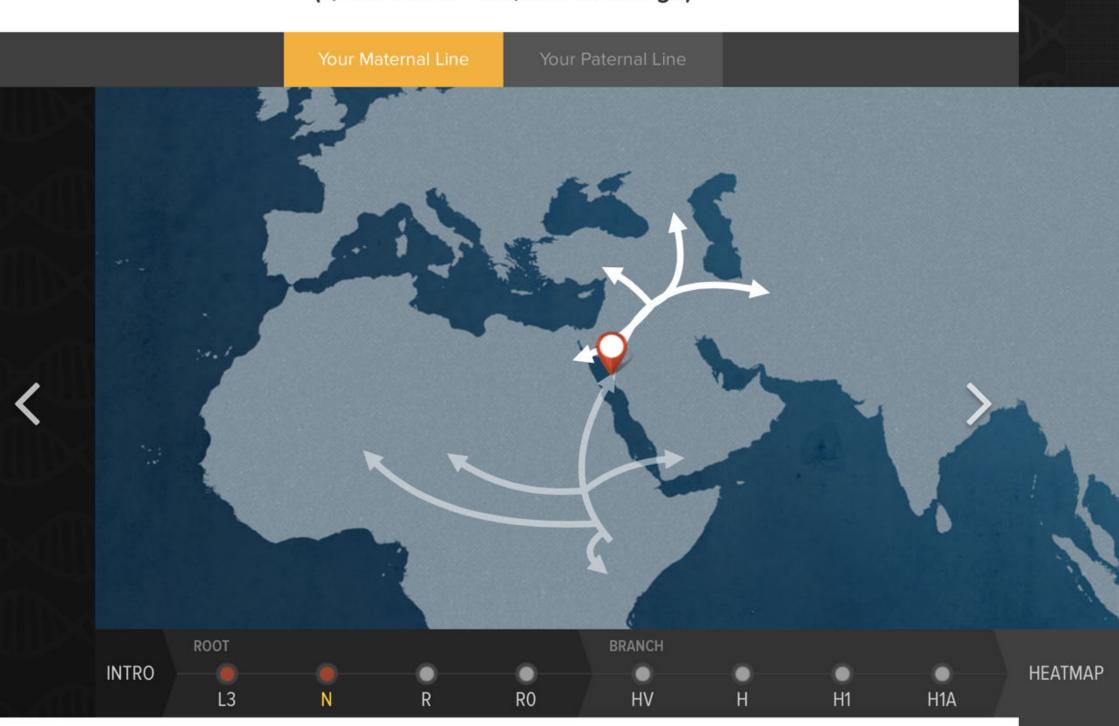
Photos From This Region

Despite their rugged appearance, Northern Ethiopia's spectacular Simien Mountains have been inhabited for at least 2,000 years and sit at the crossing of ancient trade routes.



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Your Deep Ancestry





Photograph by Helene Rogers, Alamy

Branch: N

Age: About 60,000 Years Ago

Location of Origin: East Africa or Asia

Your next ancestor is the woman whose descendants formed **haplogroup** N. Haplogroup N comprises one of two groups that were created by the descendants of L3.

One of these two groups of individuals moved north rather than east and left the African continent across the Sinai Peninsula, in present-day Egypt. Also faced with the harsh desert conditions of the Sahara, these people likely followed the Nile basin, which would have proved a reliable water and food supply in spite of the surrounding desert and its frequent sandstorms.

Descendants of these migrants eventually formed haplogroup N. Early members of this group lived in the eastern Mediterranean region and western Asia, where they likely coexisted for a time with other hominids such as Neanderthals. Excavations in Israel's Kebara Cave (Mount Carmel) have unearthed Neanderthal skeletons as recent as 60,000 years old, indicating that there was both geographic and temporal overlap of these two hominids. This likely accounts for the presence of Neanderthal DNA in people living outside of Africa.

Some members bearing mutations specific to haplogroup N formed many groups of their own which went on to populate much of the rest of the globe. These descendants are found throughout Asia, Europe, India, and the Americas. However, because almost all of the mitochondrial lineages found in the Near East and Europe

the Americas. However, because almost all of the mitochondrial lineages found in the Near East and Europe descend from N, it is considered a western Eurasian haplogroup.

After several thousand years in the Near East, members of your group began moving into unexplored nearby territories, following large herds of migrating game across vast plains. These groups broke into several directions and made their way into territories surrounding the Near East.

Today, haplogroup N individuals who headed west are prevalent in Turkey and the eastern Mediterranean, they are found further east in parts of Central Asia and the Indus Valley of Pakistan and India. And members of your haplogroup who headed north out of the Levant across the Caucasus Mountains have remained in southeastern Europe and the Balkans. Importantly, descendants of these people eventually went on to populate the rest of Europe, and today comprise the most frequent mitochondrial lineages found there.

Point of Interest

This line and its sister lineage are the only two founding lineages to expand out of Africa.

Notable People

Ann Curry of the Today Show belongs to this lineage.

