April 23, 2024

Dear Mr. Smith,

This **Basic Haplotype Test** completes your order **Rxxxx**. Any matches or terms highlighted in your PDF are clickable. Follow the link to get more information or an explanation. You can order a **Single Haplotype Report** for any of your haplotypes. This will give you the top 100 matches, inferred origin and history, and worldwide distribution.

Now that you know your haplotypes you may wish to visit DNA Ancestor Communities. Here you can meet others from the same corner of the world, upload pictures, post family stories and genealogies and follow one or more discussions in different forums, including World, Europe, Melungeon, Cherokee, Jewish and Haplotypes. It's free, so join today!

We hope you enjoy your report for years to come and thank you for entrusting us with your DNA testing needs. Deluxe Certificates are available for any population or result named in your reports, along with a large selection of books to help you pursue your interests. Remember you have a 10% discount on any future orders with the code **dnaplus**. This discount never expires, and you can pass it on to family and friends.

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Best Regards,
Donald Yates

Donald N. Yates, Ph.D.
Principal Investigator and Chief Scientific Officer
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John Smith
Basic Haplotype Test

Rxxxx – 800xxxxx

Method

Deoxyribonucleic acid (DNA) was isolated from a specimen submitted to our accredited laboratory. Several different locations on separate chromosomes were used to create a genetic profile for the individual. Specifically, distinct genetic systems (loci) were characterized using polymerase chain reaction (PCR) technology. Nine standard CoDIS markers were tested, and the subject's variations (alleles) were determined. A basic autosomal DNA profile with nine sub-profiles was thus constructed. This unique personal "DNA fingerprint" was analyzed in our computer program atDNA 11.1 to generate the subject's individual haplotypes, along with a frequency occurrence throughout the world.

Based on the observed scientific evidence, it is concluded, for practical purposes, that the chance is 1 in one quadrillion for a random person in the general population other than the subject tested to have a combination of haplotypes identical to those provided in this report. Statistical analysis for these haplotypes is more than 99.9% reliable. Rare alleles are shown in red. The validity of population matches and ethnicities is the same as the reference samples published in forensic science literature—extremely high.

Your Unique Haplotypes

Locus	*Alleles*		Frequency of Occurrence in World (%)		*Range (in number of repeats)*
	A	B	A	B	
D8S1179	13	13	**7.3**		7 – 24
D21S11	29	30	21.5	24.9	12 – 41.2
D7S820	11	12	26.4	24.9	5 – 17
D3S1358	14	15	**7.6**	33.1	9 – 21.1
D13S317	8	10	13.4	**8.7**	5 – 17
VWA	17	18	26.4	18	8 – 24
D18S51	12	14	**9.8**	17.7	7 – 31
D5S818	11	11	**11.7%**		**6 – 17**
FGA	22	24	16.1	16.0	6 – 48.2

Definitions

Short Tandem Repeats (STRs) are the basis of your test. They are segments of DNA with repeat units differing person to person and population to population. Variation in their repeats (alleles) makes them a useful tool for performing individual human identification, ancestry comparisons, ethnic composition and many other purposes.

A haplotype is a variation on a single chromosome or genetic system that can be easily inherited. The exact variant is passed down and shared by all others who have that variation at that location. Because of the stability of DNA from generation to generation, all instances of the haplotype come from a common ancestor, the first human to possess that particular mutation. Ultimately, as the Lakota Sioux Indians say, "We are all related." Haplotypes are spread all over the world. Thus we speak of the "Polynesian haplotype," a single-point mutation in the mitochondrial B haplogroup shown to be protective against malaria. This motif was identified by Stephen Oppenheimer in New Guinea in 1980. It has a high incidence in Polynesians and Southeast Asians but also Mediterranean peoples and American Indians. The patterns of its frequency and distribution document prehistoric travels, colonization efforts and migrations.

The mutation rate of STRs is about the same as for mitochondrial DNA—virtually unchanging. The time depth is very deep. A haplotype usually reflects the last 5,000 years or more, since the end of the last Ice Age before the beginning of recorded history.

Your Autosomal Alleles

It used to be thought that STRs were non-coding in nature. While useful as identification markers, they were, generally speaking, neutral in nature. They didn't actually "do" anything. But in 2007, a team of population geneticists at the University of California at Davis discovered otherwise. It seemed that a repeat of 9 at the location known as D9S1120 was present in Native Americans at an average frequency of around 30%. It was absent in other populations. Thus it qualified as "a private allele ubiquitous in the Americas." Later, a list of private alleles specific to American Indian tribes was published.

