

Genetic Genealogy Journey

Triangulating Autosomal DNA

by Debbie Parker Wayne, CGSM, CGLSM

In the last column, we analyzed Joyce's autosomal DNA segments shared with Ryan, Bob, and Gina. All three descend from a common ancestral couple, Samuel and Mary Parker. We used a matrix tool to determine which of these matches share DNA In Common With (ICW) each other and a chromosome browser to display one chromosome where some of the cousins share overlapping segments with Joyce. This column describes the triangulation technique of shared DNA analysis.

Triangulating Autosomal DNA Segments

Triangulation is the process of comparing a DNA segment common to three or more people to verify that all share DNA along the same or an overlapping segment of a particular chromosome with *all* the others.¹ When the segment is of a significant size (usually defined as 7 to 10 centiMorgans or cM),² this shared DNA indicates that all may have inherited that DNA segment from a shared common ancestor. A triangulated group consists of those test-takers who all match each other. Because we have one copy of each chromosome from our mother and one from our father, two triangulated groups can exist for each segment of each chromosome. One of those groups should share our maternal ancestry; the other should share our paternal ancestry.

Figure 1 illustrates the analysis process for three cousins, Joyce, Ryan, and Bob. When we view the chromosome browser display for Joyce as we did in the last column, we see the DNA she shares with Ryan and Bob on chromosome 10. This shared DNA is shown in the triangle with arrows between Joyce to Bob and Joyce to Ryan and in the chromosome marked as "Joyce 10" in figure 1. This data does not tell us whether Bob and Ryan share DNA on this segment or not. If Bob and Ryan are In Common With (ICW) each other and the DNA segment appears to overlap between Joyce and the other two test-takers, it is likely that Bob and Ryan also match each other on this segment. However, it is always possible that Bob and Ryan are ICW each other on some other ancestral line, and one matches Joyce on her maternal line while the other matches Joyce on her paternal line on chromosome 10.

¹ Blaine T. Bettinger and Debbie Parker Wayne, *Genetic Genealogy in Practice* (Arlington, VA: National Genealogical Society, 2016), 84.

² A centiMorgan is a relative segment-length that incorporates the statistical probability of a segment being separated during recombination.

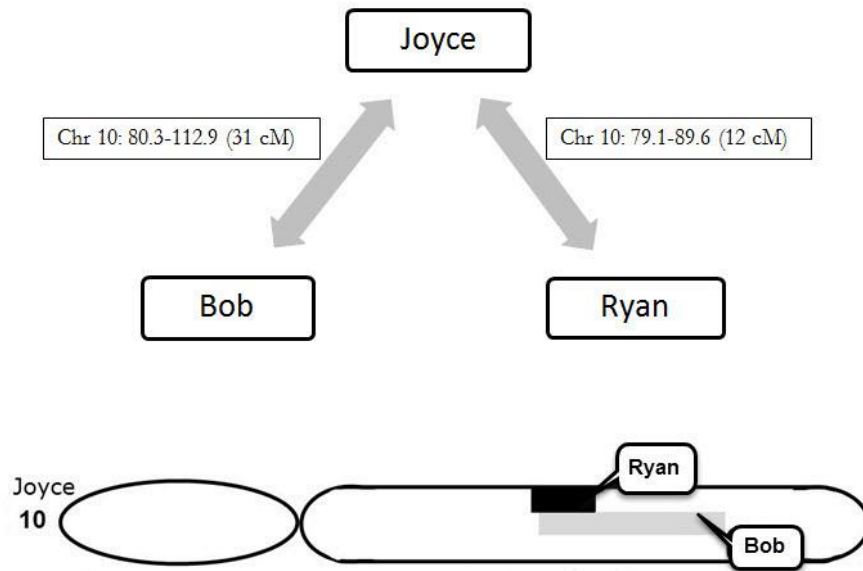


Figure 1.

To determine if Bob and Ryan both inherited this segment from the same ancestral couple, we must look at the shared segment data between the two. We can look at the shared segment data by logging into the account of Bob or Ryan, by asking one of them to gather the data from his account and send it to us, or by using a third-party tool that allows comparison of one test-taker's data to another test-taker (such as GEDmatch.com).

