Collection of sample and DNA extraction

We collect a cheek swab sample from you after you have had an opportunity to read this document and discuss the nature of the test with a scientist and/or counsellor. If you are happy to proceed with the testing, it is necessary for you to sign an **INFORMED CONSENT FORM** indicating that you requested our laboratory to conduct tests to assist you in tracing your ancestry using genetic methods. The sample will be immediately assigned a laboratory code to protect your identity, and will be processed using conventional methods to extract DNA from the cheek cells.

Both chromosomal DNA found in the nucleus of the cell (contributed from both parents) and mitochondrial DNA (mtDNA) found in the cytoplasm of the cell (inherited only from the mother), make up the total genomic DNA found in every cell (Figure 1).

![Figure 1](image)

**Figure 1.** Schematic structure of a cell showing the nucleus, which harbours chromosomal or nuclear DNA inherited from both parents, and mitochondrial DNA which is inherited only from our mothers. Humans have 46 chromosomes, which consists of 22 pairs of autosomes, and one pair of sex chromosomes (males XY and females XX). The autosomes carry genetic information that determines our physical appearance and information driving biological function.
The mitochondrion is the “power-house” of the cell whose function is to produce energy that drives cellular function.

**Maternal ancestry testing (mtDNA analysis): both females and males**

Mitochondrial DNA (mtDNA) is passed on from mothers to both her sons and daughters. However, only her daughters will transmit their mtDNA in successive generations. Both males and females can be tested for mtDNA to trace their maternal ancestry. We sequence a region of about 1000 base-pairs (bp) of the mtDNA control region (also called the hypervariable region of which there are two, HVRI and HVRII). The sequence is then compared to a published reference sequence (also referred to as the Cambridge Reference Sequence, CRS) to identify the positions at which your sequence differs from the CRS. This information is used together with an internationally adopted nomenclature to identify the name of your mtDNA lineage. These lineages are also called haplogroups. Haplogroups are continent specific and subdivisions of these haplogroups have a regional geographic distribution (Figure 2).

![Figure 2. Geographic distribution of mtDNA haplogroups.](image)

**Database Matches**

After we obtain your mtDNA sequence and deduce the haplogroup, we then compare the sequence to two international databases of mtDNA sequences in individuals we have examined for our research as well as other published data collected on individuals sampled throughout the world by other researchers. This comparison allows us to find matches or close matches to your sequence; to give you information about the distribution of your mtDNA haplogroup, and the most likely region where your mtDNA profile originated.
Y chromosome analysis (only males)

Fathers pass on their Y chromosome to their sons only, who then pass on their Y chromosome to their sons, and so on. We make use of two types of markers on the non-recombining portion of the Y chromosome to resolve the Y chromosome lineages in males. The first type of marker, so-called bi-allelic variants (two states or alleles can be found at one site on the chromosome) are used to classify Y chromosomes into lineages or haplogroups. There are 13 Y chromosome haplogroups (labelled A to R) that have been defined (Figure 3). These haplogroups, or major branches of the Y chromosome tree, show specific ethnic and/or geographic distribution patterns. The second type of marker, microsatellites or short tandem repeats (STRs) consist of repetitive DNA elements that are tandemly repeated and are highly variable in humans. STRs are used to define haplotypes (like a DNA fingerprint, but on the Y chromosome) within the haplogroups.

![World Distribution of Y Chromosome Haplogroups](image)

**Figure 3.** Global distribution of Y chromosome haplogroups A-R.
Database Matches

After we deduce your Y chromosome haplogroup, we use the STR data to derive your haplotype. We then compare your haplotype to our database and with information from a global database (www.ystr.charite.de). This comparison allows us to find matches or close matches to your Y chromosome lineage; to give you information about the distribution of your Y chromosome haplogroup, and the most likely region where your Y haplotype originated.

Limitations of genetic ancestry testing

The limitation of using mtDNA and Y chromosome DNA for genealogical testing is that this DNA will trace only two genetic lines on a family tree in which branches double with each preceding generation (Figure 4). For example, Y chromosome tracing will connect a man to his father but not his mother, and it will connect him to only one of his four grandparents: his paternal grandfather. In the same way it will connect him to one of his eight great grandparents (see figure below). Continue back in this manner for 14 generations and the man will still be connected to only one ancestor in that generation. Y chromosome DNA testing will not connect him to any of the other 16,383 ancestors in that generation to whom he is also related in equal measure. The same scenario applies when using mtDNA.

