GENEALOGICA & HERALDICA XXXV

REFORMATION REVOLUTION RESTORATION

CAMBRIDGE
2022

ISBN 978-0-904858-07-5

Congress logo by Tania Crossingham

Photographs on the rear cover: Congress banners in Clare College Scholars' Garden by Jack Sain, plaque created for the Congress baton by Paul A. Fox

Printed in Great Britain by 4word Ltd, Bath

Correspondence to coatofarms@theheraldrysociety.com

www.theheraldrysociety.com

DNA TESTING: THE GENEALOGICAL REVOLUTION

LAURA ANN HOUSE, M.Sc.

Abstract

The field of genealogy has experienced two major cultural and scientific changes in the last 30 years. The first is the advent of the World Wide Web, which has forever changed the way we access information, conduct research, and store our data. The second is the sequencing of the human genome, which was closely followed by the development of affordable and effective direct-to-consumer (DTC) genetic testing. Professional genealogists are currently re-evaluating the 'genealogical proof standard' in light of this new technology. We are learning to view traditional historical records with scepticism when the DNA evidence leads us in a different direction. The revolution that has taken place since the accessibility of direct-to-consumer DNA testing means that we must now approach genealogical research as both historians and scientists. Any methodology that does not incorporate both elements may be lacking, and if researchers wish to remain at the cutting-edge of the field, they must learn to work with this new and invaluable resource.

DNA testing serves its greatest purpose when it restores the histories of those who do not have access to the documentation that makes traditional research possible. Every person has a right to information about their heritage, and genetic genealogy has enabled researchers to connect both modern and historical adoptees, foundlings, and people with unknown paternity, to their missing roots. It is hoped that someday genetic genealogy will become a better resource for other disenfranchised groups, such as those whose personal histories have been rendered inaccessible by wars, the transatlantic slave trade, and colonialism.

DNA For Genealogy

There are several different DNA tests currently available to genealogists. The autosomal DNA (atDNA) test analyses the markers inherited across the 22 pairs of autosomes, and at the time of this writing, the companies offering this test to people in Europe and the United States include AncestryDNA, MyHeritage, 23andMe, and FamilyTreeDNA. There are companies catering specifically to Asia and Africa, but some of these do not offer the matching of relatives, which is an essential component of genetic genealogy.[1] The autosomes recombine with every reproductive event (meiosis), which results in the quantity of atDNA inherited from an ancestor decreasing by 50% with every new generation.

Except in the case of rare birth anomalies most people have two sex determining chromosomes. Those who are born biologically male usually have one X and one Y chromosome, and those who are born biologically female usually have two X chromosomes. Markers from the X chromosome are included in an atDNA test, as the X chromosome recombines like an autosome when it is passed from mother to child. The X chromosome does not recombine when passed from father to daughter, so X-DNA follows a slightly different pattern of inheritance when compared with atDNA.

Y-DNA is located on the male determining Y chromosome, which is passed almost perfectly intact from father to son. Y-DNA tests analyse short tandem repeats (STRs) and single nucleotide polymorphisms (SNPs). The Y chromosome does not recombine, but the STR and SNP markers can mutate during a meiosis event. These mutations are measured in genetic distance (GD). At the time of this writing, the market leader offering Y chromosome sequencing for genealogical purposes is FamilyTreeDNA.[2]

Mitochondrial DNA is located outside the nucleus of the cell. The function of mitochondria is to generate the energy required by the cell to power its biochemical reactions.[3] Mitochondria are present in human eggs but not in spermatozoa, and are passed directly from a mother to all her children, mutating approximately once every 500 years.[4] Mitochondrial DNA is not located on a chromosome, and it does not recombine during a meiosis event. It is useful when researching deep matrilineal ancestry, but it has limited applications to genealogical research. At the time of this writing, the market leader offering mitochondrial DNA sequencing for genealogical purposes is FamilyTreeDNA.

The Genealogical Proof Standard

According to Tyler S. Stahle, "the Genealogical Proof Standard is a process used by genealogists to demonstrate what the minimums are that genealogists must do for their work to be credible."[5] In practice, this is usually applied by locating a minimum of two primary sources before determining that a recorded fact is likely to be accurate. For example, if a census record states that Ann Smith was born in about 1886 in Lancashire, to John and Mary (Jenkins) Smith, we would search for a corresponding civil birth record before disseminating this information in print or online. If a civil birth record was not available, we would at least need to obtain a corresponding parish baptism entry, or another census record. If we can only locate one source referencing this specific historical event, we need to explicitly state in all publications that Ann Smith may have been born in about 1886 in Lancashire to John and Mary, but that the evidence supporting this assertion does not meet the genealogical proof standard.