It was not until 2020 that researchers discovered STRs had associations with health risks. For instance, about a quarter of the population have a reading of 6 at the location THO1. If you have 10 repeats on that location, you are in a tiny minority. Only 0.8% of people have this rare allele. But in this small group, there is a risk factor for male impulsive violent behavior, one admittedly small, but clinically important. This same marker, abbreviated THO1=10, is the same as the Sundaland Gene. In fact, all 33 of the Rare Genes from History are based on single STR haplotypes. They will be noted in your report if present.

Increasingly, STR haplotypes are being reviewed and catalogued much like genome-wide association studies (GWAS) in medicine. They represent the disentangled strains of your biogeographical diversity as a human being. In genetic genealogy, they are the cutting edge.

Your Leading Population Matches

As in your charts for your DNA fingerprint results, at any given locus, you receive one allele from your mother and one from your father. Siblings can receive a slightly different array because each parent also has two alleles. Every biallelic chart represents a 50-50 combination of both parents' ancestry. These alleles are termed allele A and allele B, though outwardly they are not aligned by parent. Only if you get a double allele can you be sure it comes from mother *and* father. Still, overall, half your haplotypes are genes representative of your father's ancestry, half, your mother's. For more information, references, and photos of any given ancestry, click on the link or see All Populations. Rare ancestries are in red.

Locus	Leading Matches	
	A	B
D8S1179	Russia – Yakut (n=58) 57%, Caucasus (Metapop)., North Asian (Megapop)	
D21S11	Russia – Yakut (n=58) 43.3%, Egyptian. North Asia	U.S./Mex. – Kumeyay/Digueno Indians (n=15) 76.7%, Evenk (Meta), North Asian (Mega)
D7S820	Romani- Northwestern Croatia (n=100) 64.5%, Romani (Meta, Mega)	Mexico – Mexicaneros – Durange (n=84) 50.6%, Chinese Chaozhou (Meta), American Indian (Mega)
D3S1358	Java (n=60) 58.3%, Scottish (Meta), European American (Mega)	Canada- Northwest Territories – Dogrib (n=6) 83.3%, Native American (Meta), American Indian (Mega)
D13S317	Vietnamese – British Columbia (n=50) 38%, Borneo Dyak (Meta) Australoid (Mega)	India – Indo-Mongoloid – Garo (n=110) 50.1%, Taiwanese Aboriginal (Meta), American Indian (Mega)
VWA	Canada- Northwest Territories – Dogrib (n=6) 58.3%, Melungeon (Meta), Melungeon (Mega)	Taiwan – Atayal (n=25) 42%, Taiwanese Aboriginal (Meta), Central European (Mega)
D18S51	Mississippi Choctaw Indians (n=7) 28.6%, Basque (Meta), Melungeon (Mega)	South Dakota – Sioux Indians (n=5) 60%, Taiwanese Aboriginal (Meta), North Asian (Mega)
D5S818	Mexico – Oaxaca – Zoque (n=32) 72.9%, Turkic (Meta), American Indian (Mega) 11, 11 = 11.7%	
FGA	Bhutia, India (n=75) 51.5, Borneo Dyak (Meta), Melungeon (Mega)	Kumeyay/Diegueno Indians (n=15) 46.7%, Evenk (Meta), North Asian (Mega)

The following chart summarizes your best metapopulation and megapopulation matches for each intertwined global lineage in your DNA profile. Together, these biogeographical results help define your personal ethnic mix. Our database contains data of roughly every single forensic scientific study published in the whole world since 1995—more than 400 papers in learned journals. As a statistical tool, atDNA satisfies the highest standards of comprehensiveness,

accuracy, reliability and validity. A metapopulation can be thought of as constituent populations within a country. By definition, a megapopulation contains STR frequencies for a larger unit, for instance an entire continent or ethnic bloc.

Your Biogeographical Results

Locus	Top Metapopulation		Top Megapopulation	
	A	B	A	B
D8S1179	Caucasus		North Asian	
D21S11	Egyptian	Evenk	North Asian	North Asian
D7S820	Romani	Chaozhou Chinese	Romani	American Indian
D3S1358	Scottish	Native American	European American	American Indian
D13S317	Borneo Dyak	Taiwanese Aboriginal	Australoid	American Indian
VWA	Melungeon	Taiwanese Aboriginal	Melungeon	Central European
D18S51	Basque	Taiwanese Aboriginal	Melungeon	North Asian
D5S818	Turkic		American Indian	
FGA	Borneo Dyak	Evenk	Melungeon	North Asian

Conclusion

The subject shows five haplotypes of rare occurrence in the world (in red). These haplotypes can be expected to run in the extended family. There were no private alleles found. The nine genetic systems studied combine matches from the Caucasus, Egypt, Gypsies, China, American Indians, Scotland, Vietnamese, Borneo, India, Australoids, Melungeons, Taiwanese Aboriginals, Central Europe, Basque, the Turkic region of Eurasia and North Asia. The subject carries the following Rare Genes from History: the Ancient One, Denisovan, Lake Baikal and Crazy Horse.

