

**DNA SEGMENT SHARING in DESCENDANTS of
ADAM YOUNG (1717-1790) and CATHARINE E. SCHREMLING (1720-1798)**

By

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The following manuscript is an interpretive guide to the data from the autosomal and X chromosome DNA testing of descendants of Johann Adam Jung (Young) and wife Catharine Elizabeth Schremling. Adam was born 1717 Schoharie NY, died 1790 Seneca Township, Haldimand County, Ontario, Canada. Adam was the son of Johann Theobald Young (born 1691 Dunzweiler Germany, died 1763 Canajoharie New York). Adam's wife was Catharine Elizabeth, daughter of Hendrick Schremling and Elizabeth Landgraff. They, with their 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. The data is shown in an Excel spreadsheet by [clicking here](#). The associated spreadsheet by Gerald Kenney showing the specific blocks where sharing occurs can be seen by [clicking here](#). To date there are 30 participants in the study, all descendants of Adam and Catharine Elizabeth. 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 segment comparisons to attempt to pinpoint the block 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) – for two reasons, and an infidelity is only one of them, the other relates to the mechanisms of genetic inheritance.

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. There are other important discoveries to be made, as will be seen, with examples, later in this work.

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 or paternal lineage despite testing cousins to the level of 8th cousins – we all have the same Y chromosome 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 (or are undetectable via today’s technology) – but may be “found” in a sibling. 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 Adam’s sons Lt. John Young (Larry Young) and Sgt. Daniel Young (Ken Young) were recruited. Family Tree DNA did the initial Y chromosome testing. The two descendants with the surname Young matched on 36 of 37 YSTR (short tandem repeat) genetic markers. This meant that we had captured the ‘DNA signature’ (minus one marker) of Adam Jung, the father of the above John and Daniel (as well as Henry). It remained to ascertain the Young family 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 six individuals via 23andMe, showed that the Youngs belonged to haplogroup R-U152/L2* other wise known as R-S28/S139 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 direct female 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. Here we determined that Elizabeth was haplogroup J1c (via her mother Mary Terryberry, the later’s mother Ann (Young) Terryberry, and her mother Sophia (Young) Young of New Jersey and so on). This finding was cross-validated with the testing of a direct female line descendant of the above Sophia’s sister, Elizabeth (Young) Huffman, with a resulting exact match for the J1c signature of Bob and Gerry – meaning the hypervariable regions (HVR) 1 and 2 mutations that make up a haplotype.

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 are 'closest' to the early Youngs, being only three meiotic recombination events from Lt. John Young's wife Catharine Hill and Sgt. Daniel Young's wife Elizabeth Windecker. 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). Others in the "X line" are the author, Jackie Yorke (niece of Dale and first cousin of the author); as well as Robert Nelson, Gerald Kenney, and Norman Sones for the line of Sgt. Daniel Young's wife Elizabeth Windecker.

The only X chromosome match in the entire study is between Norman Sones (first cousin once removed of the above Robert Nelson), and the author's first cousin Jackie Williamson Yorke, who share a 15.5 cM segment between positions 96 and 115 Mb. Since Norman Sones is not a descendant of Lt. John's wife Catharine Hill, the sharing can only be via Sgt. Daniel's wife Elizabeth Windecker, or one generation upstream being Catherine Elizabeth Schramling, or one generation downstream (the most recent common ancestor), Elizabeth (Young) Young (whose mother was Mary Terryberry hence the match could be from this direction).

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 (including Robert Young in the study) are only five generations back to a child of Adam Young (in this case Lt. John Young); and Archie Young the same number of generations back to Pvt. Henry Young. To the best of the author's knowledge, these represent (as with Robert Nelson and Dale Williamson with the X chromosome) the branches of the family that are presently the closest (fewest generations removed) to one of the three children of Adam Young who emigrated to Canada.

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) versus males in the formation of sperm. The ratio here is 1.6 in females to 1.0 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%) but the blocks are likely small and perhaps undetectable – 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. Oddly, this prediction is not born out in the Young study, as seen below.
- h) Even the location of recombination varies as a function of sex. 78% of male recombinations (via recombination “hotspots”) are at the far telomeric end of the chromosome (the tips). In females there is the same general tendency, but only 18% of recombinations are found in these same concentrated areas as males, with most occurring toward the tip but more likely than males to take place anywhere along the chromosome.
 - i) Some chromosomes will be passed intact from a single grandparent, with no recombination. The tendency appears to differ (as do the above tendencies) by family. Thus it is possible to inherit unchanged even more than one chromosome from a great grandparent, or even further back – as seen through multiple generations in some participants in the present study. An example is Mike Young and Jackie Yorke who share one half (the central section) of chromosome 12 despite 6 independent recombination events on each branch for a total of 12 “opportunities” to recombine it leaving nothing to share (as is the case on the other 21 chromosomes).
 - j) An unknown number of ancestors will be represented by say blocks of 3 cM (centiMorgans – a measure of genetic distance) or 3 Mb (Megabytes – a measure of physical distance on the chromosome). However, as discussed later, the need to “set the bar” to avoid false positives means some valid matches will be missed.
 - k) 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) – even siblings or first cousins can vary dramatically. Chance plays a large role in genetic inheritance. The opportunity to “see” these extant blocks depends on the number of other Young descendants with whom one can compare – in other words the number who have tested.

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. SNPs are single nucleotide polymorphisms and in a string may be AACGGTATT – it is that matching patterns that tell the story of whether there is a relationship (matching segment of a significant length) or not. What this amounts to in the 23andMe 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 will find out that we share far more Young DNA than predicted by statistics. Hence they 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. Low matching could change significantly 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 600 matches (say 3rd to 5th or distant cousins according to 23andMe) of a database of 150,000 people, only about 10% of the 600 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.

Discovering the Unknown:

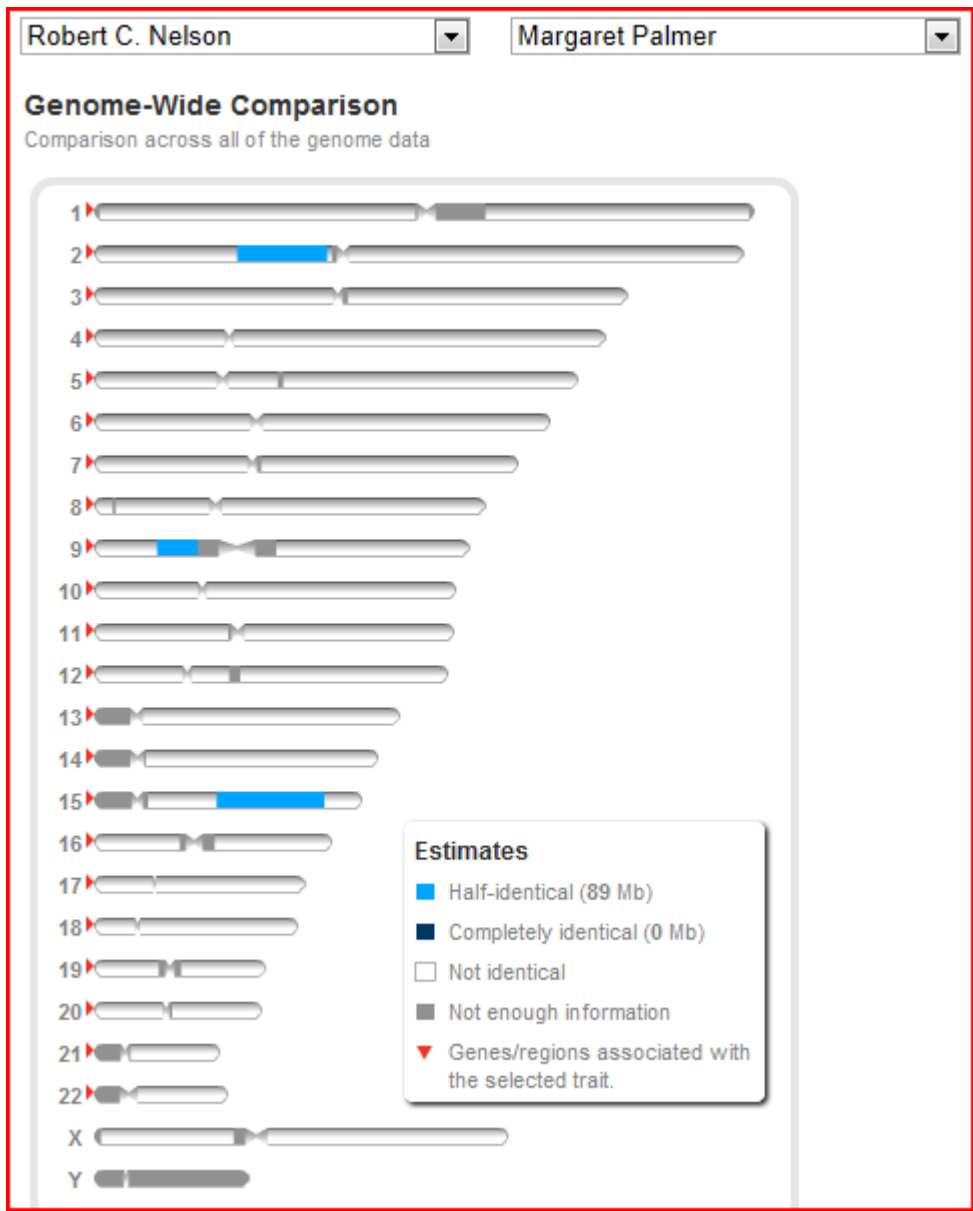
The DNA testing done here can also be used to test genealogical hypotheses. For example there were multiple sources of genealogical evidence indicating that the eldest sister in a family of 9 siblings in one Young family was not the biological child of the father to the rest (i.e., there were indications 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. In the “known” category are Dale Williamson and family as direct descendants of Elizabeth Young (daughter of George, son of Sgt. Daniel) via daughter Hannah Adelia (Young) Dawson (born 1854); and that his 3rd cousin Tom Nelson was a direct descendant of the above Elizabeth’s first child, Celestia Jane (Young) Hines (born 1849), but of an unknown male who “left his mark” a few months before the marriage of Elizabeth to her first cousin Henry Young (son of Henry Young Sr. and his first cousin once removed Rachel Young) – the ancestor of the Williamson group (including the author). The genealogical evidence (three sources) suggested that Celestia Jane and Hannah Adelia were half sisters. In the case under consideration, the matching profile strongly suggested that the biological father of Celestia was a Young – but little else. The only hope was that by chance some Young who tested at 23andMe, or was recruited as a participant, would be the key to unlock the mystery - and determine the identity of the “mystery man” who fathered the eldest daughter in the family. This rather improbable event came to fruition via one recruited Young, and two who “happened” to test.

Thanks to the testing of Ken Young, and later Margaret Palmer (and her daughter Karen, and granddaughter Lindsey), as well as FM, both of whom are second cousins to Ken, we now have the proof we needed. The biological father of Celestia was David Peter Young, born 1819 Ancaster, son of Frederick Young (son of Sgt. Daniel Young) and Catharine Young (daughter of Frederick and Sophia (Young) Young of New Jersey – no kin to the Mohawk Valley family). Ken Young, Margaret, and FM matched Robert Nelson (uncle of Tom Nelson) at the second cousin once removed level, and Tom at the 3rd cousin level (the same relationship as the Williamson group). Now, all the other bits of evidence already available started to add up and everything fell into place. Mystery solved, thanks entirely to this form of genetics testing.

An even more dramatic example of converting the unknown to the known emerged when the test results of Ken Young became available. An entire family learned not only that they had Young ancestors, but which specific Young male was their progenitor.

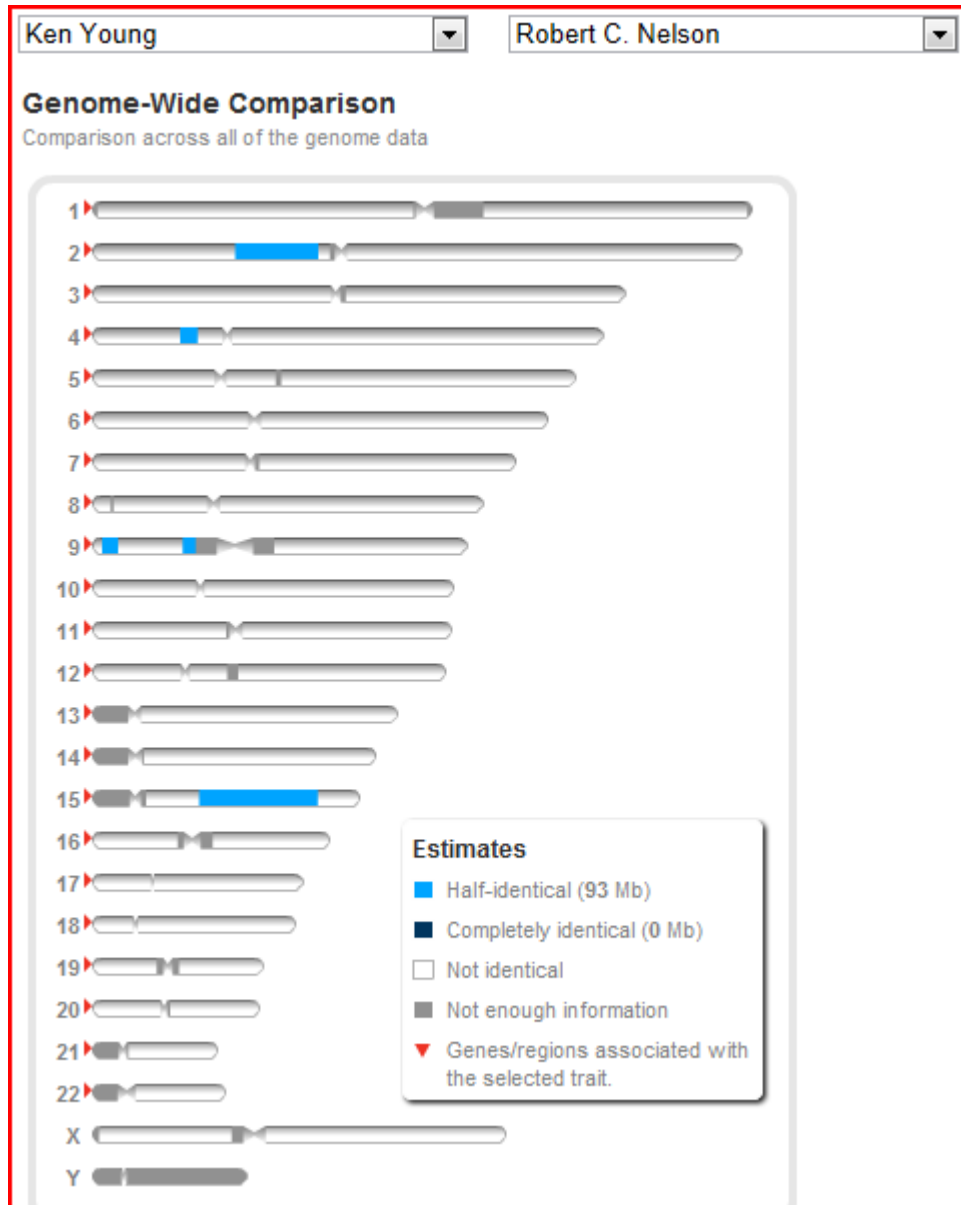
The following charts illustrated the degree of sharing between:

- 1) Robert Nelson sharing with Margaret Palmer – Relationship at the time unknown:



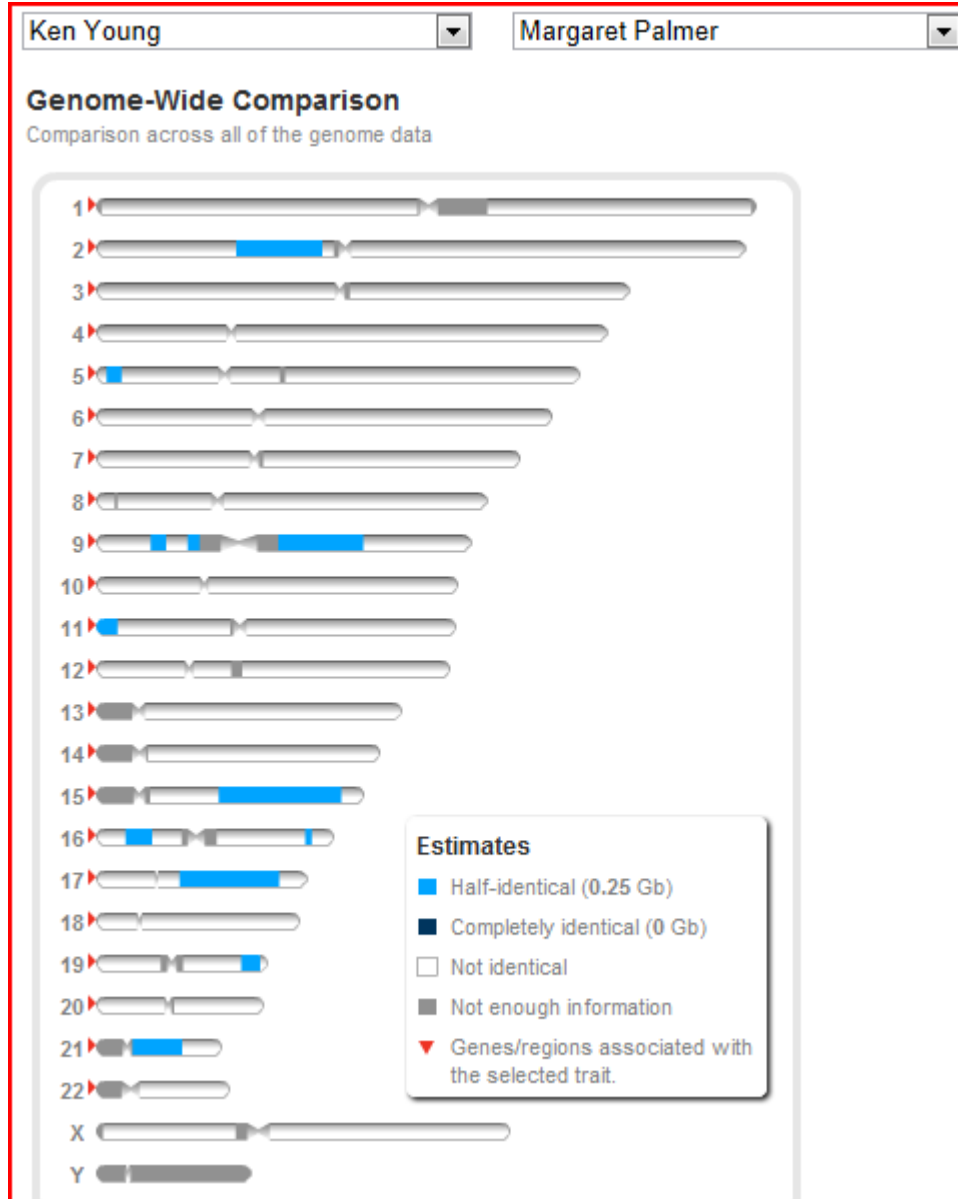
Clearly there is a strong sharing relationship here, but since there is an “irregularity” in Margaret’s genealogy, we will need to find someone else with whom to “triangulate”, such that the relationship comes into sharper focus. It turned out that that person was Ken Young – he was tested because the author has known him for many years, and is a member of the Young Tract Burying Ground Committee.

2) Robert Nelson and Ken Young:



3) Ken Young and Margaret Palmer:

Initially (before the testing of Ken) it was assumed that the relationship between the Nelsons and the Palmers related to the unknown biological grandfather of Robert Nelson. This hypothesis was quickly dispelled when the chart below emerged.



This sharing is at the level of second cousins! Now combining the sharing with the Palmers, the Nelsons, and Ken Young allowed us to make clear conclusions based on the power of DNA evidence.

Conclusion: Ken and Robert share at the level of second cousin once removed. Ken’s great great grandfather and Robert’s great grandfather are one in the same. Ken has incontrovertible evidence that the man is David Peter Young, born 1819 Ancaster, son of Frederick Young (son of Sgt. Daniel Young).

The family of Margaret Palmer knew there were “irregularities” in their genealogy. The matching with Ken Young at the level of second cousin for Margaret and second cousin

once removed for her daughter Karen (4.12%, her daughter 2.87%), plus the latter two matching both Robert Nelson and Tom Nelson, as well as Ken Young, on the same specific parts of chromosomes 9 and 15 provides conclusive evidence as to the depth of relationship. A search of all relevant genealogical records allowed a story (right place, right time) to be assembled to mesh with the genetic data. This significant amount of sharing (including overlap with segments shared with Robert Nelson and his relatives) suggest a relationship between Ken and Margaret that is one generation closer than with the Nelsons. The genetic evidence of percentage sharing, combined with some clues that have been located concerning what is possible based on time and place, indicate strongly that Ken and Margaret share a great grandfather, in this case David Francis Young. What is fascinating is that before this testing Margaret had no awareness of the Young relationship since a non-paternal event intervened and her Young ancestor (her father) actually bore a French Canadian name throughout his life.

FM, a Mexican whose mother was a Young is a known second cousin to Ken Young, and also tested with 23andMe. His data serves to entirely confirm the Young ancestry of the Nelsons and the Palmers (it is always a good idea to seek cross – validation), as well as that of the Nelsons.

