Time to the Most Common Recent Ancestor and Mutation Rates

By Roberta Estes (copyright 2008)[1]

One of the most frequently asked questions is how to effectively determine and use the Time to the Most Common Recent Ancestor (MCRA) and the TIP tool provided by Family Tree DNA.

You can access your TIP reports by clicking on the "My Matches" line on your Family Tree DNA personal page. Those with a similar surname will have a little red box that looks like a pedigree chart to the right. Click on that box and it will run the Tip report for you and the individual whose red box you clicked.

The results will be presented to you in percent of probability and will look like this:

In comparing 37 markers, the probability that Garmon Estes and Leroy F. Eastes, Jr. shared a common ancestor within the last...					
4 generations is 31.08%	**8 generations is** 71.35%	**12 generations is** 90.73%	**16 generations is** 97.39%	**20 generations is** 99.33%	**24 generations is** 99.84%

The two men in question above do in fact share a common ancestor 8 generations ago.

This tool was created by Family Tree DNA to give individuals a broad brush idea of when they might related to another participant, or conversely, if they are not related. Clearly, this is not an exact science, and furthermore, it relies heavily not only on your own results, but on statistical calculations of probability. While these calculations are very useful in population genetics, the closer one moves in time to the present, the less useful these calculations become. Why? Let's take a look.

Let's talk first about using mutations and mutation rates to determine the length of time that two individuals might converge in a common ancestor.

Mutation rates on the average and for various markers vary WIDELY, and I do mean widely. In one case, I know of a particular family whose mutation rates in 19 generations are 250 times greater than the average mutation rates. I know of another family whose rates are significantly lower, nearly zero, in about the same number of generations. Obviously, both of these are the outliers, but remember that average mutation rates are made up of just these things.....everyone's rate is put into the pot and they are all added together and then divided by the total number. So that rate may or may not be relevant to you or your ancestors. I

[1] TIP is trademarked by Family Tree DNA. The charts and graphs reproduced here are from the Estes surname project and are copyrighted by Family Tree DNA.

strongly discourage people from trying to figure out or correlate a genealogical connection between two individuals by using these rates or the number of generations given. It's just not a science refined enough for that yet.

The good news is that when you run the Tip report for 37 markers or higher, Family Tree allows you to modify the information using genealogical information, if you have it at your disposal, which will make the numbers more meaningful, but still nothing approaching what we would like to see.

So the next logical question is why some of your ancestral families (typically within surname projects) have no mutations and others have several. Let's look at how averages are constructed. If any given marker is on the average (remember what an average was from above) going to mutate once in every 15 generations, that means that some will not mutate at all, some will mutate more than once, but on the average you will see one mutation in 15 generations for that particular marker. This 15 generation number is just an example, as each marker has its own mutation rate. So a mutation could happen in the first generation, or the second, or the third, etc. If on the average you have 1 mutation every 15 generations, you don't know what "click the clock is on", you only when you started looking. This means that the mutation could have happened is the generation just before you began looking (i.e. your next oldest ancestor whom you have yet to find) and you won't see another one for 14 generations, or it could mean that you're "due" and the mutation happens immediately. It can also mean that you're NOT due, but you can still have a mutation anytime.

So, we have several factors at play here and whether or not we can measure, understand or change these factors.

First, the calculated average mutation rate for all markers. This number can be calculated and is often used, but bears little relevance to individual marker or family mutation rates.

Second, the individual mutation rate for any particular marker. This can be calculated and is used by Family Tree DNA. However, several unknowns remain, specifically, whether or not a marker is more likely to mutate in one direction or the other, or whether markers on the higher or lower end of the spectrum are more likely to mutate that markers in the middle of their spectrum.

Third, the personal mutation rate of your own family's DNA. This can be calculated but you'll need several individuals with solid genealogy connecting to a proven ancestor to be able to do this. Family Tree DNA calculations don't include this information as they have no information with which to calculate it.

Fourth, the personal mutation rate of any particular marker in your family. Same commentary as three above.

Fifth, the "click of the clock". This remains unknown.

Sixth, the mutation rate of the haplogroup. This variable is undocumented for the most part, but the fact that there is a variance is accepted in scientific circles. How much bearing this has on the rate of the click of the clock is at this time unknown, and the degree of effect that would come to bear from variations in the haplogroup mutation rate versus the individual family mutation rate could be very difficult to determine.

Seventh, generational length, which you could modify somewhat based on any knowledge about your ancestors and family patterns if known. For example, in some cultures, generation length average was much shorter as women began producing as soon as they were physically able. In other cultures and times, women didn't marry until they were between 21 and 25, which greatly affects the number of children they can expect to produce within their lifetime, and the average generational length. This variable can indeed be tweaked within the Family Tree DNA tip calculator when evaluating over 37 markers.

Eighth, where the mutations happen to fall in the three panels. For an example of this, see the final example below.

