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Introduction

When the 37 marker genetic results of Kit #535078 are compared to other Members of the Project placed in Group 1, he is a perfect match to 14, each recorded as a descendant of Aaron Stark [1608-1685] - their earliest known ancestor with the surname Stark. Table 1 presents a genealogical lineage from #535078 back to Aaron Stark [1608-1685]. His earliest known Stark ancestor when he submitted his genealogy was Isaac Stark [1805-1874], presented in Gen 5 of Table 1; and the genealogy submitted by Group 1 Member #203166 has the same Isaac Stark [1805-1874] as an ancestor. The Father of #203166 would be a 4th cousin of #535078. Using the genealogy submitted by #203166, Gens 6 thru 10 were assigned to the Genealogical Lineage of #535078; completing his detailed Lineage presented in Table 1.

This analysis will review the following related to #535078, #203166, and other Members of Group 1.

1) Compare the genetic matches over 37 markers of these Group 1 Members.

Table 1: n Descendant Lineage of Kit #535078 S Aaron Stark I; b. 1608, England; d. before June 1685 New London Co., CT; m. Sarah Unknown / about 1654 William Stark I; b. 1664, New London Co., CT;d. 09/08/1730, Groton, New London Co., CT m. Elizabeth Unknown / before 1689 / New London Co., CT Christopher Stark I; b. Before 1695, New London Co., CT; d. 1777, Northumberland Co., PA m. Joanna Walworth / 04/01/1722 / Groton, New London Co., CT Christopher Stark II; b. 09/27/1728, New London Co., CT; d. 1781-1785, Albany Co., NY m. ?Susanna Price / Before 1755 / ?NY or CT Nathan Stark; b. 1762, Dutchess Co., NY; d. 09/19/1812, Washington Co., NY m. Jemima Farnsworth / 06/??/1782 / Washington Co., NY Isaac Stark; b. 1805, Washington Co., NY; d. 04/27/1874, Washington Co., NY m. Betsey Ann Winchell / abt. 1825 / Washington Co., NY John J. Stark; b. 03/20/1846, Washington Co., Milo Stark; b. 10/14/1829, Washington Co., NY NY; d. 1/11/1912, Rutland Co., VT d. 03/20/1918, Washington Co., NY John W. Stark; b. 04/20/1875, Clarendon Co., Jared H. Stark;10/01/1858, Washington Co. VT; d. 03/28/1939, Hampden Co., MA NY; d. 1911, Washington Co., NY Jay W. Stark; b. 06/11/1897, Washington Co. Walter R. Stark; Mar. 1897, Rutland Co., VT; d. 06/02/1935, Hampden Co., MA NY; 01/11/1960, Washington Co., NY Earle H. Stark; b. 03/20/1922, Washington Co. Father; Private 1 NY; 07/05/1988, Washington Co., NY Kit #535078; Private Father Kit #203166

2) Use the FTDNATiP[™] calculations to evaluate the Time to the Most Recent Common Ancestor (TMRCA). These calculations return statistical probabilities, in percent, #535078 and #203166 could share a common ancestor within a specific generation with other selected Members from Group 1.

3) Kerchner's Triangulation Method for "*deducing*" the Ancestral Haplotype of a common ancestor will be utilized to genetically determine #535078 could share Aaron Stark [1608-1685] as a common ancestor with the Group 1 selected Members.

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Kit # ID Code	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37
203166 A	13	24	14	11	12	14	12	12	13	13	13	29	16	9	10	11	11	25	14	19	29	15	15	16	17	11	11	19	22	16	16	17	17	36	38	12	12
535078 B	13	24	14	11	12	14	12	12	12	13	13	29	16	9	10	11	11	25	14	19	29	15	15	16	17	11	11	19	22	16	16	17	17	36	38	12	12
78078 C	13	24	14	11	12	14	12	12	12	13	13	29	16	9	10	11	11	25	14	19	29	15	15	16	17	11	11	19	22	16	16	17	17	36	38	12	12
76234 D	13	24	14	11	12	14	12	12	12	13	13	29	16	9	10	11	11	25	14	19	29	15	15	16	17	11	11	19	22	16	16	17	17	36	38	12	12
233230 E	13	24	14	11	12	14	12	12	12	13	13	29	16	9	10	11	11	25	14	19	29	15	15	16	17	11	11	19	22	16	16	17	17	36	38	12	12

Table 2: 37 Marker Y-DNA comparison of #535078 & #203166 to the Selected Members

Table 2 presents the 37 marker Y-DNA Results of #535078 and #203166 and those of the selected Members for Analysis.

