DNA Consultants

John Q. Smith
DNA Fingerprint Plus
18 Marker Ethnic Panel

Sxxxx- xxxxxxx

A sample of the Y-chromosome DNA was extracted, amplified and genotyped by DNA Diagnostics Center. 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 or STR markers for 43 loci or specific regions on your DNA were reported as follows on a separate page.

In YHRD, a search found 756 matches in 216,560 Haplotypes. This is one in 286. According to haplotype prediction, the haplogroup is R1a. The haplotype is most commonly reported as Eastern European or Eurasian, with the highest number in Poland, Germany, Russia, the Ukraine, and the Czech Republic.

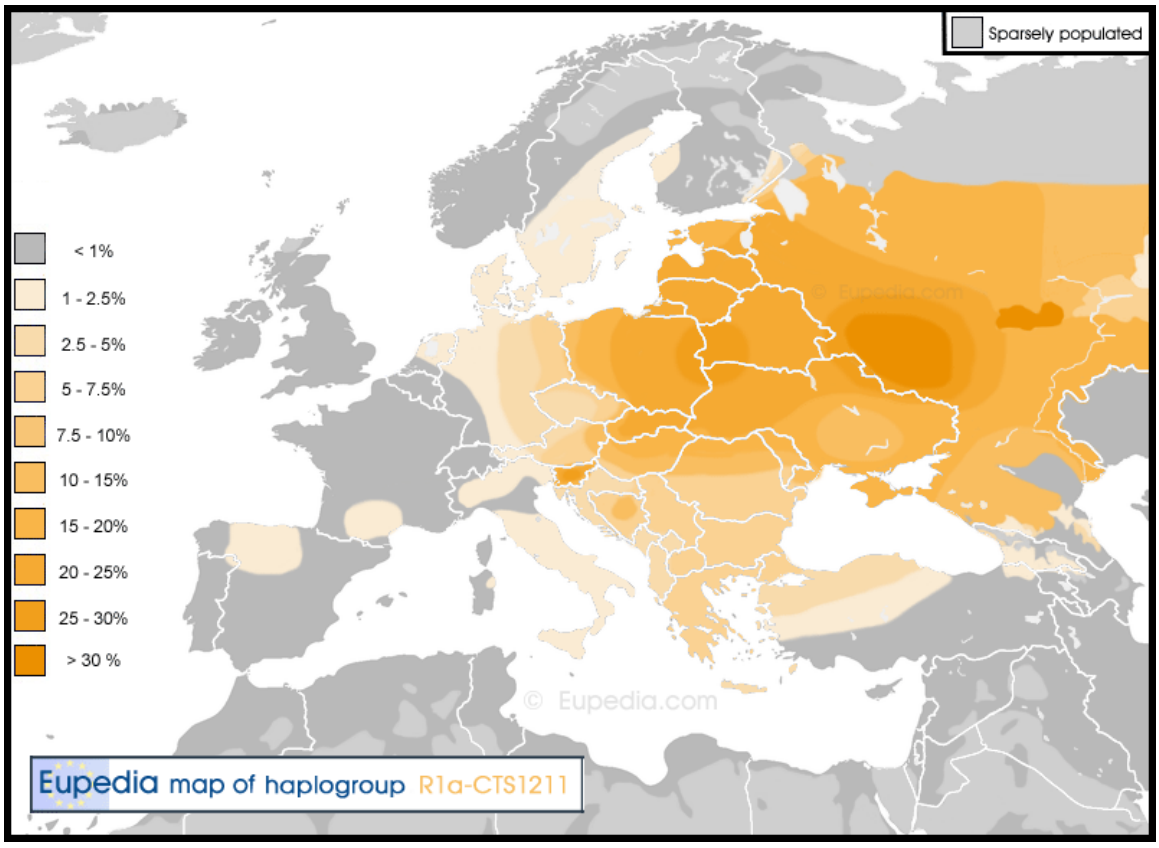
Surname History

Smith is a surname with origins in Anglo-Saxon Britain. It and its variations are the most surnames in the world. It is derived from "smite" and referred to a soldier or warrior.

