Joan Jones
Single Haplotype Test – VWA=13

Jxxxx – 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. One of these is studied further in this report.

Your Haplotype in Brief

Allele	Popula-tions with This Value	World Freq.	Top Population Match and Frequency
VWA=13	261/ 524	0.8%	Russia - Mongol (n = 42) 6.7%

Allele	Top Metapopulation Match	Freq.
VWA=13	Mongol	13.0%

Allele	Top Megapopulation Match	Freq.
VWA=13	Central Asian	5.4%

Background

Short Tandem Repeats (STRs) are the focus of this 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.

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

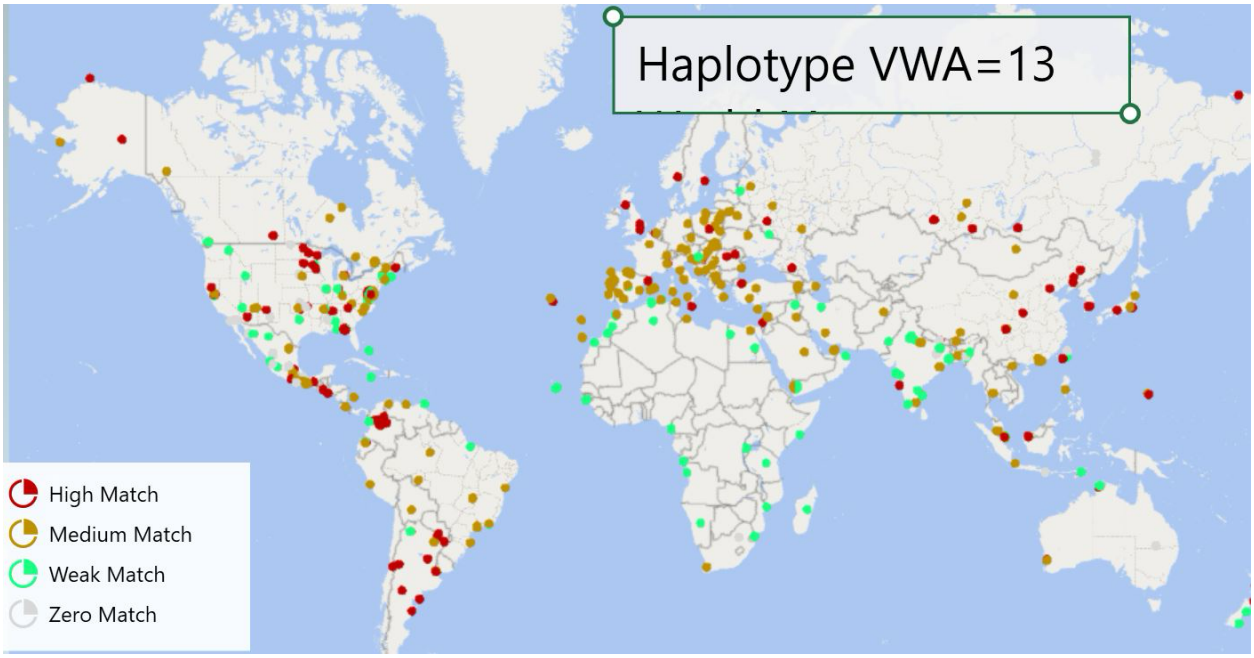
A haplotype is a variation on a single chromosome or genetic system that can be easily inherited. The exact variant is passed down and shared by all others who have that variation at that location.

Because of the stability of DNA from generation to generation, all instances of the haplotype come from a common ancestor and are related, if remotely.

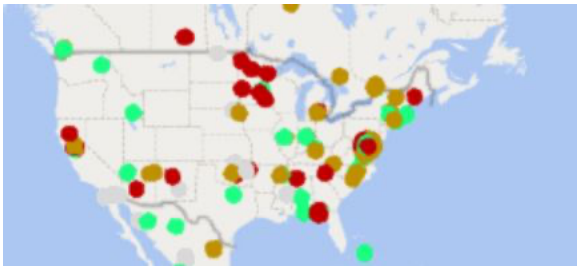
The mutation rate is about the same as for mitochondrial DNA—virtually unchanging. Thus the time depth is very deep. A haplotype usually reflects the last 5,000 years or more, since the end of the last Ice Age before the beginning of recorded history. All matches, on the contrary, are to living populations.