A Haplotype is defined as a collection of two or more DYS markers (DNA Y-chromosome Segment number). The Row under the table title with cells having a black background are the numbers assigned by the project to each DYS marker tested by FTDNA. DYS Marker #1 would be DYS393, with each of the other markers having similar scientific identifications. To review, visit the Stark FTDNA Public page published on the Internet. In Column 1 are the Kit # Identifications of the Members selected for this analysis. Under each Kit # is a letter Id Code which will be used in the analysis that follows. This simplifies the discussion to, example, a comparison of A to B; rather than a comparison of #203166 to #535078.

The number values presented under each Marker # are referred to as Allele values, the values defined as the number of repeats of a short base sequence. Geneticists refer to these sequences as Short Tandem Repeats (STR); each sequence assigned a unique DYS number by the Project as previously defined. STR's are scientifically defined as multiple copies of an identical DNA sequence arranged in direct succession in a particular region of a Y-chromosome.

When genetically comparing two Members to each other, different allele values can reveal mutations. Comparing A to B reveals they differ at Marker #9, A having the value 13 while B has the value 12 - this a mutation relative to each other. Over their 37 marker Haplotypes, Members B, C, D and E match at all 37 Markers revealing no mutations. Let's now analyze genetic comparisons using the FTDNATiPTM program.

Table 3: Summary Lineages

Table 3 presents summary lineages of the Members selected for analysis. The rows of Table 3 have been organized in the same sequence as Table 2.

Table 3: Lineages of #535078 & #203166, and Selected Members of Groups 1											
IDs	Gen 0	Gen 1	Gen 2	Gen 3	Gen 4	Gen 5	Gen 6	Gen 7	Gen 8	Gen 9	Gen 10
А	Father 203166	Earle H. 1922-1988	Jay W. 1897-1960	Jared H. 1858-1911	Milo 1829-1918	Isaac	Nathan				
В	535077 Private	Father Private	Walter R. 1897-1935	John W. 1875-1939	John J. 1846-1912	1805-1874	1762-1812	Christ' II 1728-1785	Christ' I 1696-1777	William I	
С	78078 Private	Father Private	William O. 1869-1951	John L. 1848-1926	Asahel L. 1817-1881	Daniel R. 1788-1820	Asahel 1755-1821	1720-1705	1070-1777	1664-1730	Aaron Stark I
D	76234	Father Private	Samuel G 1888-1967	James M 1824-1905	Moses 1793-1860	Jonathan J. 1778-1850	James 1741-1821	Jonathan I 1712-1764	William II 1690-1736		1608-1685
Е	233230	Father Private	Elmer M. 1906-1996	Homer 1883-????	James W. 1844-1912	Aaron 1804-1864	Isaac 1758-1824	Amos 1717-1767	Aaron III 1678-1744	Aaron II 1654-1701	

Members B, C, D, and E have matching 37 marker Haplotypes. Each of their rows have gray background cells for each person in their lineage through Gen 8. Member A, presented in the first row, has a mutation at Marker #9 as recorded in Table 2. His lineage cells from Gens 0 through 4, have a white background, revealing the probability a mutation occurred at Marker #9 relative to the other Members. Column 1 presents the same ID Code for each of these Members as presented in Table 2.

FTDNA TMRCA Tip Calculations

FTDNATiP[™] is a program that predicts the time to the most recent common ancestor for two men based on their Y-chromosome matches at each of the 37 markers tested. FTDNATiP[™] uses specific mutation rates that have been proven to vary from one marker to another. These calculations improve the power and precision of estimates of Time to the Most Recent Common Ancestor (TMRCA).

Table 4 presents the statistical possibilities two persons compared could share a common ancestor WITHIN a generation chosen for analysis. The GENS column records the generations that can be chosen for analysis. Column A to B is a Tip comparison of Member A to Member B through 11 generations. Column B to C is a Tip comparison of Member B to C over the same number of generations

In Table 3, Member A and Member B share a common ancestor, Isaac Stark, in Gen 5. The Tip calculations return a percentage value two persons could share a common ancestor WITHIN the generation chosen for analysis. Isaac Stark in Gen 5 is a son of Nathan Stark in Gen 6. Observe Member A and Member B cannot share a common ancestor in Gens 1 through 4. Presuming the genealogy of Members A and B are correct — *Isaac Stark would be the only common ancestor of Members A and B they could share as a common ancestor in Generation 5*. This suggests the Gen 6 percentage value would be the probably Members A & B could share Isaac Stark as a common ancestor in Generation 5. Therefore, selecting Gen 6 for Analysis, there is a 77.85% probability Members A and B could share Isaac Stark as a first common in Generation 5. Because Members B, C, D, and E are a perfect match, any comparisons of C, D, or E to A or B will result in the same Tip values as A to C and B to C.

Referring to Table 3, the following are Tip comparisons of Member A to Members B, C, D, and E.

1) 77.85% probability A and B share a common ancestor WITHIN Gen 6; or Isaac Stark as a common ancestor in Gen 5.

2) 92.11% probability A and C share a common ancestor WITHIN Gen 9; or Christopher Stark I as a common ancestor in Gen 8.