Analysis and Conclusion

The subject descends from a male ancestor who belonged to haplogroup R1a1, an Eastern European type that is spread as far eastward as India, where it is the genetic signature of Brahmins. Haplogroup R* originated in North Asia just before the Last Glacial Maximum (26,500-19,000 years before present). This haplogroup has been identified in the 24,000-year-old remains of the so-called "Mal'ta boy" from the Altai region, in south-central Siberia (Raghavan et al. 2013). This individual belonged to a tribe of mammoth hunters that may have roamed across Siberia and parts of Europe during the Paleolithic. Autosomally this Paleolithic population appears to have contributed mostly to the ancestry of modern Europeans and South Asians, the two regions where haplogroup R also happens to be the most common nowadays (R1b in Western Europe, R1a in Eastern Europe, Central and South Asia, and R2 in South Asia).

Haplogroup R1a probably branched off from R1* during or soon after the Last Glacial Maximum. The most likely place of origin of R1a is Central Asia or southern Russia/Siberia. From there, R1a could have migrated directly to eastern Europe (European Russia, Ukraine, Belarus), or first southward through Central Asia and Iran. In that latter scenario, R1a would have crossed the Caucasus during the Neolithic, alongside R1b, to colonize the Pontic-Caspian Steppe. In England it is considered the signature of Vikings (Wilson). Ultimately, the haplogroup is believed to go back to the Kurgan culture of western Asia, which is often credited with spreading the Indo-European languages to northwestern Europe and India. Oppenheimer (2006) discusses its important role in helping populate the British Isles. Its highest frequency is 68% in Poland (Ploski R. et al. 2002).



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Disclaimers

This Test is a probabilistic prediction of ancestry for personal knowledge only. It is a non-chain of custody form of testing and is not intended for legal or official purposes. Its results may or may not confirm expected ethnic composition, family history or genealogical determinations. Alone, it may not be used to prove identity, biological relationships, nationality, citizenship, immigration or tribal enrollment.

References and Suggestions for Further Reading

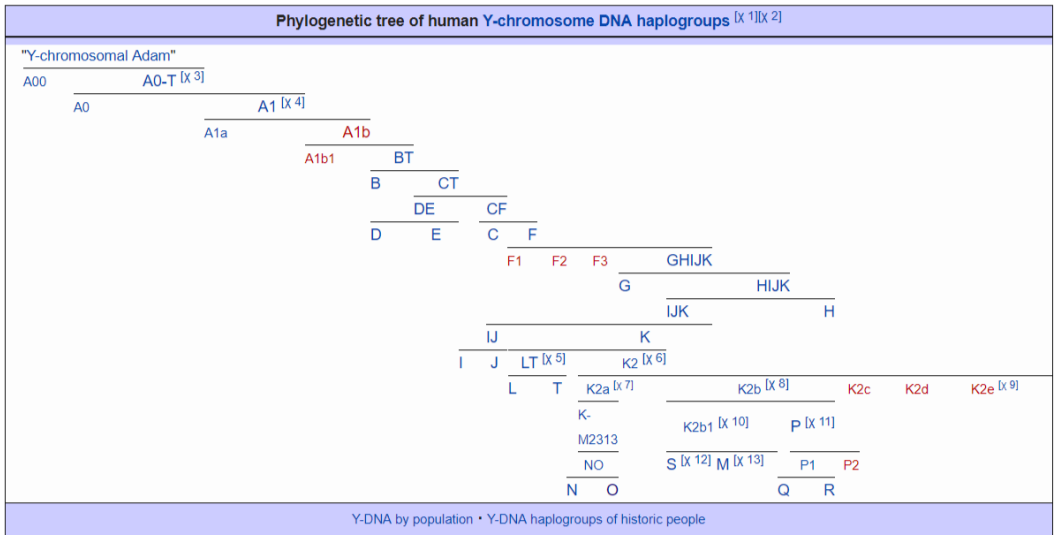
1. Capelli, C. et al. (2003). "A Y Chromosome Census of the British Isles." *Current Biology* 13:979–984.
2. Jobling, M. A. & Tyler-Smith, C. (2003). "The Human Y Chromosome: An Evolutionary Marker Comes of Age." *Nature Rev. Genet.* 4:598-612.
3. Karafet T. M. et al. (2008). "New Binary Polymorphisms Reshape and Increase Resolution of the Human Y Chromosomal Haplogroup Tree." *Gen. Res.* 18:830-8.
4. Manco, Jean (2014). *Ancestral Journeys. The Peopling of Europe from the First Venturers to the Vikings.* London: Thames & Hudson.
5. Oppenheimer, Stephen (2006). *The Origins of the British. A Genetic Detective Story*.
   New York: Carroll & Graf. ----------(2005). *The Real Eve.* New York: Carroll & Graf. -------- (1999). *Eden in the East: The Drowned Continent of Southeast Asia*. New York: Orion. Brilliant Oxford professor's books.
6. Semino, O. et al. (2000). "The Genetic Legacy of Paleolithic Homo sapiens in Extant Europeans: A Y Chromosome Perspective". *Science* 290 (5494): 1155–9.
7. Sykes, Bryan (2013). (2013). *DNA USA: A Genetic Portrait of America.* New York: Liveright. --------- (2001). *Saxons, Vikings and Celts.* New York: Norton. -------- (2001). *The Seven Daughters of Eve. The Science that Reveals Our Genetic Ancestry.* New York, Norton. Names the founders of Europe's major female haplogroups Helena, Jasmine, Katrine, Tara, Velda, Xenia, and Ursula.
8. Wells, Spencer (2006). *Deep Ancestry: Inside the Genographic Project.* Washington: National Geographic.
9. Willuweit S. and L. Roewer on behalf of the International Forensic Y Chromosome User Group, Y chromosome haplotype reference database (YHRD): "Update." *Forensic Science International: Genetics* (2007) 2. Abstract. YHRD 3.0 Release 50 with 154,329 haplotypes within 991