Distribution of This Haplotype

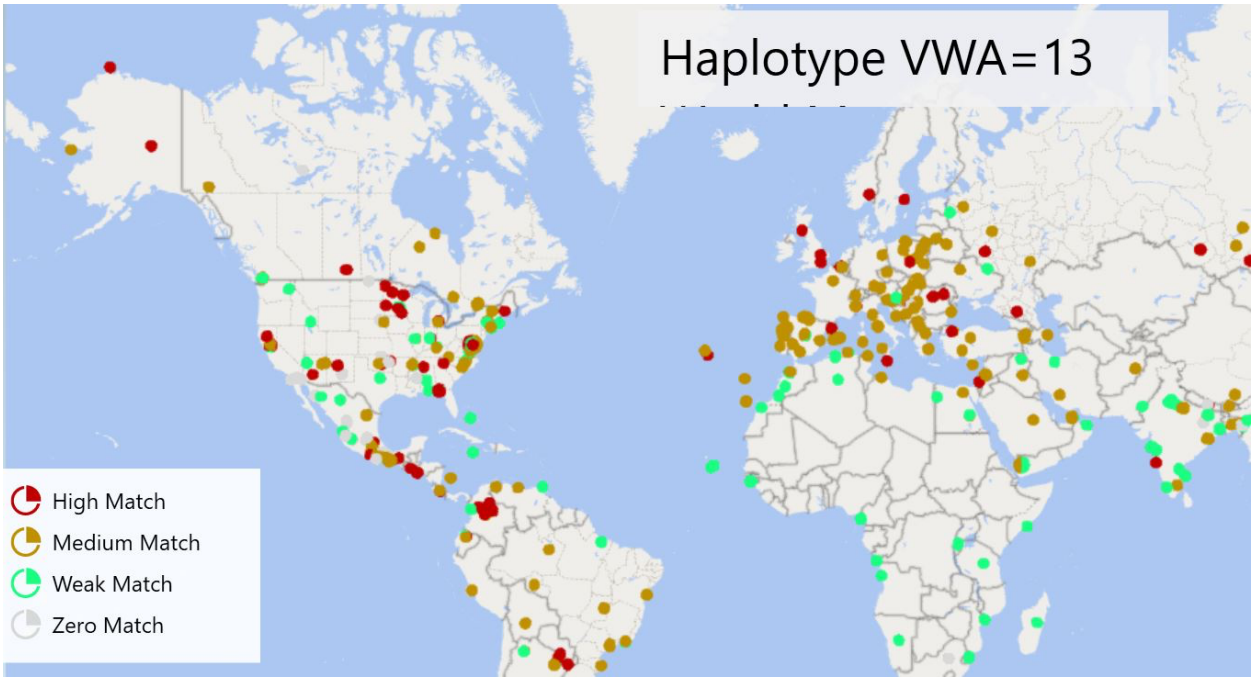
The following distribution maps of the haplotype were generated with atDNA 11.1.



From this world map it can be seen that the haplotype is weakly attested in Africa, most of India and most of southern Europe and the Mediterranean. It could be called a non-African haplotype.



From this detail, it can be seen that the haplotype has high matches among some U.S. Native Americans but not others (red dots). Prominent are White – U.S., Hispanic – U.S., Native American – Minnesota, U.S. – Shawnee – Admixed, U.S. Cherokee- Enrolled, Mississippi – Choctaw Indians, Brazilian – Non-Black – Florida, California – Miwok Indians and Native American – Alaska – Athabaskan.



From this medium range map it can be seen that the haplotype is very common among certain Central and South American Indians as well as U.S. Native tribes.

