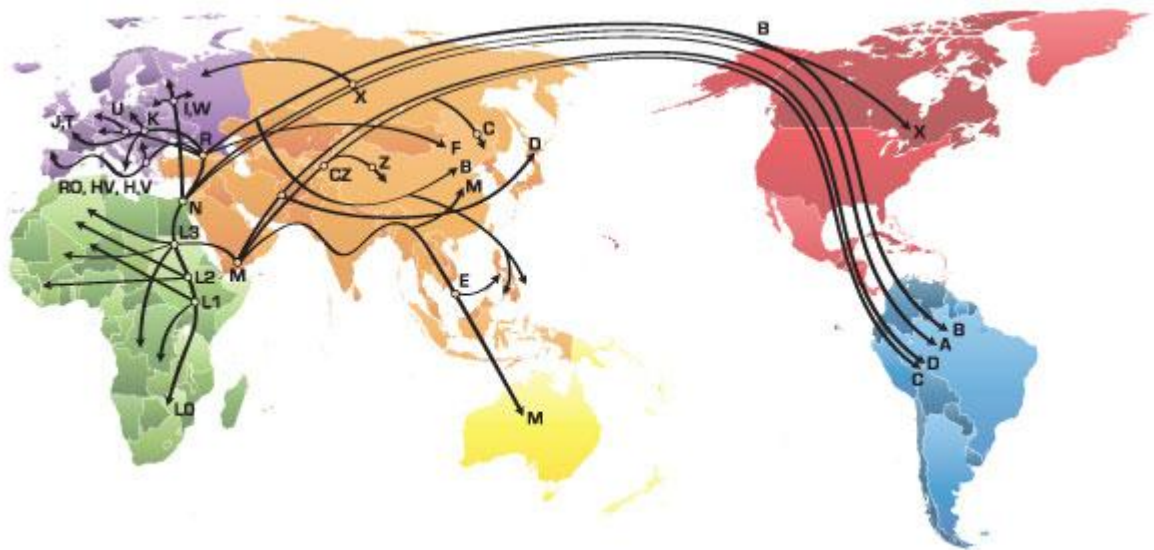


Maternal Lineage Testing- בדיקת מוצא לפי אם

Maternal Lineage (mtDNA) Testing The maternal lineage test is based on the fact that mitochondrial DNA is passed down from mother to child relatively unchanged through several generations. Our mitochondrial DNA contains markers that can be traced to our early ancestors and where they settled thousands of years ago.

Results of a maternal lineage test are expressed in terms of haplogroups—genetic groups of people who share the same set of DNA markers and can be traced to a certain geographic area that they settled at a particular point in human history.



There are three possible areas in our mtDNA that can be tested:

- **HVRI** Testing this region is usually sufficient to determine a person's haplogroup.
- **HVRII and HVRIII** Testing these two regions can provide more detail if HVSI testing is not sufficient to determine affinity to a haplogroup; it could also further refine a haplogroup into sub-groups, also called sub-clades.

Maternal Lineage (mtDNA) Biology What makes mitochondrial DNA special? Several characteristics of mitochondrial DNA distinguish it from the rest of your cells' DNA, called nuclear DNA.

Results of a maternal lineage test are expressed in terms of haplogroups—genetic groups of people who share the same set of DNA markers and can be traced to a certain geographic area that they settled at a particular point in human history.

Mitochondrial DNA is:

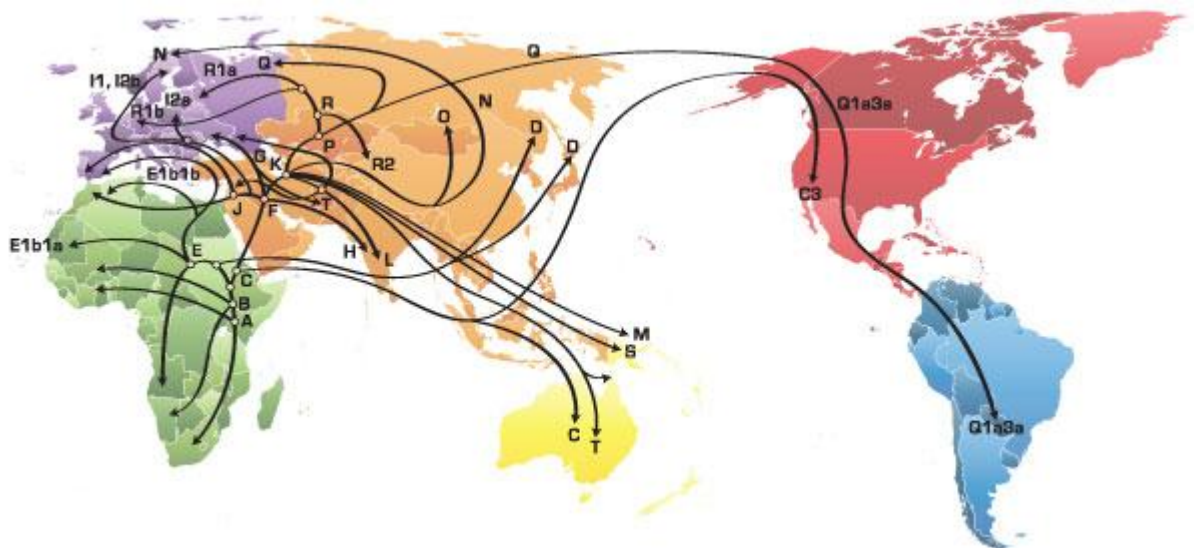
- Found in the cytoplasm, outside the nucleus.
- Only passed through the mother. During fertilization, only nuclear DNA from the sperm enters the cell; thus the father does not make any contribution to the mitochondrial DNA.
- Abundant in number. While your nuclear chromosomes are only found in 2 copies per cell, one from your mother and one from your father, mtDNA is found much more abundantly—anywhere between hundreds to thousands of copies per cell.
- Small and circular. While nuclear DNA is made up of much longer strands of DNA that are tightly coiled into chromosomes, mitochondrial DNA is found as a small, circular chromosome.

Mitochondrial DNA codes for proteins that are involved in cellular respiration. In addition, certain regions of the mtDNA are useful for ancestry research. These regions are called hypervariable regions (HVR).

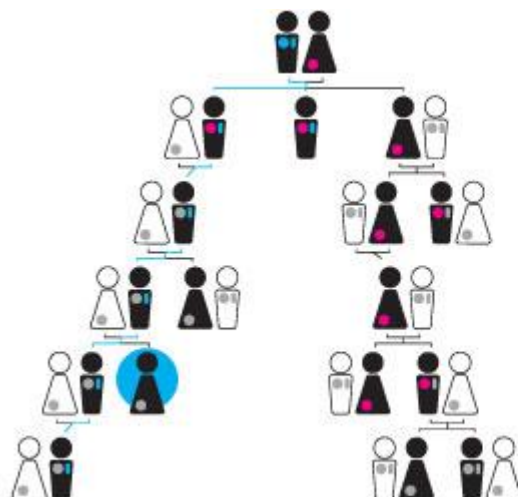
HVRs are the site where the most mutations occur in mtDNA. On average, one letter in the sequence of mtDNA changes every 1,500 years. This change is then passed on to succeeding generations. The changes in an individual's mtDNA comprise his or her haplotype—the mitochondrial DNA profile—that allows scientists to assign a person to his or her haplogroup, a group of people with similar haplotypes. The haplogroup is associated with a historical and geographical origin.

בדיקת מוצא לפי אב - Paternal Lineage Testing


Paternal Lineage (Y-STR) Testing The paternal lineage test is based on the fact that the Y chromosome is passed down from father to child relatively unchanged through several generations. Special sections on the Y chromosome, called short tandem repeats (STRs), are examined to determine a person's Y haplogroup—revealing the geographic origins of his ancestors as evidenced by common DNA markers.



Only males have the Y chromosome, but if a female wants to find out about her paternal ancestry, she can ask her brother, father, or other relative along the same paternal line to take the test.



Any of the men with a blue marker, connected by the blue line, can take a paternal lineage test for the female highlighted by the blue circle.



Ancestry by DNA- בדיקת היסטוריה משפחתית

Ancestry by DNA tests are performed to determine an individual's bio-geographic ancestry. Whether you're interested in researching your family history, or just simply want to learn more about yourself, this test can provide you with a better understanding of your genetic ancestry and provide a window into further research about your possible ancestors.

This test gives an estimated percentage of ancestry from four population groups:

- **Indigenous American.** This group is composed of people who migrated to inhabit North, South and Central America.
- **European.** This people group includes Europeans, Middle Easterners, and South Asians.
- **East Asian.** This people group includes the Japanese, Chinese, Koreans, and Pacific Islanders.
- **African.** This group includes people with roots in the Sub-Saharan region of Africa.