Until the introduction of DTC genetic testing, the genealogical proof standard referred to the quality and quantity of documentary evidence, but in 2019, the Board for Certification of Genealogists revised their publication *Genealogy Standards* to include DNA-based evidence.[6] Genetic evidence is invaluable for verifying genealogical relationships, but crucially, DNA can supersede documentary evidence by confirming that a documented relationship does not exist, and by demonstrating that the true genetic relationship is not recorded in any traditional sources.

Let us explore a hypothetical scenario, in which Ann Smith's birth certificate, baptism register entry, and census records all state that she was born in 1886 to John and Mary (Jenkins) Smith. In this case, the documentary evidence meets the genealogical proof standard by any traditional measure. Ann's living grandchildren take an atDNA test and they are matched with genetic relatives descended from the ancestors of each of their great-grandparents, except one – Ann's father, John Smith. They are matched with descendants of Mary (Jenkins) Smith's parents, Griffin and Sarah Jenkins, but they do not match with any descendants of John Smith's parents, James and Alice Smith (**Figure 1**).

To complicate matters further, they are matched with several great-grandchildren of a man named Richard McAllister, who is not a documented ancestor. The quantities of DNA shared by Ann's grandchildren and the grandchildren of Richard McAllister show

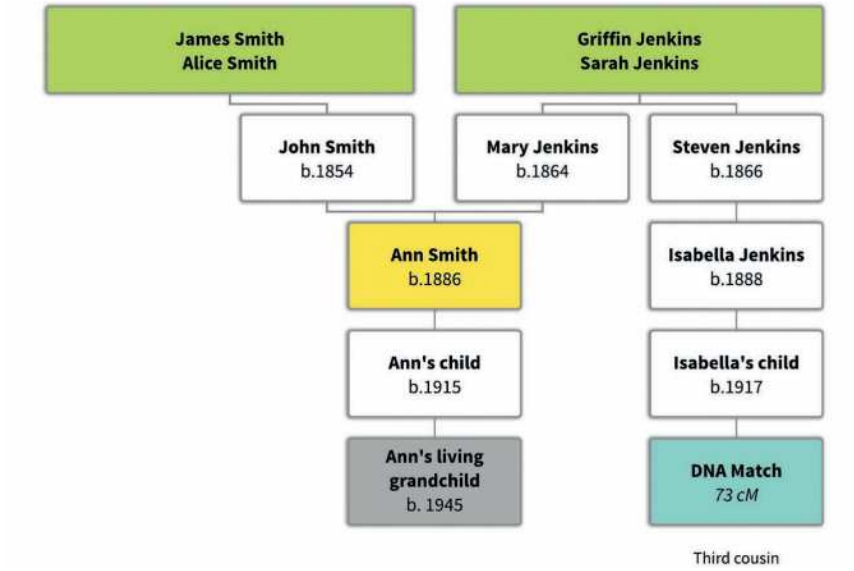


Figure 1: Family tree demonstrating the documented relationships between members of the hypothetical Smith family.

that they are likely to be half-second cousins. The 1881 and 1891 England and Wales census shows that Richard McAllister lived on the same road as Mary (Jenkins) Smith around the time that Ann Smith was conceived. The DNA and documentary evidence show that Ann Smith was not fathered by John Smith, and that she was likely to have been fathered by Richard McAllister, or a brother of Richard (**Figure 2**). In this scenario, the evidence produced by autosomal DNA analysis demonstrates that the birth certificate,

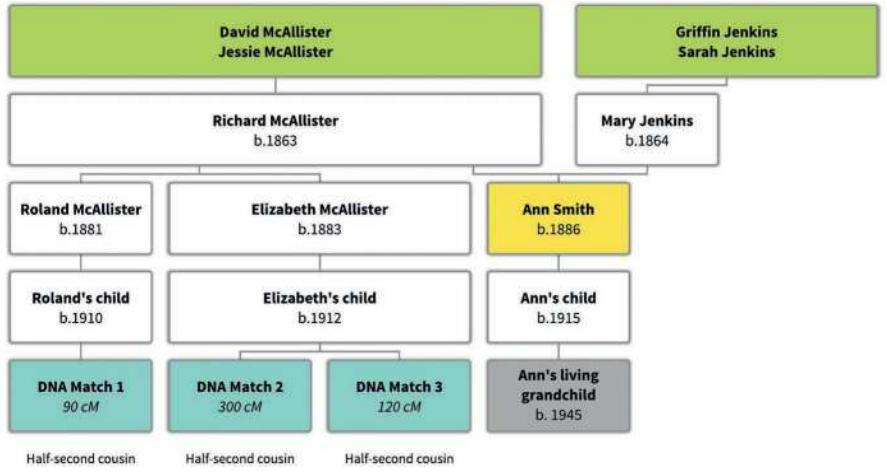


Figure 2: Family tree demonstrating the undocumented genetic relationship between Ann Smith and the McAllisters.

baptism register entry, and census records are all incorrect with regard to the paternity of Ann Smith. Despite meeting the genealogical proof standard, the documentary evidence led to a false conclusion, and this could only have been revealed by testing the DNA of living descendants.