Photos From This Region

Azerbaijan and the lands between the Caspian and Black Seas were partially populated by Levant hunters who headed north with game, later crossing the Caucasus Mountains to the Balkans.



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Branch: R

Age: About 55,000 Years Ago

Location of Origin: West Asia

Photograph by Chris Willson, Alamy

After several thousand years in the Near East, individuals belonging to a new group called haplogroup R began to move out and explore the surrounding areas. Some moved south, migrating back into northern Africa. Others went west across Anatolia (present-day Turkey) and north across the Caucasus Mountains of Georgia and southern Russia. Still others headed east into the Middle East, and on to Central Asia. All of these individuals had one thing in common: they shared a female ancestor from the N clan, a recent descendant of the migration out of Africa.

The story of haplogroup R is complicated, however, because these individuals can be found almost everywhere, and because their origin is quite ancient. In fact, the ancestor of haplogroup R lived relatively soon after humans moved out of Africa during the second wave, and her descendants undertook many of the same migrations as her own group, N.

Because the two groups lived side by side for thousands of years, it is likely that the migrations radiating out from the Near East comprised individuals from both of these groups. They simply moved together, bringing their N and R lineages to the same places around the same times. The tapestry of genetic lines became quickly entangled, and geneticists are currently working to unravel the different stories of haplogroups N and R, since they are found in many of the same far-reaching places.

Point of Interest

Descendants of this line dominate the European maternal landscape, making up 75 to 95 percent of the lineages there.

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Point of Interest

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Photos From This Region

Many people in Turkmenistan are descended from a 64,000 year-old Asian woman at the root of this branch. Some of her descendents left their West Asian homeland to settle in Central Asia.

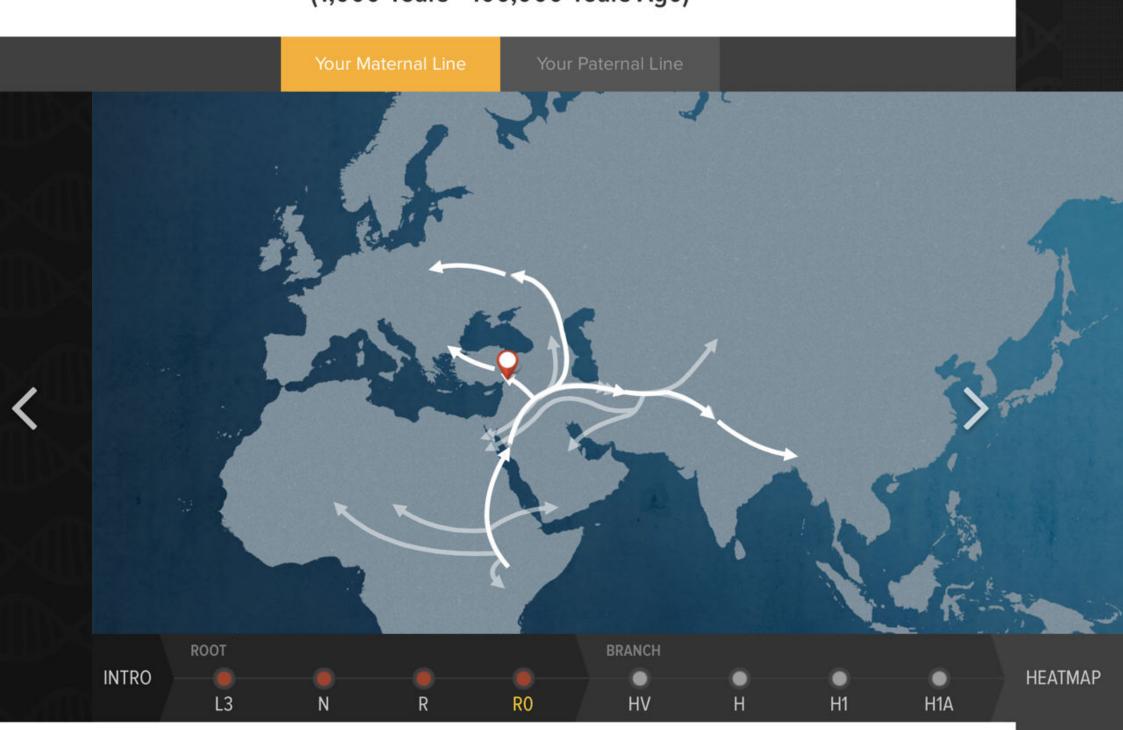
Photograph by Marcia Chambers,



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Your Deep Ancestry





Branch: R0

Age: About 41,000 Years Ago

Location of Origin: West Asia

Photograph by Peter Essick, Aurora / Getty Images

Some individuals moved across West Asia into Central Asia and then the Indus Valley. Others moved south, heading back into the African homeland from where their ancestors had recently departed.

Later, members of this lineage moved north across the Caucasus Mountains and west across Anatolia into Europe. These were Cro-Magnon. Their arrival in Europe heralded the end of the era of the Neanderthals.

