

Genetic Genealogy Demystified: Reading and Understanding Your Family Tree DNA Results Part 1: Y-DNA

Presented By
Elise Friedman, Relative Roots

You've taken the plunge and ordered a genetic genealogy DNA test from Family Tree DNA, but now that you have your results, you don't understand them? This webinar is for you! Join us to learn how to read and understand your Y-DNA results.

DNA Tests for Genealogy

- Y Chromosome (Y-DNA)
 - o Direct paternal line (father's father's father, etc)
 - o Only men can test for it
- Mitochondrial DNA (mtDNA)
 - o Direct maternal line (mother's mother's mother, etc)
 - o Both men and women can test for it
- Autosomal DNA (Family Finder)
 - o Identify cousins via any ancestral line
 - Both men and women can test for it

This webinar focused on Y-DNA tests.

Review of DNA Basics

Our DNA consists of:

46 chromosomes (23 pair)

22 pair = autosomal chromosomes, or autosomes

1 pair = gender chromosomes (X,Y) (women have XX, men have XY)

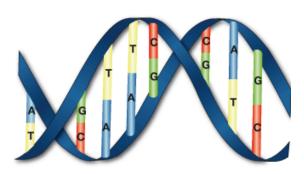
Mitochondrial DNA (mtDNA)

DNA Sequences & Mutations

DNA is made up of four (4) bases (nucleotides):

- **Adenine**
- Cytosine
- <u>Guanine</u>
- Thymine

Mutations (changes) in the DNA happen over time. Mutations happen randomly, but always between a parent/child pair. Mutations are what enable us to do



Thymine (Yellow) = T Guanine (Green) = G

Adenine (Blue) = A Cytosine (Red) = C

genealogy and ancestry studies. They differentiate us from people who we're not closely related to, while matching us with people who we are closely related to. Genetic genealogy uses two types of mutations: STR and SNP.

DNA Sequence – a string of consecutive bases

Example: TAGCAAAGTCCCATGCCCCAGTCAGTCGGGA

Short Tandem Repeat (STR) - DNA sequence of short repeating segments.

Example: GATCGATCGATCGATCGATCGATCGATC

Great for genealogy. Family Tree DNA's Y chromosome markers are STRs.

Alleles - Number of repeating segments at an STR marker

The above sequence has 7 alleles (GATC repeated 7 times).

Example: DYS393=12 means you have 12 alleles (repeats) at marker DYS393.

Haplotype – Sequence of alleles

Example: 12 23 14 10 13 17 11 16 11 13 11 30

Single Nucleotide Polymorphism (SNP) - Base change at a single location in the DNA

Example: $C \rightarrow G$, or $A \rightarrow T$

Rare occurrences in Y-DNA and mtDNA, so great for deep ancestry studies.

Great for autosomal studies when used in large quantities.

Haplogroup – Broad division of the human population, defined by Y-DNA and mtDNA SNPs.

Represents deep/ancient ancestry (thousands to tens of thousands of years).

Separate Y chromosome and mtDNA haplogroups.

Can be divided into subgroups, known as subclades.

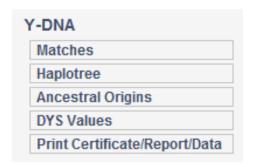
Haplogroups are hierarchical, similar to an outline.

Haplogroup names start with a capital letter, then alternate numbers and lower case letters.

Example: J1e. J is the main haplogroup name, J1 is a subclade of J, and J1e is a subclade of J1.

Reading & Understanding Y-DNA Results

Family Tree DNA currently offers five (5) levels of standard Y-DNA testing – 12, 25, 37, 67 and 111 STR markers – as well as a wide variety of advanced STR and SNP tests.