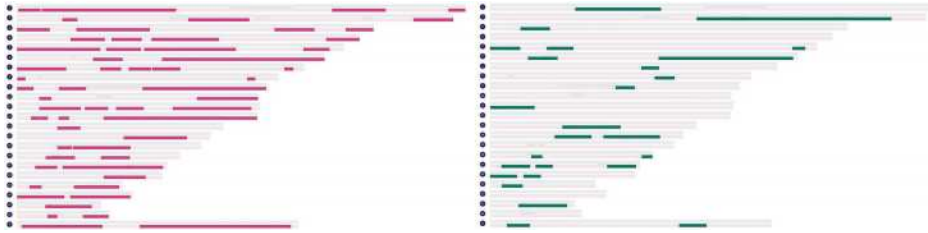
Case Study: Magda, Mari, and Juanita

As DTC- DNA testing grows in popularity, discoveries of this nature are becoming commonplace. This case study concerns three sisters: Magda, Mari, and Juanita, all of whom are now deceased. They were born in Gran Canaria, Canary Islands, to a woman named Maria del Carmen. Their documented father was their mother's husband, Luis, and the sisters never had any reason to question their paternity (**Figure 3**). After Mari and Juanita died, Juanita's three children took direct-to-consumer autosomal DNA tests. Mari's daughter also took a test, as did Magda, who at this time was the only surviving sister.

Figure 3: The documented parentage of Magda, Mari, and Juanita.

Shared autosomal DNA is measured in centiMorgans (cM). The quantity of centiMorgans shared by two individuals indicates the closeness of their genealogical relationship. A parent and a child share 3,400 cM of DNA. It is possible for two people who share zero DNA to have no recent genealogical relationship, but they might potentailly be third (or more distant) cousins.[7] A full aunt and niece should share autosomal DNA in the region of 1,201 to 2,282 cM. The DNA test results show that Magda and Mari's daughter share 2,149 cM (26%) of autosomal and X chromosomal DNA, perfectly within the expected (**Figure 4**).

Juanita's daughter, however, shares just 807 cM of autosomal and X chromosomal DNA with Magda, significantly below the lower threshold for an aunt/niece relationship. This quantity of DNA is indicative of a half-aunt/half-niece relationship, for which the expected range is 493 to 1,315 cM. Juanita's daughter shares 398 cM with Mari's daughter, placing them at the lower threshold for a full first cousin relationship (396–1,397 cM) and perfectly within the expected range for a half-first cousin relationship (156–979 cM).(Figure 5).The DNA test results of other family members confirmed that the only explanation for this event was a half-sibling relationship between Juanita and her sisters, Magda and Mari, suggesting that Magda and Mari were fathered by Luis, and that Juanita was fathered by someone other than Luis. The documentation supporting a



Left: Figure 4: the autosomal and X-DNA shared by Magda and the daughter of Mari; right: *Figure 5:* the autosomal and X-DNA shared by Magda and the daughter of Juanita. Both © DNA Painter . https://dnapainter.com.

father/daughter relationship between Juanita and her purported father, Luis, meets the genealogical proof standard, but the documentation in this case is incorrect. If researchers had relied solely on historical records when studying the family of Magda, Mari, and Juanita, they would have drawn false conclusions about the nature of the relationship between Juanita and Luis.

It is possible that any given documented relationship could be invalidated by DNA analysis; however, some researchers do not want to engage with genetic genealogy and consider documentation to be sufficient evidence of kinship. *Genealogical Standards* addresses this by differentiating between 'genetic relationships' and documented relationships. It defines a genetic relationship as "A familial relationship reported by a DNA testing company or resulting from a genealogist's use of DNA evidence to estimate the relationship."[8] The standards state that, "Genealogists declare that a relationship is genetic only when their evidence supports a genetic relationship. If DNA evidence could overturn a conclusion, genealogists explain that limitation."[9] Therefore, the Board for Certification of Genealogists does not insist that all available DNA-based evidence is obtained before a conclusion is reached, but it does suggest that researchers should be transparent when a relationship is not supported by genetic evidence.

