

# Vance Y-DNA Project: Group 1 Overview: DNA Analysis

by Adam Bradford (adam.bradford@gmail.com)

## Lineages

### 1a

- Barnbarroch (1300s)
- George of Raneel (d.1711, Donegal)
- David of Wigton (m.Agnes Jones)
- William of Smyth Co., VA b.1826
- John of Frederick 1760
- William of Yalobusha (b.c.1811, SC)

### 1b

#### **Chambersburg Group**

- Patrick of Chambersburg 1803
- David of Mecklenberg 1800
- Sihon Vance (b.1802, Claiborne Co, TN)
- Robert (b.c.1810, TN) m.Tempe Brewer
- William (b.1833, McMinn Co., TN)

#### **Frederick County Vances**

- David of Frederick 1768
- James of Frederick 1751
- Maj. William of Cross Creek (1718-1788)
- Samuel (wife Alice Carr) 1789
- Samuel (wife Sarah Colville) 1778
- Andrew of Frederick 1754
- James of Frederick 1762

#### **Miscellaneous**

- Hugh (1799-1870) m.Virginia Capps
- Elihu (b.1802, SC)
- Benjamin (d.1834-36, Carroll Co, MS)
- Joseph (d.1798, VA) m.Rachel Alexander
- Samuel of Orange, NY 1793
- John (d.c.1814, Springfield, OH)
- Joseph (d.1838, IL) m.Nancy Bradley

## Members

### 1a

- 39200 – Barnbarroch (1300s)
- 198026 – George of Raneel (d.1711, Donegal)
- 92592 – David of Wigton (m.Agnes Jones)
- 54198 – William of Smyth Co., VA b.1826
- 67952 – John of Frederick 1760
- 73264 – William of Yalobusha (b.c.1811, SC)

### 1b

#### **Chambersburg Group**

- 39459 – Patrick of Chambersburg 1803 (Wm)
- 57216 – Patrick of Chambersburg 1803 (Joseph)
- 149061 – David of Mecklenberg 1800 (Sam)
- 142808 – David of Mecklenberg 1800 (John)
- 154808 – Sihon Vance (b.1802, TN) (Jas)
- 150126 – Sihon Vance (b.1802, TN) (Rich)
- N20182 – Robert (b.c.1810, TN) m.Tempe Brewer
- 68535 – William (b.1833, McMinn Co., TN)

#### **Frederick County Vances**

- 140826 – David of Frederick 1768
- 39128 – James of Frederick 1751
- 82147 – Maj. William of Cross Creek (Joseph, Wm)
- 44166 – Maj. William of Cross Creek (Joseph, Jno)
- 43864 – Samuel (m.Alice Carr) 1789
- N21545 – Samuel (m.Sarah Colville) 1778 (John)
- 61862 – Samuel (m.Sarah Colville) 1778 (Sam)
- 160200 – Samuel (m.Sarah Colville) 1778 (Robert)
- 65717 – Andrew of Frederick 1754
- 116886 – James of Frederick 1762

#### **Miscellaneous**

- 85014 – Hugh (b.1799) m.Virginia Capps (John)
- 155538 – Hugh (b.1799) m.Virginia Capps (David)
- 87508 – Elihu (b.1802, SC)
- 107849 – Benjamin (d.1834-36, Carroll Co, MS)
- 100812 – Joseph (d.1798-9, VA) m.Rachel Alexander
- 44884 – Samuel of Orange, NY 1793
- 113168 – John Vance (d.c.1814, Springfield, OH)
- 114890 – Joseph (d.1838, IL) m.Nancy Bradley (John)
- 120759 – Joseph (d.1838, IL) m.Nancy Bradley (Jas.)
- 7555 – unknown/different surname