Figure 4. mtDNA and Y chromosome DNA inheritance. Note, a male would inherit his mtDNA from his mother and his Y chromosome from his father. He will only pass on his Y chromosome to his sons. A female only inherits the mtDNA from her mother and will pass it on to both her male and female children. Autosomal DNA, on the other hand, is contributed equally (22 chromosomes, excluding the sex chromosomes X and Y) by both parents to the offspring. This DNA will carry information contributed from four grandparents, eight great grandparents, 16 great great grandparents, etc. (see text above).
GENETIC ANCESTRY TESTING REPORT

NAME: Sample Report

SEX: Male

MtDNA analysis

MtDNA HVRI variation: 16172T-C, 16224T-C, 16311T-C, 16519T-C

MtDNA HVRII variation: 73A-G, 263A-G, 385A-G

MtDNA haplogroup: K

MtDNA matches: When we compared your mtDNA profile with about 10,600 mtDNA haplotypes from 2 international databases, we found 1 identical match in an Orcadian individual (Metspalu et al. 2004, http://www.bioanth.cam.ac.uk/mtDNA/). A search of our database yielded 5 identical matches in 5 South African Whites.

Haplogroup information

It is possible for us to reconstruct the evolutionary history of all mtDNA lineages found in living peoples to a common ancestor, sometimes referred to in the popular press as “Mitochondrial Eve”. This ancestor lived in Africa, about 150,000 years ago. She lies at the root of all the maternal ancestries of every one of the six billion people in the world. We are all her direct maternal descendants. The various “patterns” of mtDNA sequence variation found in living people are referred to as “haplogroups” that are defined by the presence of certain changes (mutations) when compared to a published
sequence referred to as the reference sequence. These mutations are random and not associated with any disease. These haplogroups, or branches, are represented in the tree below, and your branch is indicated within the ring.

Your mtDNA profile is consistent with a European ancestry. Brian Sykes (2001) at Oxford University introduced names to personalize the mtDNA types found among people of European origin and referred to the seven common haplogroups (U, X, H, V, T, K and J) as the “Seven Daughters of Eve”. These seven women have been given the names Ursula (Latin for “she-bear”), Xenia (Greek for “hospitable”), Helena (Greek for “light”), Velda (Scandinavian for “ruler”), Tara (Gaelic for “rock”), Katrine (Greek for “pure”) and Jasmine (Persian for “flower”). The first letter of the name corresponds to the haplogroup designation. http://www.oxfordancestors.com/
Today, about six percent of native Europeans belong to the clan “Katrine”. Katrine lived in Italy about 15,000 years ago, but present-day members are found throughout Europe with frequencies of ~ 12-20% found in Belgium, Bulgaria, Georgia and Norway. Iceman is the most celebrated of this clan’s members (Sykes 2001). Haplogroup K is seen at a frequency of 23% in the South African White population.

Y chromosome analysis

Two kinds of Y chromosome data were used to resolve your Y chromosome lineage. The first involved screening for certain mutations to elucidate the Y chromosome haplogroup (groups of lineages that are identical by descent since they share a common defining mutation). The second involved the use of faster evolving DNA called short tandem repeats (STRs) that we use to further resolve the haplogroup. By screening for several of these STR markers it is possible to derive a haplotype, a combination of the patterns observed for each region on the Y chromosome tested. The haplogroups, or branches, are represented in the tree below, and your branch is indicated within the ring.
Y chromosome haplogroup:  R-M343 (R1b)

Haplogroup information:

Haplogroup R-M343 is the most common haplogroup in European populations. It is believed to have expanded throughout Europe as humans re-colonized after the last glacial maximum, 10 to 12 thousand years ago. This lineage is also the haplogroup containing the Atlantic Modal haplotype. R-M343 has a frequency of about 72% in British, 65% in the Orkney Islands (Wells et al. 2001), 70.4% in Dutch, 52.2% in French and 50% in Germans (Semino et al. 2000). In Asia, R-M343 is much less common, occurring...
sporadically in a number of populations. The frequency of R-M343 is about 65% in South African Whites.

STR profile:

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STR Matches:

We compared your Y chromosome STR profile with about 57,000 Y chromosome haplotypes from a STR database (http://www.yhrd.org). When using all ten markers, we found 117 identical matches in 69 Europeans, 25 North Americans and 23 Latin Americans.

A search of our database using all ten markers yielded 4 identical matches to 3 South African Whites and 1 European individual.

References

Metspalu et al. (2004) BMC Genetics 5:26