

Interim DNA Analysis Report (Work in Progress)

Research Question and Answer Status:

Q: Is Irena R. Burke a descendant of Agnes and John C. Burke?

— Irena R. Burke: (http://www.txsgs.org/TXSGS_DNA/getperson.php?personID=I3530&tree=txsgs)

— John C. Burke: (http://www.txsgs.org/TXSGS_DNA/getperson.php?personID=I223&tree=txsgs)

— Agnes can be accessed as the wife on John's page.

A: Additional research is needed before reaching a conclusion. This report details analysis to date.

Notes:

While most genealogical case studies are not presented until complete, the Early Texans DNA Project provides interim reports on work in progress. This makes the analysis available even when not enough test takers are included to reach a sound conclusion and it allows other researchers to advance the work when the initial researcher is no longer available. The long-term nature of DNA projects encourages sharing incomplete information. This is seen on many blog posts and also in journal articles by respected genealogists.¹

Because the analysis in these reports may be continued by others in the future and the reports can be used as a learning tool, information is included here that may not be needed in a case study once the research is complete. For example, in this report a test taker in a family cluster does not share DNA with a focus person in the report; future analysis could make this important therefore all family members are included. This report also demonstrates how chromosome browser images might make it appear as though two test takers share DNA when they do not and how to avoid erroneous assumptions from misleading images.

¹ Donn Devine, "Thomas, John, and Francis Baldwin of Chester County: A Rare DNA Marker," *Pennsylvania Genealogical Magazine* 49 (Fall/Winter 2014): 102-118.

This report also uses chromosome diagrams as displayed by the testing company tools to illustrate how to analyze what is seen using the company tools. Publications sometimes use different representations for the shared DNA segments.

Cousin relationships are abbreviated as 3c2r for third cousin twice removed, 4c1r for fourth cousin once removed, and so on.²

EARLY TEXANS DNA DATABASE TIPS

See the Early Texans DNA Project database at http://www.txsgs.org/TXSGS_DNA/ for additional lineage information and sources. Project members provide permission to use their DNA and lineage in analysis when submitting applications. Project member names are anonymized as TX000013, TX000114, and so on for the given name with the surname as Member. Ancestors of project members born after 1900 also have anonymized given names such as TX9900123 and the surname as AncestorOfMember. Database entries for people can be accessed using the search features of the database and the name or alias of a person.

DNA KNOWLEDGE BASE

Basic DNA knowledge is required to fully understand this DNA analysis. The Early Texans DNA Project maintains a DNA Knowledge Base Repository with links to basic and advanced DNA information. This includes links to online versions of articles, blog posts, example projects, and other useful resources.

Readers may benefit from studying these background articles if there are portions of this report that are not clear because of a lack of DNA knowledge. The DNA Knowledge Base will be frequently updated with new links.

The project home page at http://www.txsgs.org/TXSGS_DNA/ contains links to the DNA Knowledge Base near the top of the text. The knowledge base is contained in the same database as the people in the project; it can be accessed at any time by using the search button at the top of each page and entering dna as the first name or surname search term. Each category of DNA information is accessed as a “child” of a person with “DNA Knowledge Base” as the given name and “DNA-Genetics” as the surname of the pseudo-parent. Inclusion of “DNA” in both name parts allows the knowledge base to be found no matter which name search box is used.

² For more on cousins and removes see “Cousin,” *International Society of Genetic Genealogists (ISOGG) Wiki* (<https://isogg.org/wiki/Cousin>).

Burke Case Background

Project member TX000114 submitted lineage back to Irena R. Burke (1841-1881) and Andrew Harrison Seargeant (1838-1906) and another generation back on the Seargeant line.

Project member TX000013 submitted lineage back to John C. Burke (1809-1847) and wife Agnes unknown (1806-1864) through their son James Burke (1829-1857).

TX000013 believes Irena R. Burke is also a child of John C. and Agnes Burke. No response was received from TX000114 after email contact to discuss this. Evidence from documentary research so far is consistent with this hypothesis but does not yet meet the Genealogical Proof Standard (GPS).³

Analysis in this report is to determine if DNA evidence is consistent with or contradicts the hypothesis. If the DNA is consistent with the hypothesis additional research can be done to meet the GPS and reach a credible conclusion.