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## DNA Analysis

Group 1 is the largest and most diverse group in the Vance DNA project, containing 33 Vance members who represent 22 distinct earliest known ancestors. The group is most notable for containing member 39200, the lineal heir of Barnbarroch, who has a reliable paper trail leading back to Robert Vaus of Barnbarroch, the first of the line for whom documentary records survive. The group is clearly related within a genealogical timeframe and likely descends from a common ancestor who carried the name Vaus or Vaux. We can be confident of this conclusion owing to the relatively short genetic distance obtaining between members of the group, as displayed in the following chart:

		Genetic Distance																															
ID	3	5	6	7	9	1	1	3	5	N	6	1	1	6	4	1	4	1	1	8	N	6	1	1	1	8	1	8	4	3	1	1	7
	2	4	7	3	2	5	5	9	7	2	8	4	4	5	4	0	3	1	2	7	2	1	6	1	5	5	4	2	4	9	1	0	5
	0	9	5	6	9	8	1	5	1	1	3	0	8	1	8	8	6	8	7	0	5	6	2	1	5	1	8	4	6	2	8	8	5
	0	8	2	4	2	0	2	9	6	8	5	6	0	7	4	1	4	9	5	8	4	2	0	6	3	4	2	7	6	8	8	4	
						8	6			2		1	8			2	0	9		5	0	8	8										
39200	67	2	4	5	5	5	6	7	7	6	6	5	6	5	8	6	7	5	6	4	4	6	6	5	5	5	9	2	6	8	6	7	5
54198	2	67	2	3	5	5	4	5	5	4	4	5	6	5	8	6	7	5	6	4	4	5	4	5	5	5	9	0	4	7	6	7	5
67952	4	2	67	1	4	5	3	4	3	4	4	5	4	5	6	4	5	4	5	4	4	3	5	4	3	4	8	0	2	5	4	7	5
73264	5	3	1	67	4	6	3	5	3	5	5	6	5	6	7	4	6	4	6	4	5	4	5	4	3	5	9	0	2	6	4	8	6
92592	5	5	4	4	37	6	7	7	5	7	7	6	5	5	6	5	6	6	6	4	4	5	7	6	5	3	7	2	4	4	4	4	3
154808	5	5	5	6	6	67	2	3	4	2	2	1	2	3	4	4	4	3	3	2	3	4	5	3	3	3	7	1	4	5	3	5	4
150126	6	4	3	3	7	2	37	1	3	2	2	3	3	4	4	5	5	4	4	4	4	4	5	4	4	4	8	0	3	4	4	5	5
39459	7	5	4	5	7	3	1	67	2	1	1	2	2	3	4	5	5	4	4	4	4	4	5	4	4	4	8	0	3	5	3	5	5
57216	7	5	3	3	5	4	3	2	37	2	2	3	2	3	3	4	5	5	5	3	4	4	6	5	4	4	8	1	1	2	1	2	3
