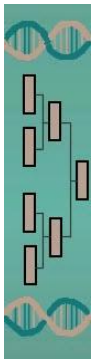
MAXY DNA:
Correlating mt-at-X-Y DNA with the GPS



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Case studies demonstrate principles and techniques that beginner to intermediate level genealogists can use to correlate DNA test results with documentary research. The focus here is on two elements of the Genealogical Proof Standard (GPS): (1) reasonably exhaustive research as applied to using DNA information and (2) correlating the DNA analysis with documentary information to answer a genealogical question.

All URLs were accessed 26 April 2017.

BASIC DNA INHERITANCE PATTERNS

Humans inherit several "types" of DNA—X, Y, mitochondrial (mtDNA) and autosomal (atDNA). Each type can help genealogists research and confirm different portions of a family tree. Multiple types of DNA used together can provide more conclusive evidence to answer a genealogical question.

Y-DNA Inheritance (Males) traces one specific line back thousands of years (patrilineal or father's father's father's father)

mtDNA Inheritance (Both) traces one specific line back thousands of years (matrilineal or mother's mother's mother's mother)

X-DNA Inheritance (Both, differ) traces a specific sub-set of lines that is **different in males and females** (charts identify potential X-contributing ancestors)

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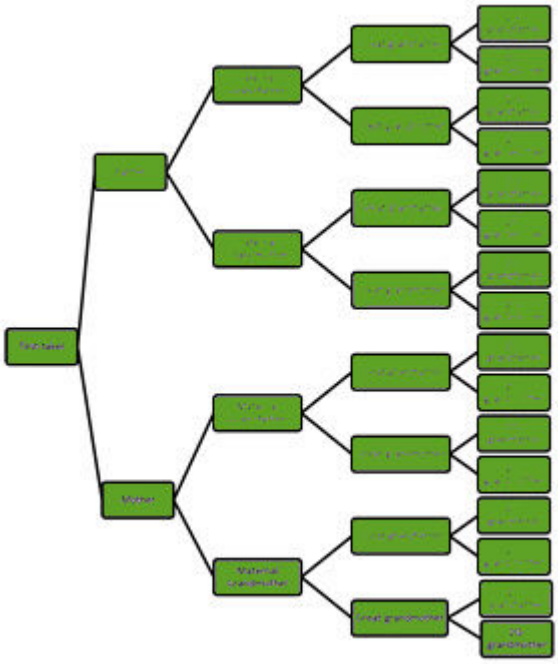


atDNA Inheritance

atDNA is composed of chromosomes 1–22.

DNA test-takers likely have some atDNA from all ancestors back five to nine generations; further back, due to random recombination and inheritance factors, test-takers may or may not have inherited DNA from a specific ancestor at a level detectable by current testing and analysis methods.

All ancestors make up the genealogical tree.

Only anestors from whom DNA was inherited make up the genetic tree.

FACTORING DNA INTO THE GPS

DNA is a critical piece of evidence when there is **a question of kinship**

- that **could be** resolved using DNA
- **and** there are living persons in the right line of descent to provide the answer (genealogical problems require multiple testers—one person's DNA is compared to another's)
- **and** those persons agree to provide a DNA sample for testing

Ethical considerations require discussion of factors with a test-taker prior to testing, such as

- how to handle unexpected findings (which can be revealed by documentary records as well as DNA)
- what information may be shared publicly and/or with those who shared DNA
- whether the test-taker approves uploading his or her data to third-party websites
- and other items discussed in the *Genetic Genealogy Standards*[1]

[1] Genetic Genealogy Standards Committee, *Genetic Genealogy Standards* (http://www.geneticgenealogystandards.com/).

DNA evidence can be used to support or reject a genealogical hypothesis, just like evidence from a census record, a birth certificate, or a deed. As with any traditional documentary source, DNA evidence is never used on its own; instead, it is evaluated, analyzed, and correlated with other evidence to arrive at a credible conclusion.

The proper use of DNA evidence to support a genealogical conclusion must allow those who did not directly perform the research—that is, those who did not see the DNA test results—to evaluate the strength of the conclusion without having to repeat the research.