Top World Matches and Frequencies for VWA=13

Population	1/RMP	Freq.
Russia - Mongol (n = 42)	7.500E+00	6.667E-02
Russia - Novgorod (n = 59)	8.429E+00	5.932E-02
U.S. Shawnee Admixed (n = 53)	1.060E+01	4.717E-02
Russia - Belgorod (n = 66)	1.267E+01	3.947E-02
Black - U.S. (n = 139)	1.389E+01	3.600E-02
Russia - Pskov (n = 62)	1.550E+01	3.226E-02
India - Nepali (n = 110)	1.613E+01	3.100E-02
Egyptian Berbers - Siwa (n = 98)	1.613E+01	3.100E-02
Black - Minnesota (n = 75)	1.667E+01	3.000E-02
Black - Minnesota (n = 157)	1.745E+01	2.866E-02
Colombian - North Pacific Coast (n = 123)	1.786E+01	2.800E-02
Black - Bahamian (n = 81)	1.800E+01	2.778E-02
India - Northeastern - Bihar - Rajput (n = 58)	1.852E+01	2.700E-02
Black - New York (n = 75)	1.873E+01	2.670E-02
U.S. /Canada Abenaki Indians (n=19)	1.900E+01	2.632E-02
India - Indo-Caucasoid - Brahmin (n = 110)	2.000E+01	2.500E-02
India - Indo-Caucasoid - Kayastha (n = 103)	2.000E+01	2.500E-02
Guinea-Bissau (n = 100)	2.000E+01	2.500E-02
Black - Texas (n = 151)	2.174E+01	2.300E-02
Black - Virginia (n = 100)	2.212E+01	2.260E-02
Black - Canadian (n = 179)	2.273E+01	2.200E-02
India - Lepcha (n = 48)	2.273E+01	2.200E-02
Guinea-Bissau (n = 92)	2.304E+01	2.170E-02

Turkish - Anatolia (n = 140)	2.381E+01	2.100E-02
Black - North Carolina (n = 383)	2.500E+01	2.000E-02
Ecuadorian - Black (n = 104)	2.632E+01	1.900E-02
Mozambique (n = 110)	2.778E+01	1.800E-02
Equatorial Guinea (n = 134))	2.778E+01	1.800E-02
Black - U.S. (n = 3,927)	2.959E+01	1.690E-02
Black - Connecticut (n = 182)	3.034E+01	1.648E-02
Guinea-Bissau (n = 92)	3.067E+01	1.630E-02
Black - U.S. (n = 195)	3.247E+01	1.540E-02
Spanish - Black - Central West African (n = 132)	3.311E+01	1.510E-02
Black - Florida (n = 50)	3.333E+01	1.500E-02
Black - Virginia (n = 194)	3.333E+01	1.500E-02
Black - Florida (n = 100)	3.333E+01	1.500E-02
Brazilian - Belem Amazonians (n = 325)	3.333E+01	1.500E-02
India - Pallar (n = 33)	3.333E+01	1.500E-02
Namibia - Windhoek (n = 195)	3.333E+01	1.500E-02
Brazilian - Black - Florida (n = 117)	3.499E+01	1.429E-02
Mozambique - Maputo (n = 154)	3.571E+01	1.400E-02
Portuguese - Porto region (n = 39)	3.846E+01	1.300E-02
Turkish (n = 500)	3.846E+01	1.300E-02
Omani (n = 79)	3.846E+01	1.300E-02
Black - Illinois (n = 78)	3.876E+01	1.290E-02
Equatorial Guinea (n = 129)	3.937E+01	1.270E-02
Black - Kentucky (n = 357)	3.968E+01	1.260E-02
Black - California (n= 100)	4.000E+01	1.250E-02
Mongolia - Ulaanbaatar - Lai (n = 92)	4.545E+01	1.100E-02
Eastern Turkey (n = 802)	4.545E+01	1.100E-02
Mozambique (n = 92)	4.587E+01	1.090E-02
Hispanic - Connecticut (n = 187)	4.673E+01	1.070E-02