N20182	6	4	4	5	7	2	2	1	2	67	0	1	2	3	4	5	5	4	4	3	4	4	4	4	4	4	8	0	3	5	3	5	5
68535	6	4	4	5	7	2	2	1	2	0	67	1	2	3	4	5	5	4	4	3	4	4	4	4	4	4	8	0	3	5	3	5	5
149061	5	5	5	6	6	1	3	2	3	1	1	67	1	2	3	4	4	3	3	2	3	4	5	3	3	7	1	4	5	2	4	4	
142808	6	6	4	5	5	2	3	2	2	2	1	67	1	2	3	3	3	3	3	2	3	6	3	2	2	6	1	3	4	1	3	3	
65717	5	5	5	6	5	3	4	3	3	3	3	2	1	67	3	4	4	4	4	4	1	4	6	4	3	2	6	1	4	5	2	2	2
44884	8	8	6	7	6	4	4	4	3	4	4	3	2	3	67	2	4	3	4	4	4	5	7	4	3	4	6	1	4	6	2	5	5
100812	6	6	4	4	5	4	5	5	4	5	5	4	3	4	2	37	3	3	3	3	3	4	7	4	3	3	5	2	3	3	3	4	3
43864	7	7	5	6	6	4	5	5	5	5	5	4	3	4	4	3	67	3	3	4	3	4	7	2	3	3	6	1	4	5	4	6	4
114890	5	5	4	4	6	3	4	4	5	4	4	3	3	4	3	3	37	0	3	3	4	6	2	3	3	6	1	4	4	4	5	4	
120759	6	6	5	6	6	3	4	4	5	4	4	3	3	4	4	3	0	67	3	3	4	6	2	3	3	6	1	4	5	4	6	4	
87508	4	4	4	4	4	2	4	4	3	3	3	2	3	4	4	3	4	3	3	37	3	4	5	3	3	3	7	2	2	2	2	3	2
N21545	4	4	4	5	4	3	4	4	4	4	4	3	2	1	4	3	3	3	3	3	67	3	5	3	2	1	5	1	3	4	3	3	1
61862	6	5	3	4	5	4	4	4	4	4	4	4	3	4	5	4	4	4	4	4	3	67	6	4	3	3	7	1	3	3	4	6	4
160200	6	4	5	5	7	5	5	5	6	4	4	5	6	6	7	7	7	6	6	5	5	6	37	6	6	4	8	2	5	6	7	7	6
113168	5	5	4	4	6	3	4	4	5	4	4	3	3	4	4	4	2	2	2	3	3	4	6	37	3	3	7	1	4	4	4	5	4
155538	5	5	3	3	5	3	4	4	4	4	4	3	2	3	3	3	3	3	3	2	3	6	3	37	2	6	1	3	3	3	4	3	
85014	5	5	4	5	3	3	4	4	4	4	4	3	2	2	4	3	3	3	3	3	1	3	4	3	2	67	4	1	3	4	3	4	2
140826	9	9	8	9	7	7	8	8	8	8	8	7	6	6	6	5	6	6	6	7	5	7	8	7	6	4	67	2	7	8	7	8	6
82147	2	0	0	0	2	1	0	0	1	0	0	1	1	1	1	2	1	1	1	2	1	1	2	1	1	1	2	14	1	2	2	2	2
44166	6	4	2	2	4	4	3	3	1	3	3	4	3	4	4	3	4	4	4	2	3	3	5	4	3	3	7	1	37	1	2	3	2
39128	8	7	5	6	4	5	4	5	2	5	5	5	4	5	6	3	5	4	5	2	4	3	6	4	3	4	8	2	1	67	2	5	3
116886	6	6	4	4	4	3	4	3	1	3	3	2	1	2	2	3	4	4	4	2	3	4	7	4	3	3	7	2	2	2	37	1	2
107849	7	7	7	8	4	5	5	5	2	5	5	4	3	2	5	4	6	5	6	3	3	6	7	5	4	4	8	2	3	5	1	67	2
7555	5	5	5	6	3	4	5	5	3	5	5	4	3	2	5	3	4	4	4	2	1	4	6	4	3	2	6	2	2	3	2	2	67

