

**JOHANN THEOBALD YOUNG (1691-1763):
DNA AUTOSOMAL STUDY OF DESCENDANTS**

By

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The following manuscript represents an interpretive guide to the raw data of the autosomal DNA testing of descendants of Johann Theobald Young (born 1691 Dunzweiler Germany, died 1763 Canajoharie New York) shown in the Excel spreadsheet accessed by [clicking here](#). To date there are 12 participants in the study, all descendants of Theobald's eldest son Johann Adam Young (1717-1790) who with his wife and three sons settled on lands in Ontario Canada given to them by the Crown and the Six Nations Indians for service during the American Revolution. Also two participants are additionally descended from Theobald's youngest son Theobald Jr. (circa 1735 to 1771) whose son John D. Young (1766-1856) came to Ontario after the War of 1812. The testing of each participant was completed using the new chip technology with more than half a million DNA markers and the platform offered by [23andMe](#).

Rationale for the Present Work –

The present work was inspired by the research of Dr. Ann Turner who used the same comparisons to attempt to pinpoint the segment of DNA responsible for the genetic form of hearing loss which affected her family. The study described in the following pages focuses only on the use of this methodology in the exploration of sharing of ancestral segments of DNA by members of the extended Young family.

Knowledge of how the testing of DNA can help us better understand our relationship to our early ancestors is not widely known. Most people would be satisfied with a well-researched paper trail assembled via genealogical procedures (written and oral records of family members). What more would be needed? The answer is that it depends on how comfortable one is with uncertainty. No one wants to contemplate the possibility that their cherished genealogy is misleading or erroneous, but with each passing generation the probability of such a scenario increases. Alas, the third great grandfather carefully recorded on a pedigree chart may be nowhere to be found in the descendant's genome (array of genes and chromosomes – one's DNA).

The present study uses cutting edge DNA technology to determine how and in what way members of the extended Young family are biologically connected. The data are able to 'tell a story' when properly interpreted. It comes as no shock to those familiar with the principles of genetic inheritance that the 'predicted' and 'observed' DNA sharing seldom match beyond the level of second cousins. Some third cousins will have no matching segments, and some 5th cousins will have multiple matching segments – presumably due to chance.

So what can we learn about living descendants and early ancestors by conducting an autosomal DNA study of the Young family? In essence, if we have a large and diverse enough sample (number of participants from the extended family and a variety of 'cousinship' relationships) we can literally (in theory) rebuild the genomic sequences of each chromosome for each Young ancestor. Secondly we will be able to compare the specific predicted and observed matching of each of our Young cousins – seeing how much DNA we share, and specifically where along our chromosomes this sharing takes place.

Some Problems with Traditional Genealogy -

It is often assumed that the paper trail (via traditional genealogical sources) can be assumed correct if there is more than one confirmatory source. In reality, 'non – parental events' (e.g. adoptions, half-siblings, children from earlier marriages for which no record was kept, etc.) were not uncommon, meaning that one's genetic link would not match one's paper link to a particular ancestor. The number of these occurrences which break the biological link between a paper trail descendant, and their supposed ancestor, varies dramatically by family, place and time. The author has never encountered an event of this nature in his paternal lineage despite testing cousins to the level of 8th cousins – we all have the same DNA signature (allowing for a number of mutations expected in that time frame). A second 'problem' is that after a mere 5 generations, ancestors who are in your genealogical tree begin to fall off your genetic tree. You may have 32 third great grandparents 'on paper', but the stark reality could be that perhaps two (for example) are no where to be seen in your genome – they have 'left the building' forever. Much more will be said about this issue. Ultimately, it is only the cross validation offered via DNA testing that can provide the 'ultimate proof' of biological lineage.

So, are your Young ancestors from more than 5 generations ago in your genetic tree? There is only one way to find out – using one or more of the 4 types of DNA testing. The focus here is on autosomal testing.

Types of DNA Testing -

1) Y – Chromosome DNA –

Some years back (2001), the present author decided that it was important for posterity to determine the genetic ancestry of the Young family from Dunzweiler, Germany who emigrated to the Mohawk Valley, New York, USA (circa 1712), and subsequently Haldimand County, Ontario, Canada (circa 1783). In 2001, the only way to address this aim was to determine the **Y chromosome DNA signature** (haplotype) of the emigrant Johann Theobald Jung, and later his "deep ancestry" (haplogroup). To this end, descendants of Theobald's grandsons Lt. John Young and Sgt. Daniel Young were recruited and the DNA testing was completed by Family Tree DNA. The two descendants with the surname Young (Larry and Ken) matched on 36 of 37 YSTR (short tandem repeat) genetic markers. This meant that we had captured the 'DNA signature' (minus one marker) of Johann Theobald Jung and his son Johan Adam Jung (born 1717

Schoharie New York), the father of the above John and Daniel (as well as David, Henry and Elizabeth). It remained to ascertain the Young haplogroup and this was done via YSNP (single nucleotide polymorphism) testing for key genetic markers which would allow us to place the Youngs within the human Y chromosome family tree. Testing of one person (all males with the surname Young would have the same grouping) by Family Tree DNA, as well as three individuals via 23andMe, showed that the Youngs belonged to haplogroup R-U152/L2* or more precisely R1b1b2a1b2d3*. This grouping is concentrated in the region of Switzerland and appears to be associated with the Hallstatt and LaTene Celtic peoples of Central Europe. If the Youngs had resided in the same area back to Roman times, then they were probably members of the Celtic Treveri Tribe.