The genealogical proof standard could be revised further to the extent that the standard can only be met if all relationships have been tested using any attainable DNA data. In practice, this would mean that any descendants of the ancestors in question are offered the opportunity to participate in DNA testing. The DNA data of any consenting participants is then collated and compared. If this analysis produces any evidence to suggest that the hypothesised genealogical relationships are false, the documentary evidence cannot be considered to meet the genealogical proof standard. If the hypothesised relationships withstand DNA analysis (even as the result of an absence of conclusive evidence), they can be considered to meet the genealogical proof standard. This would be optimal in terms of verifying kinship, but the dependence on living people raises some ethical issues. This may be one reason that *Genealogical Standards* emphasises 'genetic relationships' as a distinct category of genealogical relationship, rather than insisting that all genealogical events are confirmed with DNA testing.

The Limitations of DNA as a Component of the Genealogical Proof Standard

It is important that all attainable evidence is collated and analysed before researchers draw conclusions about genealogical relationships; however, there are limitations to consider when applying DNA data to the genealogical proof standard. DNA analysis provides us with evidence of genetic relationships, but it does not provide us with the context needed to identify the precise degree of a relationship. Two people who share 2,000 cM of autosomal DNA could be half-siblings, aunt/uncle and niece/nephew, or grandparent and grandchild.[10] To interpret the precise nature of a genetic relationship, we need the total quantity of centiMorgans, the ages of the two test-takers, and we may also need other information, such as circumstances of birth, that can only be provided by traditional records. This contextual information is more important when analysing smaller quantities of DNA, which are easier to misinterpret due to the larger number of potential relationships that can account for a smaller quantity of shared DNA.

Two people who match closely on the Y chromosome could be siblings, parent and child, patrilineal first cousins, second cousins, third cousins, or more distant. Two people with matching mitochondrial DNA are related on the matriline at some point within the last 500 years, but we cannot interpret the nature of the relationship without more information.[11] Therefore, when we use DNA as evidence of a relationship, it is important to understand the limitations, and to frame the evidence in its context.

Autosomal, Y, and mitochondrial DNA are also limited in their scope. With Autosomal DNA as segments of ancestral DNA are lost with each new generation it is possible to inherit zero autosomal DNA from a fourth great-grandparent, which means that a test-taker will not be able to use their own autosomal DNA to investigate the identities of all their 64 fourth great-grandparents.[12] If these ancestors have other descendants who have inherited their autosomal DNA, then it may be possible to use these segments as evidence of a relationship, but there will be many ancestors in the average person's tree from whom they have inherited no autosomal DNA. The genealogical proof standard must allow for this situation, and we cannot expect researchers to produce autosomal DNA-based evidence of relationships this distant.

Y-DNA is passed from father-to-son and does not recombine, so while it can be used to evidence distant genealogical relationships, an individual researcher can only use their Y-DNA data to analyse their patriline. This data may be entirely inaccessible to biologically female researchers with no living male relatives, and it may not be possible to obtain Y-DNA data for every male line in a family tree.

The same issue exists with mtDNA. People of all sexes carry the mtDNA of their own matrilineal ancestors, but it may not be possible to obtain mtDNA for every female line in a family tree, and as outlined above, Y-DNA and mtDNA cannot be used to determine precise degrees of relatedness.

The Genetic Revolution

Developing Methodologies for the Application of Y and Autosomal DNA

The field of genealogy was fairly stable for centuries, utilising oral history, physical documentation, and archival collections, until the advent of the World Wide Web in the 1990s, closely followed by the sequencing of the human genome, which was completed in 2003.[13] In 2000, FamilyTreeDNA launched the first commercial direct-to-consumer

genetic testing service, which offered members of the public the opportunity to purchase a 12-marker Y-STR test.[14] Since 2000, both the World Wide Web and DTC genetic testing have grown in scope, accessibility, and affordability, forcing leaders in genealogy to adapt in order to remain at the cutting-edge of the field.

In addition to being adept historians, genealogists must now be technologically and scientifically literate. Most professionals and academics have been using computers and the internet for decades and find that these enable access to record collections and resources all over the world, but many have struggled with the introduction of genetics to genealogy. DTC genetic testing websites are user-friendly and highly commercialised, and there are excellent tools designed to simplify processes such as chromosome mapping and calculating relatedness, but even with these resources, a certain level of knowledge is required to optimise genetic data, which is not required to utilise traditional historical sources.

To avoid further alienating traditional historians and genealogists, we should ensure that tools and resources continue to improve, and that educational programmes (particularly at undergraduate and postgraduate levels) emphasise both traditional and genetic genealogical research methods, so that future professionals and academics do not have to navigate this transition. Where applicable, a thorough genealogical research methodology must incorporate both documentary and genetic evidence, and the training of new genealogists should reflect this.