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The color coding indicates the magnitude of the genetic distance, with green closest and white the most distant. Most members of Group 1 are within a close genetic distance from every other member, although there are few outliers (92592, 160200, and 140826), which is to be expected in a group of this size.

## Time to Most Recent Common Ancestor (TMRCA)

There are various methods in use for arriving at an age estimate for a group of haplotypes. All of these methods rely in one way or another on combining marker mutation rates with the genetic distance between individuals to arrive at an estimated number of generations that have passed since those individuals shared a common ancestor. I like to use these age estimates to set an upper bound for a possible range of years during which the MRCA probably lived and I rely on two tools for making these MRCA estimates: Dean McGee's online utility and a spreadsheet designed by Tim Jantzen.

Dean McGee's utility yields 95% estimates between individual members that range as high as 31 generations (about 1100-1225 AD). [Per Dean McGee, the "probability is 95% that the TMRCA is no longer than indicated" by these estimates.] Tim Jantzen's spreadsheet yields age estimates ranging as high as 21 generations. If we average the upper bound estimates from both methods (31 generations and 21 generations), we get an estimate of 26 generations, or 780 years (i.e., 1220AD) using a generation length of 30 years. This can probably serve as a comfortable upper bound estimate, although it remains possible that the MRCA of the group lived before that time. For a lower bound estimate, it is enough to note that Group 1 contains well over a dozen lineages that were distinct by the mid-1700s. This makes it unlikely that the MRCA of the whole group could have lived at any point after about 1650 AD. Thus, a broad estimate for Group 1's age would be in the period from 1200 to 1650 AD, which would place the common ancestor of the whole group either in the following generations of 39200's lineage, or possibly some generations before the founding of Barnbarroch:

1. Robert Vaus (d.aft.6 Mar 1459)
2. Blaise Vaus (d.bef.26 Feb 1482)
3. Patrick Vaus (d.1528)
4. John Vaus (d.1547, battle of Pinkie)
5. Sir Patrick Vaus (d.22 Dec 1597)
6. Sir John Vans (c.1574-Jun1642)
7. Sir Patrick Vans (d.1673)

It's worth noting that the average estimate provided by Tim Jantzen's spreadsheet is 15 generations, which would indicate an MRCA in the period from 1400 to 1700 AD.

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## Group Structure: DYS607 and DYS572

For the sake of convenience, I have split Group 1 into two subgroups based around the markers DYS607 and DYS572. Although the entire group shares a common Vans or Vaus ancestor, these two markers reveal a distinct genetic divide within the group, with one portion having both 607=16 and 572=12 and the other having both 607=15 and 572=11. There is a perfect correlation on these markers, with all of Group 1 on one side or the other of this 2-mutation divide on what are fairly stable markers with low mutation rates. There are four possible ways to account for this divide, and they depend on what the ancestral values of those markers were for the group. These four possible scenarios entail two broad ways to think about the structure of Group 1.

### Scenarios 1 & 2: ancestral values were 607=16, 572=11 or 607=15, 572=12

In terms of Group 1's branching structure, these scenarios are identical. Both would mean that Groups 1a and 1b each represent distinct branches. In other words, somewhere in the line leading from the MRCA of Group 1 a man had one mutation that gave rise to the Group 1a lineage; another man, on a collateral branch, had another mutation that gave rise to Group 1b.

### Scenarios 3 & 4: ancestral values were 607=15, 572=11 or 607=16, 572=12

In contrast to the "two different branches" scenarios, these two scenarios would each indicate that one of the groups represents the main body of Group 1 while the other represents an offshoot.

If the group's ancestral values were 607=15, 572=11, then we could be sure that Group 1a represented a distinct branch off the main Group 1 line. This originally seemed like the most plausible scenario, for two reasons. First, the Group 1b values of 607=15 and 572=11 are also the modal values of all of R1b; the simplest explanation of this state of affairs would be that they were also the ancestral values of Group 1, and that the rarer 607=16 and 572=12 held by Group 1a represent mutations. This interpretation seemed to be bolstered by the fact that Group 1b contains over 5 times as many individuals as Group 1a, the kind of ratio one might expect to find between a main body and its satellite branch. Pretty much the only argument against this scenario was that Group 1a contains the lineal heir of Barnbarroch as well as another Vans line originating in Scotland, whereas Group 1b consists entirely of American Vance lines that everyone assumes were later offshoots.

If the ancestral values were 607=16, 572=12, it would mean that Group 1b, rather than 1a, represented an offshoot. In this scenario, Group 1b would simply be a subset of Group 1a. Although this originally seemed the less plausible scenario, in fact it is correct. Despite having values on 607 and 572 that are rare in R1b, Group 1a really does represent the "main body" of Group 1, and group 1b represents a later branch. At some point the lineage leading to 1b branched away from the main Group 1 trunk; then in the lineage leading to the Group 1b MRCA there were mutations on 607 and 572. In order to explain how we can possibly know this, I need to describe the genetic evidence in some detail and explain what it has to say about the more ancient origins of Group 1.