The best you can do with all of this is to use the tools provided by Family Tree DNA in their TIP program, but understand just how general these tools are (by the necessity of the above factors) and only use them as a very general reference. In particular, do not run the tip calculator and begin counting up the pedigree chart to the 10th generation and decide that surely this must be the common ancestor. You may be right, but chances are, you'll be wrong. The TIP calculator and common ancestors are much more reliable when working with very large timeframes over which to smooth out the effects of the outliers. For example, in the Estes example shown initially, the calculator is correct that the two men do share a common ancestor within 24 generations, and within 20, 16, 12 and 8. However, that calculation is based on 2 mutations in 37. If those 2 mutations fell within the first 25 markers, their report would look like this if run against only 25 markers instead of 37:

In comparing 25 markers, the probability that Garmon Estes and Roberta Estes shared a common ancestor within the last...					
4 generations is 25.59%	**8 generations is** 55.32%	**12 generations is** 75.65%	**16 generations is** 87.44%	**20 generations is** 93.74%	**24 generations is** 96.96%

If the mutations for these two gentlemen fell only in the third panel, then they would match at 100% if they had only tested 25 markers, and then their report would look like this:

In comparing 25 markers, the probability that Garmon Estes and Geoffrey D. Estes shared a common ancestor within the last...					
4 generations is 61.17%	**8 generations is** 84.92%	**12 generations is** 94.15%	**16 generations is** 97.73%	**20 generations is** 99.12%	**24 generations is** 99.66%

Remember that this example is using the same number of mutations but placing them in different panels and running the tip against either the 25 or 37 panel models.

The moral of this story is that we should use all of the tools available to us, with our eyes wide open, and always, always evaluate the scientific data in light of the genealogical information available. However, like most everything else in life, there is an exception to the rule.

If the DNA says you're not related, then you're not related. I have intentionally selected two men who I know are not related to demonstrate this phenomenon.

In comparing 12 markers, the probability that James Estes and Garmon Estes shared a common ancestor within the last...					
4 generations is 0.00%	**8 generations is** 0.00%	**12 generations is** .05%	**16 generations is** .19%	**20 generations is** .53%	**24 generations is** 1.21%

DNA can disprove genealogy, but genealogy cannot disprove DNA. However, these statistical tools are not infallible.

Another handy feature provided by Family Tree DNA is a chart that gives rules of thumb for matches and mismatches. Generally, I would agree with this, but again, averages are compiled by including all of the data, including outliers, and this is not gospel, it is a statistical guideline. Looking at the following chart provided at http://www.familytreedna.com/gdrules_12.html, keeping in mind that while we do call 3 mutations in 12 generally "unrelated", if these same 3 mutations were the only ones out of 37, we'd be calling the two people "related". It is possible, if improbable, that someone could have 3 mutations in the first panel and match on the rest. The only way to know is to perform further testing.

Distance	Relatedness	Explanation
0	Related	Your perfect 12/12 match means you share a common male ancestor with a person who shares your surname (or variant). These two facts demonstrate your relatedness, however if your name is one of the most common surnames, i.e. Smith, Tailor, Miller, etc, (trades or towns) then we always suggest you utilize additional markers to eliminate the possibility of a coincidental surname and genetic match.
1	Possibly Related	You share the same surname (or a variant) with another male and you mismatch by only one 'point' on only one marker. For most closely related or same surnamed individuals, the mismatch markers are either DYS 439 or DYS 385 A, 385 B, 389-1 and 389-2. To ensure that the match is authentic you should utilize additional markers.
2	Probably Not Related	You share the same surname (or a variant) but are off by 2 'points' or 2 locations on just 12 markers. It is only possible that you and another related family members' line each have had a mutation. There are two ways with DNA testing to confirm or deny. One is to test additional family members to search for a line that shows a mutation that is 1 point closer to your sample. The other is to test additional markers. Refining greatly enhances science's ability to determine relatedness -- geared towards the most accurate assessment of the number of generations to a shared ancestor. Only by further testing can you find the person in between each of you...this in 'betweener' becomes essential for you to find, and in their absence we feel you are not related.
3	Not Related	9/12 - is too far off to be considered related. Unlikely but vaguely possible that the rule for Probably Not Related applies.
4	Not Related	8/12 - You are not related and the odds greatly favor that you have not shared a common male ancestor with this person within thousands of years.
5	Not Related	7/12 - You are not related and the odds greatly favor that you have not shared a common male ancestor with this person within thousands of years.
>5	Not Related	You are totally unrelated to this person.

For more detailed information about the TIP calculator, refer to the FAQ page at http://www.familytreedna.com/faqtip.html.

Under what circumstances can we best utilize these tools? I use these tools most often to determine whether people with differing surnames are related in a genealogical timeframe, especially if I find them co-located. Again, TIP is most accurate the further back in history you can reach. It is particularly useful in answering questions like are the McMahon family and the Estes family really descended from a common ancestor and if so, in what timeframe might we reasonably expect to find that common ancestor. I also use TIP as a sanity check when the genealogy is questionable.

TIP is useful if we don't expect it to perform more than it can, don't use it to mis-set our expectations and or to "confirm" things like "two men share an ancestor within the last 8 generations". TIP can't do that, and this type of misconception and over-interpretation is all too common with excited first time participants who have just received their results. Using this tool correctly and understanding the results can indeed help us move our genealogy project forward by accurately utilizing both genetics and statistics.