Developing Methodologies for the Application of Y and Autosomal DNA

An unpublished 2019 dissertation titled '*What are the Limitations of Y and Autosomal DNA When Applied to the Investigation of Surname Changes?*' focuses on developing accessible methodologies applicable to a range of common scenarios faced by genetic genealogists in their work, such as undocumented adoptions, illegitimacies, surname changes, and other situations in which individuals did not assume their patrilineal family name.[15]To develop these methodologies, five undocumented surname change cases were resolved using a combination of documentary research and genetic genealogy, and the steps taken to identify the original patrilineal surname are outlined in a series of flowcharts, depicting the methodologies in their simplest form. These flowcharts could be adapted to create a guide or a computer programme (such as an app) that would enable genetic genealogists at all levels of expertise to navigate these complex scenarios. Genetic genealogy is most powerful when knowledgeable test-takers collaborate, and it is therefore to everyone's advantage if casual genealogists understand the benefits and limitations of these techniques (**Figures 6 and 7**).

The internet has democratised genealogy, giving access to those who might previously have been prevented from carrying out research, for example, people with disabilities who cannot physically travel to archives; those living in rural communities without access to a major archive; and people without the financial means to travel to archives. DNA testing should similarly democratise genealogy by restoring the personal histories of those who do not have access to the traditional resources many researchers take for granted.

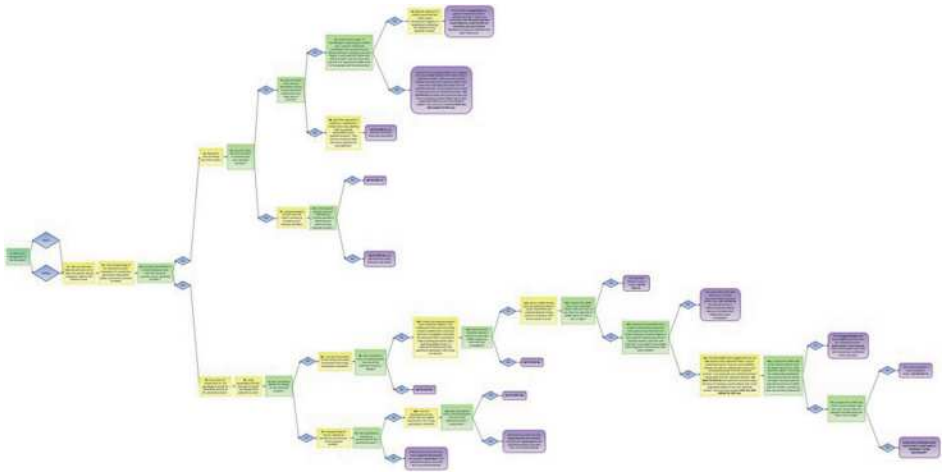


Figure 6: a full view of one flowchart (the text is not visible in this view because the chart is too large). Source: author's unpublished M.Sc. dissertation.

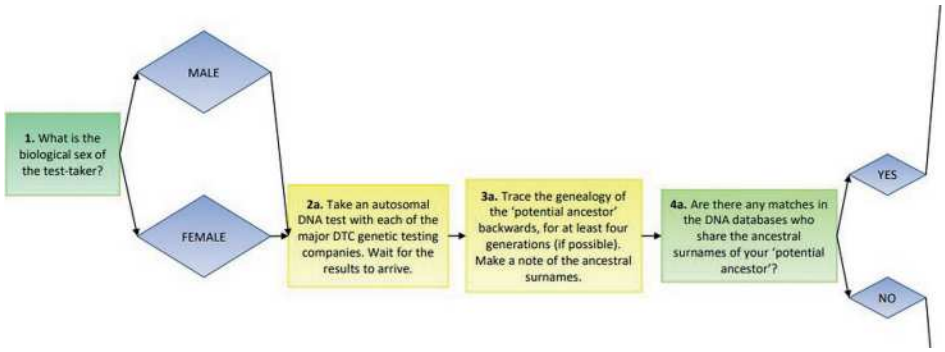


Figure 7: a close-up view of the first four steps in the above flowchart.

Restoring the Personal Histories of Disenfranchised Peoples

There are several groups of people for whom traditional genealogical research sometimes serves no function:

- People with unknown paternity, who often have no father recorded on their birth record
- Adoptees, particularly those without accurate adoption records
- Foundlings, for whom no birth documentation exists
- Descendants of enslaved peoples, for whom few useful genealogical records exist
- Descendants of refugees, who have lost access to any relevant archives, and whose genealogical records may have been destroyed in conflict
- Descendants of ancestors whose lands were colonised, whose names were forcibly changed, and whose original autonomous governments were overturned

For some people in these groups, genetic genealogy is the only means by which their personal histories can be restored. It is when working on cases like these that we can appreciate the extraordinary potential of genetic genealogy, even for people with no accessible documented history.

