Cristi Reed

So, what about DNA matches?

DNA testing can help extend genealogy, but how? Genealogical research and the DNA test correlate genealogical results. So how does one use DNA data to push a pedigree chart further back? Genetic Genealogy is a tool of elimination and indirect evidence to improve genealogical efforts. The DNA matches show how people are connected and who shares DNA. The DNA is conveyed through a common ancestor and becomes evidence of connection when analyzed correctly. The point is determining the common ancestor and the different descendants of the ancestor to prove common relationships. Every person has two family trees, genetic and genealogical (records). Comparing and using those trees can increase positive genealogical results by sorting matches, connecting the matches, and analyzing the data.

Each person has two family tree types: a genetic and a genealogical family tree. The sourced or genealogical tree is traced through traditional genealogical methods. The genetic is traced through DNA. When compared, the two trees can fill in each other's holes or expand further generations back. DNA Matches are when a person shares some portion of genetic information with another. The shared data means there is a shared ancestor at some point.

Sorting matches into four groups by ancestral grandparent couples is the first step to utilizing the DNA matches. A test taker should organize the different matches by their groups. The organization allows the test taker to know which matches pertain to which part of their pedigree. If a person or researcher is trying to find one specific ancestor and determines that the match is on a different line, that match is irrelevant to the current project. The Leeds Method is a system of sorting the matches that the researcher could explore.[1]

Genealogists then connect the matches by the amount of shared DNA for the appropriate relationship. Next, the researcher sorts the matches by an ancestral grandparent couple; the resulting groups help determine the relationships. For example, when the match is related to the paternal grandfather, the connection can be determined by the amount of shared DNA. A specific number of centimorgans is a first cousin on a great-niece. Centimorgan (cM) is the measurement for shared DNA matches; it is the unit of DNA, like inches in length. The amount of shared DNA and the possible relationships appears in charts like the shared chromosome project.[2] The primary testing sites also give potential connections based on that measurement of DNA between matches. Finally, the genealogist must build the family trees to connect to see how the matched people are related.

---

[1] Dana Leeds Creator of The Leeds Method, "DNA Color Clustering: The Leeds Method for Easily Visualizing Matches," (www.danaleeds.com; 17 November 2021), Dana Leeds.

[2] The Genetic Genealogist, "Version 4.0! March 2020 Update to the Shared cM Project!", (www.thegeneticgenealogist.com: 17 November 2021), Blaine Bettinger.

When the groups and the different relationships are determined, the genealogist can use that relationship to search more records or eliminate brick walls. For example, suppose one is searching for the female ancestor's father's name and can prove the genetic similarities with that person's son who had a sister by that name. In that case, the problem is resolved through the DNA and the genealogical records together. Some genealogical records include some of the children but not all the children, so the DNA becomes the mission piece of evidence.

DNA shared matches are where the power of genetic genealogy lies. It is fun to know ethnicities' origination to explore the DNA matches to use genetic genealogy. Shared matches are how DNA can help extend the family tree. Public trees allow matches to find the common ancestors more easily. Comparing public genealogical trees with genetic trees can increase positive genealogical results by sorting matches, connecting the matches, and analyzing the data.