Summary of Findings

There are not yet enough Burke descendants in the ETDNA project to meet particularly, Genealogy Standard 53, Extent of Evidence.⁴ This affects evaluation of all other DNA standards and does not allow a conclusion to be reached as to whether the DNA shared by TX000013 and TX000114 was inherited through their Burke ancestor. Pedigree analysis was not completed to determine if there are other potential shared ancestors between these project members. Before attributing this shared DNA to the common Burke ancestors (1) other potential shared ancestors should be eliminated, (2) additional Burke descendants should be identified, if possible, and (3) research should meet the GPS.

However, the shared DNA with some triangulated segments through multiple lines of descent from John C. and Agnes Burke make it probable that Irena R. Burke also descends from this ancestral line as long as there are no other ancestors shared by the test takers.

³ Board for Certification of Genealogists (BCG), *Genealogy Standards*, 2nd ed. revised (Nashville, Tennessee: Turner Imprint, Ancestry.com, 2021).

⁴ BCG, *Genealogy Standards*, 2nd ed. revised (Nashville, Tennessee: Turner Imprint, Ancestry.com, 2021), 31.

Limitations

Parent-child links for project members, parents, and some grandparents are accepted as submitted for the ETDNA Project. Verification of these recent parent-child links often requires sources not available to the public and DNA analysis should clearly indicate if these recent links are incorrectly stated. Whenever possible, potential discrepancies discovered will be discussed with project members before reaching conclusions.

The known data reveals no pedigree collapse or endogamy⁵ resulting in multiple relationships between the test takers discussed here. However, as stated earlier, pedigree analysis may not meet *Genealogy Standards*.⁶ The Early Texans DNA database does not include all ancestral lines for all project members and outside trees are not available for all test takers or all ancestral lines.

DNA data for this report was gathered after FamilyTreeDNA implemented their new matching scheme on 13 July 2021.⁷ This new algorithm removed segments smaller than 6 centiMorgans. Data was confirmed on 12 August 2021 because of the possibility the entire database of test takers had not been updated earlier.

Resources Used

- Ancestry.com trees (shared with the DNA committee) for Early Texans DNA Project members, where available. A preliminary and cursory review of tree completeness and potential for multiple shared ancestors was done. Not all project members have complete trees and some have no trees available other than the lineage information in the Early Texans DNA Project database (http://www.txsgs.org/TXSGS_DNA/).
- Blaine T. Bettinger, "Shared cM Project," *The Genetic Genealogist* (<https://thegeneticgenealogist.com/>). Search the blog posts for the most recent update to the project such as the March 2020 update at <https://thegeneticgenealogist.com/2020/03/27/version-4-0-march-2020-update-to-the-shared-cm-project/>. The project charts are periodically updated.⁸
- Blaine T. Bettinger, Leah LaPerle Larkin, and Jonny Perl, "The Shared cM Project 4.0 tool v4," *DNA Painter* (<https://dnainter.com/tools/sharedcmv4>).⁹

5 "Pedigree collapse, *ISOGG Wiki* (https://isogg.org/wiki/Pedigree_collapse).

6 BCG, *Genealogy Standards*.

7 "Updates To Family Finder, Featuring Improved Matching And A Soon To Be Released Chromosome Painter," *FamilyTreeDNA*, 1 July 2021 (<https://blog.familytreedna.com/updates-to-family-finder-matching-and-chromosome-painter/>). Also see Roberta Estes, "FamilyTreeDNA Relaunch - New Feature Overview," *DNAeXplained*, 1 July 2021 (<https://dna-explained.com/2021/07/01/familytreedna-relaunch-new-feature-overview/>).