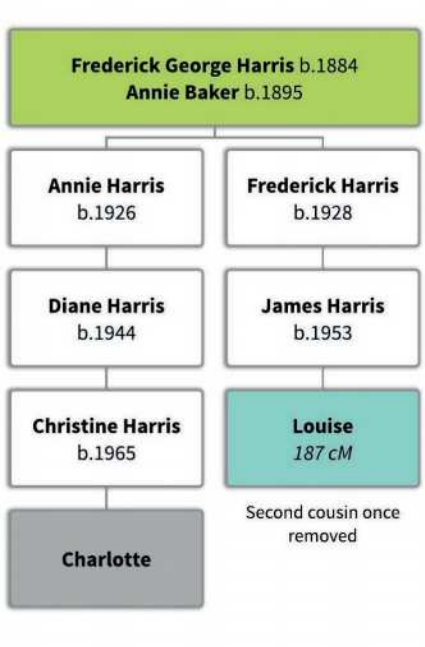
Restoring Personal Histories: A Case Study

During the Second World War, approximately 240,000 African American servicemen (GIs) passed through the United Kingdom. Many of these men had relationships with white-British women, and an estimated 2,000 children were born as a result. Servicemen needed the permission of their commanding officer to marry, and the United States Army had forbidden them to grant this permission to interracial couples, which meant that all these children were born to unmarried mothers, despite many of these couples wanting to remain together.[16]

The children born from these relationships were referred to in the African-American press as Britain's 'Brown Babies,' and many were subject to rejection, discrimination, and injustice throughout their lives. One of these babies was Diane Harris, who was born in about 1944 to Annie Harris, an unmarried woman. Annie was seventeen years old when she became pregnant by an African-American GI, and unlike many of the children born in these circumstances, Diane remained with her mother's family for some time. According to oral history, Diane was raised by her grandparents Frederick George and Annie (Baker) Harris. Frederick died in 1949, and Diane was entered into the care system soon after, although she maintained contact with her family into her adult years.

Diane eventually had a daughter of her own whom she was unable to raise, and her daughter was adopted out, losing all contact with the Harris family. Diane later died young in tragic circumstances, and her daughter eventually had children of her own, before also dying young in tragic circumstances. This series of events meant that Diane Harris's grandchildren lost all access to their maternal family history. As descendants of two generations of adopted Black women, they were multiply disenfranchised.

In 2020, Diane's granddaughter Charlotte[17] took a DTC-DNA test with AncestryDNA and was matched with a great-granddaughter of Frederick George and Annie (Baker) Harris. Charlotte and her DNA match, Louise, share 187 cM of DNA, suggesting a relationship in the range of second-to-third cousins, with second cousins once removed being the most likely degree.[18] Their respective family trees were reviewed, and it was determined that Charlotte is a granddaughter of Diane Harris, who in turn, is a granddaughter of Frederick George and Annie (Baker) Harris. Charlotte and Louise are second cousins once removed, and Charlotte has been reconnected with her matrilineal ancestors and their stories (**Figure 8**). In this case, DNA testing restored Charlotte's matrilineal family history under circumstances that would have been difficult to navigate using documentation alone. By connecting Charlotte with her second cousin once removed, it was possible to identify her previously unknown grandmother, great-grandmother, second great-grandparents, and the ancestors who precede them.



Left: Figure 8: family tree outlining the relationship between Charlotte and her DNA match Louise; right: *Figure 9:* Charlotte's DNA Story™ © Ancestry.co.uk

The Current Limitations of DNA Testing for Disenfranchised Peoples

This is not, however, the only example of a disconnect in Charlotte's family tree.The identity of the African-American GI who fathered Diane remains unconfirmed, and furthermore, as the descendant of an African-American man, it is likely that Charlotte is also descended from enslaved peoples. Genealogists with enslaved ancestors face challenges and obstacles, both with traditional documentary research, and when utilising genetic genealogy. Enslaved people were viewed as property, and consequently, their names rarely appear in historical records.[19] Where names are included, genealogical relationships are often excluded, especially relationships between fathers and their children. This can create genealogical 'brick walls' for researchers attempting to extend family trees beyond the American Civil War in the 1860s, and in theory, genetic genealogy is the ideal resource for navigating these obstacles; however, there are also unique challenges when researching African-American ancestors using genetic genealogical techniques.

