A little more on atDNA and SNP testing

Regarding DNA testing, there are different tests that you can use. For some basic things about DNA testing, please see the following hyperlink. https://carpentercousins.com/DNATesting.pdf

A quick summary follows.

Y-Chromosome DNA (Y-DNA) – passed from father to son virtually unchanged. It is excellent for surname studies.

Mitochondrial DNA (mtDNA) – passed down from the mother to her children via her X-Chromosome, but only her daughters can pass it to the next generation. Because this is the most common DNA in the body, it is most often the DNA that survives in ancient remains.

Autosomal DNA (atDNA) – This is DNA you get from both parents and they in turn get it from their parents. It is excellent for immediate family and close cousins. It is not so great for more distant cousins. It is considered by many as a short range DNA test compared to Y-DNA and mtDNA tests.

Let me briefly expand on this last one …

You own 100% of your atDNA but only get 50% from your parents, 25% from your grandparents and each generation back is halved. At the sixth generation in the past you are at 1.5625% and this 1% range is where you start to get random matches or matches "identical by state."

You – 100% of your atDNA
Parents 50% from each <– 1 generations back in time
Grand Parents 25% <- 2 gen - most matches are 1st cousins or uncles & aunts
2GP 12.5% <- 3 gen - most matches are 2nd cousins
3GP 6.25% <- 4 gen - most matches are 3rd cousins
4GP 3.125% <- 5 gen - most matches are 4th cousins
5GP 1.5624% <- 6 gen - most matches are 5th cousins ← 1% range
6GP 0.78125% <- 7 gen - most matches are 6th cousins
7GP 0.390625% <- 8 gen - most matches are 7th cousins

Yes, it is possible to go a few more generations past this, but it takes many atDNA tests and good triangulation of genealogy with the tiny centimorgan atDNA segments compared by a super computer. Such a computer is used at GEDMATCH.com. But most people can usually go just five generations in the past.

I attach two different images regarding atDNA testing. See the bottom of this report. One is to better refine atDNA centimorgan (cMs) segments in regards to relationships. But, it assumes that you have only one common ancestor with the other person.

When you have two or more common ancestors it is possible for the small cMs segments to over lap, thus appearing larger. For example a segment of 18 could appear as something larger such as 30 cMs in size. When you know you have two or more common ancestors, this requires

selective atDNA testing to help determine the true size of the atDNA segments by identifying and focusing on those specific segments.

The other image above shows the probability of NOT matching a more distant cousin. For each generation, you loose one half of the atDNA segments from that generation of ancestors. This is through the recombination of the egg and sperm and over time, it is possible that you will NOT match a documented genealogical cousin.

For example, a fourth cousin has a 30.7% probability of not being detected with atDNA testing. And a sixth cousin has an 89.9% chance of not being detected.

SNPs (Single Nucleotide Polymorphisms called snips) are a hick up or burp, so to speak in the short tandem repeats (STRs) in the X (X-SNPs) and Y (Y-SNPs) Chromosomes coding. Many of these SNPs are genetically inherited and can be traced back into times mathematically. These SNPs helps with our understanding of our human ancestry and where we came from.

SNPs do come in different flavors and some are temporary or transient in our coding. Those are a story for another time. For the purpose of this brief, we are focused on Y-SNPs because it is often tied into Y-DNA testing above 111 markers at FTDNA and at other DNA testing companies.

Remember that Genetic Genealogy is using genetic testing to help over come road blocks in genealogical research and helping determine genetic relationships. But, some people are interested in the anthropologic side of genetic DNA testing which is often called our Deep Ancestry. Another way of looking at it is that this is before most genealogical records and well documented history.

Briefly, Deep Ancestry is measured by Haplogroups and they are which is measured thousands and in tens of thousands of years in age along with its “younger” subtypes. It is possible through SNP (Single nucleotide polymorphism) testing to further refine the Haplotype more precisely in time.

You can use the first 10 or 12 Y-STR (aka Y-DNA) markers to help determine the basic Haplogroup type. We called that an estimated Haplogroup.

The only way to confirm your Haplotype is by testing for your SNPs and getting confirmation by a positive value for each one in a series. There are thousands of SNPs, and you do not have all of those known. When you get positive SNP confirmations that means they are derived or tested for. Again, Haplotyping is defined by a specific set of derived SNPs (aka Snips) or SNP markers that have been positively tested for back to the last or terminal SNP you test positive for.

In some haplotypes, such as the major Haplogroup R1b1 and its Haplotype R1b1a1a2 (long hand version), and defined by the specific SNP marker M269. Some of those confirmed SNPs have mathematically been confirmed within historical times (plus or minus x number of years at x percent probability). This Y-Chromosome Haplogroup is the most common one in Western

Europe with up to 80% of the males in some countries having it. Naturally, it is the one most studied!

Please note that in many DNA testing companies like FTDNA, they use a short hand code and label the Haplogroup and its sub-type as R-M269. See more at: https://carpentercousins.com/R-M269.pdf

In conclusion and to put it in perspective, I provide my real deep ancestry at the following hyperlink. Please be aware that this was done in tongue in cheek or with a bit of humor. This is because it uses several different formats to show the deep ancestry.
https://carpentercousins.com/RealDeepAncestry.pdf

Only three lines on that report are genetic genealogy related. They are those starting with: Group 3:, MRCA: and ME:. All the rest is anthropological in nature.