Figure 2 illustrates the shared segment data and chromosome browser display for Joyce, Ryan, and Bob. This figure shows that the shared segment overlaps on chromosome 10 for all three test-takers. We have now triangulated this segment. We have confirmed that all three test-takers share the same or an overlapping segment with all of the others in the group. We also must confirm that they all share only one common ancestral line before assuming this DNA segment came from that line. If any of the test-takers has an inaccurate tree, we could attribute the shared DNA to the wrong ancestral couple. Ideally, each tree has been well-researched by the individual genealogist with strong documentary confirmation. If any of the test-takers have incomplete trees, the shared DNA could have come from a different yet-to-be-identified common ancestral line.

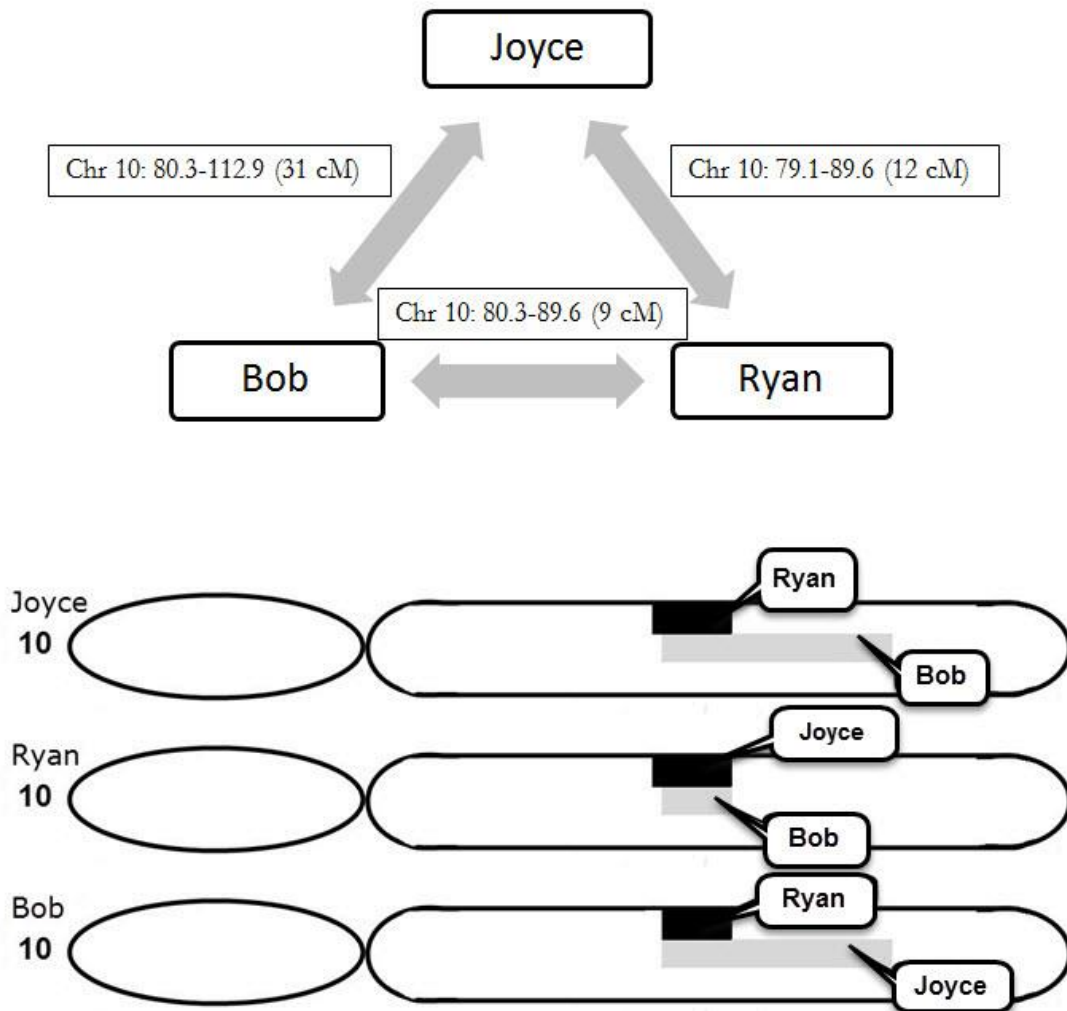


Figure 2.