2) mtDNA –

Essentially, we now had the male lineage (**Y DNA**), but were left with the reality that determining the straight line female lineage (**mitochondrial DNA i.e., mtDNA**) was not going to be easy and perhaps impossible. Mitochondria are cell inclusions, of which there are about 1000 per cell. They are mini power packs, with their own DNA separate from the nuclear (autosomes and sex chromosomes) DNA. If we wished to know the **mtDNA haplotype** (signature) of say Adam Young, we would need to find a direct line female descendant of his mother (Marie Catharine Snyder). Since female surnames have traditionally changed each generation, this has simply proven to be an impossible task – and it may be that the lineage went extinct some time in the past. It is clear that there is no known direct line mtDNA descendant of any of the early Youngs. Hence we need to explore more recent ancestors. This was accomplished for Elizabeth Young (1827-1897) by testing of two of her descendants - a great grandson (Bob Nelson, who is three generations distant from Elizabeth) and his great nephew (Gerry Kenney, who is five generations distant from Elizabeth), both in the direct female line, to determine that Elizabeth was haplogroup J1c (via her mother Mary Terryberry, the later's mother Ann Young of New Jersey and so on).

3) X – Chromosome DNA –

Another approach to understanding the relationship between family members (and verifying hypotheses if that is the goal) is to explore matches on segments of the **X chromosome**. This sex chromosome occurs in pairs in females but males have only one. Recombination occurs only in females during meiosis (when eggs are formed) – no meiotic recombination occurs in males. In a pedigree, two males (father and son) will break the link since a father gives his son only his Y chromosome not his X (which goes to his daughters intact). Thus within the extended Young family, there will be some who have inherited segments of the X chromosome from say Lt. John Young (only via his daughter Elizabeth Nelles) but others (such as direct male descendants) will have inherited nothing from this ancestor on their X. Among all of the known Young descendants, the present author's Uncle Dale Williamson is 'closest' to the early Youngs, being only three meiotic recombination events from Lt. John Young's wife Catharine Hill. Due to the inheritance patterns of this chromosome, although his predicted percentage of DNA from Catharine is 12.5%, Dale could have received his X intact from

Catharine, or zero percent, or some combination in between (via potential recombination in Catharine's granddaughter Rachel Young, Rachel's granddaughter Hannah Adelia Young, and Hannah's granddaughter Eva Fern Dawson, the mother of Dale).

4) Autosomal DNA –

Facts about Autosomal Inheritance, the Genealogical Tree and the Genetic Tree:

The DNA testing where all Young descendants can participate is the testing of **autosomal DNA**. There are 22 pairs of non sex chromosomes that are recombined in each generation (during the formation of eggs or sperm) such that anyone, male or female regardless of inheritance pattern (e.g., male to female to female to male ancestor), may have inherited segments of DNA (haplotype blocks) from an early Young ancestor. The fewer the number of intervening generations, the more likely it is that there will be some inheritance from a particular ancestor. Larry Young and his siblings are only five generations back to a child of Adam Young (in this case Lt. John Young). To the best of the author's knowledge, this represents (as with Dale Williamson and the X chromosome) the branch of the family that is presently the closest (fewest generations removed) to one of the four children of Adam Young.

Concerning the bulk of your DNA, arranged on the 22 pairs of autosomes, there are some important facts that are seldom recognized. For example, as noted above, although an individual may correctly appear as an ancestor in your recorded family tree, they may be only a genealogical or "paper ancestor" not a genetic/biological ancestor. After 5 generations, ancestors start dropping off your genetic family tree due to the process of DNA recombination. You have a:

- 1) 99.6% chance of sharing with all 16 great great grandparents.
- 2) 54% chance of sharing a DNA segment with each of your great great great (3rd great) grandparents (of which you have 32).
- 3) 0.01% for sharing DNA with all 64 of your great great great great (4th great) grandparents.

At the 10 generation level, although everyone will have 1024 ancestors as plotted on a chart, an unknown percentage of your genealogical ancestors will remain as genetic ancestors embedded in your DNA. Some have calculated that the number will be about 125 ancestors – a relatively small number – possibly as low as '12% of your genealogical tree is in your genetic tree'.

In fact these calculations or simulations have not been tested empirically, so remain only an assumption at this point. Some related facts about genetic ancestors to 10 generations include:

- a) The true number of genetic ancestors is likely between 125 and 377.
- b) There are approximately 470 segments on the 44 chromosomes.

- c) If we split the difference we could have about 250 ancestors, or 1 of 4, contributing to about 500 segments of DNA.
- d) Each remaining ancestor would likely provide between one and possibly 20 segments of various lengths.
- e) Perhaps the number of actual ‘haploblocks’ (and contributing ancestors) is even greater if the segments have been ‘shredded’ by recombination to the point where there are many scattered small (e.g., one million nucleotide ACTG bases of the three billion in the genome) segments that unfortunately cannot be assigned to a specific ancestor with today’s technology.
- f) These calculations will ultimately have to consider the average versus the extremes since there are considerable differences between individuals, and differences between the sexes.
- g) To some degree male-to-male inheritance is more likely to preserve lengthy DNA segments versus female-to-female inheritance. This is due to the higher ratio of female recombination during meiosis (egg formation), which is 1.6 times higher relative to sperm formation in males. This means that over the generations, a series of female direct line ancestors will likely chop DNA-inherited segments into smaller units (which at some point will become undetectable). Hence after 10 generations you will have a 30% greater chance of being related via a maternal Young ancestor than a male line ancestor (14% versus 11%) – this number is via simulations not empirical observations. However this estimation may be cancelled out by the tendency of genes close to one another not to recombine and so favour male transmission (being less likely to recombine at any time). Some, however, will depend on factors such as the parameters of the individual chromosome – chromosome 1 is the largest, and chromosome 22 is the smallest and least likely to retain a large number of recombinations.
- h) Please note that this is all in the realm of educated guesswork and subject to change as new empirical observations are published.

