

Early (Pre-) History of the Johannesson Family Tree

The following is the National Geographic Profile of the mitochondrial genome (DNA) from Hazel Ruby (Nelson) Krause. The DNA sample was submitted to the Genographic Project during the summer of 2005. Results are recorded on the following pages. The Setterberg (Johannesson/Nelson) lineage belonged to Haplogroup U, which originated about 55,000 years ago in the Near East. Today it is found in that region, and in Europe, at frequencies of about seven percent. The mitochondrial genome is the most accurate trace for the maternal side of a family tree as it is passed unchanged from mother to daughter.

-THE-
GENOGRAPHIC
PROJECT

Certificate of mtDNA testing

In recognition of your participation in the Genographic Project, we hereby certify that

Hazel Ruby (Nelson) Krause




belongs to:

Haplogroup U

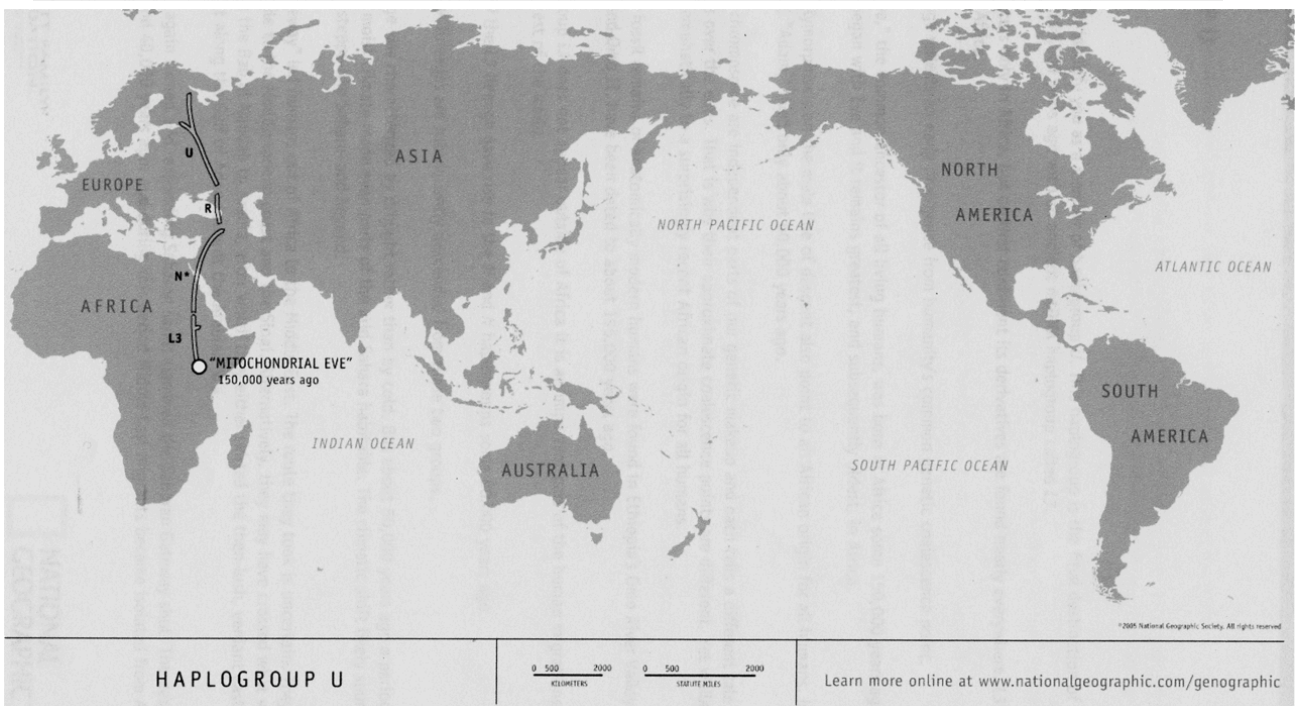
The letters designating the bases adenine, cytosine, guanine, or thymine of your mtDNA differ from Cambridge Reference Sequence (CRS) at each of the following positions:

16172C, 16183C, 16189C, 16219G, 16278T

October 13, 2005

Global field science supported by the Waitt Family Foundation A research partnership of National Geographic and IBM



HAPLOGROUP U

Your mtDNA results identify you as a member of 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 humans, 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.

Y chromosome polymorphisms on the male line of descent also point to an African origin for all humans, but our male common ancestor, "Adam," lived only about 60,000 years ago.

MtDNA and the Y 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 anatomically modern humans 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 human migrations from that continent to the rest of the world.

A single person of the *L3* lineage 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 humans 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.



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From their new Middle East location, however, they 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 Neandertals. Excavations in Israel's Kebara cave (Mount Carmel) have unearthed Neandertal 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 outcompete and eventually replace evolutionary dead-end lineages such as Neandertals.

The macro-haplogroup *N* is composed of many subclades, which are often geographically distinct.

Learning more about these subclades will add further clarity to the big picture of human genetic diversity, and is a primary goal of the Genographic Project.

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.

This lineage is divided into many subhaplogroups which reflect more limited geographic distributions. Some of these appear in North Africa and India.

Subhaplogroup *U6*, which is common in North Africa, presents an interesting possibility. It may evidence a "reverse migration" into that region from the Near East or Europe.

HAZEL R. KRAUSE

YOUR MITOCHONDRIAL HVR I SEQUENCE
16172C, 16183C, 16189C, 16219G, 16278T

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ATTCTAATTTAAACTATTCTGTTCTTTTCATGGGGAAGCAGATTTGGGTACC
ACCCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTGCTACATTACT
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CAGGGTCATAAAGCCTAAATAGCCACACGTTCCCTTAAATAAGACATCA
CGATG
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Key C Sub. (transition) C Sub. (transversion) C Insertions — Deletions

YOUR RESULTS

PARTICIPANT ID: FW358FVS6H

Type mtDNA

Haplogroup U



EXPLORE YOUR ROUTE MAP

How to Interpret Your Results

At left is displayed the sequence of your mitochondrial genome that was analyzed in the laboratory. Your sequence is compared against the Cambridge Reference Sequence (CRS), which is the standard mitochondrial sequence initially determined by researchers at Cambridge, UK. The differences between your DNA and the CRS are highlighted, and these data allow researchers to reconstruct the migratory paths of your genetic lineage. Substitution (transition): a nucleotide base

Your sequence
 CRS
 Mitochondria diagram

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ACCCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTGCTACATTAC
TGCCAGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTA
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ACTTCAGGGTCATAAAGCCTAAATAGCCACACGTTCCCTTAAATAAGAC
ATCAGATG
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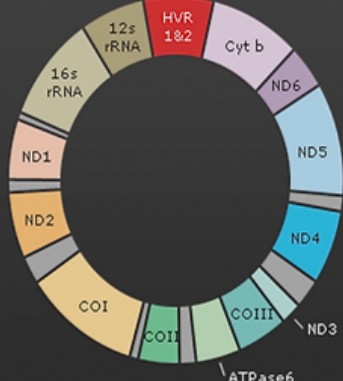


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