



John James Doe Premium Combo DNA Ancestry Report

D2550 – T222111

A sample of the subject’s Y-chromosome DNA was extracted, amplified and genotyped by Sorenson Genomics. Chromosomes are the double-helix genetic structures by which hereditary information is physically transmitted from one generation to the next. The Y chromosome is passed only from a father to sons; its entire purpose is to determine maleness. Because of its stability over time, it is useful in tracing paternal ancestry (Jobling and Smith 2003). The allele values for 43 key markers on the DNA were reported as follows:

Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele
DYS19a	15	DYS437	15	DYS452	30	DYS464a	15
DYS19b	-	DYS438	12	DYS454	11	DYS464b	15
DYS385a	11	DYS439	13	DYS455	11	DYS464c	16
DYS385b	14	DYS441	14	DYS456	14	DYS464d	17
DYS388	12	DYS442	17	DYS458	17	DYS464e	-
DYS389I	13	DYS444	12	DYS459a	9	DYS464f	-
DYS389II	29	DYS445	12	DYS459b	9	DYS635	23
DYS390	23	DYS446	13	DYS460	10	GGAAT1B07	10
DYS391	10	DYS447	25	DYS461	12	YCAIIa	19
DYS392	13	DYS448	18	DYS462	11	YCAIIb	23
DYS393	13	DYS449	30	DYS463	24	Y-GATA-A10	14
DYS426	12					Y-GATA-H4.1	22

To explore geographical origins of the subject’s type in history, we compared 11 of these scores, representing the subject’s haplotype, with the worldwide forensic gene bank known as the Y Chromosome Haplotype Reference Database (YHRD) in Berlin. There were 31 matches found in 74,742 haplotypes within 565 populations, as follows:

Population Summary

n of N	Geoposition [Population]
3 of 738	Cologne, Germany [German]
2 of 743	Chemnitz, Germany [German]
2 of 1239	United States [Hispanic American]
2 of 1301	United States [European American]
2 of 293	Aguascalientes, Mexico [Mestizo]
2 of 384	Ravenna, Italy [Italian]
2 of 55	Uppsala, Sweden [Swedish]
1 of 62	Caracas, Venezuela [Mestizo]
1 of 792	Central Portugal, Portugal [Portuguese]
1 of 125	Lyon, France [French]
1 of 645	Prague, Czech Republic [Czech]
1 of 103	Valle de Cauca, Colombia [Mestizo]
1 of 125	Brussels, Belgium [Belgian]
1 of 1277	United States [African American]
1 of 657	Berlin, Germany [German]
1 of 317	Central Norway, Norway [Norwegian]
1 of 447	Sao Paulo, Brazil [European]
1 of 122	Bulgaria [Bulgarian]
1 of 84	Lunca de Sus, Romania [Csángó]
1 of 281	Munich, Germany [German]
1 of 134	Pyrenees, Spain [Spanish]
1 of 287	London, United Kingdom [English]
1 of 248	Denmark [Danish]

These 23 males are genetic cousins descended from the same male ancestor as the subject within about the past 2,000 years. The haplogroup is R1b, and the modal (most common) matches were Germany and the United States. A map of the distribution of the haplotype throughout European populations is shown below, with the height of the red bar within each blue square indicating the frequency of the haplotype in that population.

In [Ysearch](#), there were two close matches, a descendant of Moses Davison, born 1804 in Lancaster County, Pa. ([49TKZ](#)) and a descendant of John Gary, born about 1785, origin unknown ([YYQW7](#)). There was no exact match nor close match of the same or similar surname who could be considered a cousin in a genealogical as well as genetic sense, that is, descended from the same Vandergriff male within about the past 400 years.

Surname Origin and Meaning

Doe (Dow) is an English surname that was a nickname for David (*Dictionary of American Family Names*).

Mitochondrial DNA

A mitochondrial DNA specimen was extracted, amplified by the PCR process and sequenced by Family Tree DNA for markers or mutations in the control sections of the D loop known as Hypervariable Regions I and II containing several hundred base pairs of DNA. The following differences from the reference series mutations were reported (rCRS; Andrews; Anderson). A mutation is any inheritable change in a nucleotide in the DNA sequence of genes. Although mutations in the D loop of mitochondrial DNA do not change the individual or have any effect, they have been found useful in tracing female, or mitochondrial, lineages (Richards and Macaulay):