To summarize, of the hundreds of descendants with a firm paper trail to say Lt. John Young seven generations back, he will simply not be represented in a detectable way in the genome of some of these present day descendants. However by chance a sizeable amount of his DNA may be found on multiple chromosomes in another person who is at the same generational distance (number of generations away from a particular ancestor). Chance plays a large role in genetic inheritance.

Facts about Cousin Sharing:

As of the current date, all of the descendants from the Young family who settled in Haldimand County in 1783 are 5 or more generations (typically 7 or more generations) from ‘the source’. Hence, the author wanted to embark on this DNA testing as soon as possible, as in the not too distant future it is going to become more difficult to determine the autosomal DNA motif of our Young ancestors. In other words, it appeared to be important to act now while we can recover useful data.

The above reality can be looked at in terms of probability of detecting a cousin. The probability of detecting a:

- 1) 2nd cousin is >99%
- 2) 3rd cousin is ~90%
- 3) 4th cousin ~45%
- 4) 5th cousin ~15%
- 5) 6th cousin or beyond <5%.

For a match considered 'identical by descent', 23andMe requires a matching segment at least 7 cM (centiMorgan – a measure of genetic distance), roughly 7 Mb (7 million matching base pairs, SNPs, in a sequence), and that there be a minimum of 700 SNPs in this segment. What this amounts to in the feature 'Relative Finder' is that matches of 0.06% matching segments in the total genome DNA will be under the bar and about 0.07% total DNA identical or shared will trigger the 'you match' indicator in their 'Family Inheritance' feature which will be reflected in the lowest possible match shown as a blue segment (actually this is just a rough approximation of their algorithm – the mathematical decision making that decides whether you and another person are related).

As a result of the testing, some of us will find out that we share far more Young DNA than predicted by statistics. Hence we are “closer” than the genealogical documentation would suggest. The type of testing done here allows us to look at our 'closest DNA connections', all the while being aware that testing another relative, even of someone who does not reach the “matching bar” for distant relatives set by 23andMe, could result in a match at a high level. Even two siblings can differ dramatically in their matching profile to other Young descendants. Low matching could change with new participants.

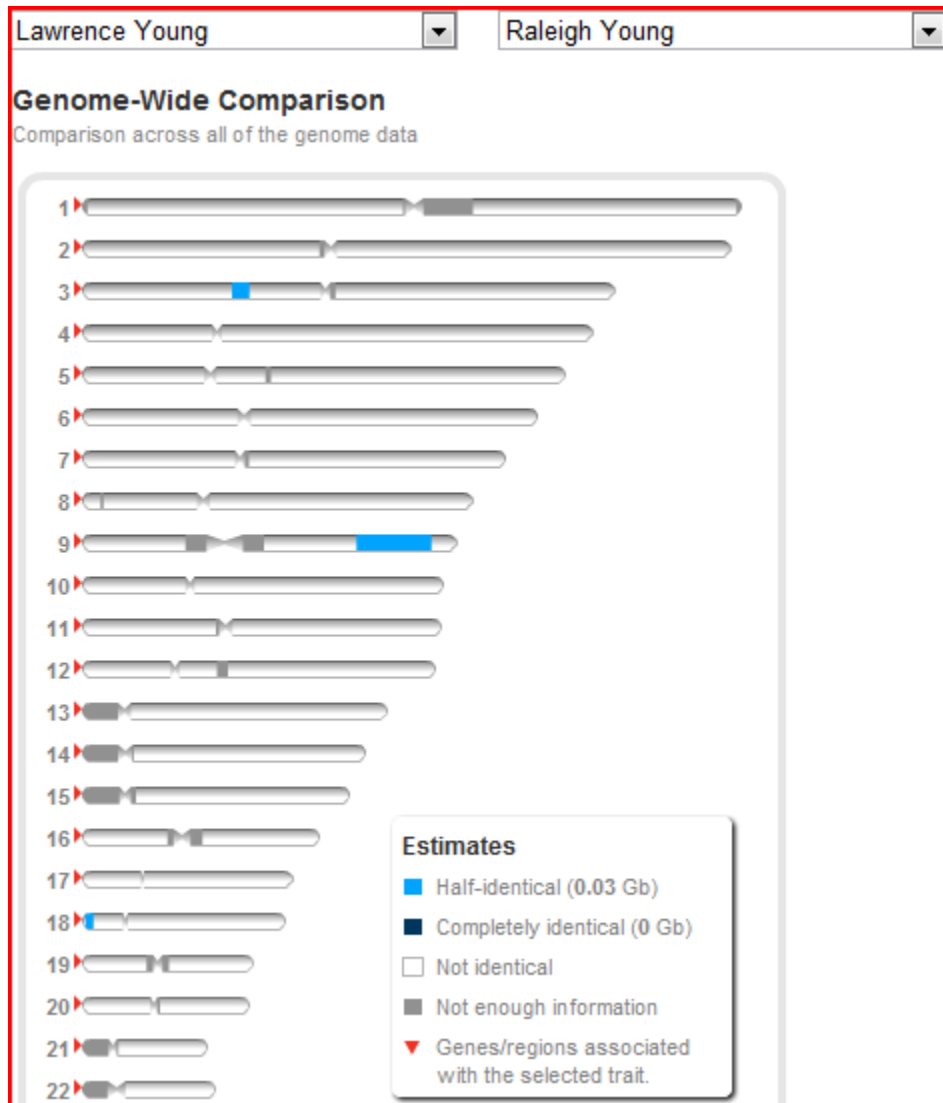
One cautionary note is that with 23andMe's current technology, there is always the possibility of a 'false positive' relationship match. In addition, we will all match people for whom there is no connection except in antiquity, before written historical records. This type of matching is particularly common among Ashkenazi, Colonial Americans, and Finns (to name a few). However if we have a list of 200 matches (say 3rd to 5th or distant cousins according to 23andMe) of a database of 40,000 people, only about 10% of the 200 23andMe matches (if that) will be true kin and others simply share common bits of Eurasian DNA and match by chance (identical by state not descent). Ironically, if you match another Young descendant at say 0.05% of your DNA (a true finding), it will not show on the 23andMe “Relative Finder” feature because of where they 'set the bar' to avoid the danger of a false positive.

