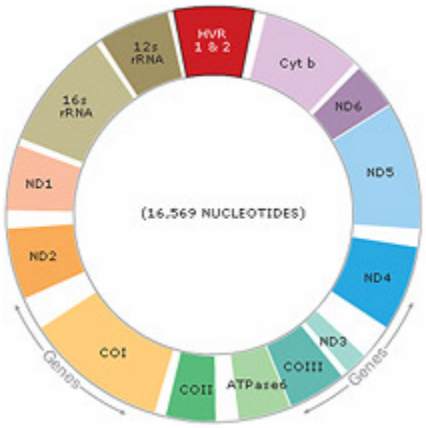
Sherwood: Where Do We Come From ?

In the modern era, dominate active Sherwood members, *Sherwoodus robustus*, originated from the Baltimore and Washington DC metropolitan areas with trace migrations from all points of the compass. In the past half century, many of these seasonal immigrants established permanent residency within the forest and are now considered indigenous to Anne Arundel County although most of disavow this classification.

All Sherwoodites originated from a common mother who lived approximately 150,000 years ago in what is now modern day Ethopia, her name was Daughter of Eve, a.k.a. Mitrochrondrial Eve. The typical dominate Sherwood female migrational track differs somewhat from the typical dominate Sherwood male. Both tracks are summarily discussed below.

Dominate Sherwood Female
Homo sapien (Sherwoodus Robustus)
Type: mtDNA
Haplogroup: U



Initial DNA Sequence With Sherwoodus Robustus Identifier Highlighted:

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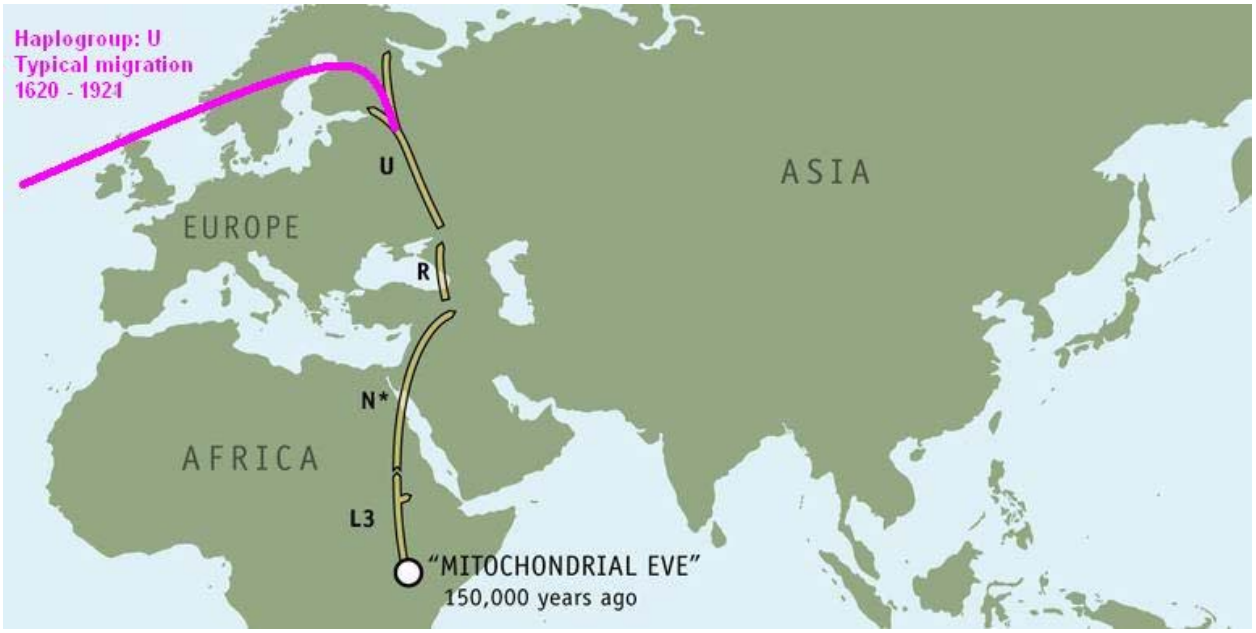


The typical *Sherwoodus robustus* female (mtDNA) results identifies members within haplogroup *U*. This haplogroup is the final destination of a genetic journey that began some 150,000 years ago with an ancient mtDNA haplogroup called *L3*. Haplogroup *L3* occurs only in Africa, but on that continent its derivatives are found nearly everywhere. *L3's* subclades are most prevalent in East Africa. This ancient lineage reflects an early divergence from humanity's common genetic coalescence point. "Mitochondrial Eve," the common ancestor of all living Sherwood members, was born in Africa some 150,000 years ago. All existing MtDNA diversity began with Eve and it remains greatest, and subsequently oldest, in Africa.