HVR I: Results of mtDNA sequencing for Hypervariable Region I

	16069	16126	16148	16519
rCRS	C	T	C	T
T222111	T	C	T	C

HVR II: Results of mtDNA sequencing for Hypervariable Region II

	73	185	188	228	263	295
rCRS	A	G	A	G	A	C
T222111	G	A	G	A	G	T

According to Richards et al. (2000), the subject's mutations belong to haplogroup J, although no exact or even close matches were found. Similarly, in the Cambridge Reference Sequence and Mitochondrial DNA Concordance there were the following matches on HVS1 and HVS2 (where red indicates a matching, blue an added, and black a missing mutation):

16069[T] 16126[C] 16148[T]	•Twgdam; 96; Cauc. Amer.(1)
73[G] 185[A] 188[G] 228[A] 263[G] 295[T] 309.1[C] 315.1[C]	•Twgdam; 96; Cauc. Amer.(1) •Twgdam; 137(92H-25); Cauc. Amer.(1)

In Mitosearch, there was an exact match on HVS1 (HVS2 not tested): a descendant of Marianne Cooper, born about 1840 in Rising Fawn, Georgia (AA4HP).

Analysis and Conclusion

On his father's side, the subject descends from a male ancestor who belonged to haplogroup R1b, sometimes (although somewhat misleadingly) called the Atlantic Modal Haplotype (AMH, Wilson). Hispanic matches suggest that the progenitor of this mega-lineage might have lived in Spain. It reaches its highest frequency on the Atlantic Fringe, in Connacht, Ireland. Bryan Sykes in his book *Blood of the Isles* (in America, Saxons, Vikings and Celts) gives the populations associated with R1b the name of Oisín for a clan patriarch, much as he did for mitochondrial haplogroups in his work *The Seven*

Daughters of Eve. Oppenheimer in his book *Origins of the British* calls this type Ruiz and maintains Ruiz was the first and most numerous male type to populate the British Isles following the last Ice Age (pp. 188f.). Haplogroup R1b is the most common male type in modern-day Europe, found in approximately 40% of all males. The mutations characterizing it are M173 and M343 (Y Chromosome Consortium; Karafet et al.). The subject's particular lineage probably originated in Germany.

Read about the [spread of R1b](#) in the National Geographic Genographic Project.

On his mother's side, the subject probably descends from a Caucasian female of haplogroup J*. Haplogroup J, termed Jasmine in the scheme of [Oxford Ancestors](#), is believed to have originated in present-day Lebanon approximately 10,000 years before present, and to have moved north and west into Europe. It is found throughout Europe with particularly high concentrations around the eastern Baltic Sea, Russia, and among the Bedouins and Yemeni, where it reaches frequencies of 25% or higher. J is a major Jewish female lineage (Thomas 2002), being the strongest maternal contributor to Jewish, Arab, Greek and Italian populations. J is also the apparent carrier of congenital longevity and a host of "Jewish" diseases that are being increasingly studied and understood by medical science. Historically, it married with male haplogroup J, and it is believed to have been instrumental in spreading agriculture to northern Europe from the Middle East about 7,000 years ago. The subject's particular [haplotype](#) is probably originally British to judge from the match in Mitosearch.

Read about the [spread of J](#) in the National Geographic's Genographic Project.

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Principal Investigator

[DNA Consultants](#)

August 15, 2009

References and Suggestions for Further Reading

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Doe Haplotype European Distribution



Source: Y-STR Haplotype Reference Database, Berlin.

Release 29 built at 21 July 2009 14:15 (GMT) consisting of 74,742 haplotypes within 565 populations.



THIS DOCUMENT CERTIFIES THAT

JOHN JAMES DOE

Ordered a DNA Ancestry Test from Our Laboratories Yielding the Following Results:

Male Lineage R1b							
Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele
DYS19a	15	DYS437	15	DYS452	30	DYS464a	15
DYS19b	-	DYS438	12	DYS454	11	DYS464b	15
DYS385a	11	DYS439	13	DYS455	11	DYS464c	16
DYS385b	14	DYS441	14	DYS456	14	DYS464d	17
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DYS390	23	DYS446	13	DYS460	10	GGAAT1B07	10
DYS391	10	DYS447	25	DYS461	12	YCAIIa	19
DYS392	13	DYS448	18	DYS462	11	YCAIIb	23
DYS393	13	DYS449	30	DYS463	24	Y-GATA-A10	14
DYS426	12					Y-GATA-H4.1	22

Female Lineage

	16069	16126	16148	16519		73	185	188	263	295
rCRS	C	T	C	T	rCRS	A	G	G	A	C
T222111	T	C	T	C	T222111	G	A	A	G	T

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