The DNA testing done here can also be used to test genealogical hypotheses. For example there were multiple sources of genealogical evidence indicating that the eldest sister in a family of 9 siblings in one Young family was not the biological child of the father to the rest (i.e., there were indications that she was a half-sister to her 8 siblings). By testing selected descendants of this particular family and comparing expected with observed percentages of shared DNA, it is possible to support or refute what the documentation is saying. Similarly, consistently high percentages of matches between

those who “should not” match at such a high level may be indicating that an unknown biological relative (e.g., the unrecorded father of the half sister) may have also been a member of the Young family – which will in turn lead to a search for likely candidates. This is precisely the scenario that was tested and the findings that led to further questions about the identity of the “mystery man” who fathered the eldest daughter in the family.

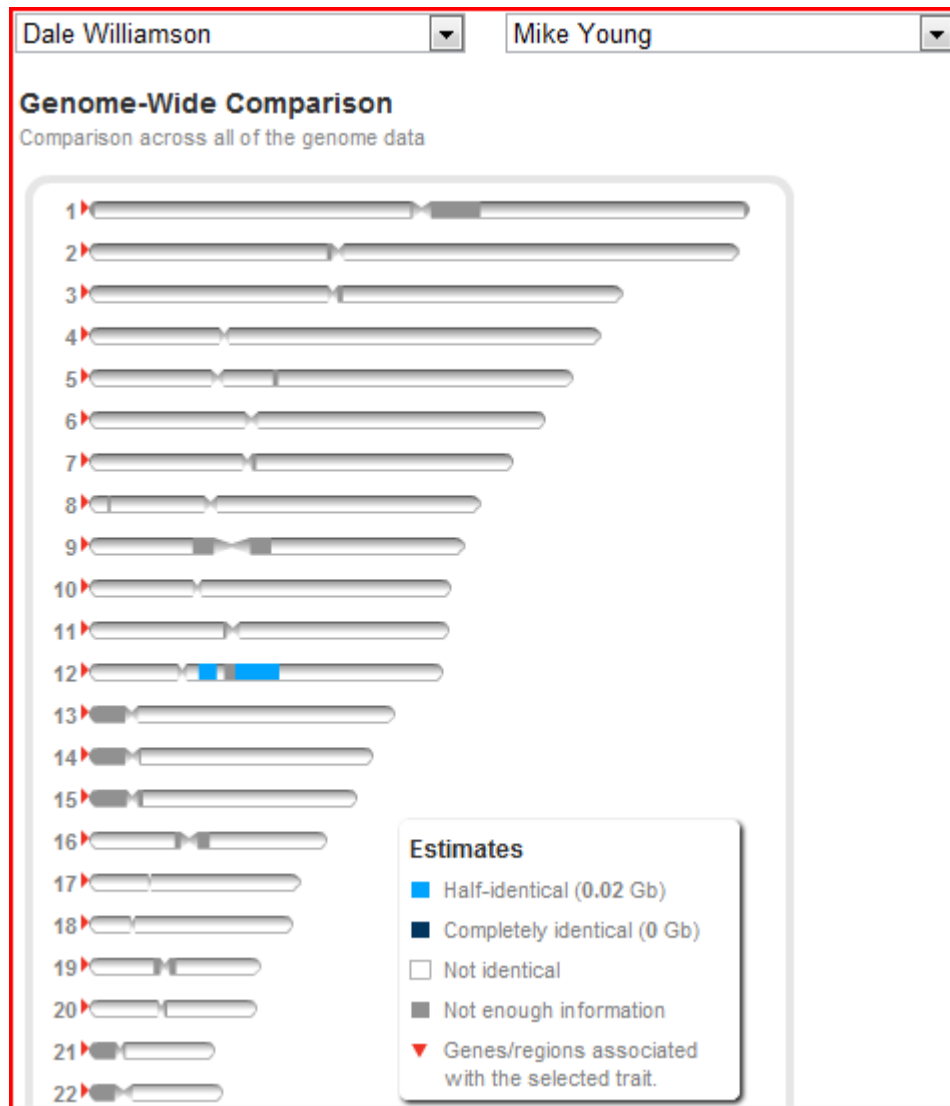
Some Concrete Examples, Observations and Further Information:

Perhaps the rationale above about the potential for the genealogical and genetic trees not matching after 5 generations has been persuasive. Each person will have their own reasons for wanting to test or not. In the case of the present author, he does not have the Young surname and even though the paper trail to the Youngs via three individuals (cousin marriages) is clear, there is something very tangible or three dimensional to see in the 23andMe results an area of a chromosome blocked out in blue which I/we share with another Young descendant – what we have inherited from our early Young ancestors.