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## Group 1 Ancient Origins

When analyzing DNA results for a group of individuals, it is helpful to identify marker values they share that are relatively rare among the general population. Not only do these shared values provide further indication of a recent common descent, they can often reveal information about a group's more ancient origins. Sometimes a larger group of individuals with different surnames will share the same rare values, and this can indicate that they share a common ancestor who lived in the time before surnames became fixed. An analysis of rare values for Group 1 reveals that they are part of just such a group and that they share with several other families of different surnames a common ancestor who probably lived in the middle ages.

Group 1 as a whole is characterized by the following marker values that are rare in R1b as a whole:

<u>Value</u>	<u>Frequency in R1b Haplogroup</u>
458=19	6% of R1b
406S1=11	11% of R1b
534=14	13% of R1b
617=13	6% of R1b
640=12	5% of R1b

Group 1a is further characterized by the following rare values:

<u>Value</u>	<u>Frequency in R1b Haplogroup</u>
607=16	14% of R1b
572=12	4% of R1b

With the exception of DYS458, all of the above markers are located on FTDNA's 67-marker panel. Without the 67-marker panel, Group 1's DNA signature, far from being rare, is actually one of the most common. The 12-marker modal haplotype of Group 1 is identical to the Western Atlantic Modal Haplotype (WAMH), which is the single most common Y-DNA signature among males of western European descent. According to FTDNA, roughly 2.5% of western European males have this precise 12-marker haplotype, the genetic signal of a prolific founder from ancient times. Groups 2a and 2b also have the WAMH, so that it is only possible to reliably distinguish these Vance groups from one another by comparing them on at least 37 markers. Being WAMH, Group 1 has over a thousand close matches on 12 and even 25 markers with men of other surnames in Ysearch, an online Y chromosome database. On 37 markers the group is more distinct, but there are still nearly 250 individuals of different surnames who are within a genetic distance of 6 on 37 markers from the Vance Group 1 modal haplotype. Even on 67 markers, the Group 1 modal haplotype yields matches with over a dozen men of different surnames. However, a closer look at these 67-marker matches reveals that they all share four of the five same rare marker values that characterize Vance Group 1. When compared specifically with Group 1a, the number of shared rare values increases to

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6. If one then isolates those 6 rare values and searches specifically for matches to those markers in Ysearch, one finds nearly 100 individuals of different surnames who are within a genetic distance of 10 or less on 67 markers and who share all of these rare marker values. These rare values are the genetic signal of a common founding ancestor, and the genetic distance between all of these men indicates that their common ancestor was relatively recent.

Several researchers independently discovered the existence of this clade, of which Vance Group 1 is a part. Indeed, it is an extremely distinct clade and easy to spot owing to the combined presence of 6 unique marker values. This clade is older than the Barnbarroch line and falls outside the traditional scope of Vance genealogy, so I have described it in a separate report. For the purposes of this paper, I want to emphasize three main points from that report:

- 1) The clade is prolific. The founder of the clade was the progenitor of the largest modern-day genetic groupings of 5 separate Scottish surnames: Vans/Vance, Elliott/Elwood, Glendenning/Clendenin, Little, and McClain. With the exception of McClain, all four of these families have traditions of descent from lowland Scotland.
- 2) The clade is relatively young. Genetic evidence indicates a probable origin of the whole clade in the period from 650 to 1250AD. Obviously this is too ancient to have an immediate bearing on our genealogical research, but it adds another dimension to Group 1's ancestry. The Barnbarroch Vaus line is not only a family in its own right, it is also one branch of a Scottish superfamily to which belong large groups of Elliotts, Glendennings, Littles, and McClains. Since the estimated age of the superfamily falls in the historical period and since it contains gentry lines of some prominence, it is not inconceivable that more could be discovered about the origins of the superfamily from the documentary record.
- 3) Although the clade falls outside what we normally think of as genealogy, we have been able to use its existence to gain insight into Group 1's genealogy by inferring the ancestral values of DYS607 and DYS572. The modal values of the "superfamily" on 607 and 572 are 16 and 12, exactly the same as the Group 1a values. These values are present in all the main family branches of the clade, including Glendenning, Elliott, Little, and McClain, which indicates that they were the likely ancestral values of the clade. Since Vance Group 1 is younger than the clade, they were also the likely values held by the Vance Group 1 MRCA. Group 1b must therefore be a later offshoot.