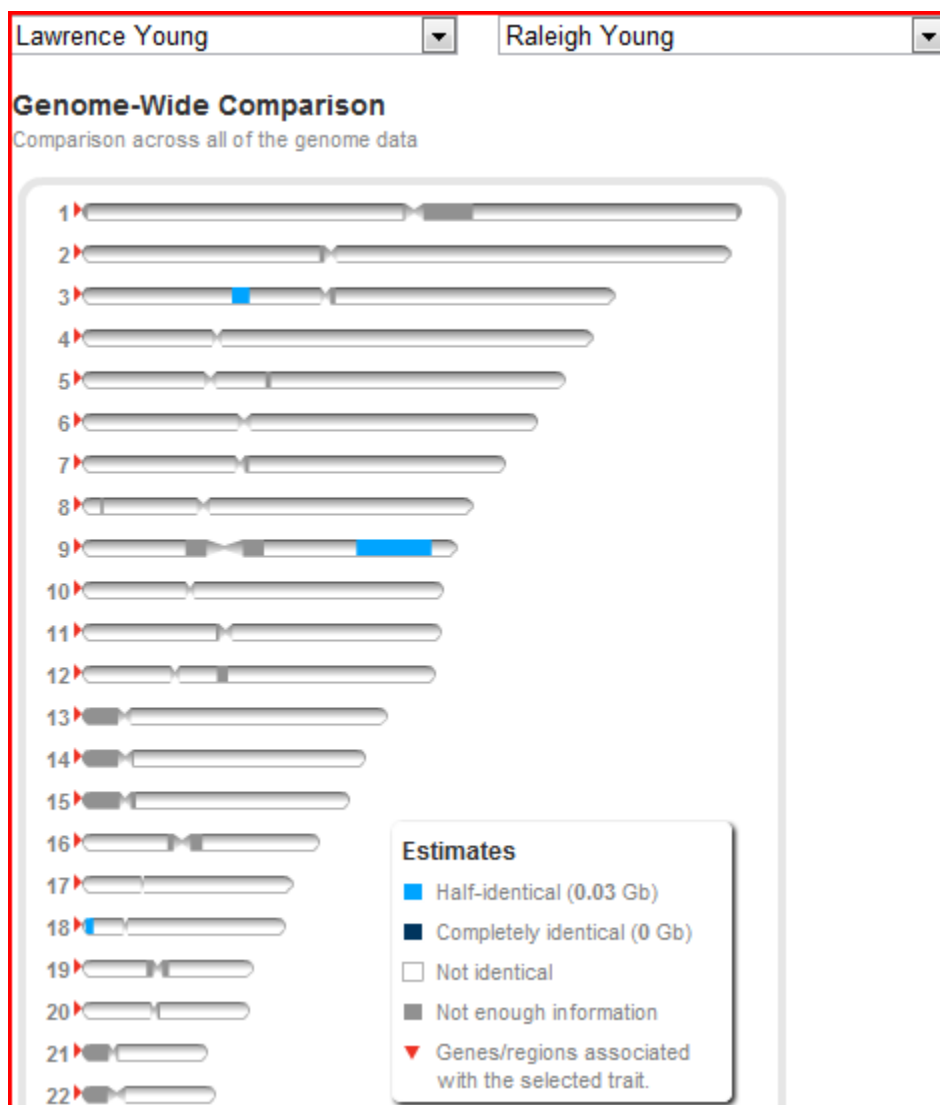
Further Concrete Examples, Observations and Additional Information:

1) Young Descendant Sharing that is Typical:

Below is the depiction (chart) of the matching segments of two descendants of Lt. John Young.

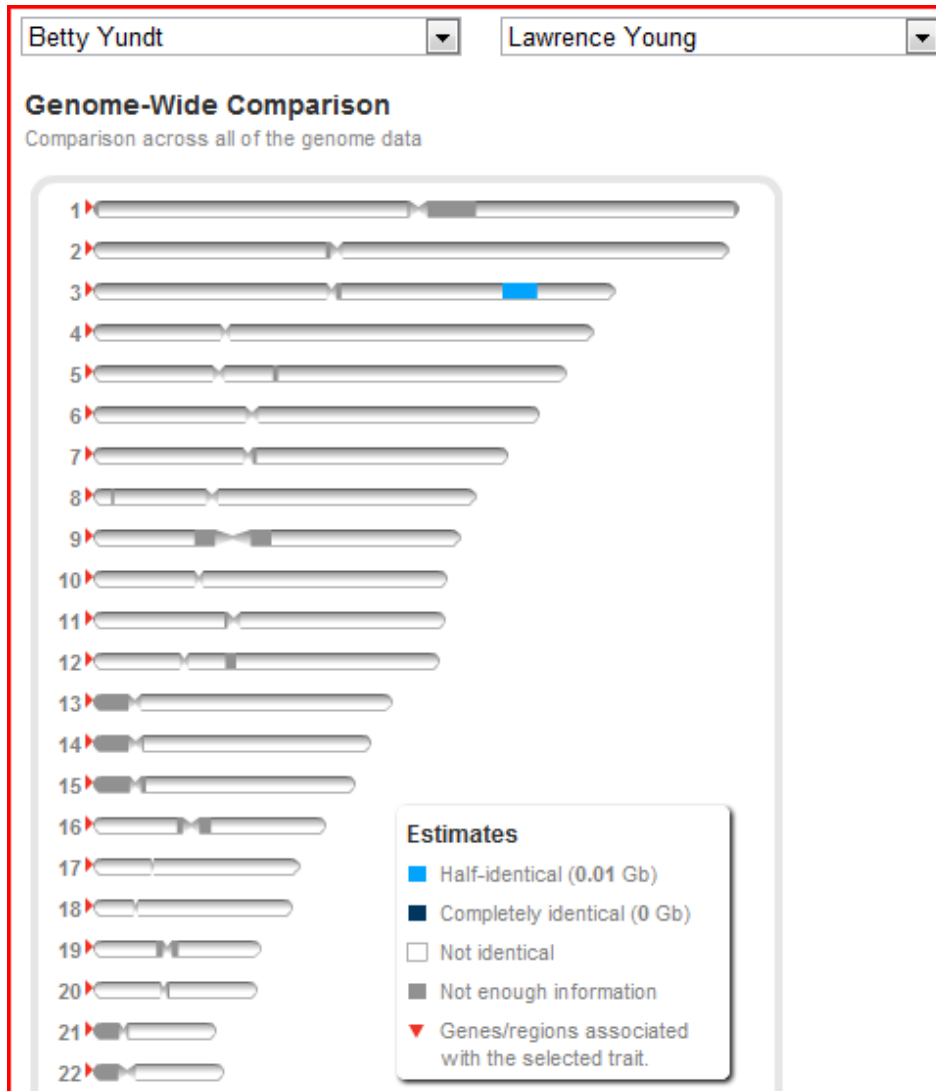
It cannot be said, based on this evidence, that the sharing is from Adam Young or Catharine Elizabeth Schremling since both Paul Fawcett and Neill Craven are descendants of Abraham Young, grandson of Adam and Catharine Elizabeth. It is impossible without some third party confirmation to assert that what we are seeing comes from Adam or Catharine Elizabeth since there are other candidates. There is the wife of John Young Sr. (Catharine Hill), and the wife of Abraham Young (Eleanor Dennis), as well as Abraham Young's son Joseph Young's wife (Rachel Wedge).

Thus it is important to note that sharing between Young descendants does not necessarily mean that they are sharing a block that can be attributed to Adam Young and Catherine Elizabeth Schramling, or even one of their sons and / or their wives. The sharing can only be assigned to the most recent common ancestor (MRCA) which, for say second cousins, includes a lot of ancestors who are not Young descendants. Much or most of the matching will have nothing to do with their Young ancestors. However if perchance the sharing is between say a descendant of Lt. John Young and Sgt. Daniel Young, then it is reasonable to denote the shared block as belonging to Adam and Catherine Elizabeth since they are the MRCA of the two descendants (assuming no other ancestors in common along the genealogical path or each). What is very typical of the Young family though was to marry either a first cousin, or someone from the Nelles family who resided next to the Youngs along the Grand River from the earliest days of settlement.



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 affecting the amount of recombination).

The “Ideal Candidate” for testing would seem to be Betty Yundt, since she is a descendant of one son of Lt. John Young (Joseph Young) via her father; and another son of Lt. John Young (John Young Jr.) via her mother. One might expect some sort of “excess” sharing. Having a Young ancestor in both the paternal and maternal lines “should” up the sharing, but the available data does not support this prediction – but there are many intervening variables that make these predictions very tentative.



Here Betty is compared to Lawrence Young (descendant of John Young Jr.) so the predicted 0.049% plus a smaller factor relating to the descent via Joseph Young emerges as 0.100% which is more or less right on the mark. However, it is important to note that both Betty and Lawrence are Nelles descendants so that it is not presently possible to know whether the blue matching sections come from the shared Young, or Nelles, or both ancestors. Thus sharing can get extremely complicated, when the goal is to offer a clear origin of each matching block. This motif once again highlights the vagaries of genetic sharing where the Nelles connection, plus Betty’s descent from two of Lt. John Young’s sons “should” have resulted in higher sharing.