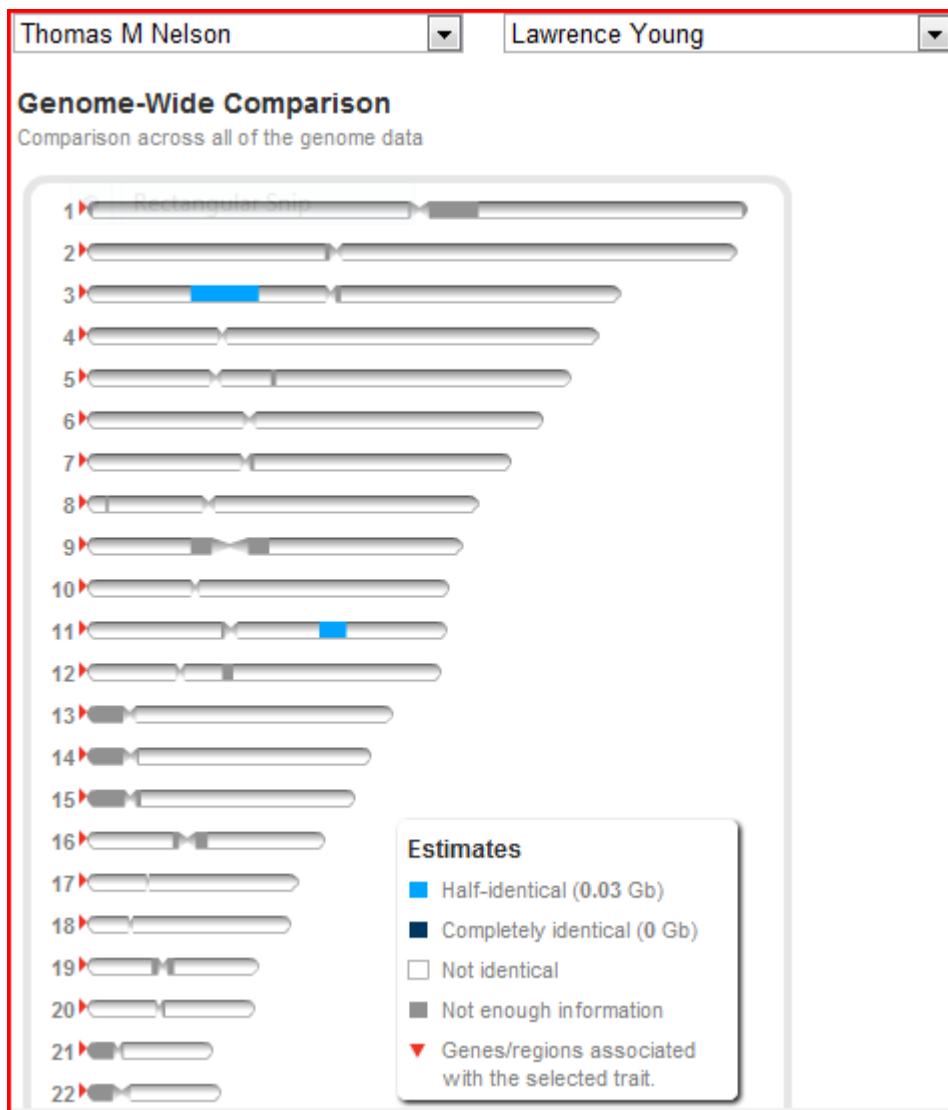
Some or most individuals will share at the predicted (based on statistical tables) percentage. One example is Larry Young and Raleigh Young who are third cousins twice removed (see chart above). Their sharing is via the direct male line. In other instances those of the same branch who are also third cousins twice removed do not share any DNA segment (likely due to the more tenuous or unpredictable results when generations go from say male to female to female to male and so on).

Another example is Mike Young and his 4th cousin Dale Williamson seen in the chart below. Despite the direct male to male transmission via Mike and the swinging back and forth between male and female ancestors in Dale, both men share an expected amount – actually somewhat more, perhaps due to their each having three Young ancestors.