Today, members of this lineage are present around the Red Sea and widely throughout the region. While this genetic lineage is common in Ethiopia and Somalia, individuals from this group are present at highest frequency in Arabia. Those living in East Africa are the likely result of more recent migrations back into the continent.

Photos From This Region

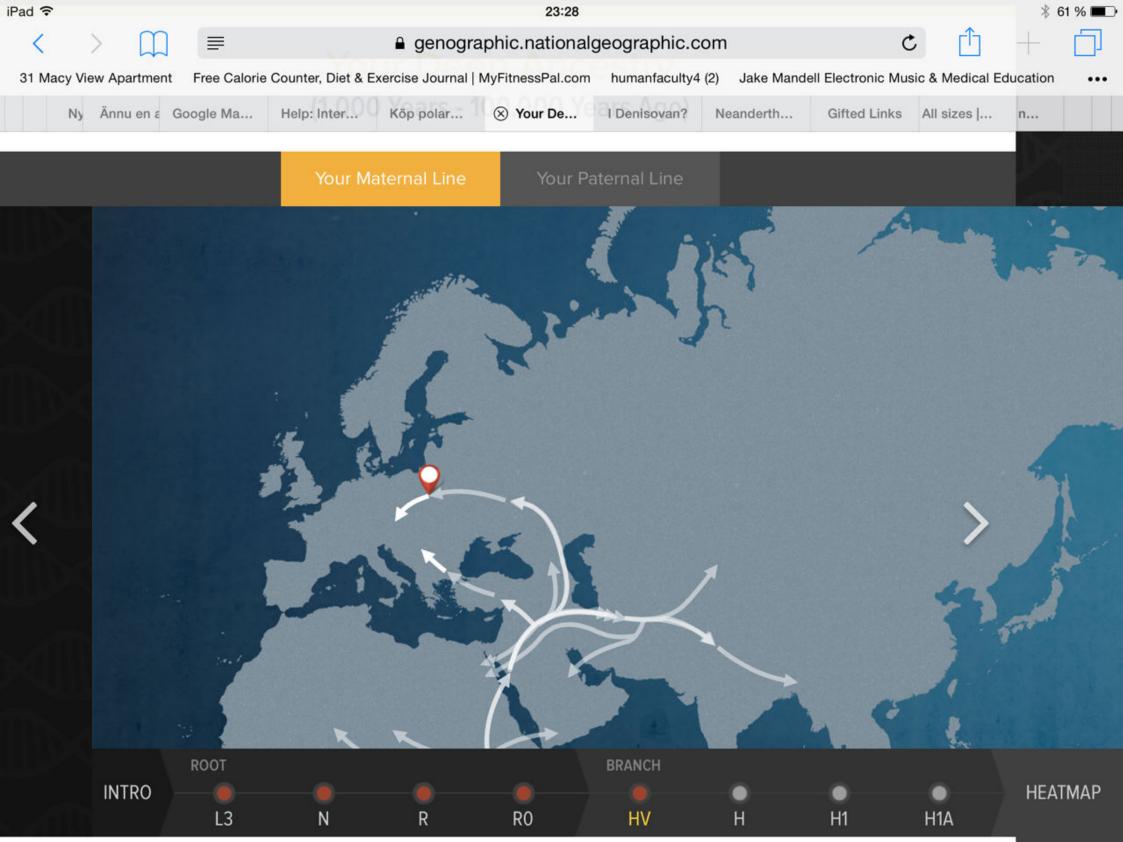
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A Saudi woman shows off her henna decorations. Haplogroup R0 is found at highest frequency in Arabia.

Photograph by Jodi Cobb, National Geographic









Branch: HV

Age: 22,350 ± 7,745 Years Ago

Location of Origin: West Asia

Photograph by Nikolay Titov, Getty Images

Descending from haplogroup R were a group of individuals who formed a western Eurasian lineage. The descendants of pre-HV live in high frequencies in the Anatolian-Caucasus region and Iran. While members of this group can also be found in the Indus Valley near the Pakistan-India border, their presence is considered the result of a subsequent migration eastward of individuals out of the Near East.

Individuals in haplogroup pre-HV can be found all around the Red Sea and widely throughout the Near East. While this genetic lineage is common in Ethiopia and Somalia, individuals from this group are found at highest frequency in Arabia. Because of their close genetic and geographic proximity to other western Eurasian clusters, members of this group living in eastern Africa are the likely result of more recent migrations back into the continent.

As we have seen from haplogroups N and R, descendants from these western Eurasian lineages used the Near East as a home **base** of sorts, radiating from that region to populate much of the rest of the world. Their descendants comprise all of the western Eurasian genetic lineages, and about half of the eastern Eurasian **mtDNA gene** pool. Some individuals moved across the Middle East into Central Asia and the Hindus Valley near western India. Some moved south, heading back into the African homeland from where their ancestors had recently departed.

Haplogroup pre-HV is of particular importance because over the course of several thousand years, its descendants split off and formed their own group, called HV. This group—thanks in large part to a brutal cold spell that was about to set in—gave rise to the two most prevalent female lineages found in Western Europe.

