

Vance Y-DNA Project – Special Report on Groups 1 and 2
By Adam Bradford (adam.bradford@gmail.com)

The purpose of this report is twofold: to assess the likelihood that the common genetic ancestor of Groups 1 and 2 in the Vance Y-DNA Project had some version of the same surname; and to assess the validity of the theory that all Vances descend genealogically (not just genetically) from a single source.

Are Groups 1 and 2 Related?

Groups 1 and 2 are clearly related in that they share a common ancestor. The question at issue is not whether they share an ancestor, but whether that ancestor bore some version of the root surname. It matters a great deal to both groups whether their most recent genetic ancestor was, say, a nobleman from Galloway named Vans or a Norman warrior named de Vaux, or whether he was an Iberian hunter-gatherer living just after the last ice age. What we're trying to establish is the possibility of the first two types of relatedness, that is, a common descent in the direct male line in the time the surname has been in use.

Groups 1 and 2 in the Vance project are for all intents and purposes identical on 12 markers and impossible to distinguish from each other. They are just barely distinguishable on 25 markers, since the genetic distance between the modal haplotypes of each group is only 2 or 3. However, on 37 markers there are more differences, enough to suggest that the two groups haven't shared a common ancestor for a very long time, perhaps not within a surname time-frame. The 67 marker panel contains mostly slow-mutating markers and on those markers the participants *within* each group are all virtually identical to each other. However, there is a large genetic distance of 7 *between* the groups on that panel. Thus, the 67 marker results tend to confirm the relatedness of the participants within each group, but they tend to strengthen the impression of a very deep split between the lineages of the two groups. Normally, this split would be too large to warrant the conclusion that the groups are related. However, unlike many surnames which didn't come into use until the late middle ages, the Vance surname is supposed have a very ancient lineage in the British Isles, stretching all the way back to the Norman Conquest in 1066. Now that we have several participants in each group tested on 67 markers and have numerous participants in each group, it is high time we try to estimate whether they might have shared a common ancestor in the direct-male line in this time frame. This in turn will allow us to assess the validity of the Vance legend of common descent from a single origin.

The Vance Legend

As the story goes, members of the Norman de Vaux family accompanied William the Bastard on his conquest of England, and one or more of these men gave rise to all the various Vaux families of England as well as the later Vaus who were lords of Dirleton, of which the Barnbarroch line is a cadet branch. The Vance surname is supposed to have arisen later in Ireland from an offshoot of the Barnbarroch line. Actually, the full narrative begins before Normandy. According to Playfair in "Baronetage of Scotland," the Norman de Vaux were descendants of a man from a Provencal de Baux family invited to take up lands in Normandy in 929 at the invitation of the duke. Prior to that, the de Baux are supposedly found in Provence as early as 749. The accompanying legend of Visigothic descent may be due to the fact that the Visigoths were granted the governance of Aquitaine, where Provence is located, as

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federate allies of the Roman government in 418 AD. Clearly some parts of this legend are more believable than other parts, but that is the legend.

The legendary narrative implies that all those men who claim descent from the original de Vaux who came over during the Conquest should descend from one man who held the name Vaux. Their Y chromosome DNA should therefore all come from this same source and the fact that there was a single origin of the surname within the last 1000 years should theoretically be supported by the DNA evidence. In other words, barring the occasional event like an adoption or infidelity, and barring phenomena like the Anglicization of unrelated German Wentz and Wantz to Vance, the DNA evidence should reflect a single origin. I imagine everyone is curious as to what the DNA might have to say on this issue, and one of the purposes of the project is to assess the evidence from that perspective. We are handicapped in this pursuit by the lack of participants who are not Vances or Vans. We have 1 Vose and 1 Vaus in the project. The other 68 participants, 97% of the whole, have the name Vance or Vans. To really assess the truth of the legend of common descent, we need to have DNA evidence from more Vaus, Vaux, and Vose men who claim descent from the lines that remained in England. However, for the purpose of gauging whether all Vances come from a single source, we may have as much information as we need, since all the Vance lines (as opposed to Vaux, &c) are supposed to have been from Ireland or Scotland as recently as the 1500s.