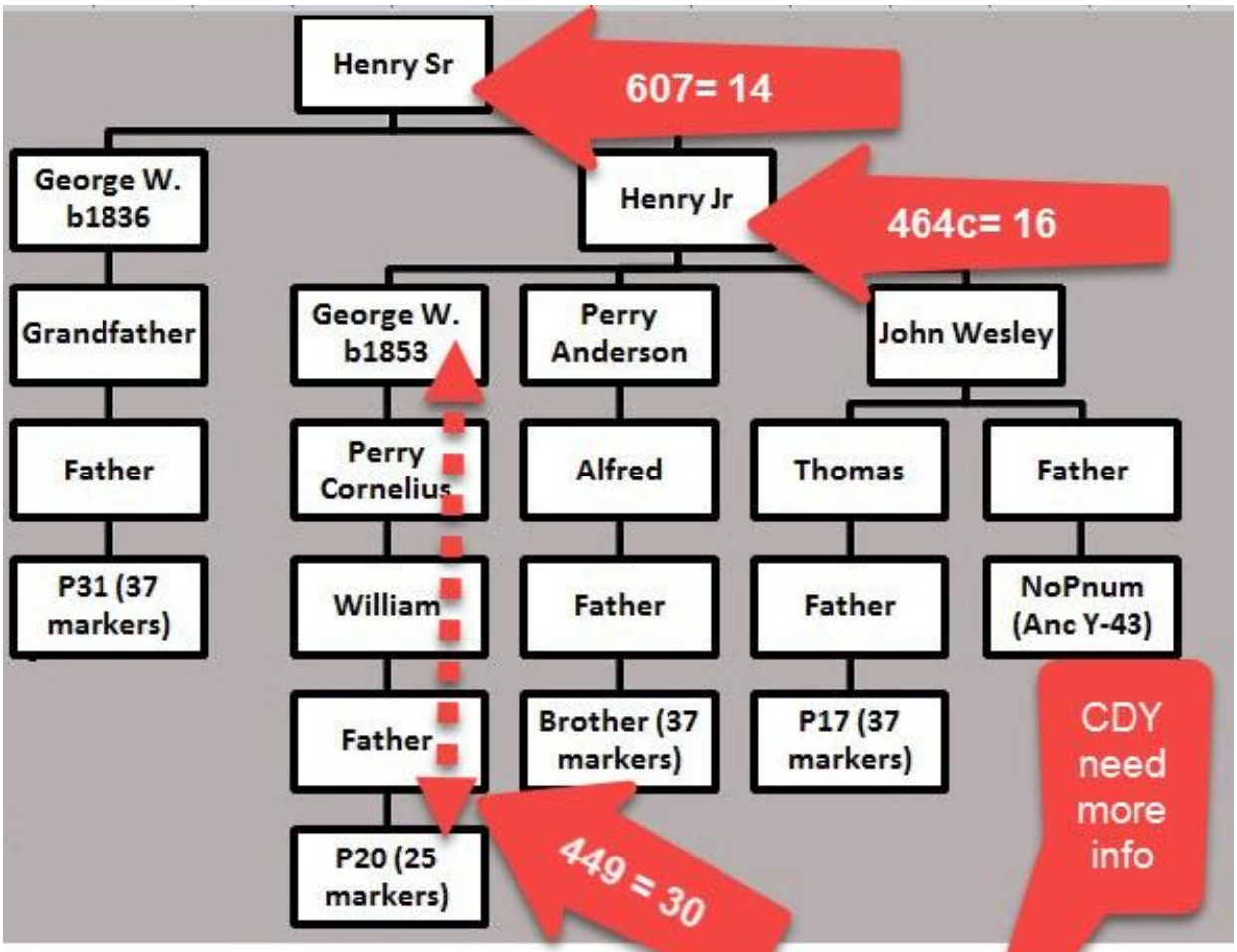
GPS element	Addressing the GPS element with DNA
reasonably exhaustive research	Focused question; which kind(s) of DNA provides evidence; what resolution test is needed; who inherited that type of DNA, is still living, and is willing to test; how many test-takers are needed for a credible conclusion
complete and accurate source citations	Test-takers and relationships, testing company, test taken and resolution, analysis tools used, sometimes versions of test, tools, or database are needed
analysis and correlation of all evidence	Analyze and consider: the shared segments or markers; the differing markers; the effect of random recombination and inheritance; the statistical probability of findings (likely and unlikely); other possible relationships that result in the same findings; effect of incomplete or inaccurate family tree
resolution of conflicting evidence	Discuss fast-moving markers, statistical probabilities, other possible relationships that could result in same DNA findings
soundly reasoned, coherently written conclusion	Explain the documentary and DNA evidence using language any genealogist can understand, define DNA concepts needed to answer this focused question

Importance of Tree Accuracy and Depth

The accuracy and completeness of family trees belonging to a test-taker and that test-taker's DNA matches impact a genealogist's ability to analyze and correlate DNA information. An inaccurate tree may make finding a common ancestor impossible or may focus on a person who is not really an ancestor. An incomplete tree may make locating a common ancestor difficult because that ancestor is not yet known. An incomplete tree might also mislead a genealogist to assume that shared DNA comes from a known common ancestor when some of the matching DNA could have come from a yet-unidentified common ancestor.