Several researchers have identified this clade as being a subgroup of a larger group of R-L21 defined by 406S1=11 and 617=13. In November 2009, Mike Walsh began a [project at FTDNA](#) dedicated to this larger group, dubbed the R-L21\* 11-13 Combo Group. He has also started a [Yahoo Group dedicated to the 11-13 group](#). In the context of the 11-13 Combo Group, Mike refers to the clade that contains Vance Group 1 as R-L21\* 11-13 A1. I have opted to maintain his usage and will refer to the clade as the A1 clade throughout this and other reports.

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## Haplogroup:

Members 39200, 65717, and 142808 have tested positive for the L193 SNP, which defines a subclade of the L21 branch of R1b. L21 is itself a subclade of the P312/S116 branch of R1b, which, with S21/U106, is one of the two main branches of R1b among those of European descent. The International Society of Genetic Genealogy maintains an up-to-date SNP tree on the R haplogroup here:

[http://www.isogg.org/tree/ISOGG\\_HapgrpR.html](http://www.isogg.org/tree/ISOGG_HapgrpR.html).

The A1 clade overlaps to a great extent with the population of men who have tested positive for the L193 SNP. Thus far, all those in the A1 clade who have tested positive for L193 fall in the 607=16/572=12 population with the exception of members of Vance Group 1b, which we know was a later offshoot. At least one individual who has 4 of the primary defining markers of the A1 clade, but not 607=16/572=12, has tested negative for L193, indicating that L193 may be actually be an identifiable subclade of the A1 clade. If L193 is a descendant of A1, the time separating their origins is not likely to be very great.

\* \* \*

## Shared Mutations:

Group 1b Branch: 607=15/572=11

Group 1b is defined by mutations to 607=15 and 572=11. Given the perfect correlation on these markers throughout the entire group, it is assumed that they are shared mutations. In fact, they are the shared mutations that define Group 1b as distinct from Group 1a.

Chambersburg Vance Branch: 576=17, 570=18, CDYb=40

Confirmed descendants of Patrick Vance of Chambersburg through two different sons (39459 and 57216) share the alternate values of 17 on 576 and 18 on 570. The best explanation of this evidence is that Patrick himself had these values and that they were inherited by the two descendant branches.

Members N20182 and 68535 do not have paper trails back to Patrick, but they do trace back to the area of Tennessee where Patrick died, and in one case (N20182) the circumstantial evidence for a descent from Patrick is compelling. The fact that they also have 576=17 and 570=18 bolsters the case for their descent from Patrick. These two have the alternate value of 40 on CDYb, while Patrick's confirmed descendants have 41 and 39. We can infer from this that 40 was probably the value held by Patrick, and that there were probably 1-step mutations on CDYb in the lineages leading to 39459 and 57216.

Patrick was the brother of David Vance of Mecklenberg, represented in the project by members 149061 and 142808, each descended from a different son of David's. One of these men has CDYb=40, which indicates that this was probably a value shared by both

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Patrick and David. However, both David's descendants have the Group 1 modal value of 576=18, which probably indicates that the mutation to 576=17 was specific to Patrick.

The two descendants of Sihon Vance (154808 and 150126) have CDYb=40 and CDYb=41. One of them also has the Patrick-specific value of 17 on 576. Their shared 19 at DYS 570 is a step away from the Patrick/David value of 18 on that marker. This evidence makes a compelling case for Sihon's descent from Patrick.