McGee Analysis

To assess the likelihood of a common Vance or Vaux descent between Groups 1 and 2, I entered the haplotypes of all those in both groups who have tested at least 37 markers into a program created by Dean McGee (<http://www.mymcgee.com/tools/yutility.html>) for estimating the time to the most recent common ancestor (TMRCA) for a given set of haplotypes. I opted to use primarily the estimates arrived at using FTDNA's per-panel mutation rates. The first chart contains estimates of the age at which the probability is 50% that the TMRCA is no longer than indicated; the second contains estimates of the age at which the probability is 95% that the TMRCA is no longer than indicated. Again, we are trying to gauge how likely it is that these individuals share a common descent within the surname time-frame, which is about 700 years for Barnbarroch and about 1000 years for de Vaux. The time frame for the Vances is supposed to be more like 500 years. The year estimates are arrived at by calculating generations at the rate of 30 years per generation. Hence an estimate of 450 years means 15 generations. An assumption of, say, 25 years per generation instead of 30 would result in estimates that are 17% smaller across the board, but it turns out that this difference wouldn't significantly alter the overall conclusions.

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Time to Most Recent Common Ancestor – 50% Probability - FTDNA Mutation Rates

ID	m	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
	o	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a
	d	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
modal	67	450	270	270	300	210	300	150	150	330	390	330	120	270	270	270	120	210	210	630	720	540	900	840	840	540	540	540	900	540	810	1050	840					
1a	450	37	210	360	360	630	540	450	450	360	540	540	360	300	450	360	540	540	360	1050	1140	930	1050	930	930	930	930	930	1050	1050	1140	1140	1050					
1b	270	210	67	150	210	450	360	270	270	330	510	450	360	270	330	330	360	450	330	840	930	720	1110	1050	1050	720	720	720	1110	840	1020	1350	1050					
1c	270	360	150	67	60	300	300	270	270	330	390	330	360	270	210	270	210	300	330	930	840	840	1200	1110	1110	840	840	840	1050	840	1140	1200	1140					
1d	300	360	210	60	37	300	300	300	300	360	360	360	360	300	210	300	210	300	360	930	840	840	930	840	840	840	840	840	720	840	1050	930	1140					
1e	210	630	450	300	300	37	210	210	210	300	300	450	300	360	360	360	120	210	300	840	720	720	840	720	720	720	720	630	720	930	630	840						
1f	300	540	360	300	300	210	37	120	120	300	300	450	360	360	360	360	300	360	450	930	930	840	930	840	840	840	840	840	840	840	1050	840	930					
1g	150	450	270	270	300	210	120	67	30	210	270	330	300	270	270	270	300	360	330	840	930	720	1050	990	990	720	720	720	1050	720	1020	1050	840					
1h	150	450	270	270	300	210	120	30	67	210	270	330	300	270	270	270	300	360	330	840	930	720	1050	990	990	720	720	720	1050	720	1020	1050	840					
1i	330	360	330	330	360	300	300	210	210	67	210	270	360	90	270	150	360	360	150	1050	930	930	1200	1110	1110	930	930	930	1050	1050	1230	990	840					
1j	390	540	510	390	360	300	300	270	270	210	67	270	360	270	330	270	360	360	330	930	840	840	1110	1050	1050	840	840	840	990	840	1140	840	720					
1k	330	540	450	330	360	450	450	330	330	270	270	67	360	210	270	210	360	360	270	1050	930	930	1200	1110	1110	930	930	930	1050	930	1230	1050	1050					
1l	120	360	360	360	360	300	360	300	300	360	360	360	37	300	360	300	210	210	210	720	840	630	720	630	630	630	630	720	630	840	720	720						
1m	270	300	270	270	300	360	360	270	270	90	270	210	300	67	210	90	300	300	90	930	840	840	1110	1050	1050	840	840	840	990	930	1140	1050	930					