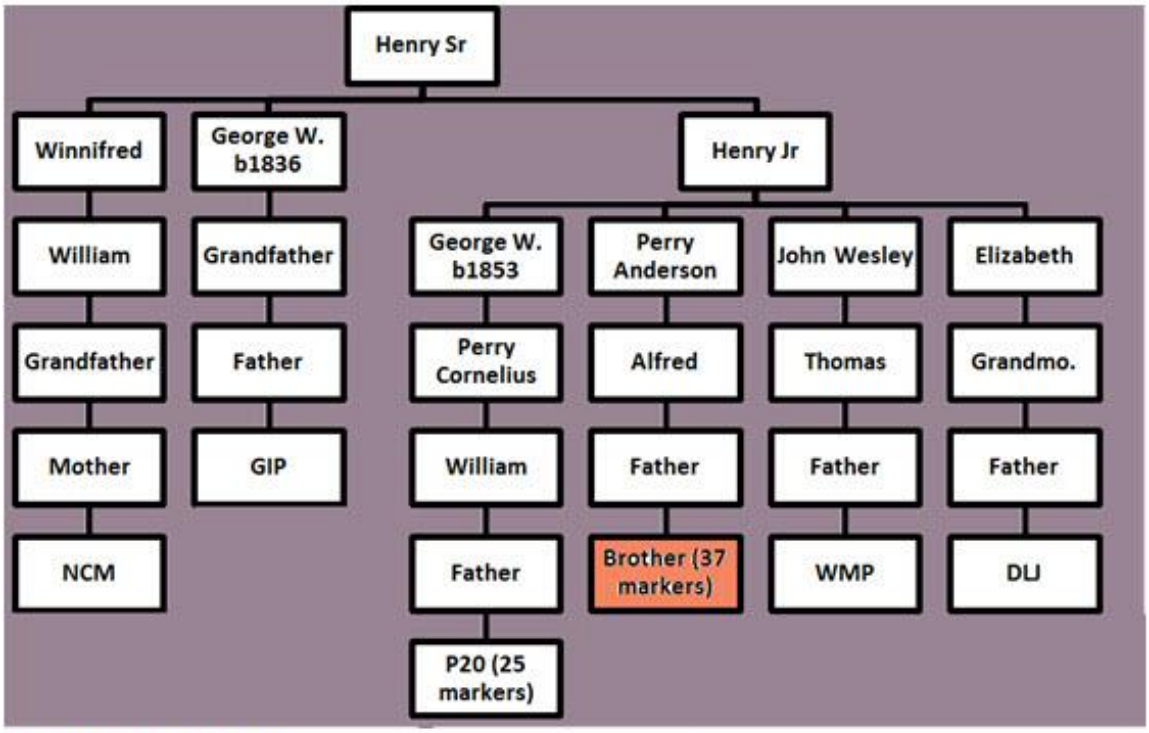
CASE STUDY CHARTS

Y-DNA Chart



607 = 14	607 unknown	607 = 14	607 = 14	7 unknown
464c = 15	464c = 16	464c = 16	464c = 16	464c = 16
449 = 31	449 = 30	449 = 31	449 = 31	449 = 31
CDYa = 35	CDYa unknown	CDYa = 34	CDYa = 35	CDY unknown

Autosomal DNA Chart



Chr#:start-stop location (cM):

NCM	GIP	P20	Bro	WMP	DLJ	
			6:18m-37m (19) 6:135m-161m (33)		6:135m-161m (33)	NCM
			1:164m-191m 11:37m-82m 12:103m-126m	3C1R: ???	3C1R: ???	GIP
			6:46m-73m (15)	3C1R: ???	6:80m-101m (17)	P20
6:18m-37m (19) 6:135m-161m (33)	1:164m-191m (24) 11:37m-82m 12:103m-126m (39)	6:46m-73m (15)		3C: 90 (4 segs)	6:134m-152m (19) 7:27m-47m (25) 10:52m-72m (20)	Bro
	3C1R: ???		3C: 90 (4 segs)		3C1R: ???	WMP
6:135m-161m (33)	3C1R: ???	3C1R: 40 / 9	6:134m-152m (19) 7:27m-47m (25) 10:52m-72m (20)	3C1R: ???		DLJ

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