8 More fully cited in the "Shared cM Tool — Ranges, Histograms, and Probabilities " section.

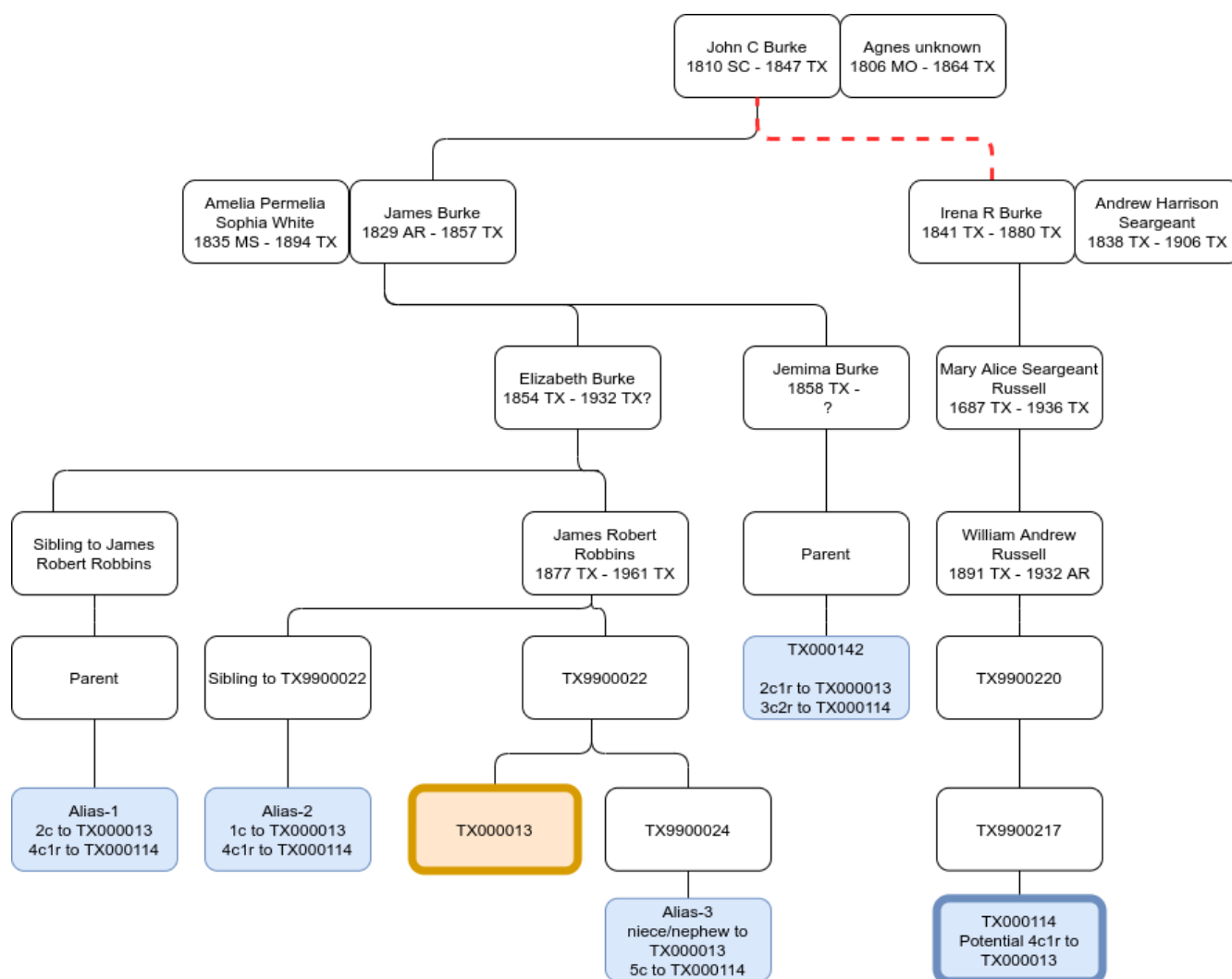
9 More fully cited in the "Shared cM Tool — Ranges, Histograms, and Probabilities " section.

- Early Texans DNA Project database (http://www.txsgs.org/TXSGS_DNA/).
- FamilyTreeDNA, TXStateGS project, match and shared DNA information (<https://www.familytreedna.com/public/TXStateGS> and private project pages with member information).

Research Notes

Figure 1. Hypothetical Family Structure Linking TX000013 and Known Relatives to TX000114

Colored boxes are DNA test takers; the orange box (TX000013) and the dark-blue outlined box (TX000114) are the focus persons of this report. The red dashed line is the hypothetical link under analysis. Names were changed to Alias-Number where permission to use the DNA, but not the identity, was obtained and the person is not yet in the Early Texans DNA Project database.



Shared cM Tool – Ranges, Histograms, and Probabilities

The Shared cM tool on the *DNA Painter* website provides three data elements for relationship possibilities based on the amount of autosomal DNA shared by two test takers:

- (1) the average amount of DNA shared and the range of values (low-to-high) reported by project participants,
- (2) the probabilities for various relationship possibilities for the amount of shared DNA entered (based on simulated data), and
- (3) a histogram of the reported data for a given relationship as calculated by the Shared cM Project.¹⁰

Details are provided below for using these elements to determine if a hypothesized relationship may be true.