1n	270	450	330	210	210	360	360	270	270	270	330	270	360	210	67	210	300	210	270	1050	930	930	1200	1110	1110	930	930	930	1050	930	1230	1110	1140					
1o	270	360	330	270	300	360	360	270	270	150	270	210	300	90	210	67	300	300	150	840	720	720	1050	990	990	840	720	720	900	930	1020	1050	840					
1p	120	540	360	210	210	120	300	300	300	360	360	360	210	300	300	300	37	120	210	720	630	630	720	630	630	630	630	540	630	840	720	930						
1q	210	540	450	300	300	210	360	360	360	360	360	360	210	300	210	300	120	37	210	840	720	720	840	720	720	720	720	630	720	930	720	930						
1r	210	360	330	330	360	300	450	330	330	150	330	270	210	90	270	150	210	210	67	840	720	720	1050	990	990	720	720	720	900	840	1020	990	840					
2a1	630	1050	840	930	930	840	930	840	840	1050	930	1050	720	930	1050	840	720	840	840	37	210	120	210	210	300	210	210	300	360	360	840	630						
2a2	720	1140	930	840	840	720	930	930	930	840	930	840	840	930	720	630	720	720	210	210	37	300	360	210	300	360	300	210	450	450	630	630						
2a3	540	930	720	840	840	720	840	720	720	930	840	930	630	840	930	720	630	720	720	120	300	37	120	120	120	120	120	210	300	300	720	540						
2a4	900	1050	1110	1200	930	840	930	1050	1050	1200	1110	1200	720	1110	1200	1050	720	840	1050	210	360	120	67	150	150	300	210	210	270	360	360	570	540					
2a5	840	930	1050	1110	840	720	840	990	990	1110	1050	1110	630	1050	1110	990	630	720	990	210	210	120	150	67	90	210	120	120	210	300	270	450	450					
2a6	840	930	1050	1110	840	720	840	990	990	1110	1050	1110	630	1050	1110	990	630	720	990	210	300	120	150	90	67	120	60	60	150	210	210	510	540					
2a7	540	930	720	840	840	720	840	720	720	930	840	930	630	840	930	840	630	720	720	300	360	210	300	210	120	37	120	120	210	210	300	720	630					
2a8	540	930	720	840	840	720	840	720	720	930	840	930	630	840	930	720	630	720	720	210	300	120	210	120	60	120	37	60	120	210	210	720	540					
2a9	540	930	720	840	840	720	840	720	720	930	840	930	630	840	930	720	630	720	720	210	300	120	210	120	60	120	60	37	120	210	210	720	540					
2a10	900	1050	1110	1050	720	630	840	1050	1050	1050	990	1050	720	990	1050	900	540	630	900	300	210	210	270	210	150	210	120	120	67	300	360	510	630					
2a11	540	1050	840	840	840	720	840	720	720	1050	840	930	630	930	930	630	720	840	360	450	300	360	300	210	210	210	210	300	37	360	720	720						
2a12	810	1140	1020	1140	1050	930	1050	1020	1020	1230	1140	1230	840	1140	1230	1020	840	930	1020	360	450	300	360	270	210	300	210	210	360	360	38	930	720					
2b1	1050	1140	1350	1200	930	630	840	1050	1050	990	840	1050	720	1050	1110	1050	720	720	990	840	630	720	570	450	510	720	720	510	720	930	67	360						
2b2	840	1050	1050	1140	1140	840	930	840	840	840	720	1050	720	930	1140	840	930	930	840	630	630	540	540	450	540	630	540	540	630	720	720	360	37					

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[The modal haplotype represented in these charts in the far left column and the top row is more accurately described as the modal of Group 1; it is skewed towards Group 1 since that group has more participants in the chart than Group 2.]

Group 1 TMRCA Data

The 50% estimates for TMRCA among the participants in Group 1 are in the 100 to 600 year range, with the average estimate being 300 and the mean estimate 350 years. Group 1's 95% estimate (which we may take to mean the point past which it becomes highly unlikely that the MRCA lived) ranges from 180 to 1080 years, with the average being 600 and the mean 630 years. This is fully supportive of a descent within the total Barnbarroch time frame of 700 years and also supportive of a descent within the 500 years during which the Vance and Vans lineages are supposed to share a common ancestor.