If our family trees are accurate and complete, we can assume this shared DNA segment came from the shared ancestral couple. In our example, we cannot yet determine whether the shared DNA came from Samuel or Mary Parker, but we know it must have come from one or both of them. As more cousins are found in the future, we may find a cousin who is only related through the paternal or maternal line of the ancestral couple. That cousin may help us determine which ancestor the DNA was inherited from. If cousins have married it can be much more difficult to assign a DNA segment to the male or female of an ancestral couple.

Cousins Not Matching in a Triangulated Group

In the last column we showed that Gina claimed this same ancestral couple, but she matched only a small portion of this segment on chromosome 10. We saw this small segment only if we lowered the threshold from 5 cM to 1 cM minimum size for a segment to be considered a match. Normally, we would not consider analysis of such small segments and Gina would not be part of this triangulated group. Not all cousins will inherit the same segments of DNA even if they do

share a common ancestral couple. It is possible there will be no shared segments of a significant size between third or greater cousins as was shown in the last column.

When we can phase the DNA data³—determine which alleles⁴ were inherited from the father and which from the mother—small segments might become more credible as evidence. Without phasing, some alleles inherited from the mother and some alleles inherited from the father can be intermixed in the analysis. This intermixing results in false-matching indications for small segments. Many of these small segments also match due to shared ancestral populations as opposed to specific ancestral couples. For example, all test-takers with ancestral origins in a specific region will share some DNA segments.⁵

