

Group 3 Overview

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

Note: This group was formerly known as Group 4. I am now designating them Group 3, due to the merging of Groups 2 and 3 into one group with two subgroups, 2a and 2b.

<u>Participant</u>	<u>Earliest Known Ancestor</u>
44944	John Vance (b.c.1760, prob. Ireland) m.Mary Allison
56896	Alexander Vance (b.Donegal, late 1800s) (son born 1903)
84477	William Vance (b.1818, Derry – d.1893, Ontario)
91181	John Vance (d.1801, Vermont) (son David born 1788)

DNA Analysis

12-Marker Analysis

All the participants in Group 3 are an exact match on 12 markers except for 91181, who differs by a genetic distance of 1 on marker DYS389ii. Given the rarity of some of the group's shared values on the first 12 markers, there is a very good likelihood of a common Vance descent. The group's shared value of 13 at DYS388 is particularly significant. In Whit Athey's review of the modal values of haplogroup R1b (<http://www.worldfamilies.net/SWAMH.html>), 98% of the sample population had the value 12 at DYS388; Group 3's shared value of 13 was present in only 1% of the sample. The group's shared value of 13 at DYS385b is also relatively rare, being present in just 8% of R1b. On DYS389ii, three of the participants have the value 18, which is present in only 2% of R1b (participant 91181's value of 17 is present in 14%). These rare shared values found in individuals who match either 12/12 or 11/12 and who have the same surname indicate a very good probability of common descent in a genealogical timeframe.

37 Marker Analysis

All participants but 44944 have upgraded to 37 markers and the match between these participants tends to confirm their common Vance descent. Following is a chart showing those markers on which there is some difference between the participants.

Kit	389ii	456b	449	460	CDYa
44944	18				
56896	18	11	30	11	34
84477	18	11	31	12	35
91181	17	10	30	11	35

Finding the ancestral values on these markers may prove useful for figuring out how these men are related. (The ancestral value is simply the value held by the most recent common ancestor of the whole group). However, we don't yet have enough information to be able to tell what the ancestral values were. Aside from marker 389ii, we only have results on these markers for 3 participants. In each case, two of the participants have one value while a third has another. At the moment it can't be determined whether the two shared values represent the ancestral values or whether they might represent a shared mutation which would indicate those men belong on their own sub-branch of the group. For this reason, it might be useful for the whole group if 44944 upgraded to 37 markers.

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TMRCAs Estimates

Using the TMRCAs tool created by Dean McGee

(<http://www.mymcgee.com/tools/yutility.html>), it is possible to come up with a range of estimates for when the group's MRCA might have lived based on observed mutation rates for all the markers tested.

The following charts represent estimates of the time to most recent common ancestor (TMRCAs) for all the individuals in Group 3. The charts on the left represent the time at which there is a 50% chance that the ancestor lived no longer ago than the time stated; the charts on the right represent the time at which there is a 95% chance that the ancestor lived no longer ago than the time stated. The top two charts were generated using FTDNA mutation rates, and the charts below were generated using mutation rates from Doug McDonald's 2004 study of the Sorensen Molecular Genealogy Foundation (SMGF) database. McDonald's estimates are theoretically more refined, since in many cases he has come up with individual mutation rates for each marker, whereas FTDNA's rates use a single rate for several markers. The actual calculations involve generations. These have been converted to years at the rate of 30 years per generation.

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

ID	m	4	5	8	9
	o	4	6	4	1
	d	9	8	4	1
	a	4	9	7	8
	l	4	6	7	1
modal	37	210	120	210	210
44944	210	12	210	210	540
56896	120	210	37	300	300
84477	210	210	300	37	360
91181	210	540	300	360	37

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

ID	m	4	5	8	9
	o	4	6	4	1
	d	9	8	4	1
	a	4	9	7	8
	l	4	6	7	1
modal	37	930	390	480	480
44944	930	12	930	930	1560
56896	390	930	37	600	600
84477	480	930	600	37	720
91181	480	1560	600	720	37

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

ID	m	4	5	8	9
	o	4	6	4	1
	d	9	8	4	1
	a	4	9	7	8
	l	4	6	7	1
modal	37	450	240	360	360
44944	450	12	450	450	1110
56896	240	450	37	510	510
84477	360	450	510	37	660
91181	360	1110	510	660	37

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

ID	m	4	5	8	9
	o	4	6	4	1
	d	9	8	4	1
	a	4	9	7	8
	l	4	6	7	1
modal	37	1890	630	840	840
44944	1890	12	1890	1890	3150
56896	630	1890	37	1050	1050
84477	840	1890	1050	37	1260
91181	840	3150	1050	1260	37

Note that since 44944 has only tested 12 markers, his comparison with 91181 is always skewed much farther back in time due to 91181's alternate value of 17 at 389ii. (When

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only 12 markers are tested, a single difference carries much greater weight.) The other participants' estimates to 91181 are not as affected by this difference, so the time estimates between them are much less drastic. If we ignore 44944's estimates, due to the 12-marker effect, FTDNA's mutation rates yield a 50% chance that the MRCA of group 3 lived no longer than 300 to 360 years ago (i.e., the 1600s) and a 95% chance that the MRCA lived no longer than 600 to 720 years ago (i.e., the 1300s/1400s). McDonald's rates result in much longer estimates: 510 to 660 (1340 to 1500 AD) for the 50% estimate and 1050 to 1260 (740 to 1000 AD) years ago for the 95% estimate.