Group 2 TMRCA Data

The spread of estimates within Group 2 is greater, mainly because Group 2 contains two subgroups with a rather deep split between them. The 50% estimates within Group 2a range from 60 to 450 years, but the range of the whole group (obtained by comparing the 2a haplotypes only with the 2b haplotypes) is from 450 to 930 years, due to the genetic distance of 4 found between the ancestral haplotypes of 2a and 2b. The mean age is 690 years. Likewise, the 95% range for Group 2a extends from 300 to 840 years, but the range for the whole group extends in some cases back to 1470 years. The mean age estimate in the 95% range is about 1125 years. Note that Group 2 appears to be significantly older than Group 1, due primarily to the split between 2a and 2b.

TMRCA Data for Both Groups

When it comes to comparing the two groups with each other, the estimates are obviously much larger. In the 50% probability chart, the TMRCA estimates for groups 1 and 2 range from 630 to 1350 years, with the average being between 850 and 900 years and the mean being about 1000 years. The 95% estimates range from 960 to 1920 years, with the average being around 1100 years and the mean 1440. Estimates to the modal are shorter – 540 to 1050 for the 50% estimates (795 mean) and 960 to 1530 for the 95% estimates (1245 mean) – but this comparison is somewhat artificial, since all the Group 1 participants have at least two (and most have more) mutations separating them from the modal. In other words, comparing to the modal is like comparing present-day Vances to the MRCA of Group 1, who lived several hundred years ago; this cancels out much of the time differential between the modal estimate and the other estimates. These estimates would seem to make a descent from the Conquest era a bare possibility, with a descent from the Barnbarroch founder a very remote possibility, and anything later than the Barnbarroch founder extremely improbable.

Other assumed mutation rates yield much older estimates and put the relatedness of the groups at the outer margins of probability. Below is the chart of 50% estimates obtained using McDonald's rates (I have removed a few haplotypes from the chart in the interest of conserving space). The 50% estimates just barely overlap the time-period of the Norman Conquest and don't support a descent

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from Barnbarroch at all. The average and mean are in the 1400 to 1500 year range. I won't include the 95% estimates, but will mention that they range from 1680 to 3090 years and are mostly over 2000 years.