## A possible 570=18 sub-branch of Group 1b

As noted above, both Patrick of Chambersburg and David of Mecklenberg had the value 18 at 570. Four other members of the project (65717, 44884, 116886, and 107849) also hold this value. Given the high mutation rate of DYS570, we can't be confident that their earliest known ancestors had this value, but it is worth keeping the possibility in mind. For now it's worth noting that all or some combination of Patrick of Chambersburg, David of Mecklenberg, Andrew of Frederick, Samuel of Orange, James of Frederick 1762, and Benjamin of Carroll might belong on a distinct sub-branch of Group 1b. In two cases (116886 and 107849), this potential shared mutation on 570 contradicts a second possible shared mutation on 458=18, which I'll discuss next.

## 458=18 and Instability of DYS458

Seven Vance members of Group 1 (92592, 57216, 44166, 39128, 87508, 116886, 107849) share the non-modal value 18 on DYS458. In over half these cases (4 out of 7) we can be sure that the value is not a shared mutation, but one that happened independently. Member 92592 is in Group 1a, so his 458=18 is clearly a mutation parallel to all those in Group 1b. Member 57216 is a descendant of Patrick Vance of Chambersburg, whom we know had the ancestral value of 19; his 458=18 is also clearly an independent mutation. Members 39128 and 44166 are likely descendants of David of Opequon, two other of whose descendants have the ancestral value of 19; values of 18 among his descendants must be parallel back mutations.

There is not much to say about the 458=18 held by the others (87508, 116886, 107849). This might be a mutation they share, or it might not. It is at least clear from the above that we are witnessing a minimum of 4 parallel mutations on 458 in Group 1. This is unusual. Although 458 is among the faster mutating markers, it is still odd that there would be so many independent mutations to the same non-modal value on a single marker in one family. This phenomenon might be explained by the fact that the Group 1 ancestral value of 458=19 is at the high end of the observed range of values for this marker, being found in only 6% of R1b in the late [Leo Little's survey of marker value frequencies](#).

There is evidence to suggest that high allele repeat counts result in more frequent back mutations. The scientific literature contains several references to this phenomenon, including the following:

[Dieringer and Schlotterer, 2003](#): “. . . the DNA replication slippage rate seems to be dependent on the length of the microsatellite. *Alleles with a high repeat number are less stable than those with a small repeat number.*



# Vance Y-DNA Project: Group 1 Overview: DNA Analysis

by Adam Bradford (adam.bradford@gmail.com)

Lai and Sun: “When slippage mutations happen . . . contractions occur more frequently if the number of repeat units is large. When mutations happen, long microsatellites are likely to mutate to shorter ones; short microsatellites are likely to mutate to longer ones. The scarcity of large number of repeat units in a microsatellite locus can be explained by the *high mutation rate and downward mutation bias when the number of repeat units is large.*”

These studies suggest that when the repeat count is very high (as it is in Vance Group 1 on DYS458), not only is there an increased chance that a mutation will happen, but if a mutation does occur it is likely to be a downward mutation. We may be witnessing this phenomenon at work in Group 1 on marker DYS458.

Joseph Vance (m.Nancy Bradley): 464d=18, CDYb=38

Based on the DNA results for two descendants of Joseph Vance (wife Nancy Bradley) through two different sons, we can be fairly certain that their alternate values of 464d=18 and CDYb=38 are shared mutations that were present in Joseph’s DNA.

\* \* \*

## Ancestral Haplotypes

We have been able to determine the likely ancestral haplotypes for Group 1 as a whole and for Group 1b. Beyond that, we have also been able to determine the actual haplotypes held by 7 of the 22 distinct ancestors in the group, since we have results from descendants of them from multiple sons (all are from Group 1b):

- Patrick Vance of Chambersburg
- David Vance of Mecklenberg
- Sihon Vance
- David Vance of Opequon (father of David 1768, James 1751, and Maj. William)
- Samuel Vance (wife Sarah Colville)
- Hugh Vance (wife Virginia Capps)
- Joseph Vance (wife Nancy Bradley)

[For space considerations I have not listed the haplotypes in the body of this report. They are available for viewing on the results page of the website.]