We shouldn't be disheartened by the length of McDonald's estimates. Although they are theoretically more refined, they are not necessarily more accurate. In those cases in the Vance project where we have been able to compare participants whose MRCA was known, the actual TMRCA has been more in line with FTDNA's predictions. This does not necessarily guarantee that FTDNA's predictions are always more accurate - it's important to keep in mind that these are only estimates, with probabilities attached. These case studies indicate that we might have the most confidence in an estimate between the 50% mean and 95% mean estimates generated by the FTDNA rates, and trending closer to the 50% mean. For Group 3, this would mean we might have the most confidence in a TMRCA of 330 to 660 years, with a bias towards the lower end of the range. In other words, our most confident estimate might be that the MRCA of this group lived between 1300 and 1700, with a bias towards the latter end of that time period.

Observations on Origin

The earliest ancestors in the group are John of Ireland (44944), who was born around 1760, and John of Vermont (91181), who died in 1801. John of Vermont's son David was born in 1788, so John of Vermont may have been born in the 1760s or before and therefore was probably a contemporary of John of Ireland. It seems likely that the common ancestor of the whole group must have lived at least two generations before these two Johns, since it would be rare for there to be two sons named John in a single family. Given a generation-length of 25 to 30 years, that would mean the latest the common ancestor of the whole group could have been born would be the early 1700s/late 1600s.

The location of the most recent common ancestor may have been northern Ireland, given that three out of four participants trace their ancestry there. In particular, 44944 and 56896 both trace back specifically to Donegal and they both have the names Alexander and Robert in their lines, which may hint at a very recent common ancestor. Participant 56896's line remained in Europe and moved to Scotland from Ireland in recent times. There appears to be a clear northern bent to those who moved to America: 91181's line migrated to Vermont, 44944's to Michigan, and 84477's to Ontario.

Group 3 is not a match with Group 1, which contains the descendants of the Barnbarroch Vans/Vance line. The average genetic distance between the groups on 37 markers is 15, which indicates an extremely low probability of a common genetic descent within the surname time frame of 1000 years. Here is a chart showing the 50% TMRCA estimates generated for the groups using FTDNA's mutation rates:

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Time to Most Recent Common Ancestor (Years)																							
ID	m	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	l	3	3	3	
	o	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	a	b	a	b	c	
	d																						
	a																						
modal	67	360	330	210	300	300	210	150	210	150	210	90	150	90	210	210	150	930	1140	840			
1a	360	37	210	360	630	540	450	360	540	540	360	300	450	360	540	540	360	1260	1500	1140			
1b	330	210	67	150	450	360	270	330	510	450	360	270	330	330	360	450	330	1260	1500	1140			
1c	210	360	150	67	300	300	270	330	390	330	360	270	210	270	210	300	330	1140	1380	1050			
1d	300	630	450	300	37	210	210	300	300	450	300	360	360	360	120	210	300	930	1140	840			
1e	300	540	360	300	210	37	120	300	300	450	360	360	360	360	300	360	450	1050	1260	930			
1f	210	450	270	270	210	120	67	210	270	330	300	270	270	270	300	360	330	1050	1260	930			
1g	150	360	330	330	300	300	210	67	210	270	360	90	270	150	360	360	150	840	1050	720			
1h	210	540	510	390	300	300	270	210	67	270	360	270	330	270	360	360	330	840	1050	720			
1i	150	540	450	330	450	450	330	270	270	67	360	210	270	210	360	360	270	1050	1260	1050			
1j	210	360	360	360	300	360	300	360	360	360	37	300	360	300	210	210	210	1050	1260	930			
1k	90	300	270	270	360	360	270	90	270	210	300	67	210	90	300	300	90	930	1140	840			
1l	150	450	330	210	360	360	270	270	330	270	360	210	67	210	300	210	270	1140	1380	1050			
1m	90	360	330	270	360	360	270	150	270	210	300	90	210	67	300	300	150	930	1140	840			
1n	210	540	360	210	120	300	300	360	360	360	210	300	300	300	37	120	210	1050	1260	930			
1o	210	540	450	300	210	360	360	360	360	360	210	300	210	300	120	37	210	1050	1260	930			
1p	150	360	330	330	300	450	330	150	330	270	210	90	270	150	210	210	67	930	1140	840			
3a	930	1260	1260	1140	930	1050	1050	840	840	1050	1050	930	1140	930	1050	1050	930	37	300	300			
3b	1140	1500	1500	1380	1140	1260	1260	1050	1050	1260	1260	1140	1380	1140	1260	1260	1140	300	37	360			
3c	840	1140	1140	1050	840	930	930	720	720	1050	930	840	1050	840	930	930	840	300	360	37			

The mean 50% TMRCA estimate is 1110 years, which is only barely approaching the era of the Norman Conquest, when the archaic version of the surname (Vaux) was supposed to have arrived in England. Furthermore, there are a few assumptions involved in this estimate which might tend to make the estimate seem younger than it actually is. One of these assumptions is that all the shared values between the groups indicate inherited values. That may not be the case. Another assumption is that when marker values differ by several steps, it may be the result of a single mutation. There are two markers where the modal values of the groups differ by 2 steps and one where the modal differs by at least 3 steps. If these steps are the result of separate mutations, it would have the effect of skewing all the estimates much farther back in time. For these reasons, it seems highly unlikely that Groups 1 and 3 share a genetic descent in the 1000-year timeframe during which the surname has been in use. The greater likelihood is that group 3 arose from a non-paternity event sometime between 1300 and 1700 or that the surname Vance arose independently in their ancestry for some reason.