Group 2 - Special Report

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Merging Group 2 and Group 3

In my first report on the DNA project in March 2006, Group 2 contained just two men, both descendants of Robert Vance of Carter Co, TN. At that time I grouped them with the descendants of Samuel Vance/Agnes Penquite (son James Vance of McDonough) and wrote, "It is not yet clear that Group II constitutes a single related group of participants, since their genetic distance from each other (as far as we can tell on 37 markers) is 7, which is a bit too distant for comfort." By the time of the next report in August 2006, two more participants had joined the project who very closely matched the Robert descendants but hadn't bridged the gap to the James of McDonough descendants. I felt a more cautious approach was called for and decided to group the James Vance descendants separately as Group 3 until such time as new evidence might allow for a more precise determination. We now have results from another participant (96768) who may clearly be placed with Group 3. His 37-marker haplotype bridges the gap between Groups 2 and 3 to the point where I feel an analysis of their relatedness is warranted.

To get a sense of whether the groups are related, it is useful to compare the genetic distance between them and to generate a range of estimates of the time to the most recent common ancestor (TMRCA) of each group separately and then of both groups together. Dean McGee has created a utility that does just that (http://www.mymcgee.com/tools/yutility.html) based on different assumed rates of mutation. Of the two methods I will be using, the first is based on mutation rates arrived at by FTDNA. FTDNA's mutation rates do not go into per-marker detail. Instead they are arranged by the average mutation rate for a particular panel of markers. For instance, for the first 12-marker panel a mutation rate of .004 is assumed for all 12 of the markers, for the next panel of 13 markers a mutation rate of .0048 is assumed for those 13 markers, and so on. The other method is based on mutation rates arrived at in most cases by Doug McDonald in his 2004 study of the Sorensen Molecular Genealogy Foundation (SMGF) Y-chromosome database. McDonald's method would seem to be more accurate, since it takes into account individual marker mutation rates; in reality it simply allows for estimates that are in theory more refined.

For this analysis I will remove from consideration those members of Groups 2 and 3 who have not tested at least 37 markers, since a comparison of their haplotypes will not provide a high level of resolution. In those cases where participants have identical haplotypes I have removed duplicates. In cases where two or more participants share a known common ancestor, I have picked the one that has the most markers tested and/or whose haplotype is closer to the ancestral hapolotype of that known ancestor (where it can be known).

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TMRCA Estimates

Using the mutation rates arrived at by FTDNA yields the following TMRCA estimates for the individual members of Groups 2 and 3. The chart on the left indicates the age at which the probability is 50% that the TMRCA is no longer than indicated. The chart on the right indicates the age at which the probability is 95% that the TMRCA is no longer than indicated. All the rows and columns but the last two belong to Group 2; the last two are the two members of Group 3 who have tested at least 37 markers. The actual TMRCA estimates are in generations and the years are arrived at by assuming a generation length of 30 years. To convert the years to generations, simply divide by 30. Assuming shorter generation lengths would have the effect of shortening the TMRCA estimates – for instance, assuming a generation length of 25 years would have the effect of decreasing the estimates by about 17%.

Time to Most Recent Common Ancestor (Years) – 50%

ID	48374	72197	N39890	82984	56883	68372	38105	56954	45791	96768
48374 (2)	37	210	120	210	210	210	300	360	840	630
72197 (2)	210	37	300	360	210	300	210	450	630	630
N39890 (2)	120	300	37	120	120	120	210	300	720	540
82984 (2)	210	360	120	67	150	150	270	360	570	540
56883 (2)	210	210	120	150	67	90	210	270	450	450
68372 (2)	210	300	120	150	90	67	150	210	510	540
38105 (2)	300	210	210	270	210	150	67	360	510	630
56954 (2)	360	450	300	360	270	210	360	38	930	720
45791 (3)	840	630	720	570	450	510	510	930	67	360
96768 (3)	630	630	540	540	450	540	630	720	360	37

Time to Most Recent Common Ancestor (Years) – 95%

ID	48374	72197	N39890	82984	56883	68372	38105	56954	45791	96768
48374 (2)	37	480	390	480	480	480	600	720	1350	1080
72197 (2)	480	37	600	720	480	600	480	840	1080	1080
N39890 (2)	390	600	37	390	390	390	480	600	1230	960
82984 (2)	480	720	390	67	360	360	510	720	930	960
56883 (2)	480	480	390	360	67	300	450	600	780	840
68372 (2)	480	600	390	360	300	67	360	480	840	960
38105 (2)	600	480	480	510	450	360	67	720	840	1080
56954 (2)	720	840	600	720	600	480	720	38	1470	1230
45791 (3)	1350	1080	1230	930	780	840	840	1470	67	720
96768 (3)	1080	1080	960	960	840	960	1080	1230	720	37

For the FTDNA rates, the 50% estimates for Group 2 range from 90 to 450 years, with the average being 230 and the mean 270 years. The 50% estimate for Group 3 is 360 years. The 50% estimates for the whole group (i.e., comparing only the overlap between the groups) range from 450 to 930 years, with the average being 615 and the mean 690 years.