MtDNA and the Y (male) chromosome are independent parts of our genetic makeup and each tells a different tale of successive genetic mutations over the eons. That is why their approximate coalescence points are different. Yet while the dates vary , both paths point emphatically to a surprisingly recent African origin for all humans.

The oldest known fossil remains of an anatomically modern Sherwood member were found in Ethiopia's Omo River Valley. The skeletons, known as Omo I and Omo II, have been dated to about 195,000 years ago.

Although haplogroup *L3* does not appear outside of Africa it is an important part of the member migrations from that continent to Sherwood Forest. A single person of the *L3* lineage, the common mother of us all, gave rise to the *M* and *N* haplogroups some 80,000 years ago. All Eurasian mtDNA lineages are subsequently descended from these two groups.

The African Ice Age was characterized by drought rather than by cold. But about 50,000 years ago a period of warmer temperatures and moist climate made even parts of the arid

Sahara habitable. The climatic shift likely spurred hunter-gatherer migrations into a steppe-like Sahara—and beyond.

This "Saharan Gateway" led our Sherwood ancestors out of Africa to the Middle East. The route they took is uncertain. They may have traveled north down the Nile to the Mediterranean coast and the Sinai. Alternatively, they may have crossed what was then a land bridge connecting the Bab al Mandab to Arabia, after which they either skirted the then-lush, verdant eastern coast of the Red Sea or headed east along the Gulf of Aden towards the Arabian Sea.

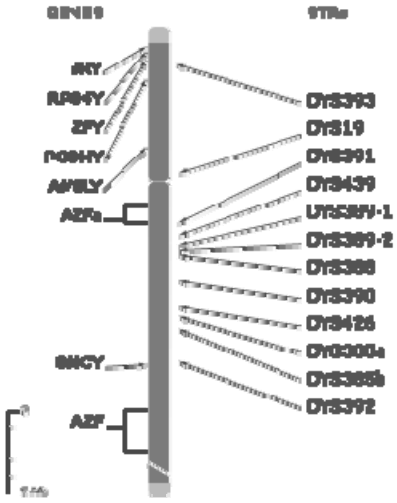
When the climate again turned arid, expanding Saharan sands slammed the Saharan Gateway shut. The desert was at its driest between 20,000 and 40,000 years ago, and during this period Middle East migrants became isolated from Africa. From their new Middle East location, however, our forebearers would go on to populate much of the world. N is a macro-haplogroup descended from the African lineage L3. This line of descent, with haplogroup M, traces the first human migrations out of Africa. The ancient members of haplogroup N spawned sublineages found across Eurasia and, eventually, the Americas.

Early members of this group lived in the eastern Mediterranean and Near East region, where they likely coexisted for a time with pre-modern hominids such as Neanderthals. Excavations in Israel's Kebara cave (Mount Carmel) have unearthed Neanderthal skeletons at least as recent as 60,000 years old. Growing cognitive abilities likely gave these Upper Paleolithic humans tremendous social advantages, evidenced by the appearance of modern thought and behavior. This "great leap forward" may have enabled our ancestors to out compete and eventually replace evolutionary dead-end lineages such as Neanderthals.

The macro-haplogroup N is composed of many subclades, which are often geographically distinct. Haplogroup R is descended from N and has since dispersed across much of the globe. The lineage, in its many subgroups, appears on all continents except Australia and Antarctica.
Subgroups preHV, U, T, and J are found in Europe and the Near East. The R5 and R6 lineages arose on the Indian subcontinent. Haplogroup U arose about 55,000 years ago (on the R line of descent) in the Near East. Today it is found in that region, and in Europe, at frequencies of almost seven percent.

Immigration from European locales during recent immigrations and centuries are to be specifically tracked by individual family genealogies and oral traditions.

Dominate Sherwood Male
Homo sapien (Sherwoodus Robustus)
Type: Y-Chromosome
Haplogroup: R1b (M343)



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TG

The typical male Sherwoodus Robustus' Y chromosome is correlated to haplogroup *R1b*, a lineage defined by a genetic marker called *M343*. This haplogroup is the final destination of a genetic journey that began some 60,000 years ago with an ancient Y chromosome marker called *M168.*

The very widely dispersed *M168* marker can be traced to a single individual his name was Son of Adam, a.k.a. "Eurasian Adam." This African man, who lived some 31,000 to 79,000 years ago, is the common ancestor of every non-African person living today. His descendants migrated out of Africa and became the only lineage to survive away from humanity's home continent.