Donald N. Yates, Ph. D.
Principal Investigator
DNA Consultants
April 23, 2024

References

1. Butler, John M. (2010). *Fundamentals of Forensic DNA Typing*. Amsterdam: Elsevier. Authoritative treatment endorsed by the National Institute of Standards and Technology.
2. Cavalli-Sforza, Luigi Luca and Francesco Cavalli-Sforza (1995). *The Great Human Diasporas.* New York: Basic. Wonderful, readable classic on human genetics and prehistory by father and son.
3. "Evolution and Ancestry: DNA Mutation Rates," blog post, Oct. 25, 2012.
4. Jones, Martin, *Unlocking the Past: How Archaeologists Are Rewriting Human History with Ancient DNA* (New York: Arcade, 2016).
5. "Junk DNA? We Don't Think So," blog post Jan. 14, 2013.
6. Kanthaswamy, S. et al., "The Enhancement of the Native American CODIS STR Database for Use in Forensic Casework," Office of Justice Programs, NCJ 253079 (2016) 17 pp.
7. National Research Council (U.S.) Committee on DNA Technology in Forensic Science, "DNA Technology in Forensic Science," (Washington: National Academies Press, 1992). Fundamental early chapter on using STR profiles for identity and relationship.

8. Oppenheimer, S. J. et al, "Alpha-thalassaemia in Papua New Guinea," *Lancet* 1 (1984) 424–26.
9. "Private Alleles Reveal Minor Ancestry," blog post, May 24, 2021.
10. Schroeder, K. B., "A Private Allele Ubiquitous in the Americas," *Biology Letters* 3 (2007) 218-23.
11. Sykes, Bryan, "The Origins of the Polynesians: An Interpretation from Mitochondrial Lineage Analysis," *American Journal of Human Genetics* 57 (1995): 1463-1475.
12. Wyner, Nicole, Mark Barash and Dennis McNevin, "Forensic Autosomal Short Tandem Repeats and Their Potential Association with Phenotypes," *Frontiers in Genetics* 11/884 (2020).

Glossary of Terms Used in This Report

https://dnaconsultants.com/dna-glossary/

Disclaimer

This DNA Test is a probabilistic prediction of haplotype association and ancestry for personal knowledge only. It is a non-chain of custody form of testing and is not intended for legal or medical 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, health conditions, nationality, citizenship, immigration, or tribal enrollment.

Statement on Ethnicity

Allelic population analysis is a science still in the early stages of development. As our understanding of human history and prehistory improves and more specific markers are discovered and reported for distinct populations, we can expect the accuracy of prediction of the ethnic constituents in our ancestry to increase.

Reliability

While the laboratory methods used to determine your DNA markers are completely accurate and their statistical analysis is reliable, interpretation of the numerical results is subjective. Conclusions will vary. To form more confident opinions, we suggest that you combine the findings in this report with other testimony, such as that of sex-linked haplotype matches, genealogical records and family history.

Confidentiality

Your testing, results and this report are 100% confidential.

Following Up

Join a Forum at DNA Communities for free. Just follow the prompts to register and set your preferences. Begin exploring your results and sharing your genealogy with others. You may find people you are related to or learn about the perfect resource. Choose from European, World, Native American, Hispanic, Melungeon, African, Jewish, Gypsy/Roma and Haplotypes discussions. Visit our blog for interesting reviews of news and research about genetics and ancestry tracing. Check out the populations where your ancestors originated on Population Pages.

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THIS DOCUMENT CERTIFIES THAT

John Smith

COMMISSIONED A PERSONAL **BASIC HAPLOTYPE TEST** FROM OUR LABORATORIES

WHICH SHOWED THE FOLLOWING RARE ANCESTRAL MATCHES

Russia – Yakut (n=58) 57%
Java (n=60) 58.3%
India – Indo-Mongoloid – Garo (n=110) 50.1%,
Mississippi Choctaw Indians (n=7) 28.6%
Mexico – Oaxaca – Zoque (n=32) 72.9%

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Donald N. Yates

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