The Shared cM Project – Version 3.0
August 2017

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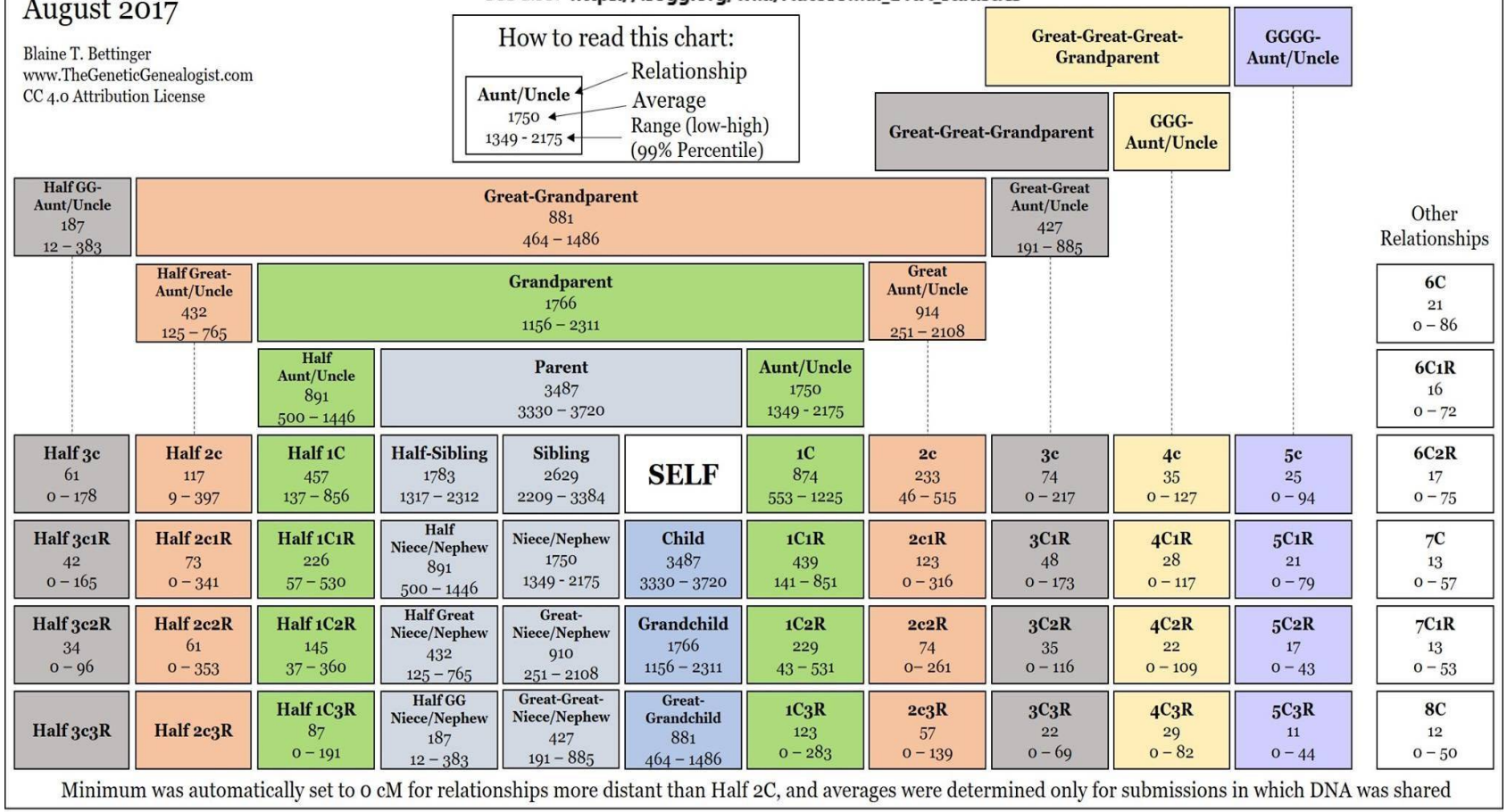
For MUCH more information (including histograms and company breakdowns) see: goo.gl/Z1EcJQ
See also: **https://isogg.org/wiki/Autosomal_DNA_statistics**



Minimum was automatically set to 0 cM for relationships more distant than Half 2C, and averages were determined only for submissions in which DNA was shared

Theoretical probabilities

Extracted from:
https://isogg.org/wiki/Cousin_statistics

The content of the following two tables is derived from Table 1 in the paper The probability that related individuals share some section of genome identical by descent by Kevin P Donnelly, Statistical Laboratory, Cambridge University, Cambridge, England. (Source: *Theoretical Population Biology* 1983: 23, 34-63) A copy of the paper is available here.

Genealogical Relationship	Probability of *No* Detectable DNA Relationship
1st cousin	0.00%
1st cousin once removed	0.00%
1st cousin twice removed	0.00%
2nd cousin	0.00%
2nd cousin once removed	0.10%
2nd cousin twice removed	2.30%
3rd cousin	2.30%
3rd cousin once removed	12.10%
3rd cousin twice removed	30.70%
4th cousin	30.70%
4th cousin once removed	52.00%
4th cousin twice removed	69.80%
5th cousin	69.80%
5th cousin once removed	82.20%
5th cousin twice removed	89.90%
6th cousin	89.90%
6th cousin once removed	94.40%

Genealogical Relationship	Probability of *No* Detectable DNA Relationship
1 x great grandparent	0.00%
2 x great grandparent	0.00%
3 x great grandparent	0.01%
4 x great grandparent	0.56%
5 x great grandparent	4.95%
6 x great grandparent	17.76%
7 x great grandparent	37.43%
8 x great grandparent	57.53%
9 x great grandparent	73.50%
10 x great grandparent	84.38%
11 x great grandparent	91.12%
12 x great grandparent	95.07%
13 x great grandparent	97.31%
14 x great grandparent	98.54%