For the FTDNA rates, the 95% estimates for Group 2 range from 300 to 840 years, with the average being 516 and the mean 570 years. The 95% estimate for Group 3 is 720 years. The 95% estimates for the whole group (i.e., comparing only the overlap between the groups) range from 780 to 1470 years, with the average being 1044 and the mean 1125 years.

McDonald's rates yield much older estimates:

Time to Most Recent Common Ancestor (Years) - 50%										
ID	48374	72197	N39890	82984	56883	68372	38105	56954	45791	96768
48374 (2)	37	360	240	360	360	360	510	660	1440	1110
72197 (2)	360	37	510	660	360	510	360	810	1110	1110
N39890 (2)	240	510	37	240	240	240	360	510	1290	960
82984 (2)	360	660	240	67	210	210	390	630	840	960
56883 (2)	360	360	240	210	67	150	300	510	660	810
68372 (2)	360	510	240	210	150	67	210	360	750	960
38105 (2)	510	360	360	390	300	210	67	630	750	1110
56954 (2)	660	810	510	630	510	360	630	38	1620	1290
45791 (3)	1440	1110	1290	840	660	750	750	1620	67	660
96768 (3)	1110	1110	960	960	810	960	1110	1290	660	37

Time to Most Recent Common Ancestor (Years) - 95%										
ID	48374	72197	N39890	82984	56883	68372	38105	56954	45791	96768
48374 (2)	37	840	630	840	840	840	1050	1260	2370	1920
72197 (2)	840	37	1050	1260	840	1050	840	1470	1920	1920
N39890 (2)	630	1050	37	630	630	630	840	1050	2130	1680
82984 (2)	840	1260	630	67	540	540	780	1260	1380	1680
56883 (2)	840	840	630	540	67	420	660	1050	1140	1470
68372 (2)	840	1050	630	540	420	67	540	840	1260	1680
38105 (2)	1050	840	840	780	660	540	67	1260	1260	1920
56954 (2)	1260	1470	1050	1260	1050	840	1260	38	2580	2130
45791 (3)	2370	1920	2130	1380	1140	1260	1260	2580	67	1260
96768 (3)	1920	1920	1680	1680	1470	1680	1920	2130	1260	37

For the McDonald rates, the 50% estimates for Group 2 range from 300 to 810 years, with the average being 400 and the mean 550 years. The 50% estimate for Group 3 is 660 years. The 50% estimates for the whole group (i.e., comparing only the overlap between the groups) range from 660 to 1620 years, with the average being 1050 and the mean 1140 years.

For the McDonald rates, the 95% estimates for Group 2 range from 420 to 1470 years, with the average being 875 and the mean 945 years. The 95% estimate for Group 3 is 1260 years. The 95% estimates for the whole group (i.e., comparing only the overlap between the groups) range from 1140 to 2580 years, with the average being 1800 and the mean 1860 years.

Which set of mutation rates is more trustworthy?

Clearly there is a large difference between the McDonald and FTDNA estimates. For the sake of testing the reliability of both models, I obtained TMRCA estimates using both FTDNA's and McDonald's rates for four groups of participants in the Vance project whose common ancestor is known: Patrick Vance of Chambersburg, Samuel Vance of Abingdon, Matthew Vance of Pittsylvania, and Samuel Vance (wife Agnes Penquite). I found that the FTDNA estimates were in each instance more accurate. If they were to be used as a guide, the estimate in which we might have the most confidence would be a time in between the 50% and 95% mean estimates, with a frequent bias towards the 50% mean and some support for the overall estimate from the McDonald 50% range of estimates.

Case 1: In the case of Patrick Vance, the actual TMRCA was 5 to 7 generations, or 150 to 210 years. This was exactly within the range of estimates given in the FTDNA 50%

chart. It was also within the range between the FTDNA 50% and 95% mean estimates, and closer to the 50% mean. It was within the 50% range supplied by McDonald's rates, but only just at or below the 50% mean. It was below the range of the 95% estimates.