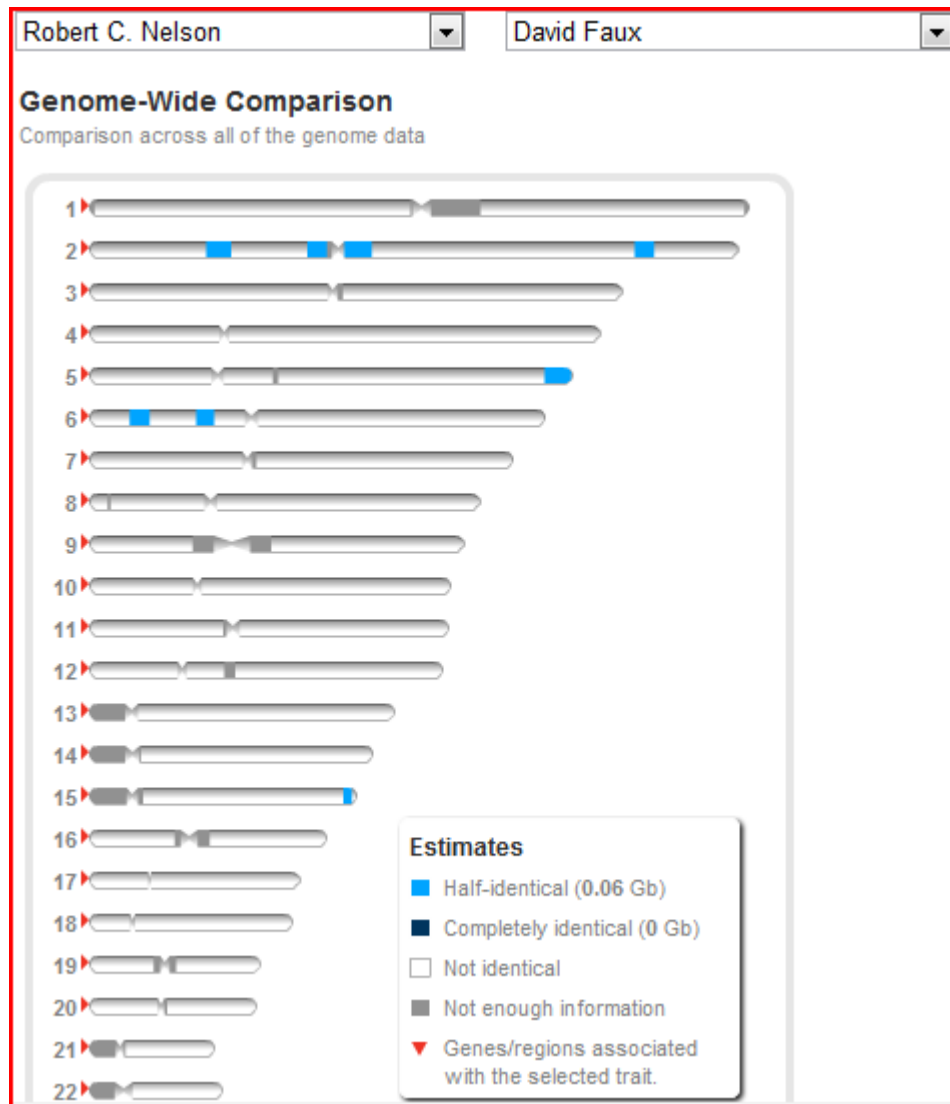


It is also apparent that some unexpected discoveries await. It was very surprising, based only on genealogy, that Tom Nelson matches a very large number in the current test group, whether from the Sgt. Daniel or Lt. John line - and often at a high level. As an

example, the sharing between he and his 5th cousin once removed Larry Young is shown in the chart below. This observation is very difficult to explain, especially since his own uncle does not show the unexpectedly strong affiliation with Young DNA, though he and Tom have the expected DNA share between an uncle and nephew. Tom must have (by chance) received a very large percentage of Young autosomal DNA from his father (his uncle Bob's brother). In another instance, Bob Nelson, his nephew Tom Nelson, and Bob's great nephew Gerry Kenney all match Paul Fawcett (a descendant of Abraham Young) on a single segment on chromosome 13. Considering that they are very remote cousins this is a fortunate find. The observation means one of two things. Either the Nelson family has another Young ancestor, likely one descended from Lt. John Young's son Abraham Young, or we are seeing a specific segment of DNA that comes from the most recent common ancestor Adam Young (born 1717) and / or his wife Catharine Elizabeth Schremling.

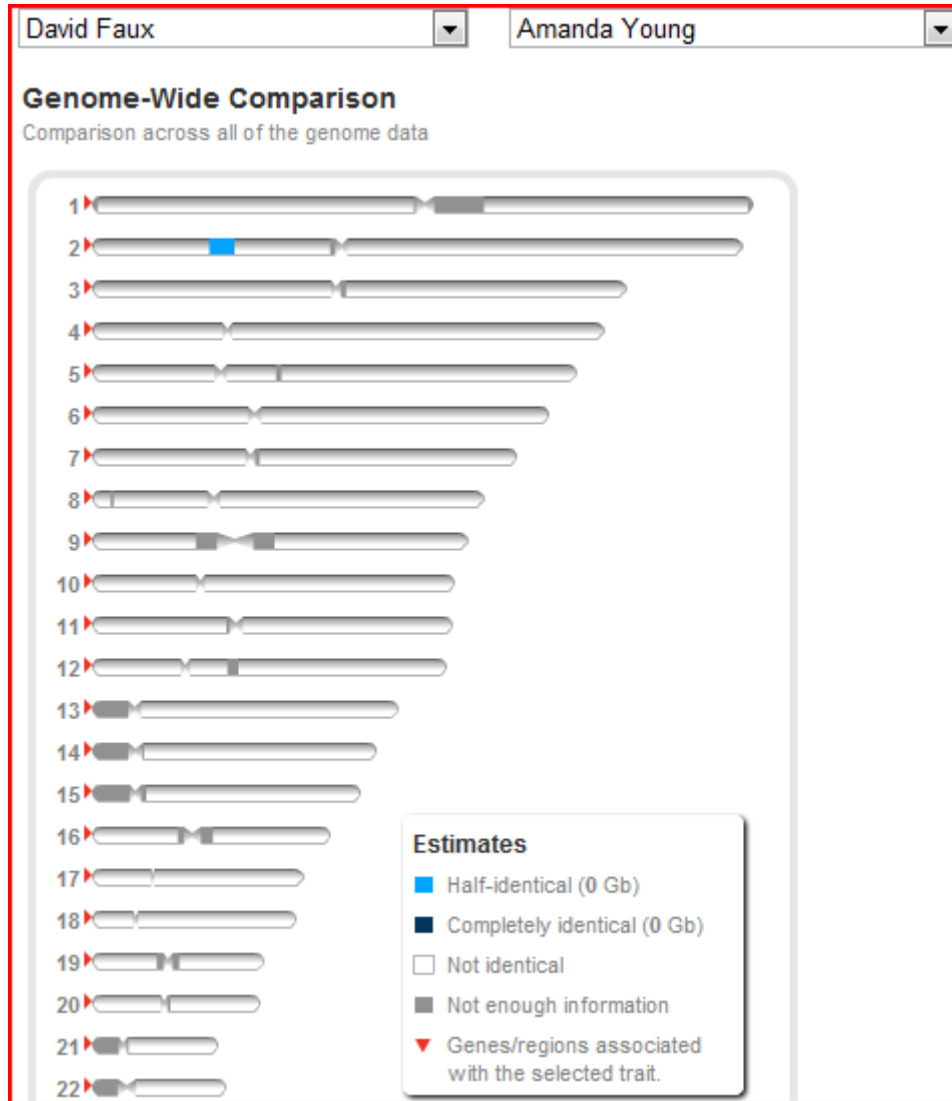


Another surprise is that it is not clearly evident that degree of sharing will be effected by how many branches of the Young family are shared, once you reach the level of third cousin. Many descend from multiple cousin marriages. While this would yield quantitatively more Young family DNA it does not seem to affect the sharing with any one individual. What would, however, undoubtedly make a strong difference would be in the case where one has Young family ancestors on both their mother and father's side which would likely significantly increase the sharing. To date we have no one tested who falls into this category.