The situation in relation to the sharing for Lawrence Young, Robert Young, Betty Yundt, John D. Anderson and his daughters Elizabeth Einig and Margaret Hegner, as well as Richard Lidzbarski and Jane Pullin can be instructive. All have both Young and Nelles ancestors. Some observations here show for example a negligible sharing between Lawrence and Richard Lidzbarski; in contrast to the strong sharing between Richard Lidzbarski and Betty Yundt. Richard is at the same “cousin level” as Elizabeth and

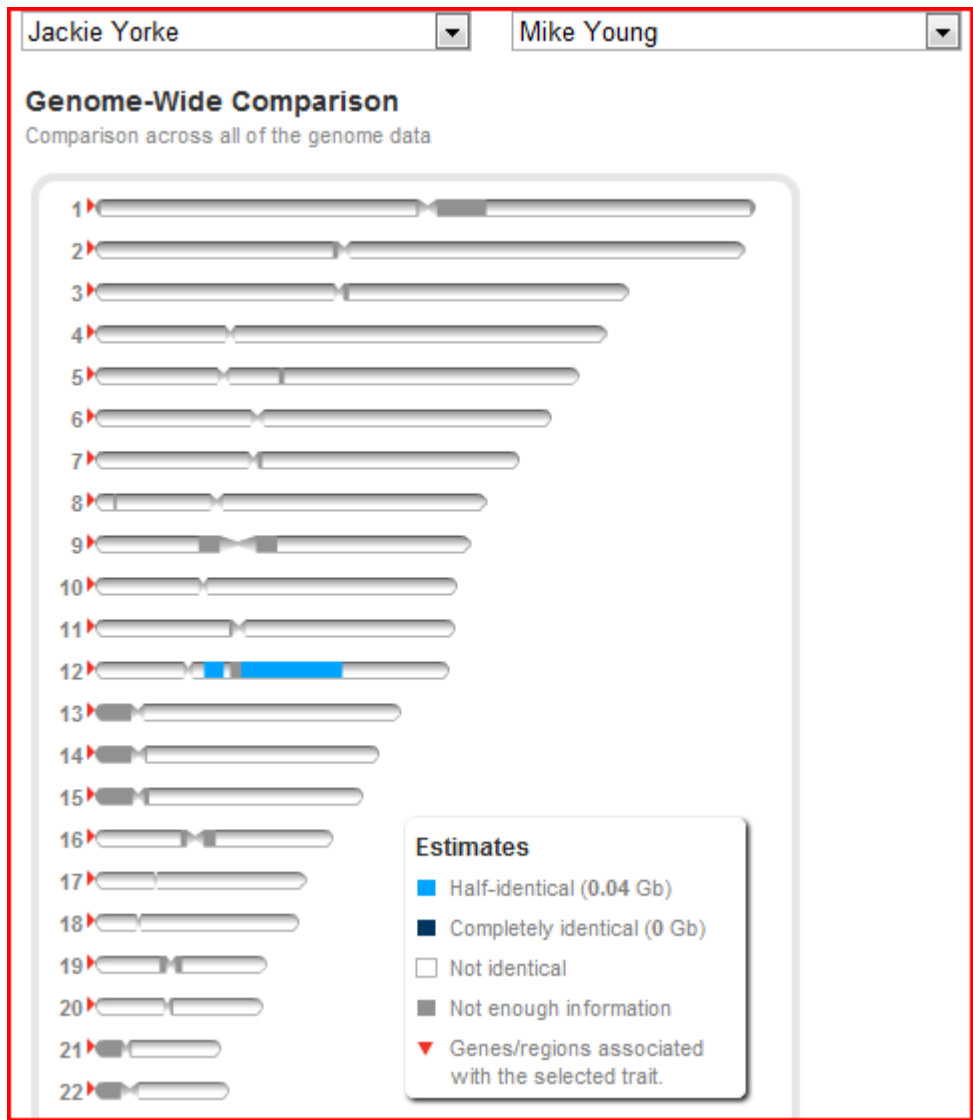
Margaret. Here the predicted sharing of 0.049% turns out to be 0.330%. What is important to note is that they not only share Young ancestors, but also the closely connected Nelles family of the Grand River. Thus, to repeat, it is unclear whether the matches are due to the Young or Nelles relationship – and this adds a layer of complexity to the matter. However the sharing between Richard with Margaret Palmer and her daughter Karen Palmer must reflect a common ancestor in Adam and Catharine Elizabeth. The sharing between Lawrence Young and Jane Pullin (two small segments) is problematic in that Jane is a descendant of Sgt. Daniel Young (not Lt. John Young as is the case with the other above named individuals), but again both have Nelles as well as Young ancestors. Thus in theory we could be seeing the DNA of Adam Young and / or Catharine Elizabeth Schremling, or, the more likely scenario is the Nelles connection, which is more proximal (fewer generations back).

It is important to recall that chromosomes are more likely to become “chopped up” in females whose recombination rate is 1.6 to 1.0 (female to male). In theory, two persons who are direct male to male Young descendants are more likely to share more (larger segments) DNA than those whose descent is all female or a blend of male and female in their descent from Adam and Catharine Elizabeth. Frequently, however, we see sharing that is more “generic” despite the mode of inheritance. For example despite the direct male to male transmission in Mike Young and the swinging back and forth between male and female ancestors in his 4th cousin Dale Williamson, both men share an expected amount – actually somewhat more, perhaps due to their each having multiple Young ancestors. The effect of having more than one Young ancestor (via for example first cousin marriages) does not seem to have a large effect – surprisingly to the author – at least based on present observations among others in the same situation. Here is a case where the statistical modeling accurately reflects real life observations – although the stats do not take into account multiple connections. Perhaps it is the relatively small sample size – perhaps there is a lot we have to learn about genetic transmission within families.

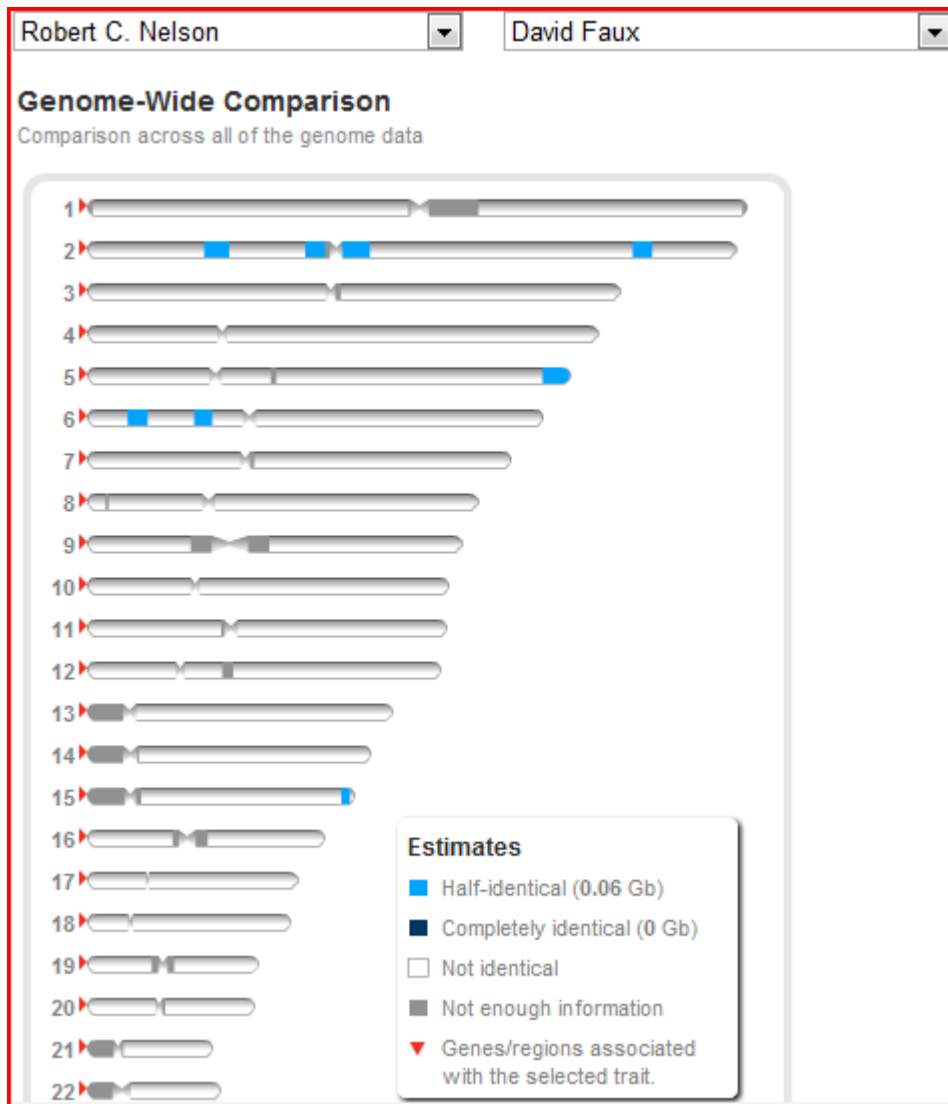
2) Sharing that Significantly Exceeds Expectation:

Of all the participants, to date, Tom Nelson shares with more individuals and at a greater depth, than what is predicted. In addition, as another example, Dale’s niece Jackie Williamson Yorke shares more with Mike than her uncle on the same chromosome. The author, first cousin to Jackie, shares zero with Mike. This once again reflects the vagaries of genetic inheritance (used as an example earlier), and also suggests that the respective parents or grandparents of these individuals would likely have shared a very considerable part of their genomes.

Below is the chart showing the matching of Jackie and Mike. As noted above, despite the fact that the author is first cousin to Jackie, he shares nothing at all with Mike. However, undoubtedly if Mike’s cousins had been tested there would have been those who matched all three. Here there is no other family line, other than Young, which can explain any matching. Their ancestors in common are Henry Young Sr. (b. 1787) and his wife (and first cousin once removed) Rachel Young (b. 1800).



It is also apparent that some unexpected observations await. While generally a member of the older generation (e.g., an uncle) shares more than a member of the younger generation (e.g., a nephew), this “rule” seems to be violated frequently in some branches of the Young family. It was very surprising, based on a known genealogy, that Tom Nelson (Sgt. Daniel line) 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. An example is the sharing between he and his 5th cousin once removed Larry Young, as noted earlier in this work. This observation is very difficult to explain, especially since his own uncle Robert does not show the unexpectedly strong affiliation with Young DNA, though Robert and Tom have the expected DNA share between and 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).

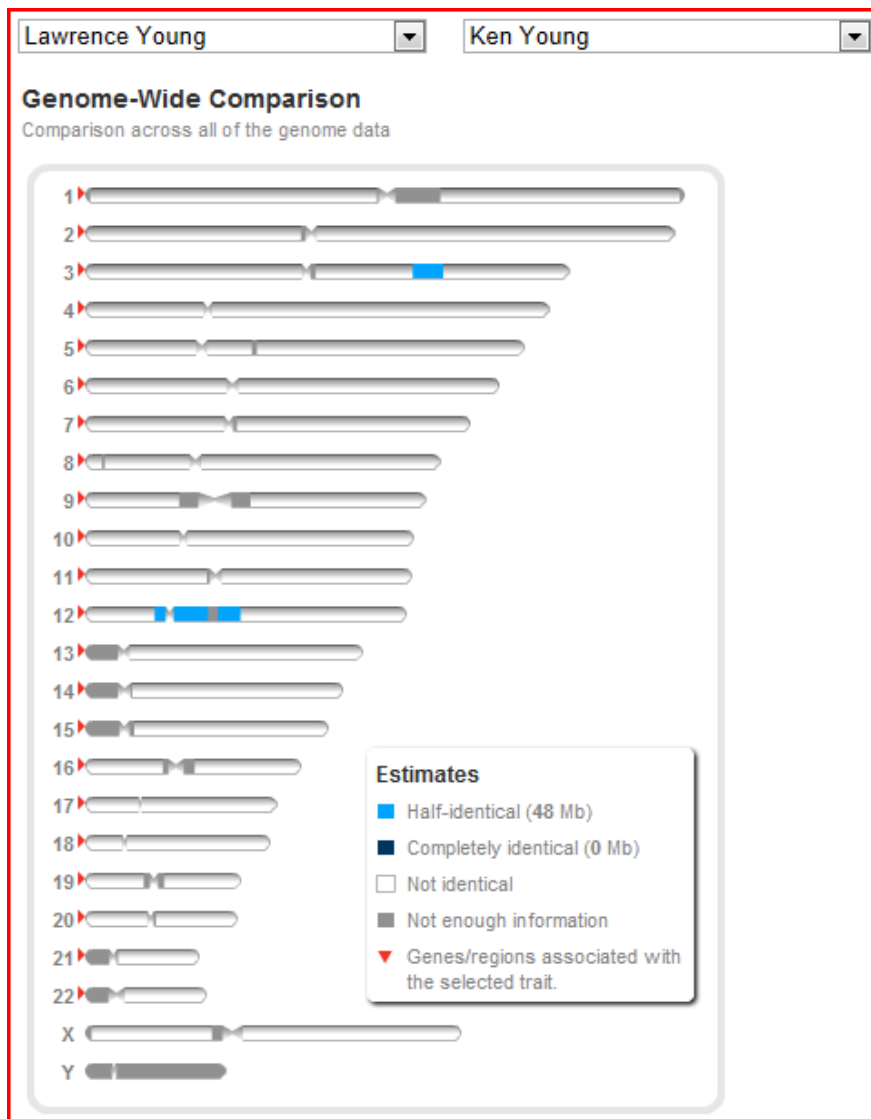


Above is another example of unexpected “over-sharing”, between Robert Nelson and his (half) second cousin twice removed, the author. The latter’s sharing at 1.15% and 7 segments almost matches that of the author’s uncle Dale Williamson at 1.28% and 5 segments. However notice the size of the segments. They are small, reflecting no doubt the fact that we are seeing the female factor of more recombination in gamete formation. Even more dramatic is the 0.90% and 4 segments between the author and 3rd cousin once removed Norm Sones. Expected is 0.391%. One wonders what sharing would have been observed had these individuals been full third cousins once removed rather than half. What is quite unusual is that the author’s uncle Dale Williamson shares zero with Norm – yet they are half 3rd cousins (so unexpected “under-sharing”) – although we now know that they are half 3rd Cousins, but there is little in the literature to help offer sharing predictions here. However it is important to note that about 10% of 3rd cousins (expected to share 0.781%) do not have any matching blocks. The author’s first cousin Jackie (same generational level) shares one segment with Norm, and on the X chromosome – within the expected range of sharing.