Case 2: In the case of Samuel Vance of Abingdon, the actual TMRCA was 7 to 8 generations, or 210 to 240 years. This was exactly in between the 50% and 95% mean estimates given by FTNDA's rates. It was within the 50% McDonald range and right around the 50% mean, but well below the 95% McDonald estimates.

Case 3: In the case of Matthew of Pittsylvania, the actual TMRCA was 7 to 8 generations, or 210 to 240 years. Again, this was within the 50% range given by FTDNA and very close to the mean 50% estimate. It was below the range of 95% estimates and well below the 95% mean. The actual TMRCA was within the McDonald 50% range of estimates but below the 50% mean; it was well below the 95% range of estimates and the 95% mean.

Case 4: In the case of Samuel Vance (wife Agnes Penquite), the actual TMRCA was 7 to 8 generations, or 210 to 240 years. This turned out to be within the range of 50% estimates given by FTDNA's rates, but below the 50% mean. It was below the 95% range and was also younger than the lowest estimate given by the 50% McDonald rates.

Analysis of TMRCA Estimates

Given the consistency between the results of these four case studies, we might have the most confidence in a TMRCA estimate between the 50% and 95% mean estimates given by FTDNA, and trending closer to the 50% mean, possibly with support from the 50% range supplied by the McDonald rates. In terms of the relatedness of Groups 2 and 3, that means we might have the most confidence in a TMRCA estimate of roughly 700 to 1100 years (900 to 1300 AD), with a bias towards the lower end (1300 AD). This estimate is, of course, within the range of time during which the surname Vance or older variants have been in use. The 1300s was the century when the founder of the Barnbarroch line lived, and the surname itself is supposed to have a pedigree in Britain stretching all the way back to the Norman Conquest, which is near the upper limit of the TMRCA estimate for the groups. In either case, a common genetic descent from a man of the same surname is possible. It must be pointed out that this range is just our most confident estimate and that the actual age might be younger or older than the range given.

Another factor linking these groups is the ancestral value of each group on DYS456. The ancestral value of this marker for both groups is 19, which is a rare value among individuals of the R1b haplogroup. (The value was not even observed in Whit Athey's study of the modal values for R1b.) The relative uniqueness of this shared ancestral value tends to strengthen the conclusion that Groups 2 and 3 share a relatively recent common genetic descent. Based on this and the TMRCA estimates above, there is a distinct likelihood that these groups share a common descent in the direct male line from some man who carried the surname Vance or an older variant (e.g., Vans, Vaus, etc.). The alternative - that the two groups match this closely and have the same surname, yet are not descended from a man with some variant of the surname - seems to be more unlikely.

We must still admit the possibility that these two groups happen to match closely but that their common genetic ancestor did not have a version of the Vance surname. It is possible that there were two independent non-paternity events where the males involved happened to have a relatively recent genetic ancestor, or that the surname just happened to arise independently in two branches of the same genetic lineage for some other reason. However, whether or not the surname descent is common, it seems likely that they do share a relatively recent common genetic descent. For that reason, from now on I will refer to the two groups as subgroups of a single group, known as Group 2. I will refer to the former Group 2 as Group 2a and the former Group 3 as Group 2b. Since there is a significant difference between the two subgroups, and since we can't entirely discount the possibility that they don't share a common surname descent, I will continue to shade them with different colors on the website.

Determining the Ancestral Haplotypes of Groups 2a and 2b

A TMRCA estimate for the group of at least 700 years happens to be consistent with an estimate arrived at by a slightly more refined method that involves comparing the MRCAs of each group to each other directly. We have been able to make this comparison by deducing each subgroup's ancestral haplotype, which is simply the haplotype held by the most recent common ancestor of each subgroup.

In determining the ancestral haplotype, we may first remove from consideration all those markers on which the participants are identical. By far the simplest explanation for their identity is that those were the values held by the MRCA and that they haven't mutated since the MRCA in any of the participants' lineages. An illustration of mutation rates should suffice to make this obvious. Since the distinction is often made between slow and fast markers, I will use two markers by way of illustration, one a so-called fast-mutating marker and the other a so-called slow-mutating marker. This should make it plain that on any marker, fast or slow, a mutation is a rare thing.