Population growth during the Upper Paleolithic era spurred the *M168* (ancestors of modern Sherwood males) lineage to seek new hunting grounds for the plains animals crucial to their survival. A period of moist and favorable climate had expanded the ranges of such animals at this time, so these nomadic peoples may have simply followed their food source.

Improved tools and rudimentary art appeared during this same epoch, suggesting significant mental and behavioral changes. These shifts may have been spurred by a genetic mutation that gave "Eurasian Adam's" descendants a cognitive advantage over other contemporary, but now extinct, human lineages.

Some 90 to 95 percent of all non-Africans are descendants of the second great human migration out of Africa, which is defined by the marker *M89*. *M89* first appeared 45,000 years ago in Northern Africa or the Middle East. It arose on the original lineage (*M168*) of "Eurasian Adam," and defines a large inland migration of hunters who followed expanding grasslands and plentiful game to the Middle East.

Many people of this lineage remained in the Middle East, but others continued their movement and followed the grasslands through Iran to the vast steppes of Central Asia. Herds of buffalo, antelope, woolly mammoths, and other game probably enticed them to explore new grasslands.

With much of Earth's water frozen in massive ice sheets, the era's vast steppes stretched from eastern France to Korea. The grassland hunters of the *M89* lineage traveled both east and west along this steppe "superhighway" and eventually peopled much of the continent. A group of *M89* descendants moved north from the Middle East to Anatolia and the Balkans, trading familiar grasslands for forests and high country. Though their numbers were likely small, genetic traces of their journey are still found today.

Some 40,000 years ago a man in Iran or southern Central Asia was born with a unique genetic marker known as *M9*, which marked a new lineage diverging from the *M89* group. His descendants spent the next 30,000 years populating much of the planet. Most residents of the Northern Hemisphere trace their roots to this unique individual, and carry his defining marker. Nearly all North Americans and East Asians have the *M9* marker, as do most Europeans and many Indians. The haplogroup defined by *M9*, *K*, is known as the Eurasian Clan.

This large lineage dispersed gradually. Seasoned hunters followed the herds ever eastward, along a vast belt of Eurasian steppe, until the massive mountain ranges of south central Asia blocked their path. The Hindu Kush, Tian Shan, and Himalaya, even more

formidable during the era's ice age, divided eastward migrations. These migrations through the "Pamir Knot" region would subsequently become defined by additional genetic markers.

The marker *M45* first appeared about 35,000 to 40,000 years ago in a man who became the common ancestor of most Europeans and nearly all Native Americans. This unique individual was part of the *M9* lineage, which was moving to the north of the mountainous Hindu Kush and onto the game-rich steppes of Kazakhstan, Uzbekistan, and southern Siberia. The *M45* lineage survived on these northern steppes even in the frigid Ice Age climate. While big game was plentiful, these resourceful hunters had to adapt their behavior to an increasingly hostile environment. They erected animal skin shelters and sewed weather tight clothing. They also refined the flint heads on their weapons to compensate for the scarcity of obsidian and other materials.

The intelligence that allowed this lineage to adapt and thrive in harsh conditions was critical to human survival in a region where no other hominids are known to have survived. Members of haplogroup *R* are descendents of Europe's first large-scale human settlers. The lineage is defined by Y chromosome marker *M173*, which shows a westward journey of *M45*-carrying Central Asian steppe hunters.

The descendents of *M173* arrived in Europe around 35,000 years ago and immediately began to make their own dramatic mark on the continent. Famous cave paintings, like those of Lascaux and Chauvet, signal the sudden arrival of humans with artistic skill. There are no artistic precedents or precursors to their appearance.

Soon after this lineage's arrival in Europe, the era of the Neanderthals came to a close. Genetic evidence proves that these hominids were not human ancestors but an evolutionary dead end. Smarter, more resourceful Sherwood forefathers of *M173* likely out competed Neanderthals for scarce Ice Age resources and thus heralded their demise.

The long journey of this lineage was further shaped by the preponderance of ice at this time. Sherwood ancestors were forced to southern refuges in Spain, Italy, and the Balkans. Years later, as the ice retreated, they moved north out of these isolated refuges and left an enduring, concentrated trail of the *M173* marker in their wake. Today, for example, the marker's frequency remains very high in northern France and the British Isles—where it was carried by *M173* descendents who had weathered the Ice Age in Spain.