¹⁰ Blaine T. Bettinger, Leah LaPerle Larkin, and Jonny Perl, “The Shared cM Project 4.0 tool v4,” DNA Painter (<https://dnapainter.com/tools/sharedcmv4>).

Bettinger provided the Shared cM data, self-reported by (and likely to contain some errors) from actual test taker data. Blaine T. Bettinger, “The Shared cM Project, Version 4.0 (March 2020),” *The Genetic Genealogist*, PDF online (<https://thegeneticgenealogist.com/wp-content/uploads/2020/03/Shared-cM-Project-Version-4.pdf>). Page 5 covers data collection methods. Pages 8-51 cover the histograms. Also see Blaine T. Bettinger, “Shared cM Project,” *The Genetic Genealogist* (<https://thegeneticgenealogist.com/2020/03/27/version-4-0-march-2020-update-to-the-shared-cm-project/>). Also see “Collecting Sharing Information for Known Relationships,” *The Genetic Genealogist* (<https://thegeneticgenealogist.com/2015/03/04/collecting-sharing-information-for-known-relationships/>) and “Collecting Sharing Information for Known Relationships – Part II”, (<https://thegeneticgenealogist.com/2015/04/06/collecting-sharing-information-for-known-relationships-part-ii/>).

Larkin provided the underlying data for the probability indications based on Ancestry.com simulated, statistical data. Also see Leah LaPerle Larkin, “The Limits of Predicting Relationships Using DNA,” 19 December 2016, *The DNA Geek* (<https://thednageek.com/the-limits-of-predicting-relationships-using-dna/>); probabilities based on simulated data citing “AncestryDNA Matching White Paper,” *AncestryDNA*, 31 March 2016 (<https://www.ancestry.com/dna/resource/whitePaper/AncestryDNA-Matching-White-Paper>).

Perl developed the website where these tools are housed, the user interfaces, and other tools on the site. These include the Chromosome Mapper that was the initial offering at DNA Painter as well as the Cluster Auto Painter, Inferred Segment Generator, cM Estimator, several tree and pedigree tools, and more. Also see the online help at <https://dnapainter.com/help>. The cM Estimator was also used during this analysis.

Using Shared DNA amounts:

Comparing the shared DNA between two people of a specific relationship is easily done using the chart at <https://dnainter.com/tools/sharedcmv4>. Obtain the number of centiMorgans shared by two test takers and determine if it falls within the range specified on the chart for the relationship believed to be shared by the two. This can be done by manually searching the chart and comparing the amount of DNA shared by the test takers to the range of values listed in the chart.

Using Probabilities:

The probabilities, displayed after entering a centiMorgan value in the “Filter” box, are best used to determine the most likely place to begin looking for a family link when the relationship is unknown. When a relationship is known, the probabilities primarily are used for a possible or not possible indication. A low probability percentage does not rule out the possibility of that relationship unless the probability percentage is zero (0).

Random recombination of DNA can result in some test takers sharing more or less than the expected amount of DNA for a specific relationship. Relationships more distant than second cousins may result in no shared DNA at all even though the genealogical relationship is real.¹¹

The probability numbers should be evaluated within the context of all of the evidence, DNA and documentary. The probabilities should not be used alone as confirmation of a relationship; any number other than 0 indicates the relationship is possible. Probabilities for relationships for which more DNA is shared are more likely to be accurate. For more distant relationships the smaller amount of shared DNA can be typical of multiple relationships. The probability percentages may be lower, but still be consistent with the hypothetical relationship as long as the probability is not zero.

Using Histograms:

As shown in figure 2, histograms, displayed by clicking on one of the relationship boxes in the Shared cM Chart, are used to determine if the amount of shared

¹¹ Blaine T. Bettinger, “Q&A: Everyone Has Two Family Trees - A Genealogical Tree and a Genetic Tree,” *The Genetic Genealogist*, 10 November 2009 (<https://thegeneticgenealogist.com/2009/11/10/qa-everyone-has-two-family-trees-a-genealogical-tree-and-a-genetic-tree/>). Also see “Cousin statistics,” *International Society of Genetic Genealogists Wiki* (https://isogg.org/wiki/Cousin_statistics).