Doug McDonald's mutation rate for marker DYS19, one of the "slow" markers, is .0015, which means there is a .15% chance for that marker to mutate each generation. That means it ought to mutate about once every 600 to 700 generations, or 18,000 to 21,000 years (assuming 30 years per generation). McDonald's rate for DYS458 (a "fast" marker) is .0053, or about a half-percent chance of a mutation each generation. Therefore, DYS458 ought to mutate about 3 to 4 times faster than DYS19. In that sense, it is "faster," but in absolute terms it should still only mutate once every 200 or so generations, or about 6,000 years or so. Clearly fast and slow are relative terms, since even the "fast" markers are slow in terms of a genealogical time-frame. In any case, it should be apparent that when all the participants' values are the same on a marker, the odds highly favor that the value was the same one held by the MRCA of the group.

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Removing the markers on which all the participants are identical yields the following 11 markers on which there is some difference among the participants:

Kit ID	Earliest Vance Ancestor	385b	439	3891	392	459b	455	449	456	576	570	CDYaa	CDYbb	442	444
48374	Thomas (b.c.1820, OH)	14	12	13	**12**	10	11	30	**18**	17	17	37	**40**	13	
72197	Thomas (d.1886, Caribou, ME)	14	12	13	**12**	10	11	30	**19**	17	17	37	**39**	13	
N39890	George of Orangeville, PA 1847	14	12	13	13	10	11	30	**18**	17	17	37	**40**	13	
82984	John Thomas Vance (b.c.1824, PA)	14	**13**	13	13	10	11	30	**18**	17	17	37	**40**	13	**14**
85380	Abner (d.1819)	14	12	13	13	x	x	30	**19**	x	x	x	x	x	
56883	Abner (d.1819)	14	12	13	13	10	11	30	**19**	17	17	37	**40**	13	**14**
94893	David (m.Elizabeth Rose)	14	12	13	13			30	**19**					13	
68372	Matthew of Pittsylvania (son Matthew)	14	12	13	13	10	11	30	**20**	17	17	37	**40**	13	**14**
71598	Matthew of Pittsylvania (son Matthew)	14	12	13	13	10	11	30	**20**	17	17	**36**	**40**	13	
80341	Matthew of Pittsylvania (son Matthew)	14	12	13	13	10	11	30	**20**	17	17	37	**40**	13	
72769	Matthew of Pittsylvania (son John)	14	12	13	13	10	11	30	**20**	17	17	37	**40**	13	
38105	Matthew of Pittsylvania (son John)	14	12	13	13	10	11	30	**20**	17	17	37	**39**	13	**13**
75086	Matthew of Pittsylvania (son John)	**13**	12	13	13	10	11	30	**20**	17	17	**38**	**40**	13	
56954	George (d.1845-50, MS)	14	12	**14**	13	10	11	30	**20**	17	17	37	**40**	13	**14**
45791	Samuel Vance/Agnes Penquite	14	12	13	13	10	**12**	31	19	18	18	**38**	**39**	12	14
Sor2	Samuel Vance/Agnes Penquite	14	12	13	13	10	11	31	19					12	
Sor3	Samuel Vance/Agnes Penquite	14	12	13	13	10	11	31	**18**					12	
Sor5	Samuel Vance/Agnes Penquite	14	12	**12**	13	**9**	11	31	19					12	
96768	John F. Vance of Smith Co., TN (1801)	14	**11**	13	13	10	11	31	19	18	18	**37**	**40**	12	

We can easily pare this down further. There are certain markers on which only a single participant from a subgroup differs from the others in the subgroup. These are markers with a very pronounced modal value. (The modal value is simply the value held by a majority of the participants on that marker.) If only 1 participant out of many differs on a given marker, we may safely assume that these isolated differences are probably instances of mutations away from the ancestral value that are peculiar to the participant's lineage, and that the modal value is identical to the ancestral value. Removing those markers from consideration leaves the following 8 markers on which there is either some difference between the subgroups or for which the ancestral value of one of the subgroups can't be automatically determined:

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Kit ID	Earliest Vance Ancestor	392	449	456	576	570	CDYa	CDYb	442
48374	Thomas (b.c.1820, OH)	12	30	18	17	17	37	40	13
72197	Thomas (d.1886, Caribou, ME)	12	30	19	17	17	37	39	13
N39890	George of Orangeville, PA 1847	13	30	18	17	17	37	40	13
82984	John Thomas Vance (b.c.1824, PA)	13	30	18	17	17	37	40	13
85380	Abner (d.1819)	13	30	19	x	x	x	x	x
56883	Abner (d.1819)	13	30	19	17	17	37	40	13
94893	David (m.Elizabeth Rose)	13	30	19					13
68372	Matthew of Pittsylvania (son Matthew)	13	30	20	17	17	37	40	13
71598	Matthew of Pittsylvania (son Matthew)	13	30	20	17	17	36	40	13
80341	Matthew of Pittsylvania (son Matthew)	13	30	20	17	17	37	40	13
72769	Matthew of Pittsylvania (son John)	13	30	20	17	17	37	40	13
38105	Matthew of Pittsylvania (son John)	13	30	20	17	17	37	39	13
75086	Matthew of Pittsylvania (son John)	13	30	20	17	17	38	40	13
56954	George (b.1780/90, SC - d.1845-50, MS)	13	30	20	17	17	37	40	13
45791	Samuel Vance/Agnes Penquite	13	31	19	18	18	38	39	12
Sor2	Samuel Vance/Agnes Penquite	13	31	19					12
Sor3	Samuel Vance/Agnes Penquite	13	31	18					12
Sor5	Samuel Vance/Agnes Penquite	13	31	19					12
96768	John F. Vance of Smith Co., TN (1801)	13	31	19	18	18	37	40	12

Since we have determined that these subgroups probably share a relatively recent common genetic descent, we can now employ one subgroup to infer the ancestral values of the other. In other words, if a value is present to a considerable extent in one subgroup and is also present in 100% of the other subgroup, we may assume that value was the ancestral value despite the presence of alternate values on that marker in one of the subgroups. This is because it is highly likely that the two subgroups split apart from each other well before any later branching within the subgroups. Therefore, any values shared between the subgroups stand a very good chance of being the ancestral values. The alternative is that ancestors in each group experienced the same mutation in parallel – a more unlikely possibility.

On marker DYS392, the first two participants differ from the Group 2a modal. Since the Group 2a modal (13) is shared by all those in Group 2b, we may safely infer that 13 was the ancestral value on DYS392 for the whole group and that the value 12 shared by 48374/72197 is probably a mutation away from the ancestral value. On marker CDYa, the modal of for group 2a is 37; since one of the two members of 2b who have tested for that marker also has the value 37, we can assume for now that 37 was the probable ancestral value for both groups. The same is true for CDYb, where we can infer that the value 40 was that held by the common ancestor of both groups. The conclusions

regarding CDYa and CDYb are less secure since only two participants in Group 2b have tested those markers and since these are fast-mutating markers and more prone to parallel mutations.

The ancestral value of marker DYS456 is less obvious to deduce. The modal in Group 2a is actually 20, since it is present in more participants than the other values 19 and 18. However, in this case we happen to know the value of 20 is held only by the descendants of Matthew of Pittsylvania, whose descendants are very heavily represented in the group, and by the descendant of George Vance of MS, who is probably also a Matthew descendant. The most reasonable explanation for the spread from 18 to 20 in Group 2a is that the ancestral value of the group at DYS456 was 19, and that some lines underwent a mutation to 18 and some (namely, Matthew of Pittsylvania's line) to 20. This conclusion is confirmed by the fact that 19 is clearly the ancestral value of Group 2b. (We know that the single instance of 18 is a mutation away from the ancestral value held by James Vance of McDonough Co, IL.)

Having inferred the likely ancestral values on 392, CDYa,b, and 456, we may remove them from consideration. We have now effectively determined the probable ancestral haplotype of each subgroup. However, we are left with the following 4 markers on which the ancestral values of the two subgroups differ from each other:

Kit ID	449	576	570	442
Group 2a	30	17	17	13
Group 2b	31	18	18	12

On these four markers, it is impossible to tell which values were held by the MRCA of the whole group, but it is clear that these were the ancestral values of the different subgroups. In other words, we have effectively discovered that there was at least a genetic distance of 4 between the MRCAs of each subgroup. What this indicates is a relatively deep split between the subgroups, enough of a split for 4 mutations to accumulate between the time of the MRCA of each subgroup and the MRCA of the group as a whole. This split was of course already hinted at in the TMRCA estimates above, but this genetic distance between the two MRCAs serves to highlight it.