3) DNA Traced Specifically to Adam Young and Catherine Elizabeth Schremling

a) Segments Which Can and Cannot be Attributed to the Family Patriarch and Matriarch:

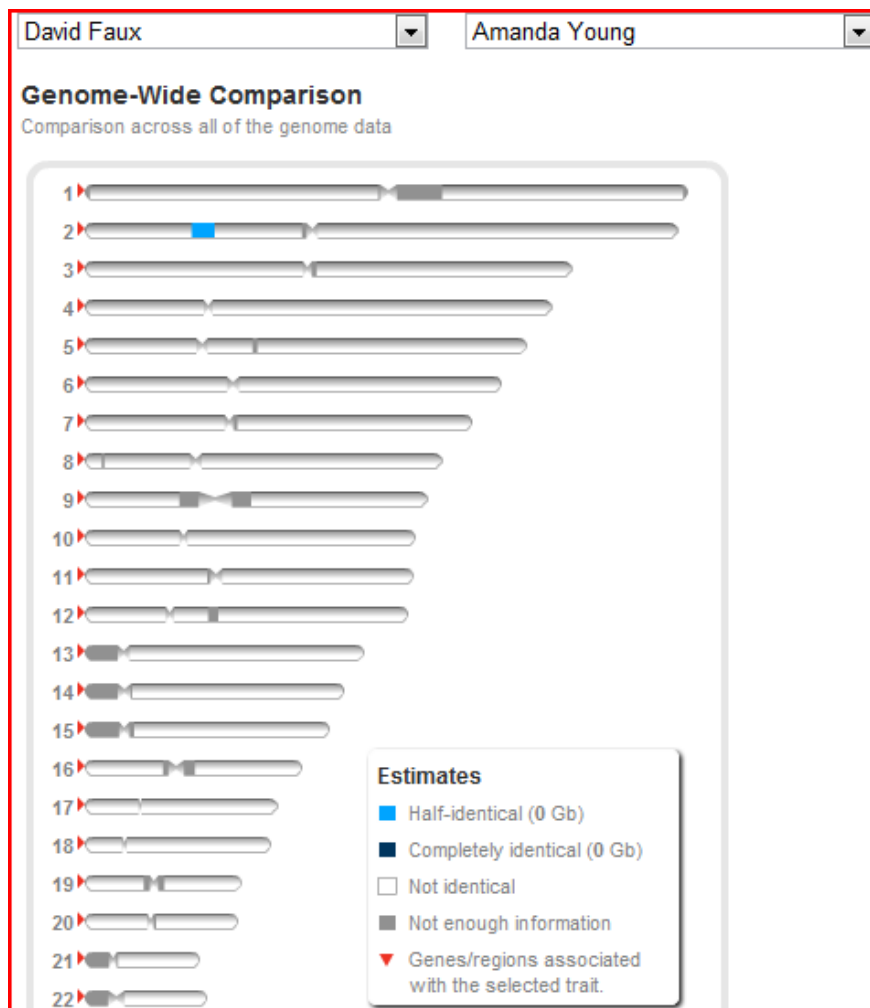
Below is a chart depicting the sharing between a descendant of Lt. John Young (Lawrence Young) and a descendant of Sgt. Daniel Young (Ken Young). See diagram below. Tom Nelson, also a descendant of Ken's ancestor David Peter Young also shares two segments with Larry. The Nelsons (Sgt. Daniel Young) additionally share a small segment with Paul Fawcett (Lt. John Young). There is only one reasonable interpretation. We are seeing segments that came from the Loyalist patriarch of the family, Adam Young, and / or his wife Catharine Elizabeth Schremling.



Generally if a matching segment is seen between two descendants of Adam and Catharine Elizabeth it is going to be very difficult to prove that this block of DNA came from them and not for example from the wife of one of the three sons, Lt. John (Catharine Hill), Sgt. Daniel (Elizabeth Windecker) and Pvt. Henry (Phoebe Van Every), or another ancestor which may be shared in common. The only way this can be done is to have someone who is a descendant of say only Daniel, match someone who is a descendant of only John, at precisely the same location on the same chromosome.

b) The Importance of “Triangulation” for Determining the Origin of Some Shared Segments:

Here we can once again illustrate the important point that sometimes it may be impossible (given the specific participants) to know whether a segment comes from a Young ancestor, or one of the other family lines (e.g., Nelles, Wedge, Terryberry) that are shared. An example of this effect is the small block on chromosome 2 shared by the author, Robert Nelson and Norm Sones. These three also share Terryberry ancestors. However there is a technique that can “come to the rescue” here. The example of how Amanda Young can “solve the mystery” is given here.



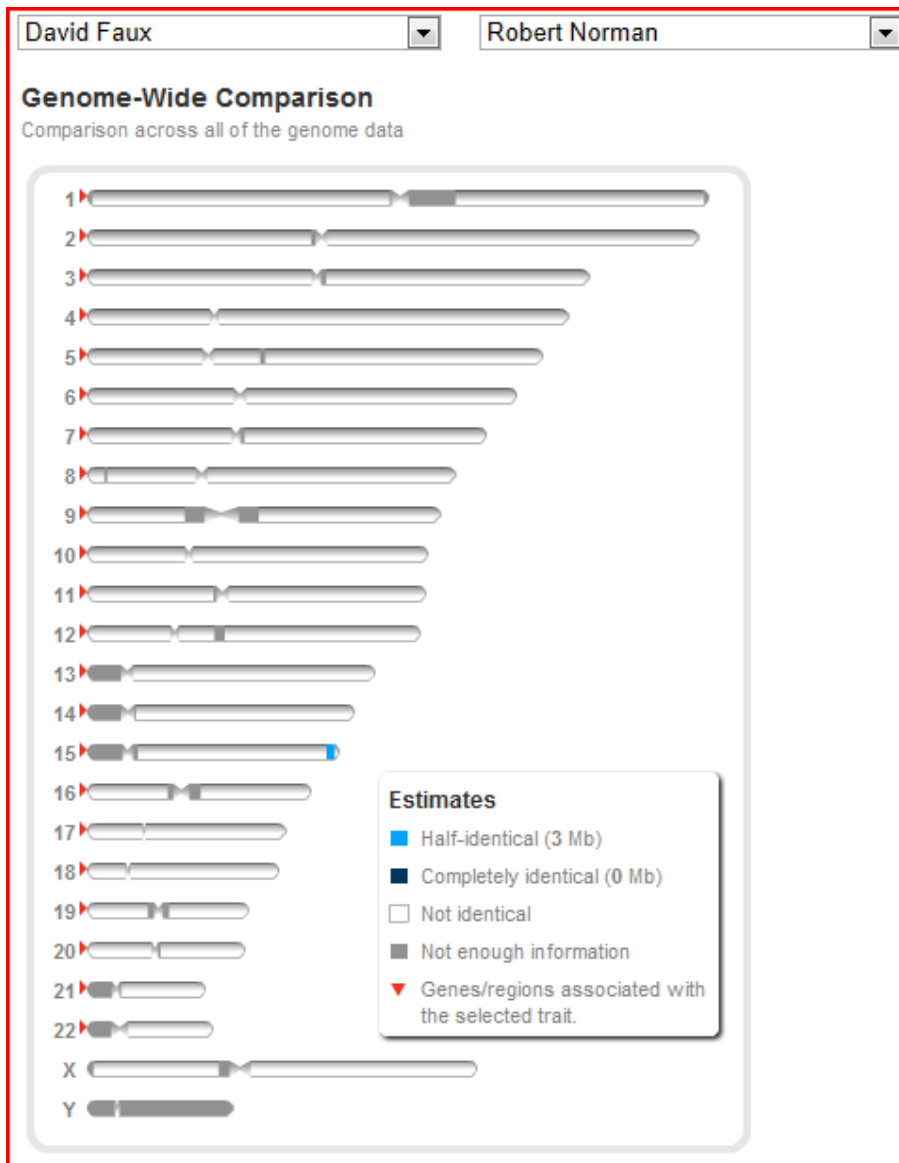
Via a process called triangulation it is possible to parse out which ancestor of a genealogical couple (husband and wife) or which cousin if a cousin marriage is in the genetic picture, and represented in the blue segment, is responsible for the sharing. For example, Dale Williamson and his nephew David Faux (Bob Nelson'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. At this point the relationship gets complicated since the descent splits via Elizabeth having had relationships with two males/husbands. Bob descends from Celestia, a daughter of David Peter Young a married first cousin of Elizabeth. Dale and David descend from Henry Young Jr, the husband of record, and also another first cousin to Elizabeth Young. The point here though is that, as with the Nelles example above, it is often impossible to know which of these shared segments come from Young ancestors and which from for example Terryberry ancestors. Again, only a “triangulation” maneuver will uncover the identity of the shared segments.