While some descendants of these ancestral lineages moved out across Central Asia, the Indus Valley, and even back into Africa, your ancestors remained in the Near East. Descending from haplogroup pre-HV, they formed a new group, characterized by a unique set of mutations, called haplogroup HV.

While some descendants of these ancestral lineages moved out across Central Asia, the Indus Valley, and even back into Africa, your ancestors remained in the Near East. Descending from haplogroup pre-HV, they formed a new group, characterized by a unique set of mutations, called haplogroup HV.

Haplogroup HV is a west Eurasian haplogroup found throughout the Near East, including Anatolia (present-day Turkey) and the Caucasus Mountains of southern Russia and the republic of Georgia. It is also found in parts of East Africa, particularly in Ethiopia, where its presence there indicates recent Near Eastern gene flow, likely the result of the Arab slave trade over the last two millennia.

Much earlier, around 30,000 years ago, some members of HV moved north across the Caucasus Mountains and west across Anatolia, their lineages being carried into Europe for the first time by the Cro-Magnon. Their arrival in Europe heralded the end of the era of the Neanderthals, a hominid species that inhabited Europe and parts of western Asia from about 230,000 to 29,000 years ago. Better communication skills, weapons, and resourcefulness probably enabled them to outcompete Neanderthals for scarce resources. Importantly, some descendants of HV had already broken off and formed their own group, haplogroup H, and continued the push into Western Europe.

Today, members of this line are part of the populations of Europe, West Asia (including Anatolia), and the Caucasus Mountains of South Russia and the Republic of Georgia.

This lineage accounts for around 21 percent of maternal lineages in Armenia. It is about 8 percent of those in Turkey and about 5 percent of those in Croatia. Across much of Europe, this line is present at low frequencies of around 1 percent. This lineage accounts for about 7 percent of the population of both India in South Asia and the United Arab Emirates in West Asia.

Point of Interest

Some descendant branches that are now part of the populations of East Africa were introduced by the Arab slave trade of the last two millennia.

Photos From This Region

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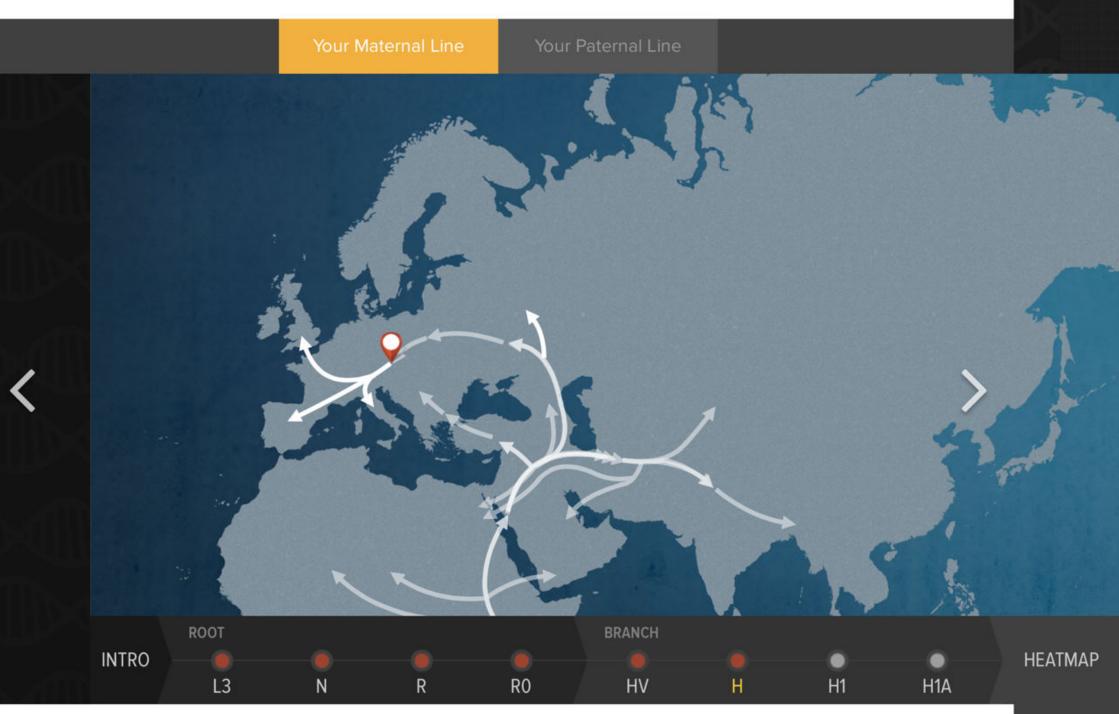
Some descendant branches that are now part of the populations of East Africa were introduced by the Arab slave trade of the last two millennia.

Photos From This Region

India is home to many descendents of the West Asian woman who founded this haplogroup some 25,000 years ago. Her genes still occur here at a frequency of about 7 percent.