Matches

Family Tree DNA provides names and email addresses of other customers who your results match. You can contact your matches to share your family trees and work together to identify your common ancestor. FTDNA displays the following match levels:

12 Markers: 11/12 (only for people in the same project as you), and 12/12

25 Markers: 23/25, 24/25, 25/25

₹ 37 Markers: 33/37 through 37/37

№ 67 Markers: 60/67 through 67/67

№ 111 Markers: tba/111 through 111/111

DYS Values

Family Tree DNA provides the STR allele values on the *Y-DNA DYS Values* page of your MyFTDNA account:

PANEL 1 (1-12)												
Locus	1	2	3	4	5	6	7	8	9	10	11	12
DYS#	393	390	19*	391	385a	385b	426	388	439	389-1	392	389-2 ****
Alleles	12	23	14	10	13	17	11	16	11	13	11	30

How to Read the Results

DYS393=12, DYS390=23, DYS19=14, etc.

Example: DYS393 = 12

At marker DYS393

Which has the repeat structure AGAT [This info isn't shown on the FTDNA pages]

* "AGAT" is repeated 12 times:

Comparing Results

Y-DNA matches do not necessarily have to be exact to be significant. Since mutations happen randomly – always between a parent/child pair – a father and son can have a mismatch on a marker.

So relationship predictions are always provided in terms of probabilities.

Locus	1	2	3	4	5	6	7	8	9	10	11	12
DYS#	393	390	19	391	385a	385b	426	388	439	389-1	392	389-2
Male 1	14	24	14	10	17	19	11	12	12	12	11	30
Male 2	14	24	14	10	17	18	11	12	12	12	11	30

In the above example, Male 1 and Male 2 match on 11 out of 12 markers. At DYS385b, they have a mismatch. This example came from two people who are known to be recently related, but an 11/12 match could also exist between two people who aren't recently related.

50% probability that the MRCA was no longer than this number of generations	90% probability that the MRCA was no longer than this number of generations	95% probability that the MRCA was no longer than this number of generations		
16.5	56	72		
17	39	47		
7	23	29		
11	23	27		
7	16	20		
3	10	13		
6	12	14		
4	8	10		
2 to 3	5	7		
6	12	14		
4	8	9		
2	4	6		
	MRCA was no longer than this number of generations 16.5 17 7 11 7 3 6 4 2 to 3 6 4	MRCA was no longer than this number of generations MRCA was no longer than this number of generations 16.5 56 17 39 7 23 11 23 7 16 3 10 6 12 4 8 2 to 3 5 6 12 4 8		

Time to Most Recent Common Ancestor

How to Read

An 11/12 match has a 90% chance of being related within 39 (from 1 to 39) generations.

A 36/37 match has a 90% chance of be related within 8 (from 1 to 8) generations.

37 markers and higher is best for identifying matches within genealogical timeframe (hundreds of years vs thousands of years).

Haplotree

Family Tree DNA provides Y-DNA haplogroup information on the Haplotree page. Haplogroups represent deep ancestry (thousands to tens of thousands of years). They are broad groupings of the human population. Haplogroups are also divided into many subgroups, known as subclades. Haplogroups and their subclades form a hierarchical tree, similar to a family tree.

Haplogroup names start with a capital letter, and subclades have alternating numbers and lower-case letters. You can view the

Wy Haplotree By Marchies Frequency Map Migration Map My Confirmed Haplogroup: J2 Shorthand: J-M172

You Are Eligible For An Upgrade!
Haplogroup Test Based on your matches, you belong to J2. Our Deep Clade test will confirm his. It will also test for any branches to which you may belong. Click on the Continue for More Information button to order.

Continue for more information

Choose your own SNP
You may also use the Choose Your Own SNPs page to order specific SNPs. Click to continue.

Continue To Choose SNPs

Y-DNA Haplotree Chart
The chart displayed to the right represents the Y chromosome family tree of mankind, called a phylogenetic tree. Each major branch is named with a letter, and deeper branches within the tree are labeled with numbers and letters to note their relationship to one another. Each branch is thousands or lens of thousands of years old. Because members of a branching support of the first provided by the continue of the provided of of the provi

subclades for a haplogroup by clicking on a capital letter on your Haplotree page.

