



**MRC/NHLS/WITS HUMAN GENOMIC  
DIVERSITY AND DISEASE  
RESEARCH UNIT (HGDDRU)**

Division of Human Genetics, National Health Laboratory Service, P O Box 1038, Johannesburg, 2000  
Room 303 James Gear Building, Corner of Hospital and DeKorte Streets, Braamfontein  
Tel: (011) 489-9237 (Laboratory) Prof Himla Soodyall: (011) 489-9208 FAX: (011) 489-9226

## **GENETIC ANCESTRY TESTING REPORT**

**NAME:** Ryan Gregory Sheard

**SEX:** Male

### **MtDNA analysis**

**MtDNA HVRI variation:** 16293A-G, 16362T-C, 16519T-C

**MtDNA HVRII variation:** 263A-G

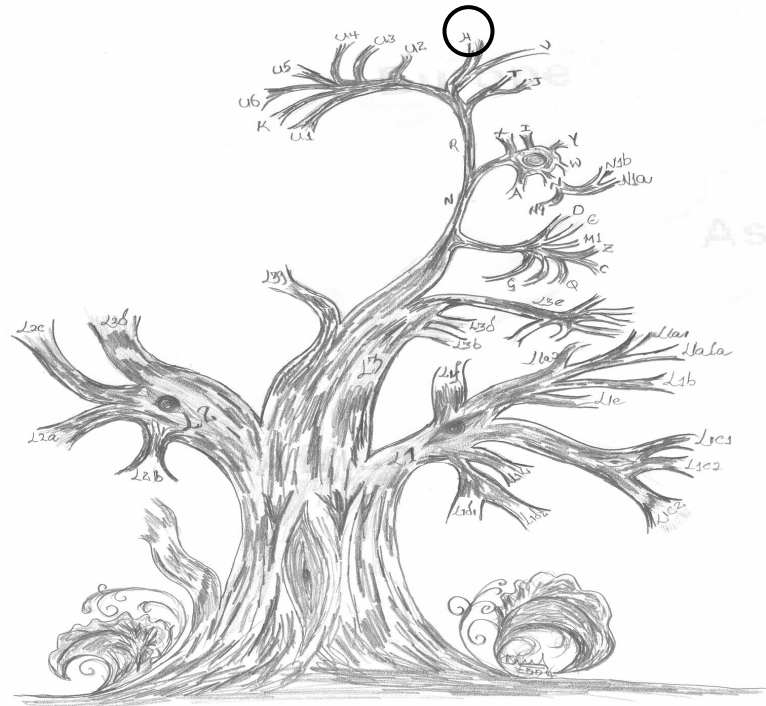
**MtDNA haplogroup:** H

**MtDNA matches:** When we compared your mtDNA profile to 2 international databases with about 10,600 mtDNA haplotypes, we found no identical matches. The closest matches differed by one position in 3 European individuals (Metspalu *et al.* 2004, <http://www.bioanth.cam.ac.uk/mtDNA/>)  
A search of our database yielded no identical matches. The closest match differed by one position in a Caucasian American individual.

### **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

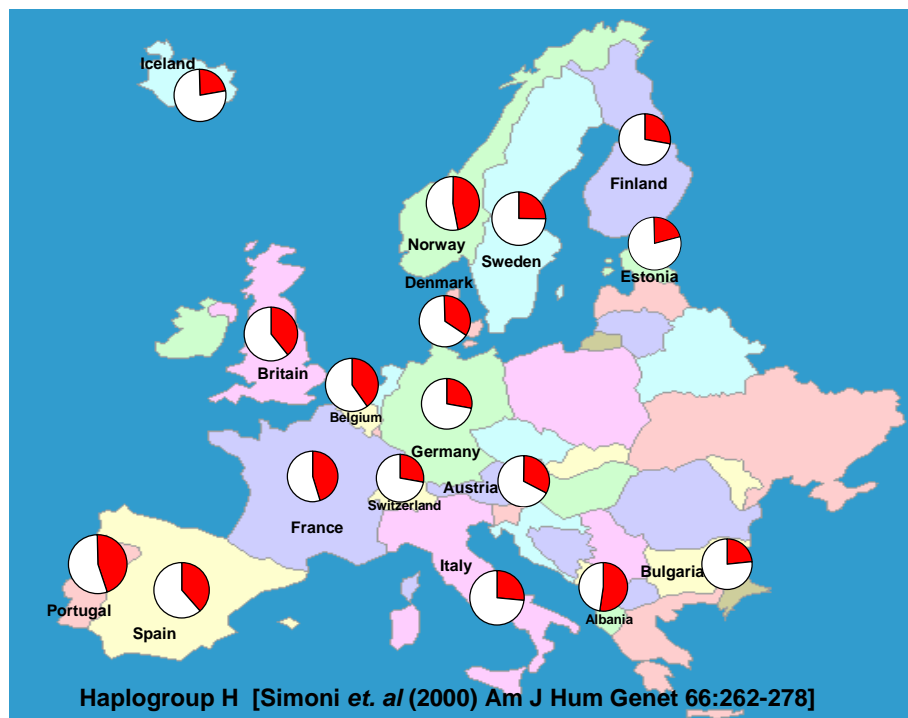
sequence. These mutations are random and not associated with any disease. The haplogroups, or branches, are represented in the tree below, and your branch is indicated within the ring.



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 forty-seven percent of native Europeans belong to the clan “Helena”. Helena’s descendants are the most numerous in Europe having started 20,000 years ago from a hunting family in the Dordogne region of southwest France. The reference sequence with which all mitochondrial mutations are

compared is Helena's sequence. Haplogroup H is found at a frequency of ~ 38% in South African Whites.



## 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.

## Y chromosome haplogroup: G-M201

### Haplogroup information:

Haplogroup G-M201 is thought to have originated approximately 30 000 years ago, likely somewhere in the northern parts of the Middle East. It occurs at its highest levels in the Caucasus region, with more than half the males in Ossetia belonging to haplogroup G-M201 (Nasidze *et al.* 2004b). It also occurs at levels of about 30% in Georgians and Azerbaijanis (Nasidze *et al.* 2004a). The distribution of Haplogroup G-M201, however, is quite wide spread; occurring at low to moderate levels from Northwest Europe to South and East Asia.

### STR profile:

Marker	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393
Profile	15	15	33	22	11	11	14
Range	10-19	9-17	24-35	12-29	6-15	6-18	7-17

Marker	DYS385	DYS438	DYS439
Profile	13,19	10	11
Range	7-25	8-12	8-15

### STR Matches:

We compared your Y chromosome STR profile with about 55,000 Y chromosome haplotypes from a STR database ([www.ystr.org](http://www.ystr.org)). Using all ten markers (both tables above), we found no identical matches. Using seven of the ten markers (first table) still yielded no matches.

A search of our database using seven of the ten markers (first table) yielded no identical matches.

## References

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

Nasidze *et al.* (2004) Ann Hum Genet 68:205-221

Nasidze *et al.* (2004) Ann Hum Genet 68:588-599

Sykes B (2001) The seven daughters of Eve. Bantam Press, London

Wells S (2006) Deep Ancestry: Inside the Genographic Project. National Geographic, Washington D.C.