DNA is at the peak of the curve, within the curve, or on the shoulders of the histogram curve. Shared centiMorgan values that fall far out on the shoulders of the histograms or outside of the reported range are known as outliers. Outliers require additional investigation and more evidence to be accepted as true (often more test takers are needed). Outliers will often lead to more tentative or qualified hypotheses and need more explanation in the analysis.¹²

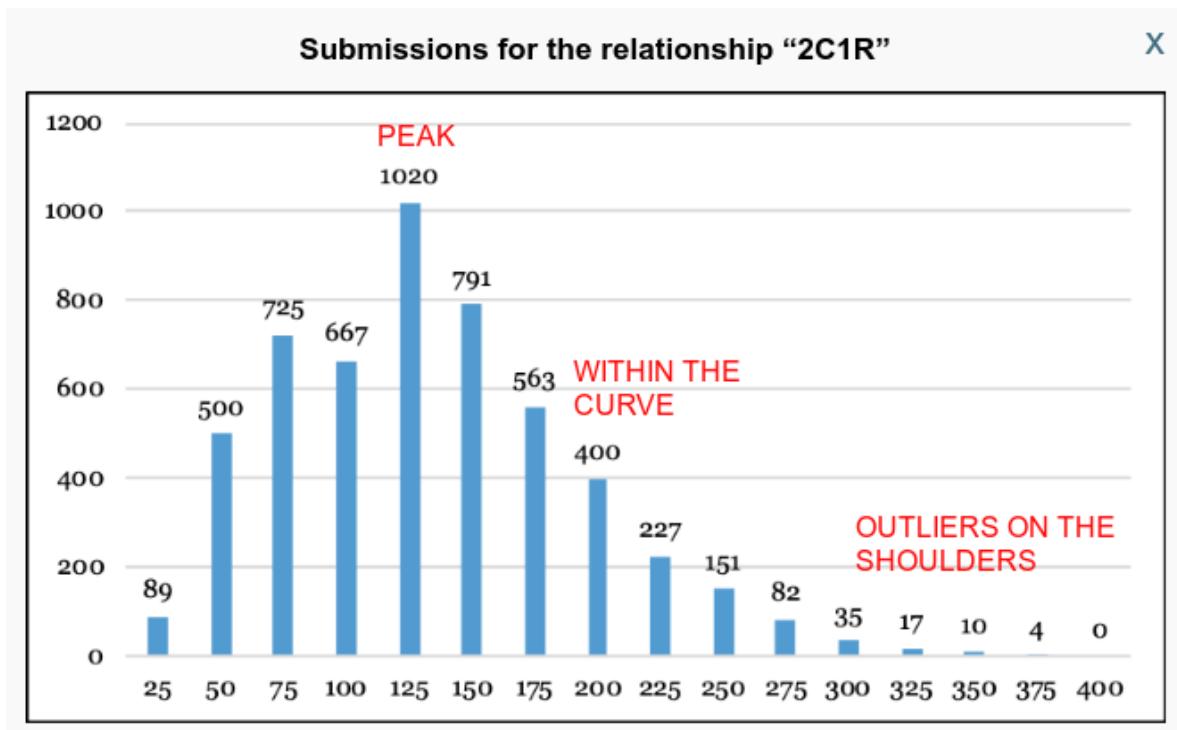
To determine where on the curve a DNA match falls, look along the horizontal axis for the numbers closest to the amount of DNA shared by two test takers. Mentally note the location for the shared cM number on the horizontal axis. Mentally draw a line up to intersect the curve. Determine if the amount of DNA shared by the two test takers is at the peak or within the curve of the histogram or if the value may be an outlier (on the shoulders of the curve or outside of the range of the curve).

If the value is not within the curve it is likely that more evidence may be needed to support the hypothesized relationship.

12 Blaine T. Bettinger, "The Shared cM Project Version 4.0 (March 2020)," PDF online (<https://thegeneticgenealogist.com/2020/03/27/version-4-0-march-2020-update-to-the-shared-cm-project/>), 8-18.

Figure 2.

Example histogram for 2c1r from Shared cM Project Display on *DNA Painter*. The added red markings indicating the peak of the curve, position of values described as “within the curve,” and outliers (on the shoulders) of the curve. Numbers outside of the range of shared values are also considered outliers.