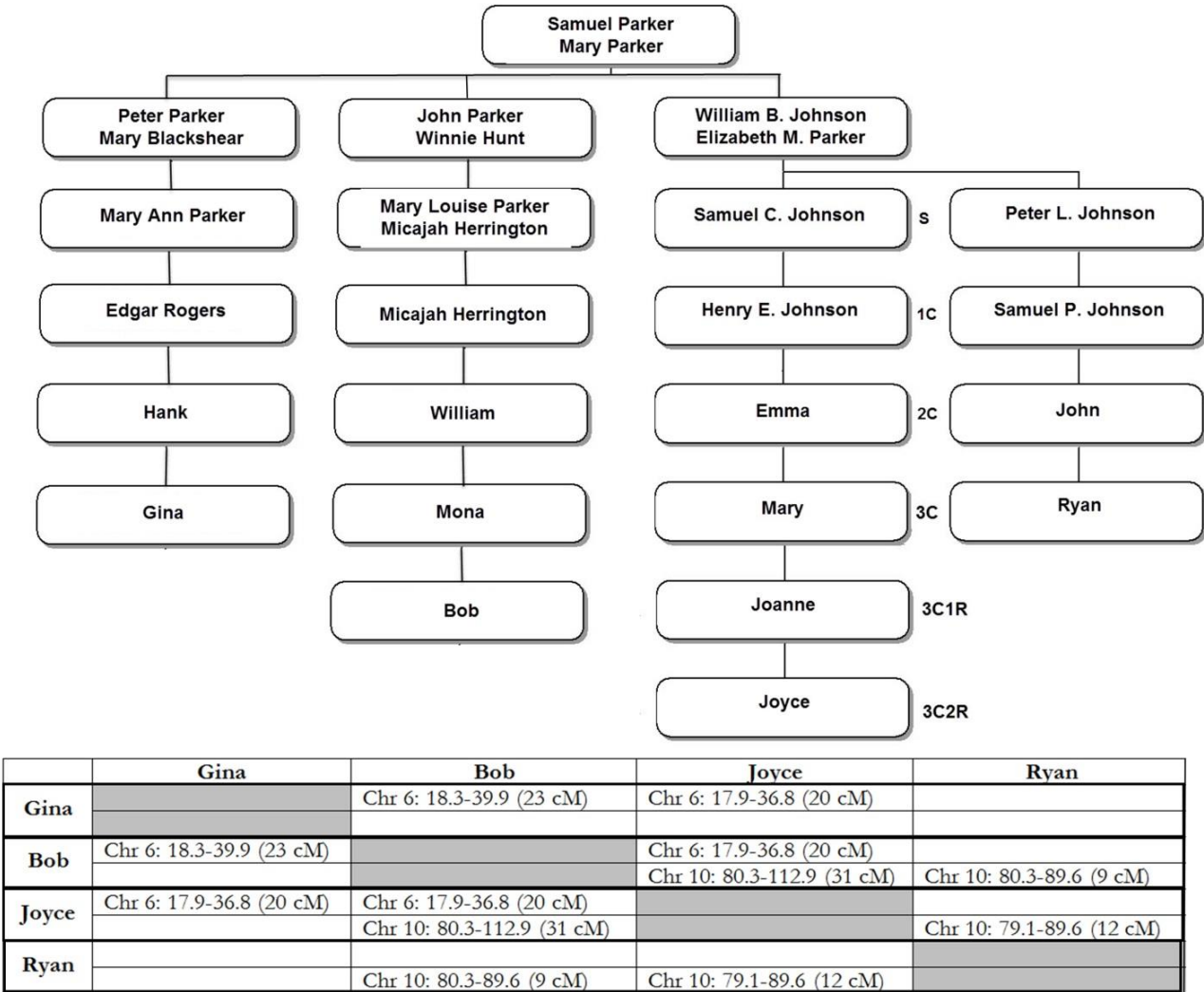


Figure 3.

³ “Phasing,” *International Society of Genetic Genealogy Wiki* (<http://isogg.org/wiki/Phasing>).

⁴ An allele is the value of a marker tested by a testing company; the allele value will be a G, C, A, or T, representing the DNA chemical at that location.

⁵ “Identical by State,” *International Society of Genetic Genealogy Wiki* (http://isogg.org/wiki/Identical_by_state).

It is possible to find multiple triangulated groups with some cousins forming one group, other cousins forming a second group, and some in both groups. Figure 3 illustrates the family trees of our four cousins. The table under the tree shows that the cousins form two triangulated groups. Each cousin is listed in a row and a column. The shaded box marks the cells where the same cousin is listed in both row and column. Other cells list the chromosome segments shared by the cousin named in the row with the cousin named in the column. Bob, Joyce, and Ryan share an overlapping segment on chromosome 10. Gina does not share a sizable portion of chromosome 10 with the others. An overlapping segment of chromosome 6 is shared by Gina, Bob, and Joyce, but not Ryan. The match on chromosome 6 forms a second triangulated group between these cousins.

More data is almost always better with genetic genealogy. While three is the minimum number of cousins needed for triangulation, more test-takers will reduce the chance of an inaccurate conclusion. The more cousins who match on an overlapping segment and share only one common ancestral couple in a well-documented and complete tree, the more credible is our conclusion as to the ancestral couple from whom that DNA segment was inherited.

Is Triangulation a Valid Analysis Technique?

Anyone who reads the DNA mailing lists or forums will see periodic discussions on the validity of triangulation. Some say it is not valid, others say it is. Genetic genealogy is still an emerging technology. Many of our DNA matching concepts are based on scientific studies and theoretical probabilities. Until we publish more case studies of the DNA findings for real families, this discussion will not likely be resolved one way or the other. Each of us believes what we have seen in our own family and client projects and may be suspicious of theories that do not match what we have seen. But remember: random, random, random. Never say never or always when DNA is involved. What we have not yet seen may become common as more people are tested.

Accurate triangulation requires multiple test-takers who all have deep and accurate family trees. Even when these conditions are met, not all real cousins will triangulate due to random recombination and inheritance factors. We can never forget the random factors affecting DNA inheritance. That randomness may result in some techniques working for some people and not others. Where it works, triangulation is a valid technique.

We should not ignore any potential evidence that can help solve a genealogical problem, but should not be surprised when evidence is not found. This statement applies to DNA as it does to documentary research. Many ancestors have not left wills or estate settlements. But will and probate indexes should not be ignored because there might not be a file for an ancestor. By that same reasoning, researchers should not ignore the possibility that DNA evidence may be found by triangulating shared segments. Triangulation may not be possible for every DNA segment, but likely will be for some segments. Once the ancestral couple is identified, that chromosome segment can be mapped to that couple. This map can provide clues as to where to look for a common ancestor for a new DNA cousin who pops up on a match list.

Conclusion

Triangulation is a powerful tool, where it is available. In the opinion of many genetic genealogists, triangulation should be considered as part of reasonably exhaustive research that can support or refute a genealogical hypothesis. Researchers must also consider the accuracy and depth of each test-taker's family tree. Unidentified or misidentified ancestors increase the likelihood that the shared DNA did not come from the focus ancestor under study. A complete and accurate tree allows the triangulated segment to be assigned to a specific ancestral couple.

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