Members of haplogroup *R1b*, defined by *M343* are the direct descendents of Europe's first modern humans—known as the Cro-Magnon people.

Recent immigration, past few centuries, from this circuitous Middle Eastern to European locales are to be specifically tracked by individual family genealogies and oral traditions

Sherwood Hereditary Glossary

Chromosome
Long strands of DNA on which genes are found. Each human cell has 46 chromosomes in 23 pairs. One member of each pair is inherited from the mother, the other from the father.

DNA (Deoxyribonucleic Acid)
The double helix-shaped molecule that holds an organism's genetic information. DNA is composed of sugars, phosphates, and four nucleotide bases: adenine, guanine, cytosine, and thymine (A, G, C, T). The bases bind together in specific pairs (see detailed entry below).

Double Helix
The shape of DNA, much like a spiral staircase or twisted ladder. The stairway's railings are composed of sugars and phosphates. Its sides contain the patterned base pairs: A, T, C, and G. When a cell divides for reproduction, the helix unwinds and splits down the middle like a zipper in order to copy itself.

Genes
Segments of DNA that are the basic functional units of heredity. Genes are determined by an ordered sequence of chemical bases found in a unique position on a specific chromosome. Their "blueprint" guides protein production, which determines how different cells in the body function. Inherited genes also control an animal's unique set of physical traits.

Genetic Marker
Random mutations in the DNA sequence which act as genetic milestones. Once markers have been identified they can be traced back in time to their origin—the most recent common ancestor of everyone who carries the marker.

Genome
The total DNA sequence that serves as an instruction manual for all proteins created in our body. Two copies of the genome are found inside each of our cells.

Haplogroup
Branches on the tree of early human migrations and genetic evolution. Haplogroups are defined by genetic mutations or "markers" found in Y chromosome and mtDNA testing. These markers link the members of a haplogroup back to the marker's first appearance in the group's most recent common ancestor. Haplogroups often have a geographic relation.

Haplotype
A person's individual footprint of all tested genetic markers. Even the difference of a single genetic marker delineates a distinct haplotype.

Heredity
The total sum of genetic information that humans pass on from generation to generation.

Mitochondria
A remnant of an ancient parasitic bacteria that now helps to produce energy inside the cell. A mitochondrion has its own genome, present in only one copy, which does not recombine in reproduction. This genetic consistency makes mitochondrial DNA a very important tool in tracking genetic histories.

Mitochondrial DNA or mtDNA
Genetic material found in the mitochondria. It is passed from females to their offspring without recombining, and thus is an important tool for geneticists.

Nucleotide
A DNA building block which contains a base, or half of a "staircase step," and sugars and phosphates which form the "railing." Nucleotides join together to form DNA's distinctive double helix shape.

Nucleus
The part of the cell in which chromosomes reside.

Phylogeny
The evolutionary development of a species. Phylogeny is sometimes represented as a tree that shows the natural relations and development of all species.

Proteins
Linear sequences of amino acids that are the building blocks of cells. Each protein has a specific function that is determined by the "blueprint" stored in DNA.

Recombination
The process by which each parent contributes half of an offspring's DNA, creating an entirely new genetic identity. This process mixes genetic signals, so that nonrecombining DNA, passed intact through the generations, is most important to population genetics.

Replication
The process by which two DNA strands separate, with each helping to duplicate a new strand. During reproduction, the DNA double helix unwinds and duplicates itself to pass on genetic information to the next generation. Because bases always form established pairs (AT and CG), the sequence of bases on each strand will attract a corresponding match of new bases. Only occasional errors occur—about one for every billion base-pair replications.

Sequencing
Determines the order of nucleotides for any particular DNA segment or gene. The order of a DNA string's base pairs determines which proteins are produced, and thus the function of a particular cell.

Single Nucleotide Polymorphism
Small, infrequent changes which help to create an individual's own unique DNA pattern. When a single nucleotide (A, T, G, or C) is altered during DNA replication, due to a tiny "spelling mistake," the genome sequence is altered.

Trait
The physical characteristics, like eye color or nose shape, which are determined by inherited genes.

X and Y Chromosomes
Chromosomes which determine sex. Females have two X chromosomes while males have one X and one Y. When chromosomes pair, the mismatched Y determines male gender. Because of the mismatch, part of the Y chromosome does not recombine with the X during reproduction. The nonrecombining part of the Y chromosome contains a sequence of DNA passed intact from males to their sons through the generations, giving population geneticists a useful tool for studying human history.