Conclusion

The VWA=13 haplotype, while it probably began its life in Africa, like all other haplotypes, expanded most dramatically over time in Central Asian, Northern European and certain North American Indian populations. Because the Black matches in North America are African Americans and matches to Africans are weak we can assume its strong distribution in U.S. blacks is attributable to admixture with American Indians. The story of the Mongol Gene, common in Europeans and American Indians, comes to mind, as well as the discovery of the Ice Age Mal'ta Boy fossil in Siberia. For more information, references, and photos of any ancestry, click on the link or see All Populations.

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April 26, 2024

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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.

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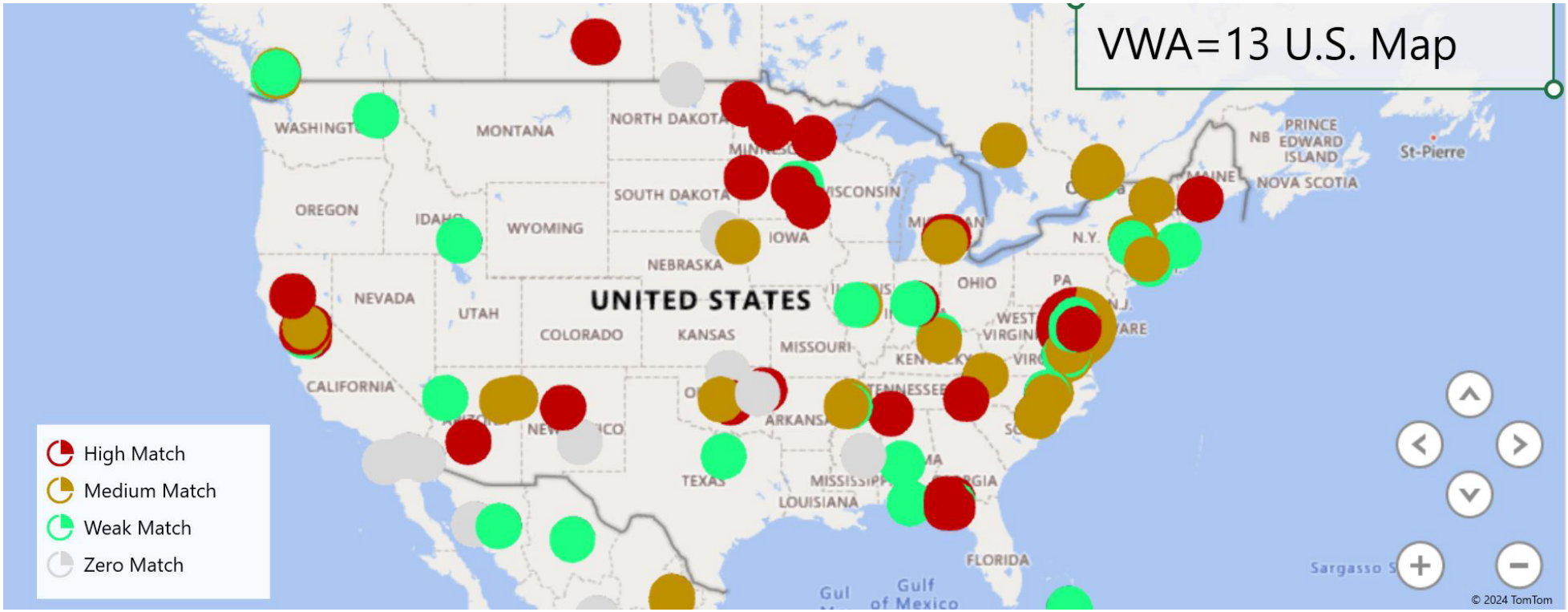

Map of American Indian, African American and Hispanic Shows Strong Common Matches for Haplotype VWA=13 in U.S. **Source: atDNA 11.1.**