Genetic Genealogy Journey
Why Is My Cousin Not on my DNA Match List?

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The CSI television shows have conditioned us to expect exact DNA matches and lead us to think DNA evidence is infallible. We think we should be able to determine quickly how we are related to every person on our DNA match lists. We are confused when we test a known cousin and she does not show up on our autosomal DNA (atDNA) match list. What caused this? Is she not the biological child of our uncle? We forget that DNA mutations and recombination events are random, random, random. Randomness introduces an uncertainty factor that many of us find confusing. Add our inexperience using statistics, because many of us avoided math as much as possible in school, and it is easy to get lost in genetic genealogy analysis.

DETERMINING COUSINSHIP — WHO GETS PLACED ON A MATCH LIST

If we could trace our genealogies back far enough we would all converge on the same ancestral pool at the beginning of humankind. Because of this, we all share some small DNA segments. Intermarriage and common ethnic origins also result in shared small DNA segments. Random recombination causes some of us to share more DNA than others at the same level of cousinship. Which other testers will be on our DNA match list is determined by match criteria selected by the testing company. Without such criteria our match list would include cousins so distant we could never find documentary research to confirm a relationship.

Testing companies use different algorithms to determine match list contents. Some companies are more willing to share their algorithms than others are; test results of those with known family relationships allow us to deduce other algorithms. The International Society of Genetic Genealogists (ISOGG) documents the deduced and stated criteria for matching segments, as well as much other information useful to genetic genealogists. The ISOGG Wiki indicates one company requires at least one DNA segment to be 7.0 centimorgans long, another requires 7.69 centimorgans, and a third requires only 5.0 centimorgans.[1] A centimorgan is a relative unit of measurement, not a physical one, related to the likelihood of a DNA segment going through recombination in one generation.[2] There are other details involved with the match algorithms not discussed here.

As shown in table 1, the testing companies provide statistical odds indicating the likelihood of a cousin of a specific level appearing in our atDNA match list. Random recombination and the match criteria both affect whether or not a cousin appears on our match list. The different odds stated by each company indicate that we still have much to learn about DNA and that random recombination

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All URLs accessed 14 May 2015.

[1] "Autosomal DNA Testing Comparison Chart," *International Society of Genetic Genealogists* (ISOGG) Wiki (http://www.isogg.org/wiki/Autosomal_DNA_testing_comparison_chart).

[2] "Centimorgan," *Genetics Home Reference*: *Your Guide to Understanding Genetic Conditions*, U.S. National Library of Medicine (http://ghr.nlm.nih.gov/glossary=centimorgan).

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can have a large effect on the calculated odds. As we go past the second cousin level, the odds of a cousin appearing in our match list get lower. We likely have many more fifth and sixth cousins in our atDNA match list. Most of us have many more cousins at that distant level than we have first or second cousins.

Table 1 clearly illustrates that we can theorize about relationships when a person does appear on a DNA match list. If two people share enough DNA to be on each other's match list, they definitely have a biological relationship. Theories about relationships of two people who do not appear on each other's match list are more problematic. Perhaps they are not related at all. Perhaps random recombination and/or the company threshold algorithms prevent appearance on the match list.

Table 1.
Odds of Matching a Known Relative with atDNA Testing
~ symbol used to indicate approximately

	FTDNA[a]	23andMe[b]	AncestryDNA[c]
2nd cousin or closer	> 99%	>99%	100%
3rd cousin	~ 90%	~90%	98%
4th cousin	> 50%	~45%	71%
5th cousin	> 10%	~15%	32%
6th cousin (and more distant for FTDNA and 23andMe)	< 2%	<5%	11%
7th cousin			3.2%
8th cousin			.91%

a. "What is the probability that my relative and I share enough DNA for Family Finder to detect?" *Family Tree DNA Learning Center* (https://www.familytreedna.com/learn/autosomal-ancestry/universal-dna-matching/probability-relative-share-enough-dna-family-finder-detect/).
b. "The probability of detecting different types of cousins," *23andMe Customer Care* (https://customercare.23andme.com/hc/en-us/articles/202907230-The-probability-of-detecting-different-types-of-cousins).
c. "Should Other Family Members Get tested?," *AncestryDNA;* accessed through help on the "Member Matches" page of a person's AncestryDNA Results page, help link indicated by a question mark button.