Each haplogroup and subclade is defined by a Single Nucleotide Polymorphism (SNP). SNP names often start with a capital letter, followed by digits.

Example:

	Defining SNP: M96
E1	Defining SNP: P147
■ E1a	Defining SNP: M132
• E1a1	Defining SNP: M44
■ E1b	Defining SNP: P177
• E1b1	Defining SNP: P2
E2	Defining SNP: M75
	 E1a E1a1 E1b E1b1

Viewing a Y chromosome tree such as the one on the *Haplotree* page of your myFTDNA account is the best way to see the correlation between Haplogroup and SNP names.

NOTE: New SNPs are still being discovered all the time. When new SNPs are discovered, sometimes they have to be inserted into the middle of a tree. When that happens, the hierarchical haplogroup names below the insertion point will need to be adjusted accordingly.

Family Tree DNA most recently updated their Haplotree on Friday, March 4, 2011.

Family Tree DNA provides a free backbone (top-level) haplogroup prediction for every customer who orders a Y-DNA test. Predictions are done by comparing your 12-marker results to Family Tree DNA's robust database of customers who have already been SNP-tested. If Family Tree DNA cannot confidently predict the backbone haplogroup, they will run a free backbone SNP test.

An optional deep-clade SNP test can be purchased to refine the haplogroup assignment to the deep subclade level.

Making the Most of Your Genetic Genealogy Experience

Receiving, reading and understanding your results shouldn't be the end of your genetic genealogy journey. Here are some ways you can make the most of this experience:

- Share. Your myFTDNA account has fields to enter your Most Distant Known Ancestor's (MDKA) name and location, as well as all the surnames in your ancestry. You can also upload a GEDCOM of your family tree. Entering all this information will enable your matches to learn something about your genealogy before they even contact you.
- Communicate. Don't be afraid to email your matches, and definitely respond to emails that you receive from your matches! All customers can choose whether to sign the green release form that Family Tree DNA provided with your swab kit, which gives FTDNA permission to provide their name and email address to matches. So everyone who you see on your Matches page had signed this form and given permission.
- Participate. Family Tree DNA has over 6,000 different projects which focus on surname, geography, heritage and haplogroups. Projects are all run by volunteer administrators and are free to join. Joining projects is the best way to stay informed about news related to the topic of the project, and you have the added benefit of getting support and assistance from your project administrator.
- Be Proactive. No project for your surname yet? Start one and recruit other people with your surname to get tested. You don't have to be an expert on genetic genealogy to start a project.
- Learn. Keep learning about genetic genealogy by attending Relative Roots Webinars, consulting the Family Tree DNA FAQ, visiting the International Society of Genetic Genealogy website, and reading discussion forums and email lists that discuss genetic genealogy. Project administrators are also invited once a year to attend a conference hosted by Family Tree DNA in Houston.

Websites

- Relative Roots
 - o http://www.relativeroots.net
 - o http://www.facebook.com/RelativeRoots
 - o http://www.twitter.com/RelativeRoots
- Family Tree DNA
 - o http://www.familytreedna.com/
 - o http://www.familytreedna.com/faq/
 - o http://www.facebook.com/FamilyTreeDNA
- - o http://www.isogg.org
- Figure Genetic genealogy mailing lists and discussion forums:
 - o http://www.yahoogroups.com/group/ISOGG
 - o http://www.yahoogroups.com/group/DNA-Newbie
 - o http://forums.familytreedna.com
 - o http://www.dna-forums.org
 - o http://lyris.jewishgen.org/ListManager (JewishGen)
 - o http://lists.rootsweb.ancestry.com/index/other/DNA/GENEALOGY-DNA.html



Ysearch http://www.ysearch.org

SMGF http://www.smgf.org

YHRD http://www.yhrd.org

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