populations in 129 countries. About 90% have been analyzed for the loci DYS438 and DYS439. Available online at http://www.yhrd.org.

10. Y Chromosome Consortium (February 2002). "A Nomenclature System for the Tree of Human Y-chromosomal Binary Haplogroups." *Genome Res.* 12 (2): 339–48.

Understanding Your Male Lineage

Your haplogroup (R1b, R1a, I, G etc.) represents the broad family of male lineages to which you belong. These genetic super-tribes have been traced back about 10,000 years to different areas of origin such as Western Europe, Northern Europe, the Middle East, Africa or the Americas. Geneticists believe all people on earth are descended directly or indirectly from a man who lived in Africa 200,000 to 300,000 years ago (Y-chromosomal Adam).



Your haplotype, as defined in your Y chromosome lab report, is a specific lineage within that haplogroup. It reflects your direct line of father-to-son descent from a common founder who lived perhaps 500-1000 years ago, when surnames first appeared. Your lab report lists the allele values or STR markers for 26 loci or specific regions on your Y chromosome DNA. This is your genetic profile.

You received this male signature from your father, your father from *his* father, and so forth, unchanged or only slightly modified from generation to generation. Variations over time are called mutations.

Many males exhibit an across-the-board match with another male of the same surname. Both are descended without question from a common male ancestor. They are male-linked cousins bearing the same original family name, and a strict pedigree can be constructed. Others, however, match on most markers but not

all. A great deal of expertise is required to judge whether a close match is due to mutations within the same lineage, or whether it represents a different lineage and surname altogether.

If no perfect match is found, your male lineage may be extremely rare. It may not be reported in the databases, and no comparisons or conclusions can be made.

Evaluating a Possible Non-Paternity Event

A "non-paternity event" indicates a break in the link between the Y-chromosome and the surname. Such a misalignment may happen in any generation. The chance of a nonpaternity event occurring accumulates as you go back in time through numerous generations. Its incidence is smallest in aristocratic lines and highest in groups of low social status. An unfamiliar surname in your male line might come from a distant adoption, illegitimacy, child known by other surname (mother's maiden name, stepfather's name), the use of an alias or a deliberate change of surname. Moreover, it may point to a time before settled surnames came into use. In the British Isles, the transition to fixed surnames handed down in patrilineal fashion began about 1100 and was not complete until after 1600. [

It is perhaps helpful to remember that the value of an STR at any given locus (DYS 393, DYS 390 etc.) can mutate up or down one unit about every 500 years. Since they can change in either direction, however, the effect tends to cancel out. The phenomenon of convergence occurs when a configuration of scores randomly mutates to correspond to an unrelated haplotype, but this statistical event appears to be extremely rare and can be ignored.

For help in evaluating your report, contact us at dpy@dnaconsultants.com or call DNA Consultants at 888-806-2588 Monday through Friday 10 a.m. to 6 p.m. Mountain Time. We pride ourselves on customized service and will be glad to walk you through your report and answer all your questions personally.

WORLD HEAT MAP FOR JOHN Q. SMITH