Shared Matches Within the Project For TX000013 and TX000114

TX000013 (orange box in figure 1) shares DNA with all other test takers in this study (blue boxes in figure 1). The shared amounts of DNA for TX000013 are listed in table 1. All of these shared amounts of DNA are “within the curves” of the histograms, not outliers far out on the shoulders, and are within the expected range of shared centiMorgan values for the relationship.

| Project Member Test Taker | Relation-ship to TX000013^a | Shared cM^b | Average shared cM for relationship^c | Range of shared cM for relationship^d | Histogram location on curve^e | Proba-bility^f |
|---|--|------------------------------|---|--|--|---------------------------------|
| Alias-1 | 2c | 317.59 | 229 | 41-592 | within the curve | 51% |
| Alias-2 | 1c | 1040.33 | 866 | 396-1397 | within the curve | 100% |
| Alias-3 | niece/ nephew | 2111.21 | 1741 | 1201-2282 | within the curve | 85% |
| TX000142 | 2c1r | 113.58 | 122 | 14-353 | near peak of curve | 43% |
| TX000114 | 4c1r | 55.08 | 28 | 0-126 | within the curve | 20% |
| a) Relationships are calculated from lineages submitted for the Early Texans DNA Project. b) Shared cM values are taken from the <i>FamilyTreeDNA</i> TXStateGS Project reports. c) Average shared cM is from Blaine T. Bettinger, Leah LaPerle Larkin, and Jonny Perl, “The Shared cM Project 4.0 tool v4,” <i>DNA Painter</i> (https://dnapainter.com/tools/sharedcmv4). This average ignores instances where true cousins share no DNA. d) Ibid. e) Ibid., click on a relationship box to access the histogram chart. f) Ibid., probability displayed after entering a value for shared cM. All relationship probabilities are non-zero and therefore possible. | | | | | | |

In this study, the relationships between Elizabeth Burke’s descendants are known. The probability of the shared amount of DNA indicating the stated relationship of TX000013 to second cousins and closer is over 50% (100%, 85%, and 51%). The probabilities for the 2c1r and 4c1r relationships are lower, but still acceptable. All relationship probabilities are non-zero and therefore possible. The lowest percentage is 20% which is acceptable, especially for a distant relationship such as 4c1r.

These numbers are consistent with the relationships indicated by project members for the tested descendants of Elizabeth Burke. The numbers are consistent with the relationship to TX000114 even though that relationship is

further out and more difficult to predict with a high probability. More test takers are needed to reach a credible conclusion.

The shared amounts of DNA for TX000114 are listed in table 2.

| Table 2. Shared cM with TX000114 | | | | | | |
|---|--|------------------------------|---|--|--|---------------------------------|
| Project Member Test Taker | Relation-ship to TX000014^a | Shared cM^b | Average shared cM for relationship^c | Range of shared cM for relationship^d | Histogram location on curve^e | Proba-bility^f |
| Alias-1 | 4c1r | 26.7 | 28 | 0-126 | within the curve | 56% |
| Alias-2 | 4c1r | 0 | 28 | 0-126 | n/a ^g | |
| TX000013 | 4c1r | 55.08 | 28 | 0-126 | within the curve | 20% |
| Alias-3 | 5c | 0 | 25 | 0-177 | n/a ^h | |
| TX000142 | 3c2r | 25.95 | 36 | 0-166 | near peak of the curve | 17% |

a) Relationships are calculated from lineages submitted for the Early Texans DNA Project.
 b) Shared cM values are taken from the *FamilyTreeDNA* TXStateGS Project reports.
 c) Average shared cM is from Blaine T. Bettinger, Leah LaPerle Larkin, and Jonny Perl, "The Shared cM Project 4.0 tool v4," *DNA Painter* (<https://dnapainter.com/tools/sharedcmv4>). This average ignores instances where true cousins share no DNA.
 d) Ibid.
 e) Ibid., click on a relationship box to access the histogram chart.
 f) Ibid., probability displayed after entering a value for shared cM.
 g) n/a: Shared DNA amounts of zero are within expectations for any relationship more distant than 2c. Values of 0 are not included on the histograms.
 h) Ibid.

TX000114 shares no DNA with Alias-2 or Alias-3. This is consistent with and within expectations for the relationships of fourth cousin once removed (4c1r) and fifth cousin (5c). About half of fourth and more distant cousins will share no detectable amount of DNA.¹³

The amount of DNA shared between TX000114 and TX000013 is within expectations. The amount of DNA shared between TX000114 and TX000142 is well within expectations—near the peak of the histogram curve. Although the probability numbers for TX000114’s match to TX000013 and TX000142 are lower (20% and 17%) neither probability is zero (0) and the amount of shared DNA is near the peak or within the curve of the histogram. Therefore, the DNA evidence supports these relationships when correlated with the documentary evidence.