Photograph by Petra Chriastelova, My

/





Branch: H

Age: About 28,000 Years Ago

Location of Origin: West Asia

Photograph by Marion Bull, Alamy

This wave of migration into western Europe marked the appearance and spread of what archaeologists call the Aurignacian culture, a culture distinguished by significant innovations in methods of manufacturing tools, standardization of tools, and use of a broader set of tool types, such as end-scrapers for preparing animal skins and tools for woodworking.

Around 15,000 to 20,000 years ago, colder temperatures and a drier global climate locked much of the world's fresh water at the polar ice caps, making living conditions near impossible for much of the northern hemisphere. Early Europeans retreated to the warmer climates of the Iberian Peninsula, Italy, and the Balkans, where they waited out the cold spell. Their population sizes were drastically reduced, and much of the genetic diversity that had previously existed in Europe was lost.

Beginning about 15,000 years ago—after the ice sheets had begun their retreat—humans moved north again and recolonized western Europe. By far the most frequent mitochondrial lineage carried by these expanding groups was haplogroup H. Because of the population growth that quickly followed this expansion, your haplogroup now dominates the European female landscape.

Today haplogroup H comprises 40 to 60 percent of the gene pool of most European populations. In Rome and Athens, for example, the frequency of H is around 40 percent of the entire population, and it exhibits similar frequencies throughout western Europe. Moving eastward the frequencies of H gradually decreases, clearly illustrating the migratory path these settlers followed as they left the Iberian Peninsula after the ice sheets had receded. Haplogroup H is found at around 25 percent in Turkey and around 20 percent in the Caucasus Mountains.

While haplogroup H is considered the Western European lineage due to its high frequency there, it is also

While haplogroup H is considered the Western European lineage due to its high frequency there, it is also found much further east. Today it comprises around 20 percent of southwest Asian lineages, about 15 percent of people living in Central Asia, and around five percent in northern Asia.

Importantly, the age of haplogroup H lineages differs quite substantially between those seen in the West compared with those found in the East. In Europe its age is estimated at 10,000 to 15,000 years old, and while H made it into Europe substantially earlier (30,000 years ago), reduced population sizes resulting from the glacial maximum significantly reduced its diversity there, and thus its estimated age. In Central and East Asia, however, its age is estimated at around 30,000 years old, meaning your lineage made it into those areas during some of the earlier migrations out of the Near East.

Haplogroup H is a great example of the effect that population dynamics such as bottleneck events, founder effect, genetic drift, and rapid population growth, have on the genetic diversity of resulting populations.

Later migrations, such as those during the Neolithic Revolution and those triggered by the Bronze Age, brought additional groups containing different descendant branches of this line to Europe.

Point of Interest

The highest percentage of this line in Europe is in Ireland, where it makes up 61 percent of the population.

Notable People

French queen Marie Antoinette and Renaissance astronomer Nicholas Copernicus were members of this lineage.

Photos From This Region

Though lush today France and much of Europe fell into a deep freeze that peaked 22,000 years ago.



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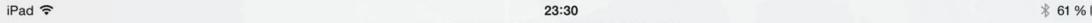
Though lush today France and much of Europe fell into a deep freeze that peaked 22,000 years ago. Haplogroup H survivors recolonized the continent

Photograph by Kathryn Massey, My Shot

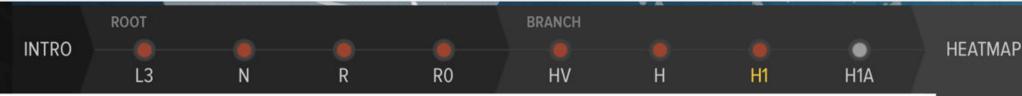
when temperatures rose.



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■ genographic.nationalgeographic.com



Branch: H1

Age: 9,900 ± 800 Years Ago

Location of Origin: West Asia

From West Asia, this line spread north into Europe and west into West Africa. Descendants of some of those who traveled to Europe expanded out of a southern Europe refugia after the last glacial maximum to recolonize the continent.

Today, this line makes up about 10 percent of maternal lineages in Denmark and around 8 percent of maternal lineages in Norway and Sweden. It accounts for around 9 percent of maternal lineages throughout the British Isles and is 12 percent of maternal lineages in Northern Ireland. It is around 8 percent of the population in Portugal. It is between 4 and 5 percent of maternal lineages in Croatia. It is about 5 percent of the Armenian population and about 6 percent of the Lebanese population.

Note: This branch is not accompanied by a major movement on the map, and research on this branch is continuing.

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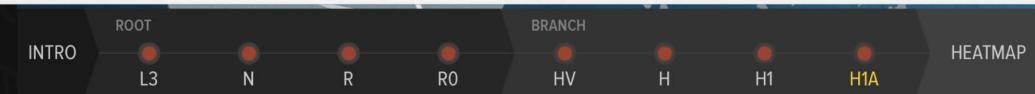
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Branch: H1a

Age: To Be Determined

Location of Origin: Europe

From Eastern Europe, members of this lineage traveled to Scandinavia, and it is most common there. Other branches spread across Europe.