Enslaved people were often given the surnames of their slaveholders, and when they were sold, their names were changed to those of their new slaveholders. No record was created to document the change. Consequently, African American test-takers may find that the surnames in the family trees of their DNA matches do not correspond to their own ancestral surnames. Even if the test-taker and their matches had the same ancestor in their respective trees, it might be difficult to confirm their relationship if the ancestor was recorded under multiple names.

This issue is exacerbated by the lower numbers of African-American test-takers in DNA databases, which mean that the majority of DNA matches are descended from white slaveholders, and the matches descended from enslaved ancestors tend to be more distant.[20] Distant matches share smaller quantities of DNA, and researchers must use extreme caution when working with small segments of DNA, as it can be difficult to determine whether they are identical by descent (indicative of a genuine genealogical relationship) or identical by state (a false-positive segment, not inherited from a shared ancestor). Genealogists use chromosome browsers to triangulate segments of DNA shared by a test-taker and two or more matches, which can enable researchers to determine whether a segment is likely to be identical by descent, but at the time of this writing, AncestryDNA does not include a chromosome browser – nor do they allow test-takers to access shared segment data.

There are legitimate reasons to withhold access to shared segment information, but the unintended consequence of their limited online tools is that AncestryDNA, which is currently the largest DTC genetic testing database, is significantly less useful to African-American test-takers and to test-takers from endogamous communities (in which unions are more likely to be consanguineous) than it is to white European test-takers, and those from non-endogamous populations. AncestryDNA counteracts some of these limitations with its segment threshold of 8 cM, which prevents genetic genealogists being led astray by small, identical by state segments, and its Timber algorithm automatically removes any segments that are likely to be identical by state; however, there are many additional means by which AncestryDNA might improve their features for descendants of enslaved people.

All DTC genetic testing companies have limitations when determining biogeographical ancestry. Each company has its own reference panels, which it uses to gauge allele frequency in specific populations.[21] This produces accurate results on a continental scale – if a DTC genetic test tells you that you have European, African, or Asian DNA, this is likely to be true; however, on a national level, it is more difficult to precisely designate biogeographical origins. This is partly due to the genetic similarities between neighbouring countries and countries with historical intermigration, but it is also caused by inadequate reference panels. In each of the main DTC genetic testing companies, the reference panels for European populations are larger than those for African, Asian, Indigenous-Australian, and Native-American populations.[22] As a result, estimates of biogeographical ancestry are more accurate for white European test-takers than they are for any other groups.

Charlotte's *Ethnicity Estimate*™ has designated her African ancestry to specific groups and countries. Her father is Nigerian, which accounts for the entirety of this designation. The remaining designations: England and North-western Europe; Ivory Coast and Ghana; Benin and Togo; Cameroon, Congo, and Western Bantu Peoples; European Jewish; Senegal; Norway; Eastern Europe and Russia; and Wales; are from her less well-documented maternal heritage (**Figure 9**).[23]

Charlotte's only documented maternal ancestors are on her matriline, extending through her great-grandmother Annie Harris to her great-grandparents Frederick George Harris and Annie Baker, and their ancestors. This line accounts for approximately 12.5% of her genetic inheritance, and we can estimate from Charlotte's documented pedigree that approximately 4.68% of her known ancestry is English, 3.12% is German, and 4.68%

is European Jewish. We do not expect Charlotte's biogeographical ancestry to perfectly reflect her documented heritage, as individuals inherit more DNA from some ancestors than they do from others, which may partially explain Charlotte's 2% European Jewish designation and the absence of any detectable German DNA.

Charlotte's remaining European and African DNA pertains to her maternal grandfather and to the African-American father of Diane Harris. In terms of her more historical African origins, the information offered by the biogeographical ancestry estimate is limited. The countries referenced, such as Ghana, Cameroon, Congo, and Senegal, are post-colonial constructs. What these designations tell us is that Charlotte's ancestors were almost certainly enslaved when they arrived in the United States. If Charlotte wanted to know more about the origins of her African ancestors, these estimates give her approximate regions, but they reveal little about the unique cultural groups to which those ancestors belonged. There is a disconnect for people with African-American heritage that does not exist for people whose countries of origin and cultural inheritance have not been impacted by colonialism and the transatlantic slave trade.

As with so many issues relating to diversity, the primary solution is to improve representation. Recent studies, such as that carried out by O'Connell, Yun, Moreno, *et al.* of 23andMe in 2021, show that progress is being made towards improving the accuracy of biogeographical ancestry estimates for African Americans, and that DTC genetic testing companies are aware of the limitations that exist for people with heritage outside Europe.[24]

DTC genetic testing will increase in popularity globally as the technology improves for people outside Europe and the United States. The increase in popularity will result in larger DNA match databases for test-takers with ancestry in non-European countries, creating a resource that can begin to compensate for the massive record loss and record destruction inflicted by colonists, wars, and corruption.