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Following are the probable ancestral haplotypes for groups 2a and 2b, as deduced above, with the markers on which they differ highlighted:

Group 2a Probable Ancestral Haplotype

393	**390**	**19**	**391**	**385a**	**385b**	**426**	**388**	**439**	**389i**	**392**	**389ii**	
13	24	14	11	11	14	12	12	12	13	13	16	
458	**459a**	**459b**	**455**	**454**	**447**	**437**	**448**	**449**	**464a**	**464b**	**464c**	**464d**
19	9	10	11	11	25	15	19	30	15	16	16	17
460	**GATA**	**YCA1**	**YCA2**	**456**	**607**	**576**	**570**	**CDYa**	**CDYb**	**442**	**438**	
10	11	19	23	19	15	17	17	37	40	13	12	
531	**578**	**395s1a**	**395s1b**	**590**	**537**	**641**	**472**	**406s1**	**511**	**425**	**413a**	**413b**
11	9	15	16	9	10	10	8	11	11	12	23	23
557	**594**	**436**	**490**	**534**	**450**	**444**	**481**	**520**	**446**	**617**	**568**	**487**
18	10	12	12	15	8	14	22	19	13	13	11	13
572	**640**	**492**	**565**									
11	11	12	12									

Group 2b Probable Ancestral Haplotype

393	**390**	**19**	**391**	**385a**	**385b**	**426**	**388**	**439**	**389i**	**392**	**389ii**	
13	24	14	11	11	14	12	12	12	13	13	16	
458	**459a**	**459b**	**455**	**454**	**447**	**437**	**448**	**449**	**464a**	**464b**	**464c**	**464d**
19	9	10	11	11	25	15	19	31	15	16	16	17
460	**GATA**	**YCA1**	**YCA2**	**456**	**607**	**576**	**570**	**CDYa**	**CDYb**	**442**	**438**	
10	11	19	23	19	15	18	18	37	40	12	12	
531	**578**	**395s1a**	**395s1b**	**590**	**537**	**641**	**472**	**406s1**	**511**	**425**	**413a**	**413b**
11	9	15	16	9	10	10	8	11	11	12	23	23
557	**594**	**436**	**490**	**534**	**450**	**444**	**481**	**520**	**446**	**617**	**568**	**487**
18	10	12	12	15	8	14	22	19	13	13	11	13
572	**640**	**492**	**565**									
11	11	12	12									

Conclusion

Having deduced the probable ancestral haplotypes for groups 2a and 2b, we may now compare them directly to get a TMRCA estimate for the MRCAs of both groups. If we use FTDNA's mutation rates, we come up with a 50% estimate of 270 years and a 95% estimate of 510 years, with a 50% McDonald estimate of 390 years. That means roughly that we might expect the MRCAs of groups 2 and 3 hadn't shared a common ancestor for at least 300 years. If we add this figure to the minimum figure for the MRCAs of Groups 2a or 2b, we should arrive at a fairly reliable lower limit for the overall age of Group 2.

We are fairly sure when the MRCA of Group 2b lived – about 300 years ago. We can also tell that the MRCA of group 2a must have lived at least 300 years ago and probably more, since at least two distinct lineages in Group 2a extend back to the 1700-1750 time period without sharing a known ancestor. If we add the TMRCA estimate of 300 years to the 300 years that is the minimum age of group 2a and the actual age of 2b, we get a minimum estimate of 600 years, or around 1400 AD. This is, of course, close to the figure seen in the lower range of estimates from our initial TMRCA estimate for both groups, which was around 1300 AD.

In light of the above TMRCA estimate, it is noteworthy that the Vance surname is only supposed to have been around for about 400 to 500 years as an offshoot of the Barnbarroch Vans line. In other words, it appears that Group 2 is probably older than the Vance surname, maybe by a hundred years or more. Not only that - it also appears from the DNA evidence that Group 2 may be older than Group 1, which is presumed to contain the genetic descendants of the Barnbarroch line. Since many in Group 2 trace their descent back to Ulster, this would seem to indicate that their surname Vance might have arisen in Ireland independently of Group 1. It may also be that the TMRCA estimates are off the mark and that these two subgroups really do share a common ancestor in the Vance timeframe of 500 years; as improbable as that is, it remains a possibility. Although it seems unlikely, another possibility is that the two subgroups arose from independent non-paternity events in the Barnbarroch Vans-Vance line in which the males involved just happened to share a relatively recent common genetic ancestor.

Regardless of the specific origin of the two subgroups, our primary conclusion is that the DNA evidence warrants viewing them as a single group with a relatively recent genetic heritage. As the range of TMRCA estimates for the subgroups falls within a meaningful genealogical time frame, there is further a distinct possibility that they share a common genetic descent from a man who had some version of the same surname.