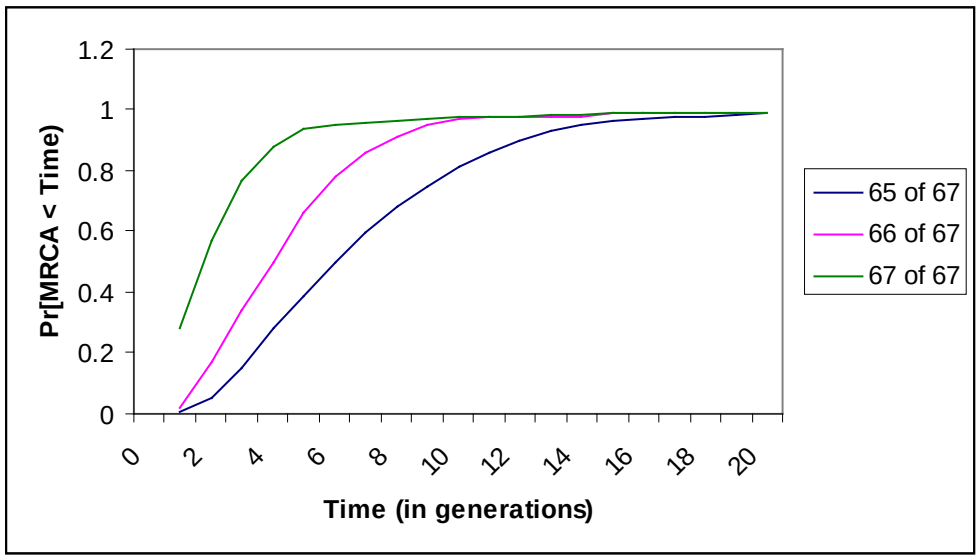
Understanding your 67 markers

You have had your Y chromosome DNA analyzed by **Family Tree DNA**. The results represent your actual allele values for 67 locations on the Y chromosome, and are listed on your certificate and in the Y-DNA DYS Values section of your personal page.

You can compare your results to other individuals to see how closely or distantly you may have shared a common ancestor. By referring to the "Y-DNA Matches" section of your personal page you will be able to compare yourself to others that are a match or close match to you. Specifically for genealogists, if you match another person with the same surname or a variant, you have a 99.9% likelihood of sharing a common ancestor with that person in a genealogical time frame. This individual is described scientifically as the Most Recent Common Ancestor (MRCA). Population geneticists then apply a term known as the Most Likely Estimate (MLE) for the time (T) when your MRCA would have lived. However, this is an estimate and in each individual case the actual generation could be nearer or further from the person tested.

The graph: In each case a common ancestor is shared between two individuals. In the case of 67/67 (a perfect match) the common ancestor is considerably more recent. For that reason, many people who share a surname will share a perfect or near perfect match. Many surnames are much older than a few hundred years and two people may share a surname but only match 66/67 or 65/67 or more. In these cases, as the graph shows, the MLE of when their MRCA lived could be much further back in time. Translation: you are related but probably much more distantly. Remember that this is an estimate, not an exact figure.



Since we are all related to one another if we go back far enough in time, it is important to only consider very close matches when we are using DNA to resolve genealogical questions. We have supplied you with both a graph (page one) and a table (below) to help you better understand the information given.

How often a marker changes or mutates varies depending on the marker. Because mutation rates may also vary between families, we provide a conservative estimate of how long ago your MRCA lived. While this may not be as satisfying, it tends to err on the side of producing false negatives rather than false positives. The science of DNA and genealogy is quite new and has been adapted from anthropology, where the MRCA is more flexibly defined.

The table: you are probably focusing on when the MRCA actually lived. We have provided a table below to help you better understand this issue. The table, along with additional information available online, tells you with statistical likelihood the generation when your MRCA would have lived. For example if two people matched exactly, there is a 50% probability that the MRCA was no longer than 2 generations ago and a 90% probability that the MRCA was no longer than 5 generations ago.

The FTDNATiP Calculator is our patent-pending time predictor. It is based on Family Tree DNA and the University of Arizona's mutation rate study of 2004 that provided us with benchmark mutation rates on a marker-by-marker basis. This study and the rates it observed form the backbone of the FTDNA-TiP. Mutation rates have been determined for the first 37 markers we test, and the next 30 are currently being added to the study. Until mutation rates for these 30 additional markers are determined, the calculator will use a conservative average mutation rate for these markers. With it, you can see a personalized prediction of the probable time to the most recent common ancestor you share rather than the approximation in the table below.