RANDOM RECOMBINATION AND THRESHOLD CRITERIA AFFECTS

Random recombination affects the size and number of segments where two descendants of an ancestral couple share DNA. The threshold criteria determine how a company interprets that shared DNA. The threshold criteria can have as much effect on the match list contents as random recombination has. The following example shows how three DNA testers can be cousins through the same ancestral couple even when two of the testers do not appear to share DNA, based on the match list at the testing company.

Figure 1 indicates that Deb and Nan share two DNA segments on the chromosome illustrated here. One segment is 12.84 centimorgans in length. A second shared segment is 5.85 centimorgans in

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length. A small unshared segment separates the shared segments. Deb and Nan can both see the other on their DNA match lists. Deb and Nan both have well-documented, thoroughly researched family trees back to one common ancestor.

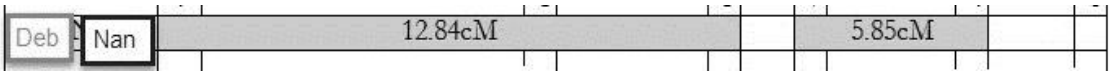

Figure 1.

Nan has a third person, Max, on her atDNA match list. After corresponding with Max, Nan determines the common ancestors could be the same as the ancestors shared with Deb. Nan contacts Deb and finds out Max is not on Deb's list of atDNA matches. How can this be if they all share the same common ancestral couple? How can Nan share DNA with Deb and Max in the same area on the same chromosome, but Deb does not share that DNA with Max?

By analyzing the segment data (the details indicating the chromosome number and the start and stop points of the matching DNA) that Nan shares with Deb and that Nan shares with Max, we can determine why Deb and Max are not on each other's match list. We can determine if all three might share a common ancestral couple. The data necessary for this analysis is available to us only if we tested at Family Tree DNA or 23andMe. AncestryDNA does not provide the necessary data, at least at this time, without uploading your data to other websites and/or using third-party tools.

TRIANGULATION

We triangulate and confirm common groups by confirming A shares a DNA segment with B, B shares the same segment with C, and C shares the same segment with A. In our example, Deb is A, Nan is B, and Max is C. We discussed the shared segments of Deb and Nan above. Now let us look at the segments Nan shares with Max and Deb may share with Max.

As illustrated in figure 2, Nan and Max share a 9.13 centimorgan DNA segment that overlaps the two segments shared by Deb and Nan. This segment bridges the segment where Deb and Nan do not match each other. We can deduce, based on a comparison of Deb to Nan and Nan to Max, that Deb and Max probably share two small segments in the range of 5–6 centimorgans each on this chromosome. If the company threshold requires at least one segment that is seven centimorgans or longer before a person is considered a match, the DNA shared by Deb and Max (figure 3) does not meet that threshold. We can confirm the match between Deb and Max using third-party tools such as those available on GEDmatch.com that allow using a smaller threshold than the testing company uses.

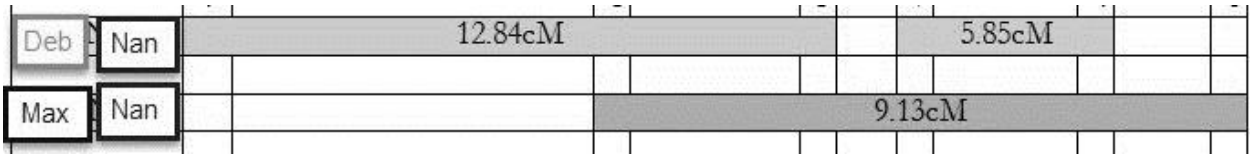

Figure 2.

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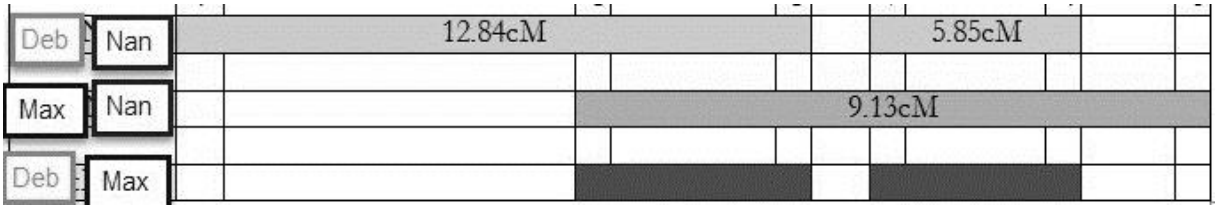

Figure 3.