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 David's ancestors George Young and Henry 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 other Youngs, we can conclude via triangulation that this discrete part of the genome of Nelson et al. came from Young ancestors, but not the wife of George Young, Mary Terryberry (who is not in Amanda's tree).

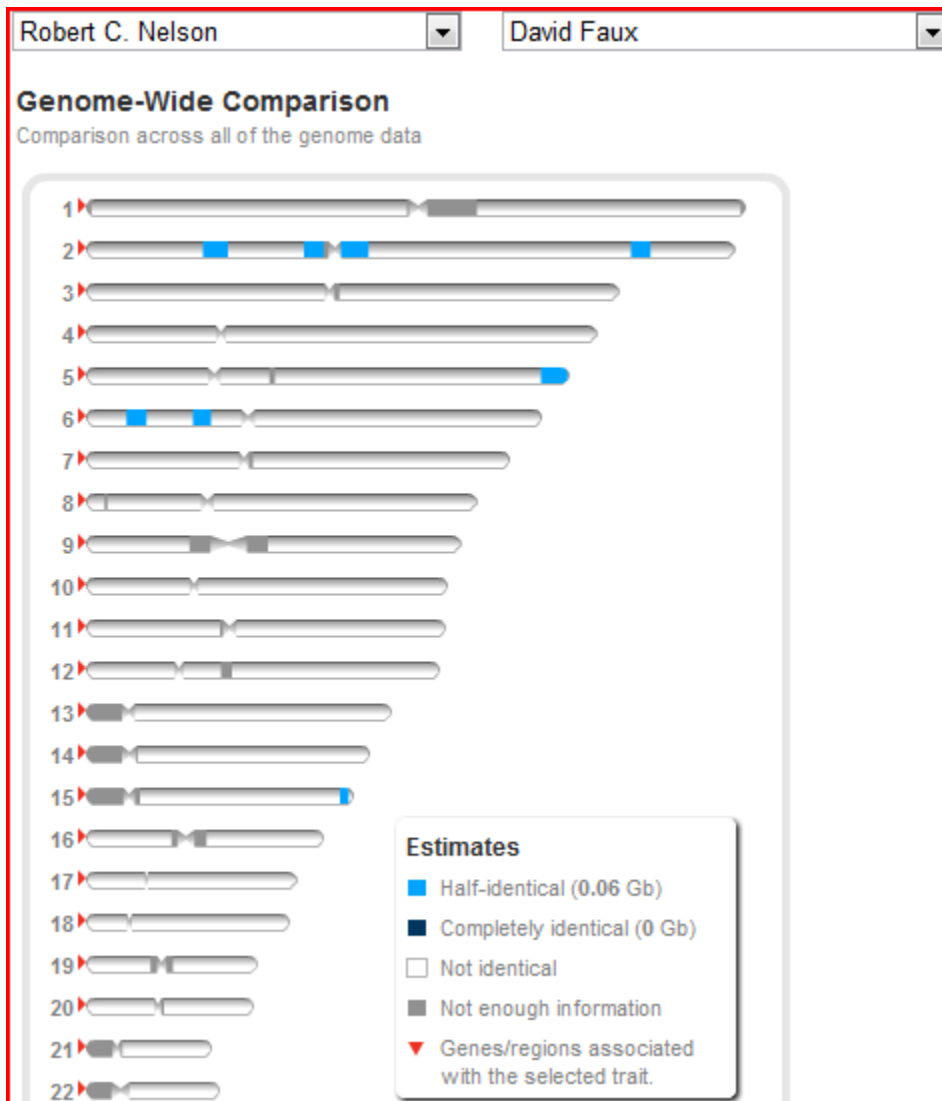
Returning to the above chart showing the sharing between Bob Nelson and his half second cousin twice removed David, what can also be concluded here is that both Bob and to a less extent David (being two generations removed) are descendants who have many times the number of 'Young segments' in their genomes than shown via sharing with any one participant. 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. The number and distribution of segments would be very different with different participants, and particularly those who descend from Elizabeth's formal husband, Henry Young. 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.

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, again, it typically does not affect the sharing with any one individual.

Another example of sharing that can be triangulated to obtain proof of descent from Young ancestors, ruling out possible Nelles sharing, but with an unusual twist, is that of the sharing of Robert Norman, David Faux, and Robert Nelson.



The above sharing diagram of David Faux and Robert Norman shows a region of matching at the q end tip of chromosome 15. Since David and Robert share the ancestors Abraham Young (son of Lt. John Young and Catharine Hill) and Eleanor Dennis, it seems probable that this is the source of the block. However, Robert Nelson shares precisely the same segment with David Faux and Robert Norman, as seen below. Robert Nelson is a descendant of Sgt. Daniel Young (as is David Faux), but not Lt. John Young.



The conclusion is that the segment may jump a generation such that it came from Adam Young and Catharine Elizabeth Schremling. Until further evidence is forthcoming, the most reasonable assessment is that in David Faux and Robert Norman the segment comes from Abraham Young (not his wife Eleanor Dennis since Robert Nelson does not have a known Dennis ancestor), and from his father Lt. John Young, and then to Adam Young and Catharine Elizabeth Schremling. With Robert Nelson the path would be back to Sgt. Daniel Young and then to his parents Adam and Catharine Elizabeth. Thus, the block can be attributed to the family patriarch and matriarch.

4) Some Thoughts and Observations on Sharing in the Young Project:

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 here we want to know 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 “Ancestry Labs”, ‘Family Inheritance – Advanced’ feature allowing users to for example see the specifics such as segment length and position on the chromosome.

By chance the process is well under way for chromosome 2 of Sgt. Daniel Young and Elizabeth Windecker. The pattern of sharing noted to date has produced an interesting observation that for descendants of James F. Young and his brothers George Young, Henry Young and Frederick Young - participants who are descendants of Sgt. Daniel Young and Elizabeth Windecker match on both arms of chromosome 2. There is something unusual about the degree and consistency of sharing. Seeing the spreadsheet, and the matching segments drawing by Gerry Kenney will illustrate the point with clarity. Perhaps the genomes of the various 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 and Frederick etc. which 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? It is also unknown why participants either have the block on one (left or right) or both sides of the breakpoint at 52-53 megabites (position on chromosome). This is by far the most commonly shared segment among the Young participants. It is also amazing that despite the fact that chromosome 1 is the largest of the 22, only two Young descendants in the study have any match whatsoever here. There seems to be no reasonable explanation for this observation. In theory the potential for sharing here should be infinitely greater than on say chromosome 21, which is miniscule in size by comparison to chromosome 1.

5) Call for More Members of the Young Family to Test:

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. In this day and age a paper trail is just one half of what is needed for a complete genealogy.

In addition, 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. The difference here, however, is that while census records will always be available, with each passing generation more of the Young genome is being lost via the process of recombination. There is no time like the present to act.

The author wishes to thank his research associates Thomas Nelson and Gerald Kenney who have each provided important guidance in this field whose level of complexity, and the sheer number of participants, requires efforts beyond what one person can offer.

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