¹³ "Cousin statistics," *ISOGG Wiki* (https://isogg.org/wiki/Cousin_statistics).

Shared and Triangulated Segments

Shared segment data analysis focuses on segments shared by TX000013 and TX000114 with overlaps shared by test takers TX000142, Alias-1, Alias-2, or Alias-3. All of these segments are over 10 centiMorgans in length and likely to be true segments.¹⁴ All include a number of matching SNPs sufficient for the analysis to be credible and useful.¹⁵

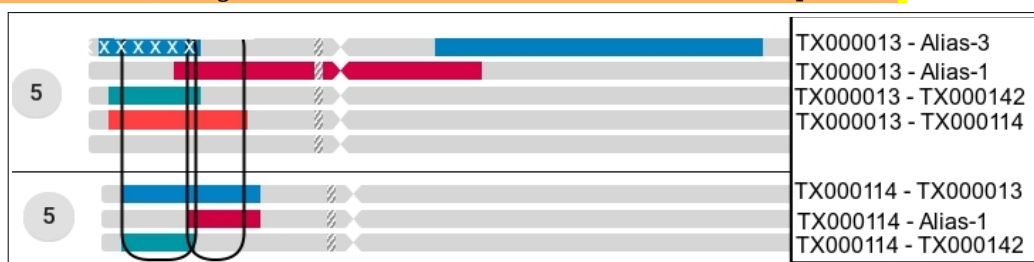
The descendants of Elizabeth Burke share additional triangulated segments,¹⁶ but only the segments that triangulate with TX000114 are outlined in the images below.

The descendants of TX990022 share additional segments not shared with the others as their relationship is much closer (aunt/uncle-niece/nephew).

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- 14 Rui Hu et al., "Family Finder Matching 5.0 Matching Algorithm and Relationship Estimation," White Paper 2021-08-18, *FamilyTreeDNA* (https://blog.familytreedna.com/wp-content/uploads/2021/08/Family_Finder_Matching_WhitePaper.pdf); see table 2, "False positive rate according to different lengths of match segments," 15. Also see Eric Y. Durand, Nicholas Eriksson, and Cory Y. McLean, "Reducing Pervasive False-Positive Identical-by-Descent Segments Detected by Large-Scale Pedigree Analysis," *Molecular Biology and Evolution* 31, no. 8 (August 2014): 2212–22 (<https://doi.org/10.1093/molbev/msu151>). Also see Blaine Bettinger, "A Small Segment Round-Up," *The Genetic Genealogist*, 29 December 2017 (<https://thegeneticgenealogist.com/2017/12/29/a-small-segment-round-up/>).
- 15 "Autosomal DNA Match Thresholds," *ISOGG Wiki* (https://isogg.org/wiki/Autosomal_DNA_match_thresholds).
- 16 Debbie Parker Wayne, "Genetic Genealogy Journey—Triangulating Autosomal DNA," *NGS Magazine* 42 (Oct-Dec 2016): 43–46; online (https://debbiewayne.com/pubs/pub_NGSMag_201608_triangularion.pdf).

| Shared Segments—Chromosome 5, with Two Triangulated Segments | | | | | | |
|--|----------|------------|------------|------------|---------|---------------|
| Member 1 | Member 2 | Chromosome | Start Loc | End Loc | cM | Matching SNPs |
| TX000013 | Alias-3 | 5 | 25,328 | 23,475,692 | 38.86 | 6,457 |
| TX000013 | Alias-1 | 5 | 18,038,790 | 77,219,131 | 56.50 | 11,802 |
| TX000013 | TX000142 | 5 | 4,396,901 | 22,046,965 | 26.55 | 4,612 |
| TX000013 | TX000114 | 5 | 4,644,270 | 31,804,216 | 36.53 | 6,466 |
| TX000114 | TX000013 | as above | | | | |
| TX000114 | Alias-1 | 5 | 17,484,038 | 31,771,147 | 14.69 | 2,701 |
| TX000114 | TX000142 | 5 | 3,663,183 | 18,853,732 | 25.95 | 4,206 |
| Yellow Triangulated Segment | | | 4,644,270 | 18,853,732 | 23.7 cM | |
| Orange Triangulated Segment | | | 18,038,790 | 31,771,147 | 13.1 cM | |

The segment portion beginning at 4,644,270 and ending at 18,853,732 is a triangulated segment of about 23.7 cM^a shared by three test takers (TX000013, TX000114, and TX000142) (yellow color in table cells marks start and end points). An adjacent 13.1 cM segment (with a minuscule overlap) shared by three test takers (TX000013, TX000114, and Alias-1) begins at 18,038,790 and ends at 31,771,147 (orange color in table cells marks start and end points).