Conclusions

DTC genetic testing is a spectacular development in the field of genealogy, creating a solution to the once-insurmountable obstacles of record loss and falsification. It has changed the way we view documentary evidence and the genealogical proof standard, and it has challenged us to broaden our knowledge of genetic relatedness and inheritance. Crucially, genetic genealogy has given disenfranchised groups (such as adoptees, foundlings, and descendants of enslaved people) access to their heritage, without the need for physical documentation or oral history. Leaders in the field must strive to make this resource useful and accessible to disenfranchised groups around the world, not only by improving the biases in the technology, but also by continuing to provide educational resources and tools for interpreting DNA data.

There will come a day when every person on our planet who wants to learn more about their history has access to this information, and the knowledge to utilise it to the best effect, and there will no longer be anyone who feels removed from their heritage and their ancestors. At the time of this writing, there are people who are not aware that DNA testing can offer material genealogical information to individuals with no documented family history – even to those with no documented parentage. As a genealogist, the genetic revolution is a source of endless wonder and fascination – the reformation of the field is a subject of enormous academic and professional weight; however, most

important of all is the restoration of history to people whose origins have been rendered inaccessible. Genealogy has deeply problematic roots; it has often been a weapon of fascism and bigotry. We must take genetic genealogy in the opposite direction by ensuring that it becomes a resource for the many, not the few.

---

[1] ISOGG. *List of DNA Testing Companies*. https://isogg.org/wiki/List_of_DNA_testing_companies.
[2] FamilyTreeDNA. https://www.familytreedna.com.
[3] National Human Genome Research Institute. *Mitochondria*. https://www.genome.gov/
[4] Stanbary, Karen, 'Drowning in DNA? The Genealogical Proof Standard Tosses a Lifeline', in Parker Wayne, Debbie (ed.) *Advanced Genetic Genealogy: Techniques and Case Studies* (Cushing, Texas, 2019), p. 221.
[5] Stahle, Tyler S. *Understanding the Genealogical Proof Standard*. www.familysearch.org/en/blog/understanding-the-genealogical-proof-standard.
[6] Board for Certification of Genealogists, *Genealogy Standards Second Edition Revised*. 2nd ed (2019), Chapter 3: Standards for Researching, section: Using DNA Evidence.
[7] DNA Painter. *The Shared cM Project 4.0 tool v4*. https://dnapainter.com/tools/sharedcmv4.
[8] *Genealogy Standards,* op. cit., Appendix D: Glossary.
[9] Ibid., Chapter 3.
[10] DNA Painter, op. cit.
[11] Stanbary, op. cit., p. 221.
[12] ISOGG. *Cousin statistics*. https://isogg.org/wiki/Cousin_statistics.
[13] National Human Genome Research Institute. *The Human Genome Project*. https://www.genome.gov/human-genome-project : accessed 17 April 2022.
[14] FamilyTreeDNA. *Improvements To The Y-DNA Matches Page.* https://blog.familytreedna.com/improvements-to-the-y-dna-matches-page/ : accessed 17 April 2022.
[15] House, Laura, *What are the Limitations of Y and Autosomal DNA When Applied to the Investigation of Surname Changes?* Unpublished MSc dissertation (University of Strathclyde, 2019).
[16] Bland, Lucy and Caballero, Chamion. *'Brown Babies': The children born to black GI and white British women during the Second World War*. https://blog.nationalarchives.gov.uk/brown-babies-second-world-war/
[17] The names of living people have been changed to protect their identities.
[18] DNA Painter, op. cit.
[19] Dockser Marcus, Amy, 'Proving a Connection to Enslaved Ancestors Through DNA', in *The Wall Street Journal* (16 April 2021).
[20] Smith, Franklin Carter, ' Ancestry's Changes Affect Those with Enslaved Ancestors: A Guest Post' *Dana Leeds*. 22 July 2020, www.danaleeds.com/affect_enslaved_ancestors/
[21] 'Scitable' by Nature Education, *Allele Frequency*, www.nature.com/scitable/
[22] O'Connell, Jared, Yun, T., Moreno, M. *et. al*., 'A population-specific reference panel for improved genotype imputation in African Americans', in *Communications Biology*. 4 (2021).
[23] Ancestry. *DNA Story*: www.ancestry.co.uk/dna/origins/
[24] O'Connell, et. Al., op. cit.