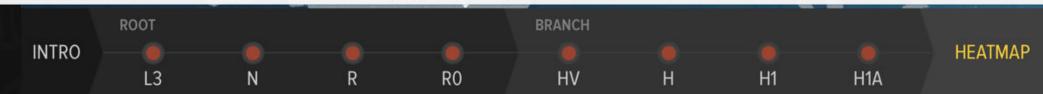
Today, this line and its subtypes are 4 percent of the population of Finland, 6 percent of the population of Sweden, and 3 percent of the population of Denmark. It is also present at trace frequencies of around 1 percent in Norway. Elsewhere in Europe, it is between 1 and 2 percent of maternal lineages. It is a striking 5 percent of the population of Austria and comprises 3 percent of the population of Greece.

Note: This branch is not accompanied by a major movement on the map, and research on this branch is continuing.

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Heatmap for H1a

This next step in your journey is a map showing the frequency of your haplogroup (or the closest haplogroup in your path that we have frequency information for) in indigenous populations from around the world, providing a more detailed look at where your more recent ancestors settled in their migratory journey. What do we mean by recent? It's difficult to say, as it could vary from a few hundred years ago to a few thousand years ago depending on how much scientists currently know about your particular haplogroup. As we test more individuals and receive more information worldwide, this information will grow and change.

The colors on the map represent the percentage frequency of your haplogroup in populations from different geographic regions—red indicates high concentrations and light yellow and grey indicate low concentrations. The geographic region with the highest frequency isn't necessarily the place where the haplogroup originated, although this is sometimes the case.

The map for H1a shows that it is most common in Scandinavia and Russia, particularly in the Finns and Saami (Lapp) people.

Does this mean you're related to people in the areas highlighted on your map? Distantly, yes! We are all connected through our ancient ancestry. In order for us to learn more ancestry information about where haplogroups settled in more recent times, please choose to contribute your results to science (check the checkbox during Login or from the Account Settings tab of your Profile), and fill out your ancestry information in the Profile section of the site. Also be sure to tell your own story in the Our Story section.

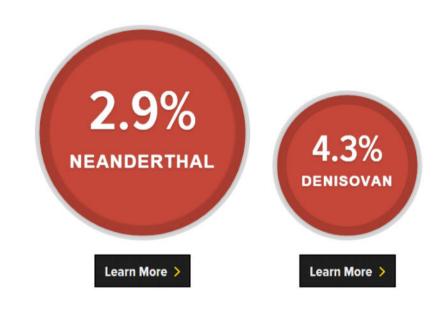
Your Hominin Ancestry

(60,000 Years Ago and Older)

Your Hominin Ancestry

When our ancestors first migrated out of Africa around 60,000 years ago, they were not alone. At that time, at least two other species of hominin—our cousins—walked the Eurasian landmass: Neanderthals and Denisovans. As our modern human ancestors migrated through Eurasia, they encountered these hominin cousins and interbred, resulting in a small amount of Neanderthal and Denisovan DNA being introduced into the modern human gene pool.

Most non-Africans are about 2 percent Neanderthal and slightly less than 2 percent Denisovan. Both percentages are calculated using a sophisticated analytical method that looks at parts of your DNA that you share with these hominin populations. The science around this calculation is very new. Thanks to participation from citizens like you, we continue to learn more and refine this method. For this reason, your result may change slightly over time as our accuracy and understanding improves.



Why Am I Neanderthal?

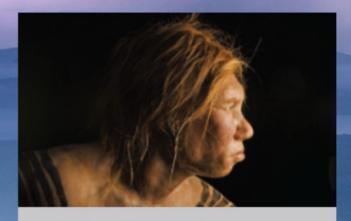
When our ancestors first migrated out of Africa around 60,000 years ago, they were not alone. At that time, at least two other species of hominid cousins walked the Eurasian landmass—Neanderthals and Denisovans. As our modern human ancestors migrated through Eurasia, they encountered the Neanderthals and interbred. Because of this, a small amount of Neanderthal DNA was introduced into the modern human gene pool.

Everyone living outside of Africa today has a small amount of Neanderthal in them, carried as a living relic of these ancient encounters. A team of scientists comparing the full genomes of the two species concluded that most Europeans and Asians have between 1 to 4 percent Neanderthal DNA. Indigenous sub-Saharan Africans have no Neanderthal DNA because their ancestors did not migrate through Eurasia.

On one level, it's not surprising that modern humans were able to interbreed with their close cousins. According to one theory, Neanderthals, Denisovans, and modern humans are all descended from the ancient human *Homo heidelbergensis*. Between 300,000 to 400,000 years ago, an ancestral group of *H. heidelbergensis* left Africa and then split shortly after. One branch ventured northwestward into West Asia and Europe and became the Neanderthals. The other branch moved east, becoming Denisovans. By 130,000 years ago *H. heidelbergensis* in Africa had become *Homo sapiens*. Our modern human ancestors did not begin their own exodus from Africa until about 60,000 years ago, when they expanded into Eurasia and encountered their ancient cousins.