Please note that this test does not predict or establish a person's race; it only gives an estimate of genetic ancestry or heritage, for example:*

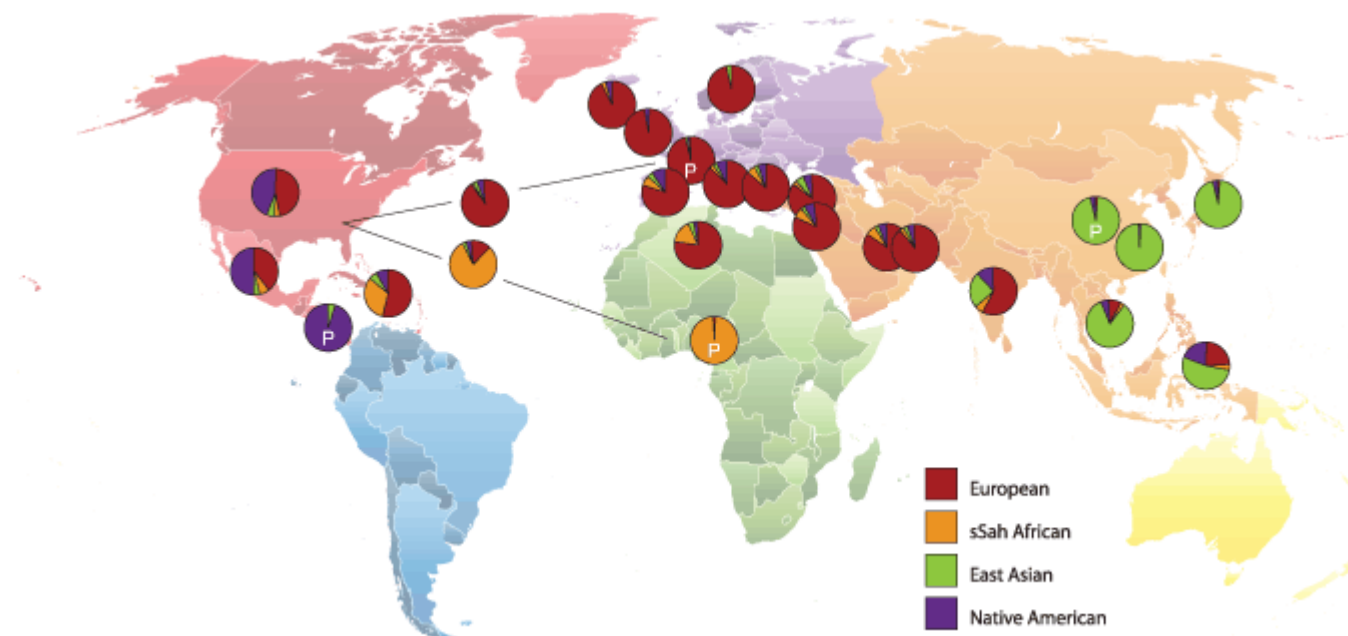
Estimate	Ancestry
87%	European
13%	Indigenous American
0%	Sub-Saharan African
0%	East Asian

What you will receive

When you order an Ancestry *by* DNA test, you will receive the following:

- An easy-to-use DNA sample collection kit containing cheek swabs and complete instructions
- Ancestry Test Certificate listing your ancestral percentage
- A detailed Ancestry *by* DNA manual that explains your results, as well as provides more information about ancestry testing and human migration history.

Average Results for Various Populations Below is an illustration and a table showing average test results for various populations around the world.



The following table lists the average population groups. **N** represents the sample size of each population.

Ethnic Group (n)	European	sSah African (s.d.)	East Asian (s.d.)	Indigenous American (s.d.)
African American (136)	14.3% (13.3%)	79.6% (14.0%)	2.8% (6.0%)	3.3% (5.1%)
North African (7)	77.4% (5.8%)	15.0% (7.3%)	5.6% (5.4%)	2% (3.4%)
Puerto Rican (64)	55.0% (20.7%)	32.6% (24.6%)	3.6% (5.4%)	8.8% (8.3%)
North Euro subset 1 (10)	97.0% (3.6%)	1.0% (2.1%)	1.9% (3.0%)	0.4% (1.4%)
Irish (17)	96.4% (4.3%)	0.7% (2.1%)	1.2% (2.7%)	1.7% (4.1%)
Icelandic (12)	93.8% (5.5%)	1.2%*** (2.2%)	0.8% (1.4%)	4.25% (5.0%)
Greek (18)	90.4% (4.0%)	4.8% (4.2%)	1.7% (5.3%)	4.7% (4.8%)
Iberians (9)	78.8% (21.0%)	6.6% (7.1%)	4.0% (7.6%)	10.7% (16.7%)
Basque (10)	93.0% (5.2%)	2.3% (3.6%)	0.8% (2.5%)	3.9% (4.1%)
Italian (12)	86.8% (8.9%)	2.3% (3.2%)	2.7% (5.5%)	7.3% (5.9%)
Turkish (40)	85.3% (5.4%)	3.2% (4.8%)	7.3% (6.7%)	5.1% (6%)
Ashkenazi Jewish(10)	86.8% (5.8%)	4.7% (3.9%)	2.0% (4.9%)	6.6% (3.6%)
Middle East vers. I (9)	88.1% (9.7%)	2.8% (5.6%)	4.8% (7.3%)	4.2% (5.1%)
Middle East vers. II (11)	82.0%	10.8% (8.9%)	4.5% (7.5%)	2.6% (6.3%)