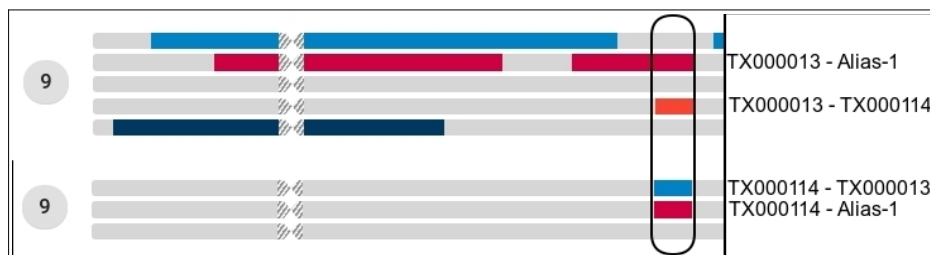
Chromosome 5 segments shared with TX000013 (top of the chromosome browser image) and TX000114 (bottom of image) with oval around triangulated segments. Other colored segments on top section are shared by TX000013 and Alias-1. Only segments shared with TX000114 are analyzed as the goal is to substantiate links between TX000013's and TX000114's Burke lines.

a) Size of the triangulated segment was estimated using Jonny Perl, "cM Estimator," *DNA Painter* (<https://dnainter.com/tools/cme>).

This chromosome browser display makes it appear that the first segment shared by TX000013 and Alias-3 would be part of the triangulation. However, it is not—indicated by the Xs added over that segment. If it were triangulated between all of these matches then Alias-3 should also be on the match list of TX000114 but the two share no detectable amount of DNA. All matches on a chromosome between selected test takers are displayed. The browser cannot differentiate between matches to a paternal or maternal copy of the chromosome. This is a known limitation of the chromosome browser display. Anomalies, such as not seeing Alias-3 in TX000114's match list, must be analyzed to determine the significance to the problem under analysis. In this case, TX000013 and Alias-3 share an aunt/uncle-niece/nephew relationship. This segment they share on chromosome 5 is likely from the spouse of James Robert Robbins or TX9900022 and is not from the Burke line ancestor shared with the other test takers.

| Shared Segments—Chromosome 9, with One Triangulated Segment | | | | | | |
|---|----------|------------|-------------|-------------|---------|---------------|
| Member 1 | Member 2 | Chromosome | Start Loc | End Loc | cM | Matching SNPs |
| TX000013 | Alias-1 | 9 | 106,798,942 | 132,786,313 | 35.14 | 7,368 |
| TX000013 | TX000114 | 9 | 124,680,367 | 133,037,273 | 10.66 | 2,010 |
| TX000114 | TX000013 | as above | | | | |
| TX000114 | Alias-1 | 9 | 124,280,991 | 133,414,224 | 12.02 | 2,168 |
| Yellow Triangulated Segment | | | 124,680,367 | 132,786,313 | 10.0 cM | |

The segment portion beginning at 124,680,367 and ending at 132,786,313 is a triangulated segment of about 10.0 cM^a shared by three test takers (TX000013, TX000114, and Alias-1) (yellow color in table cells marks start and end points).



Chromosome 9 segments shared with TX000013 (top of the chromosome browser image) and TX000114 (bottom of the image) are shown with an oval around the triangulated segment. Other colored segments on top section are shared by TX000013 and Alias-2 and Alias-3 but not TX000142. Those test takers share a closer relationship and more DNA than is shared with TX000114. Only segments shared with TX000114 are analyzed as the goal is to substantiate links between TX000013's and TX000114's Burke lines.

a) Size of the triangulated segment was estimated using Jonny Perl, "cM Estimator," *DNA Painter* (<https://dnainter.com/tools/cme>).

Suggestions for Continuing Research

1. Invite other Burke descendants who have tested DNA and show up as matches at FamilyTreeDNA to join the Early Texans DNA Project.
2. Add information to this report for additional Burke descendants as they join the project.
3. Build the pedigrees of some Burke descendants in the project back a sufficient number of generations to eliminate or identify other potential shared ancestors.
4. Additional documentary and DNA research should be performed in order to meet the GPS. Specifics will be indicated as research and analysis continues.