The revelation that our ancient ancestors mated with one another could help explain one of the great mysteries in anthropology: Why did the Neanderthals disappear? After first venturing out of Africa, Neanderthals thrived in Europe for several hundred thousand years. But they mysteriously died out about 30,000 years ago, roughly around the same

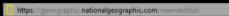


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Some scientists have suggested modern humans outcompeted or outright killed the Neanderthals. But the new

genetic evidence provides support for another theory: Perhaps our ancestors made love, not war, with their European cousins, and the Neanderthal lineage disappeared because it was absorbed into the much larger human population.



Hominin Ancestry Explained

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Why Am I Denisovan?

Discover These Ancestors >

Genographic Project / Why Am I Denisovan?

Why Am I Denisovan?

When our ancestors first migrated out of Africa around 60,000 years ago, they were not alone. At least two of our hominid cousins had made the same journey—Neanderthals and Denisovans. Neanderthals, the better known of the two species, left Africa about 300,000 years ago and settled in Europe and parts of western Asia. The Denisovans are a much more recent addition to the human family tree. In 2008, paleoanthropologists digging in a cave in southern Siberia unearthed a 40,000-year-old adult tooth and an exquisitely preserved fossilized pinkie bone that had belonged to a young girl who was between five and seven years old when she died.



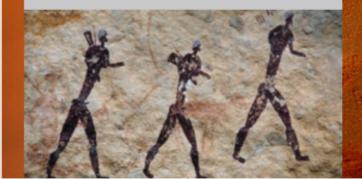
Recently, scientists successfully extracted nuclear DNA from the pinkie bone and conducted comparison studies with the genomes of modern humans and Neanderthals. Studies show the girl was closely related to Neanderthals, yet distinct enough to merit classification as a new species of archaic humans, which scientists named "Denisovan" after the cave where the pinkie bone was found. The Denisovan genome also suggests the young girl had brown hair, eyes, and skin.

Surprisingly, the scientists found genetic overlap between the Denisovan genome and that of some present-day east Asians, and, in particular, a group of Pacific Islanders living in Papua New Guinea, known as the Melanesians. It appears the Denisovans contributed between 3 to 5 percent of their genetic material to the genomes of Melanesians. Scientists think that the most likely explanation is that Denisovans living in eastern Eurasia interbred with the modern human ancestors of



Hominin Ancestry Explained

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they brought their Denisovan DNA over with them.

If this genetic mixing did occur, the fact that Denisovans were discovered in Siberia but contributed to the genomes of modern humans living in Southeast Asia suggests the species ranged widely across Asia, although their low genetic diversity also indicates their numbers were never very high.

According to one theory, Neanderthals, Denisovans, and modern humans are all descended from the ancient human *Homo heidelbergensis*. Between 300,000 to 400,000 years ago, an ancestral group of *H. heidelbergensis* left Africa and then split shortly after. One branch ventured northwestward into West Asia and Europe and became the Neanderthals. The other branch moved east, becoming Denisovans. By 130,000 years ago, *H. heidelbergensis* in Africa had become *Homo sapiens*—our ancestors—who did not begin their own exodus from Africa until about 60,000 years ago.

By comparing the genomes of apes, Denisovans, Neanderthals, and modern humans, scientists hope to identify DNA segments unique to the different groups. Early results already suggest modern humans underwent genetic changes involved with brain function and nervous system development, including ones involved in language development, after splitting from Neanderthals and Denisovans. Identifying and understanding these genetic tweaks could help explain why our species survived and thrived while our close relatives died out.

Photographs courtesy Max Planck Institute (Denisovan tooth and Siberian cave)



Why Am I Neanderthal?

Read About Our Neanderthal Connection >

>





Based on their different destinations, humans migrating out of Africa developed regional affiliations over time. These affiliations are present as patterns of DNA and are visible in the variety of physical traits humans possess. Scientists have identified typical individuals, genetically speaking, from different parts of the globe and defined them as "reference populations." Genographic participants are assigned to the reference population they most resemble genetically. The significant mixing of peoples over time, however, means that a reference population may only provide a rough estimate of an individual's ancestral diversity.

markers.

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The Keys To Discovery

Part 2: Dr Spencer Wells explains how genetic markers can be used to build a family tree for everyone alive today.

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rour Regional Ancestry

(5,000 Years - 10,000 Years Ago)

We are all more than the sum of our parts, but the results below offer some of the most dramatic and fascinating information in your Geno 2.0 test. In this section, we display your affiliations with a set of nine world regions. This information is determined from your entire **genome** so we're able to see both parents' information, going back six generations. Your percentages reflect both recent influences and ancient genetic patterns in your **DNA** due to migrations as groups from different regions mixed over thousands of years. Your ancestors also mixed with ancient, now extinct hominid cousins like Neanderthals in Europe and the Middle East or the Denisovans in Asia. If you have a very mixed background, the pattern can get complicated quickly! Use the reference population matches below to help understand your particular result.