	(11.0%)			
South Asian Indian (56)	58.9% (8.9%)	5.1% (4.7%)	26.9% (10.7%)	9.1% (8.8%)
Chinese (10)	0.7% (0.9%)	0% (0%)	98.0% (2.4%)	1.3% (2.5%)
Japanese (10)	1.1% (2.6%)	0.4% (1.8%)	95.3% (4.2%)	3.2% (4.0%)
Atayal (10)	0.5% (1.6%)	0% (0%)	97.6% (4.2%)	1.9% (4.2%)
SouthEast Asian (11)	8.0% (11.1%)	3.6% (7.3%)	82.2% (14.8%)	6.3% (6.7%)
Pacific Islander (7)	24.7% (16.0%)	3.7% (4.5%)	50.6% (21.3%)	21.0% (11.7%)
American Indian* (223)	41.9% (35.8%)	3.7% (12.4%)	6.7% (8.6%)	47.6% (33.8%)
American Indian** (170)	28.6% (27.6%)	2.2% (5.9%)	8.2% (9.2%)	61.1% (27.0%)
Mexican (60)	43.2% (19.3%)	5.6% (7.2%)	4.4% (9.3%)	46.8% (18.1%)
POPULATION COMBINATIONS				
Combined North Euro/Irish (27)	96.5%(4.0%)	0.81%(2.0%)	1.5%(2.8%)	1.2%(3.8%)
Mediterranean (Greek/Italian) (30)	89%(6.0%)	4.2%(4.4%)	2.1%(5.4%)	5.7%(5.2%)
SE European (Greek/Italian/Turks) (70)	86.9%(5.6%)	3.6%(3.8%)	6.7%(5.6%)	7.8%(5.2%)
Middle Eastern(Mid East I+II) (20)	84.8%(10.7%)	7.2%(8.7%)	4.4%(7.7%)	3.7%(5.1%)
Ashkenazi Jewish + Middle Eastern(30)	85.4%(8.9%)	6.4%(6.2%)	3.8%(6.6%)	4.4%(5.0%)
European American(207)	90.5%(10.2%)	3.0%(5.8%)	2.8%(4.9%)	3.8%(6.1%)

* includes individuals from US Government recognized tribes (Sioux, Cheyenne, Cherokee, Arapaho) as well as unrecognized tribes, without regard to "blood" percentage.

** includes individuals from US Government recognized tribes only (Sioux, Cheyenne, Cherokee, Arapaho), without regard to "blood" percentage

*** significance contributed mainly by one sample, scoring 7% AFR.

In the table above, the dark red background indicates the primary ancestry. Tan background indicates levels of non-primary admixture that is statistically significant compared to the level in the appropriate simulated parental population using Fishers Exact test. (Fishers Exact test p-values were computed in the following way: percentage p of admixture was multiplied by

the sample size (n), and this value combined with the corresponding value for $1-p$ (non group admixture) was compared against the $p*n$ and $(1-p)*n$ for the simulated parental populations. The reason p is multiplied by the sample size is to penalize low admixture estimates contributed by only a small number of samples when the sample size for a group is relatively low.)

Also, the table shows that most of the subpopulations exhibit fractional affiliations statistically different from their respective parental populations (using Fishers exact test). Of the European subpopulations, only Northern European and Irish samples show no significant affiliation; others such as Greeks, Italians, Iberians show statistically significant affiliation using the 4-population model and the basic MLE algorithm. Of the East Asians, the Chinese and Japanese are relatively unadmixed compared to the South East Asians. All Indigenous American and African populations tested in this study showed significant fractional affiliation compared to their parental group.