Just looking at the illustrations and using our deduction, we cannot determine if Nan might be related to Deb and Max on these chromosome segments through the same common ancestor. If we remember earlier columns where we discussed atDNA inheritance, we each inherit one copy of each chromosome from our mother and one from our father. It would be possible for Nan to be related to Deb through Nan's paternal line and for Nan to be related to Max through Nan's maternal line. Confirming that Deb and Max share the same DNA on the same segments where Nan and Max share DNA on overlapping segments is called triangulation.

Triangulation is the piece of this analysis that reduces the potential for later discovery of conflicting information. If we have not shown that Deb and Max share these DNA segments by examination of the DNA results we cannot make a firm conclusion whether Max is related to Nan through the same common ancestor as Deb is or if Max is related to Nan through another ancestral line, maternal or paternal. A thorough search often includes research into the relationships between associates. In this DNA example, confirming the matches of your matches through triangulation leads to a more credible conclusion.

This is just one example where understanding the biological inheritance factors of DNA, the company decisions regarding thresholds and algorithms, and how to interpret probabilities all are important. All of these elements are correlated with our well-documented, thoroughly researched family tree. The DNA match can prove we have a common ancestor. The well-documented, thoroughly researched family tree is necessary to determine who that common ancestor may be. Education in both documentary research methodology and genetic genealogy analysis techniques are needed.

EDUCATING OURSELVES

A good place to start looking for answers to genetic genealogy questions is the Wiki of the International Society of Genetic Genealogists (ISOGG).[3] The main content providers strive to provide truthful and unbiased information for the companies offering genetic tests for genealogical purposes. Information from and about all of the companies is compiled in one place. Like most Wikis, this is a volunteer effort. There may be a time delay between the discovery of new information and the time it is documented in the Wiki. DNA mail lists, forums, and blogs are another great resource for information on genetic genealogy.

[3] *International Society of Genetic Genealogists* (ISOGG) Wiki (http://www.isogg.org/wiki/).

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Many of us who avoided math in school now regret that decision. In our Internet connected world, it is easy to educate ourselves as adults and correct the errors of our youth. Ivy League universities are placing courses online for free access by the public. Massachusetts Institute of Technology (MIT) offers many online classes for which the course materials can be downloaded and studied on our own. One such is a course on Genetics.[4] Everything in this course is not applicable to genetic genealogy, but this will answer some of the biological questions that many of us have.

MIT is a little intimidating. Khan Academy, where "[o]ur mission is to provide a free, world‑class education for anyone, anywhere" may be more comfortable. Khan Academy was started by a man who was tutoring his younger relatives through math and he did such a good job that he began to get requests from others for help.[5] The "Probability and Statistics" course provides information on the algorithms and math concepts used by genetic genealogists and by all of us in our everyday lives.[6]

CONCLUSION

To use genetic genealogy effectively we may need to study some of those subjects we avoided when we were younger. Math and biology can be fun. We can find ways to learn what we need without taking classes in person or admitting that we did not pay attention in class years ago.

We need to understand the random nature of DNA inheritance and how that can manifest itself in true biological cousins; some inherit and some do not inherit certain DNA segments. In addition, we need to understand that the choices companies make about algorithms and thresholds can affect our analysis. Sometimes we may need to go beyond the tools provided by a company to find the true relationships of our DNA cousins. Luckily for us, new tools for genetic genealogy are appearing on a regular basis.

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[4] Prof. Chris Kaiser , et al., "Genetics," MIT Course Number 7.03, as taught in Fall 2004, Massachusetts Institute of Technology, *MITOpenCourseware* (http://ocw.mit.edu/courses/biology/7-03-genetics-fall-2004/).
[5] "How did Khan Academy get started?" *Khan Academy* (https://khanacademy.zendesk.com/hc/en-us/articles/202260104-How-did-Khan-Academy-get-started-).
[6] "Probability and Statistics," *Khan Academy* (https://www.khanacademy.org/math/probability).

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