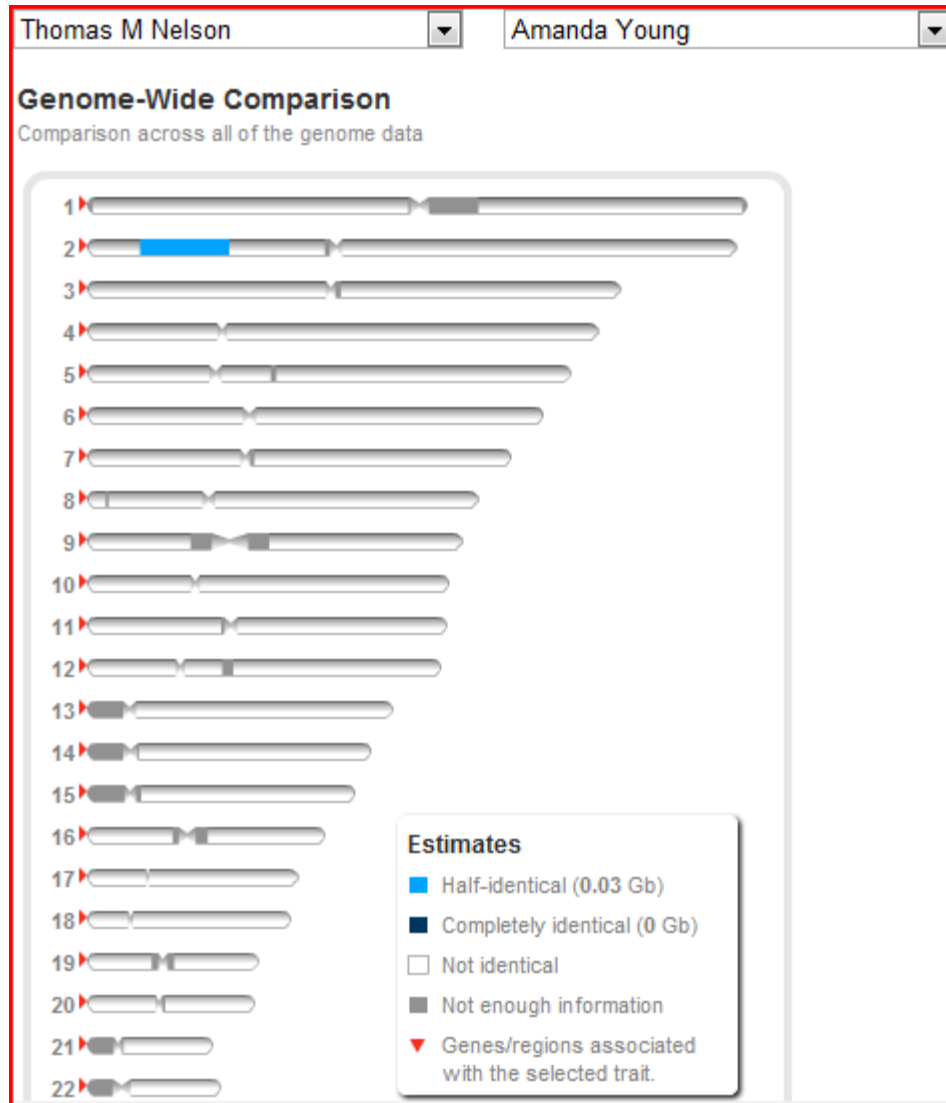
Over time we can become aware not only of the life story of an individual Young ancestor, but also know perhaps the most important detail of their life – their genetic structure. Via a process called triangulation it is possible to parse out which ancestor of a genealogical couple (husband and wife) or which cousin if a cousin marriage is in the genetic picture, and represented in the blue segment. For example, Dale Williamson and his nephew David Faux (Bob's second cousin twice removed) share 5 and 7 segments respectively with Bob Nelson – these segments come from shared ancestors George

Young (born 1795) and wife Mary Terryberry via their daughter Elizabeth. The chart above illustrates the sharing between Bob and David. At this point the relationship gets complicated since the descent splits via Elizabeth apparently having had relationships with two males/husbands (Bob a descendant from as yet unknown male number 1; Dale and David from known male/recorded husband number 2, the latter being her first cousin Henry Young).



The person who, as a third party, can resolve where at least one segment came from is Amanda Young (David’s 5th cousin once removed). Since among the grandchildren of Adam Young she is only descended from James F. Young, the brother of George Young (both sons of Sgt. Daniel Young and Elizabeth Windecker), the segment on chromosome 2 shared by her, Bob Nelson and his nephew Tom Nelson, and Dale Williamson and his nephew David Faux, we can conclude that this discrete part of the genome of Nelson et al. came from George Young and not from George’s wife Mary Terryberry. This sharing is shown in the chart above and is even more “dramatic” with the two Nelsons as seen in the chart below. We now know exactly where this particular stretch of DNA came from

and it can be recorded for posterity – particularly if the raw data or millions of bases is transferred to a spreadsheet. In a way, it is like having an artifact such as a silver tea cup that has a known provenance – owned by an ancestor – but in the case of DNA an even more personal connection will be apparent.