Your Results

Northern European Mediterranean Southwest Asian
48% 31% 17%



Northern European

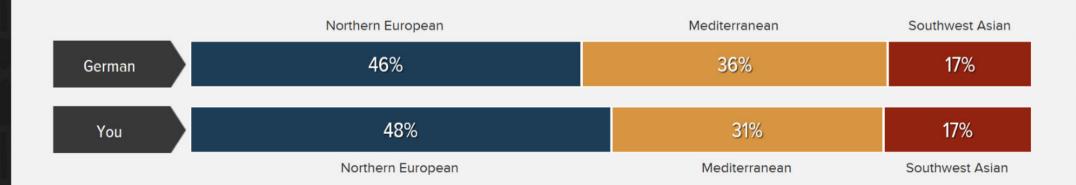
This component of your ancestry is found at highest frequency in northern European populations—people from the UK, Denmark, Finland, Russia and Germany in our reference populations. While not limited to these groups, it is found at lower frequencies throughout the rest of Europe. This component is likely the signal of the earliest hunter-gatherer inhabitants of Europe, who were the last to make the transition to agriculture as it moved in from the Middle East during the Neolithic period around 8,000 years ago.

2 What Your Results Mean

Modern day indigenous populations around the world carry particular blends of these regions. We compared your DNA results to the reference populations we currently have in our database and estimated which of these were most similar to you in terms of the genetic markers you carry. This doesn't necessarily mean that you belong to these groups or are directly from these regions, but that these groups were a similar genetic match and can be used as a guide to help determine why you have a certain result. Remember, this is a mixture of both recent (past six generations) and ancient patterns established over thousands of years, so you may see surprising regional percentages. Read each of the population descriptions below to better interpret your particular result.

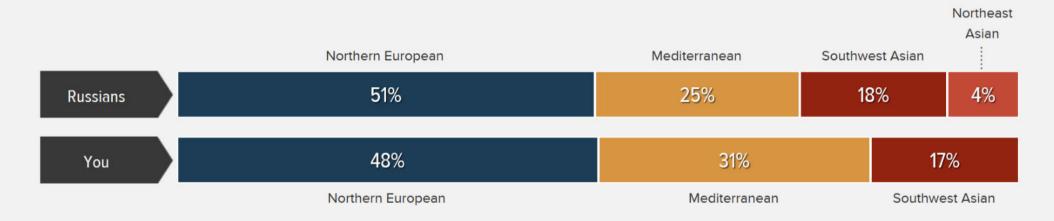
Your First Reference Population: German

This reference population is based on samples collected from people native to Germany. The dominant 46% Northern European component likely reflects the earliest settlers in Europe, hunter-gatherers who arrived there more than 35,000 years ago. The 36% Mediterranean and 17% Southwest Asian percentages probably arrived later, with the spread of agriculture from the Fertile Crescent in the Middle East over the past 10,000 years. As these early farmers moved into Europe, they spread their genetic patterns as well. Today, northern and central European populations retain links to both the earliest Europeans and these later migrants from the Middle East.



Your Second Reference Population: Russians

This reference population is based on samples collected from Russians living in Russia. The dominant 51% Northern European component likely reflects the earliest settlers in Europe, hunter-gatherers who arrived there more than 35,000 years ago. The 25% Mediterranean and 18% Southwest Asian percentages arrived later, with the spread of agriculture from the Fertile Crescent in the Middle East over the past 10,000 years. As these early farmers moved into Europe, they spread their genetic patterns as well. Today, northern European populations retain the links to both the earliest Europeans and these later migrants from the Middle East. The 4% Northeast Asian component reflects mixing with native Siberian populations, including the reindeer-herding Saami people of far northern Russia and Scandinavia.



More Information:

- How Do You Compare? See an overview of all reference Case Studies: Dr. Spencer Wells discusses example populations.
- Helping Understand Your Results: Learn more about this Region Descriptions: Read background on all nine regions. analysis and the science behind how it was conducted.
- participant results.

Asian components in Egypt are representative of that ancient migratory route, as well as later migrations from the Fertile Crescent in the Middle East with the spread of agriculture over the past 10,000 years, and migrations in the 7th century with the spread of Islam from the Arabian peninsula. The 14% sub-Saharan African indicates intermixing with African populations to the south.

FINNISH



This reference population is based on samples collected from people native to Finland. The dominant 57% northern European component likely reflects the earliest settlers in Europe, hunter-gatherers who arrived there more than 35,000 years ago. The 17% Mediterranean and 17% Southwest Asian percentages arrived later, with the spread of agriculture from the Fertile Crescent in the Middle East, over the past 10,000 years. As these early farmers moved into Europe, they spread their genetic patterns as well. Today, northern European populations retain the links to both earliest Europeans and these later migrants from the Middle East. The 7% Northeast Asian component reflects mixing with native Siberian populations, particularly the reindeer-herding Saami people of far northern Scandinavia.

GEORGIAN

