

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

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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 and mtDNA results, as well as get a virtual tour of your myFTDNA account.

# **myFTDNA**

Family Tree DNA provides every customer with a private myFTDNA account where the results of all tests you ordered at Family Tree DNA are posted. myFTDNA accounts contain the following information:

### My Project Groups

List of all projects you have joined, Join Projects, FTDNA Forum, myFTDNA Home

### My Account

Contact Information, Account Preferences, Order Tests & Upgrades, Order Personalized Report

### My Maps

Plot Ancestral Locations, Maps

### Y-DNA

Matches, Haplotree, Ancestral Origins, DYS Values, Print Certificate/Report/Data

### mtDNA

Matches, Ancestral Origins, Haplogroup Origins, Results, Print Certificate/Report/Data

# Family Finder

Matches, Chromosome Browser, Known Relationships, Population Finder, Download Raw Data

Tools

Refer Family & Friends, Interpreting Results, Ysearch.org, Mitosearch.org, GEDCOM, Genographic Project

# **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: Adenine (A), Cytosine (C), Guanine (G), Thymine (T)

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

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 offers four (4) levels of standard Y-DNA testing -12, 25, 37 and 67 STR markers - as well as a wide variety of advanced STR and SNP tests.

# STRs

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.

## **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.

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.

# Y-DNA Haplogroups/SNPs

Y-DNA SNPs define Haplogroups. SNP names typically start with a capital letter, followed by digits. Each SNP name corresponds to a hierarchical Haplogroup name. For example, haplogroup E1b1b1 is defined by a SNP called M35. The SNP or change at M35 is from a G to C. 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 SNP and Haplogroup names.

Family Tree DNA provides a free backbone (top-level) Haplogroup prediction for every customer who orders a Y-DNA test. Predictions are done using Family Tree DNA's robust database of customers who have already been SNP-tested. Predictions can be confirmed by ordering an optional SNP test. An optional deep-clade SNP test can also be ordered to refine the Haplogroup assignment to the deep subclade (subgroup) level.

# **Reading and Understanding mtDNA Results**

mtDNA contains 16,569 bases.

Family Tree DNA offers three (3) levels of mtDNA testing: mtDNA Basic, mtDNA Plus and Full Mitochondrial Sequence (FMS).

#### mtDNA Basic

Tests a section of the mtDNA known as Hypervariable Region 1 (HVR1), which has 569 bases.

#### mtDNA Plus

Tests HVR1 plus a second section known as HVR2, which has 574 bases.

## Full Mitochondrial Sequence (FMS) [previously known as FGS, Full Genomic Sequence]

Tests the entire Mitochondria – 16,569 bases.

### Cambridge Reference Sequence (CRS)

First full mtDNA sequence ever completed. Family Tree DNA reports results as differences from the CRS.

The following chart shows results for a sample Full Mitochondrial Sequence test: HVR1, HVR2 and the rest of the mtDNA, known as the Coding Region (CR). Each value shown is a difference from the CRS.

#### Haplogroup - K1a1b1a

| HVR1 diffe | rences from | CRS    | HVR2 diffe | rences from | CRS  | CR differences from CRS |        |        |  |
|------------|-------------|--------|------------|-------------|------|-------------------------|--------|--------|--|
| 16224C     | 16234T      | 16311C | 73G        | 114T        | 263G | 750G                    | 1189C  | 1438G  |  |
| 16519C     |             |        | 315.1C     | 497T        |      | 1811G                   | 2706G  | 3480G  |  |
|            | -           |        |            |             | -    | 4769G                   | 7028T  | 8860G  |  |
|            |             |        |            |             |      | 9055A                   | 9698C  | 10398G |  |
|            |             |        |            |             |      | 10550G                  | 10978G | 11299C |  |
|            |             |        |            |             |      | 11467G                  | 11470G | 11719A |  |
|            |             |        |            |             |      | 11914A                  | 12308G | 12372A |  |
|            |             |        |            |             |      | 12954C                  | 14167T | 14766T |  |
|            |             |        |            |             |      | 14798C                  | 15326G | 15924G |  |

### How to Read the Results

16224C = At location 16,224 on the mtDNA, this sample has a C instead of the reference value.

The chart to the right shows the reference (CRS) value at position 16224 as T, while this sample has a C.

### Comparing Results

In most cases, mtDNA matches should be exact. The differences from the CRS are compared:

|          | HVR1 Differences from CRS      |
|----------|--------------------------------|
| Person 1 | 16224C, 16234T, 16311C, 16519C |
| Person 2 | 16224C, 16234T, 16311C, 16519C |

| HVR1 REFERENCE SEQUENCE |  |  |  |  |  |  |  |  |
|-------------------------|--|--|--|--|--|--|--|--|
| Show All Positions      |  |  |  |  |  |  |  |  |
| CRS                     | Your<br>Result                                   |  |  |  |  |  |  |  |
| т                       | С  |  |  |  |  |  |  |  |
| С                       | Т  |  |  |  |  |  |  |  |
| т                       | С  |  |  |  |  |  |  |  |
| т                       | С  |  |  |  |  |  |  |  |
|                         | I Positions<br>CRS<br>T<br>C<br>T<br>T<br>T<br>T |  |  |  |  |  |  |  |

Genetic Genealogy Demystified: Reading and Understanding Your Family Tree DNA Results, Part 1: Y-DNA & mtDNA Webinar – February 17, 2011 Relative Roots © 2011 <u>www.relativeroots.net</u> Person1 and Person 2 have an exact match at HVR1, so they should also compare their results at HVR2 and the Coding Region.

Exact HVR1 match: 50% chance of a common ancestor within 52 generations.

Exact HVR1+HVR2 match: 50% chance of a common ancestor within 28 generations.

Full Mitochondrial Sequence match: 50% chance of a common ancestor within 5 generations.

### mtDNA Haplogroups

The backbone (top-level) mtDNA Haplogroup is determined by an included test of approximately 20 locations that define the major haplogroups. Subclades are determined by the Full Mitochondrial Sequence.

# Making the Most of Your Genetic Genealogy Experience

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

- Inform. 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, visiting the International Society of Genetic Genealogy website, and joining 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 <u>http://www.relativeroots.net</u>
- 🖋 Family Tree DNA
  - o <u>http://www.familytreedna.com/</u>
- M International Society of Genetic Genealogy (ISOGG) it's free to join!
  - o <u>http://www.isogg.org</u>

Solution Genetic genealogy mailing lists and discussion forums:

- o http://www.yahoogroups.com/group/ISOGG
- o <u>http://www.yahoogroups.com/group/DNA-Newbie</u>
- o <u>http://forums.familytreedna.com</u>
- o <u>http://www.dna-forums.org</u>
- o <u>http://lyris.jewishgen.org/ListManager</u> (JewishGen)
- o http://lists.rootsweb.ancestry.com/index/other/DNA/GENEALOGY-DNA.html

## **Public Searchable Databases**

M Ysearch

- o <u>http://www.ysearch.org</u>
- 🖋 mitoSearch
  - o http://www.mitosearch.org
- 🖋 SMGF
  - o <u>http://www.smgf.org</u>

🖋 YHRD

o <u>http://www.yhrd.org</u>

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