Bruce Walsh, Ph.D., noted population geneticist from the **University of Arizona**, provides us with this information. An expert on population genetics and statistical applications and co-author of one of the leading texts in this field, Dr. Walsh sits on the **Family Tree DNA** advisory board. His calculations are the basis for most discussions on the subject of DNA and the time to the MRCA for genealogy today. A more extensive list of calculations is available online, as are additional graphs for your benefit.

Number of matching markers	50% probability that the MRCA lived no longer ago than this number of generations	90% probability that the MRCA lived no longer ago than this number of generations	95% probability that the MRCA lived no longer ago than this number of generations
67 of 67	2	4	6
66 of 67	4	8	9
65 of 67	6	12	14

One feature offered exclusively to our customers is our database of Recent Ancestral Origins. This is a collaborative project between **Family Tree DNA** and the **University of Arizona**.

Ysearch is a public database we have created to aid genealogists who want to compare their results with other individuals worldwide, regardless of the company they tested with. Now that you have your results, you may want to add them to www.Ysearch.org and to a European Forensic database located at www.ystr.org.

Our lab is located at the **University of Arizona** where Michael Hammer, Ph.D., oversees this work as the director of the Genomic Analysis & Technology Core (GATC) facility. Dr. Hammer, who sits on the **Family Tree DNA** advisory board, also holds appointments to the Department of Anthropology and the Department of Ecology. He co-authored the first paper showing that present day 'Cohanim' are descended from a single male ancestor and discovered the marker on the Y-chromosome commonly used in population studies today (YAP marker).

Resolution: Your **Family Tree DNA** test examined 67 specific locations on your Y chromosome. The more genetic markers that are tested, the tighter the accuracy becomes. However, testing a greater number of loci does not increase the chance that you are related to someone. Scientists will tell you that if we go back far enough we are all related. On the other hand, testing a greater number of markers dramatically reduces your projected TMRCA with another person in the case of a match—the essence of most genealogical pursuits.

In the future, we hope to be able to bring forth examples of individuals related to famous persons in history so that researchers will be able to compare themselves. At that time we will begin to list those historical figures and their alleles on our web site for your comparison.

We plan to continue offering innovative ways to trace your families' anthrogenealogy in the future so it would be prudent to return to the web site from time to time to see what new opportunities exist for you. While there remember to search for your surname in our Surnames Database Library to see how our library continues to grow or whether a surname project has been established for your surname.

It has been a pleasure to serve you. If you have questions, please feel free to email us at info@familytreedna.com or to visit and read our ever-expanding Frequently Asked Questions (FAQ) page, www.familytreedna.com/faq/. For additional valuable education aids please go to: www.familytreedna.com/genetic-genealogy-tutorials.aspx.

Useful terms to know:

Allele: one of the different forms of a gene that can exist at a single locus. Since mutations in the allele value occur very slowly with time, one should see the same allele value for a male and his great-grandfather for example.

Chromosomes: bundles of tightly coiled DNA. Humans have 23 paired chromosomes; 22 pairs of autosomes and one pair of sex chromosomes. A single chromosome of each pair is passed from each parent to child.

DNA Y-Chromosome Segment (DYS): a nomenclature system which assigns DYS numbers to newly discovered markers. They are the "names" of each marker.

Gene: the functional and physical unit of heredity passed from parent to offspring.

Haplotype: a genotype of genetically linked loci that are inherited in a block as a single unit.

Haplogroup: branches in the human genetic tree (Phylogenetic tree). They are tied to deep ancestry (think 10,000s or 10s of 1000s of years). Haplogroups are predicted based on 12-marker results and using Dr. Hammer's backbone database and FTDNA's database of individuals who have had their haplogroup confirmed through SNP testing.

Locus (plural-loci): a specific spot in the genome. A variable locus will have several possible alleles.

Point Mutation: a change in a single base pair.

RAO (Recent Ancestral Origins): A database of countries of origin reported by people who have tested.

Short Tandem Repeat (STR): a region of repetitive DNA with short units of repetition (2 to 6 bases).

TMRCA: the term used by population geneticists to indicate the **T**ime to the **M**ost **R**ecent **C**ommon **A**ncestor shared with another person.

Y-DNA: non-recombining DNA which determines whether a child will be male or female. Y-DNA passes from father to son almost unaltered for long periods of time.