3) 94.50% probability A and D share a common ancestor WITHIN Gen 10; or William Stark I as a common ancestor in Gen 9.

4) 96.19% probability A and E share a common ancestor WITHIN Gen 11; or Aaron Stark I as a common ancestor in Gen 10.

Tip Comparisons of Member B to Members C, D, and E.

1) 98.26% probability B and C share a common ancestor WITHIN Gen 9; or Christopher Stark I as a common ancestor in Gen 8.

2) 98.89% probability B and D share a common ancestor WITHIN Gen 10; or William Stark I as a common ancestor in Gen 9.

3) 99.29% probability B and E share a common ancestor in Gen 11 or Aaron Stark I as a common ancestor in Gen 10.

Summarizing, my confidence criteria suggests there is increasing confidence as the A and B percentage value of 77.85% approaches 80%. My confidence A is a descendant of Aaron Stark I increases even further as A is compared to C, D, & E for there is very good confidence when the percentage values exceed 90%. While the A to B comparison has a lower confidence criteria, the value is sufficient relative to A's comparisons to C, D, and E, suggesting A and B most likely could share Isaac Stark as a common ancestor in Generation 5, provided the genealogy submitted is correct.

G E N	Table 4 Tip Calculations								
N S	A to B	B to C							
11	96.19%	99.29%							
10	94.50%	98.89%							
9	92.11%	98.26%							
8	88.77%	97.28%							
7	84.14%	95.73%							
6	77.85%	89.48%							
5	69.45%	83.49%							
4	58.56%	74.10%							
3	45.00%	59.37%							
2	29.18%	36.26%							
1	12.77%	93.29%							

Kerchner's Triangulation Method for "deducing" the Ancestral Haplotype

According to Kerchner, if descendants of two different sons of a Father are a perfect match over 37 markers, then the Father of these sons most likely would have matched his descendants over their 37 marker Haplotype. According to Kerchner's triangulation methodology, this defines the Ancestral Haplotype of a group of related Males having the same surname. Presently, 15 of a total of 33 descendants of Aaron Stark [1608-1685] have the 37 marker Ancestral Haplotype. Kerchner's triangulation rules are quite simple and can be stated as follows:

- If two genetically compared males, having the same Surname, are direct line descendants of two known and different sons of a common Ancestor — *and* — they both match at each marker of a 37 marker Haplotype, then by deduction, we presume the father of the two sons had the same 37 marker Haplotype, defined as as the Ancestral Haplotype of two sons Father.
- 2) If (1) genetically occurs and the genealogy is correct, then by deduction, we presume all individuals in their respective descendant branches from the Father have the same allele value at that DYS Marker.
- 3) If neither has the same value at one or more 37 marker Haplotypes, then the Ancestral Haplotype of the father cannot be determined; nor can the Haplotype of individuals in the respective descendant branches be determined; the exception in each branch being the known known Haplotype the genetically compared Males.

Table 2 presents the 37 marker Haplotypes of Members B and E. These Members are a perfect genetic match to each other over these Markers. Referring to Table 3, Member B is a direct line descendant of William Stark I [1664-1730] in Generation 9 of Table 3. Member E is a direct line descendant of William Stark II [1655-1701] in Generation 9. The Father of William I and Aaron II is Aaron Stark I [1608-1685] in Generation 10.

In this analysis, Kerchner's Rules 1 & 2 apply to comparisons of Members B, C, D, and E. The Y-DNA and genealogy of each suggest their 37 marker Haplotypes define the Ancestral Haplotype of Members of Group 1. Therefore, their is added confidence Member B is an ancestor of Aaron Stark I [1608-1685] and all of his male ancestors with the surname Stark most likely had his 37 marker Haplotype.

Rule Number 3 applies to Member A's genetic comparison to the Ancestral Haplotype. While his generation 5 ancestor, Isaac Stark [1805-1874] has the Ancestral Haplotype of Aaron Stark I, a mutation occurred in one of the generations beginning with Milo Stark to his descendant, Member A. Because we know the 37 marker Haplotype of Member A has a mutation at Marker 9, it would also be possible the mutation occurred in the transfer of the Y-DNA of his Father to Member A.

Conclusions

Member #535078, Y-DNA tested over 37 markers by FTDNA, when compared genetically and genealogically to other Stark Project Members placed in Group 1, is confirmed to be a descendant of Aaron Stark I [1608-1685] of New London County, Connecticut. He is most likely a 4th cousin of the Father of Member # 203166, both being descendants of Isaac Stark [1805-1874]. The genetic results of #535078 compared to selected Members of Group 1, confirm #535078 has the Ancestral Haplotype of Aaron Stark I [1608-1685] and Aaron is his earliest known ancestor. Confirmation of #535078 suggests Member #203166 is also a descendant of Aaron Stark [1=1608-1685].