Returning to the above chart showing the sharing between Bob and his second cousin twice removed David, what can also be concluded here is that both Bob and to a less extent David (being two generations removed) are descendants who have many times the number of ‘Young segments’ in their genomes than these 7 – this is the minimum. The sum total would be for example perhaps 5 times these blue segments in Bob and say 3 times in David. This is merely guesswork, only multiple comparisons with a large number of descendants could permit us to arrive at a reasonable approximation. We can see by these results that it is, for example, unlikely that any of David’s 3 great great great grandparents with the Young surname have dropped from his genetic tree.

It is apparent that some of the present participants share little with others likely due to the relatively small sample size. The only way to tell how much autosomal DNA from a particular ancestor many generations back (e.g., a third great grandparent) has come down to an individual is to find as many descendants from the extended family as possible to test. Too few descendants in the test sample can give a skewed view, for example suggesting little connection – but with the next three participants there may be matching with each. It is very important to continue expanding this project to in turn make it more worthwhile to the individual participants and generations to come. We are truly just learning how this new genetic technology can be used to supplement genealogical records. Autosomal testing of this nature has only been available for about two years and typically people have been using it for a purpose different from that of the present author. The typical reason for doing this testing is to ‘find new cousins’. New cousins are not the focus, rather how those of us who have corresponded for years and attended reunions are related in the genetic sense.

If enough participants are available, using a process such as the above, it would be possible to map out the parts of the genome that came from a specific ancestor. Again, this means that genes on this segment can then be attributed to this ancestor. Using the raw data we could determine beginning and end points of the segment. In theory, the entire genome of each of Adam Young’s children could be plotted by tapping into the shared segments of hundreds of his or her descendants. More precision and detail is available with 23andMe’s ‘Family Inheritance – Advanced’ feature allowing users to for example see the specifics such as segment length and position.

By chance the process is well under way for chromosome 2 of Sgt. Daniel Young. The pattern of sharing noted to date has produced an interesting observation that for descendants of James F. Young and his brother George Young, all but one participants match on the small arm (‘p’) of chromosome 2. There is something unusual about the degree and consistency of sharing. Perhaps the genomes of the two brothers were more similar than those of other family members. It also occurs that some of the concepts of ‘epigenetics’ may apply. Something that happened in the lives of James and George imprinted a ‘mark’ on that part of the chromosome such that through a process called methylation and the wrapping of histones around the DNA segment, it has an unusual tendency to be ‘sticky’ and ‘refuse to break up via recombination’ so that it will perhaps continue to be passed along to distant generations for reasons that are completely unknown at this point. What is so special about this one part of the genome in this part of the family?

The following segment sharing summary was completed by Thomas Nelson:

For the 15 people David has in the Excel file so far, here are the number of shared DNA segments among us, expressed in pairs, but not including the Close Kin in the Excel table (the parts marked in yellow) - ie., not including my sharing with Uncle Bob or my second cousin Gerry KENNEY (First Cousin once removed), and not including the shared segments between Dale and David (Uncle/Nephew), and not including the segments shared between Beth and Margaret (Sisters) nor the segments share between Beth,

Margaret and David Anderson (Half Sisters - Half Brother) due to the large number of segments shared between Close Kin.

Keep in mind that the size of Chromosomes is like a ranking, with Chromosome #1 being the largest and Chromosome 20 being the smallest, so that the potential to share is highest on the low numbered Chromosomes:

Chromosome 2: 10 pairs (i.e., 11 of the 15 people in David's Excel table have shared segments on Chromosome 2 - but not necessarily all on the same segment)

Chromosomes 3 and 5: 5 pairs each (i.e., 6 of the 15 have shared segments on Chromosome 3, and 6 of the 15 shared segments on Chromosome 5)

Chromosomes 9 and 13: 3 pairs each (i.e., 4 of the 15 have shared segments on Chromosome 9, and 4 of the 15 shared segments on Chromosome 13)

Chromosomes 10, 11 and 18: 2 pairs each (3 of the 15 share on Chr 10; 3 of the 15 share on Chr 11, and 3 of the 15 share on Chr 18)

Chromosomes 5, 6, 7, 15, and 16: 1 pair each (2 of the 15 share on Chr 5, 2 of the 15 share on Chr 6, 2 of the 15 share on Chr 7, 2 of the 15 share on Chr 15, and 2 of the 15 share on Chr 16).

Ancestry testing is also available via the 'Ancestry Painting' feature of 23andMe – using autosomal data. We can supplement other DNA testing to search for support for the very clear and unequivocal genealogical records that indicate that Lt. John Young's first wife Catharine, the mother of his children, was of Native North American ancestry. This assessment has been completed and integrated with the testing from other DNA tests. To see the results of both the genealogical and genetic evidence, [click here](#). Unfortunately 23andMe does not at present assess ancestry for the X chromosome. However, an analysis was completed on the X chromosome of Dale's nephew David (the present author) using a rival company, deCODEme, testing with almost one million markers. To view this analysis [click here](#).

Furthermore, some circumstantial evidence suggests that Daniel Young's wife Dorothy Windecker had a mulatto great grandmother. 23andMe will identify European, African and Asian segments in their "Ancestry Painting" feature. Although two descendants do have an African segment, they are uncle and nephew and the link may well come from another branch of their family so only if other descendants of Sgt. Daniel Young and Elizabeth Windecker show as having an African segment will we be able to support the circumstantial evidence. To date it appears that the hypothesis will have to be abandoned for lack of evidence. Here there is no substantial genealogical data that would over ride some of the problems with ancestry testing via 23andMe. The restricted reference samples (e.g., using only the Yoruba to represent all Africans; and the Han Chinese to represent all Asians and Native Americans), and the small expected percentages (meaning that 23andMe may not be able to detect ethnic ancestry that far back) being but two issues.

By joining this DNA testing venture, Young descendants can help make a contribution for future generations, and perhaps discover something of interest to add another dimension to their family history. [Click here](#) to see the Excel sheet with the raw data of this study.

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