Time to Most Recent Common Ancestor (Years) - 50% - McDonald Rates																																			
ID	m	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	2	2	2	2	2	2	2	2	2	2	2	2	2			
	o																			1	2	3	4	5	6	7	8	9	0	1	2	1	2		
	d																			a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
modal	67	810	390	390	510	360	510	210	210	480	570	480	240	390	390	390	240	360	300	1110	1290	960	1350	1260	1260	960	960	960	1350	960	1440	1560	1440		
1a	810	37	360	660	660	1110	960	810	810	660	960	960	660	510	810	660	960	960	660	1800	2010	1620	1800	1620	1620	1620	1620	1620	1800	1800	2010	2010	1800		
1b	390	360	67	210	360	810	660	390	390	480	750	660	660	390	480	480	660	810	480	1440	1620	1290	1680	1560	1560	1290	1290	1290	1680	1440	1800	2010	1800		
1c	390	660	210	67	90	510	510	390	390	480	570	480	660	390	300	390	360	510	480	1620	1440	1440	1800	1680	1680	1440	1440	1440	1560	1440	1980	1800	2010		
1d	510	660	360	90	37	510	510	510	510	660	660	660	660	510	510	810	510	660	660	1620	1440	1440	1620	1440	1440	1440	1440	1440	1440	1440	1440	1440	1800	1620	2010
1e	360	1110	810	510	510	37	360	360	360	510	510	810	510	660	660	660	240	360	510	1440	1290	1290	1440	1290	1290	1290	1290	1290	1290	1110	1290	1620	1110	1440	
1f	510	960	660	510	510	360	37	240	240	510	510	810	660	660	660	660	510	660	810	1620	1620	1440	1620	1440	1440	1440	1440	1440	1440	1440	1440	1800	1440	1620	
1g	210	810	390	390	510	360	240	67	60	300	390	480	510	390	390	390	510	660	480	1440	1620	1290	1560	1470	1470	1290	1290	1290	1560	1290	1800	1560	1440		
1h	210	810	390	390	510	360	240	60	67	300	390	480	510	390	390	390	510	660	480	1440	1620	1290	1560	1470	1470	1290	1290	1290	1560	1290	1800	1560	1440		
1i	480	660	480	480	660	510	510	300	300	67	300	390	660	150	390	210	660	660	210	1800	1620	1620	1800	1680	1680	1620	1620	1620	1560	1800	2190	1470	1440		
1j	570	960	750	570	660	510	510	390	390	300	67	390	660	390	480	390	660	660	480	1620	1440	1440	1680	1560	1560	1440	1440	1440	1470	1440	1980	1260	1290		
1k	480	960	660	480	660	810	810	480	480	390	390	67	660	300	390	300	660	660	390	1800	1620	1620	1800	1680	1680	1620	1620	1620	1560	1620	2190	1560	1800		
1l	240	660	660	660	660	510	660	510	510	660	660	660	37	510	660	510	360	360	360	1290	1440	1110	1290	1110	1110	1110	1110	1110	1290	1110	1440	1290	1290		
1n	390	810	480	300	360	660	660	390	390	390	480	390	660	300	67	300	510	360	390	1800	1620	1620	1800	1680	1680	1620	1620	1620	1560	1620	2190	1680	2010		
1o	390	660	480	390	510	660	660	390	390	210	390	300	510	150	300	67	510	510	210	1440	1290	1290	1560	1470	1470	1440	1290	1290	1350	1620	1800	1560	1440		
1p	240	960	660	360	360	240	510	510	510	660	660	660	360	510	510	510	37	240	360	1290	1110	1110	1290	1110	1110	1110	1110	1110	960	1110	1440	1290	1620		
2a1	1110	1800	1440	1620	1620	1440	1620	1440	1440	1800	1620	1800	1290	1620	1800	1440	1290	1440	1440	37	360	240	360	360	360	510	360	360	510	660	660	1440	1110		
2a2	1290	2010	1620	1440	1440	1290	1620	1620	1620	1620	1440	1620	1440	1440	1620	1290	1110	1290	1290	360	37	510	660	360	510	660	510	510	360	810	810	1110	1110		
2a3	960	1620	1290	1440	1440	1290	1440	1290	1290	1620	1440	1620	1110	1440	1620	1290	1110	1290	1290	240	510	37	240	240	240	360	240	240	360	510	510	1290	960		
2a4	1350	1800	1680	1800	1620	1440	1620	1560	1560	1800	1680	1800	1290	1680	1800	1560	1290	1440	1560	360	660	240	67	210	210	510	360	360	390	660	630	840	960		
2a5	1260	1620	1560	1680	1440	1290	1440	1470	1470	1680	1560	1680	1110	1560	1680	1470	1110	1290	1470	360	360	240	210	67	150	360	240	240	300	510	510	660	810		
2a6	1260	1620	1560	1680	1440	1290	1440	1470	1470	1680	1560	1680	1110	1560	1680	1470	1110	1290	1470	360	510	240	210	150	67	240	90	90	210	360	360	750	960		
2a9	960	1620	1290	1440	1440	1290	1440	1290	1290	1620	1440	1620	1110	1440	1620	1290	1110	1290	1290	360	510	240	360	240	90	37	240	360	360	1290	960				
2a10	1350	1800	1680	1560	1290	1110	1440	1560	1560	1470	1560	1290	1470	1560	1350	960	1110	1350	510	360	360	390	300	210	360	240	240	67	510	630	750	1110			
2a11	960	1800	1440	1440	1440	1290	1440	1290	1290	1800	1440	1620	1110	1620	1620	1620	1110	1290	1440	660	810	510	660	510	360	360	360	360	510	37	660	1290	1290		
2a12	1440	2010	1800	1980	1800	1620	1800	1800	1800	2190	1980	2190	1440	1980	2190	1800	1440	1620	1800	660	810	510	630	510	360	510	360	360	630	660	38	1620	1290		
2b1	1560	2010	2010	1800	1620	1110	1440	1560	1560	1470	1260	1560	1290	1560	1680	1560	1290	1290	1470	1440	1110	1290	840	660	750	1290	1290	1290	750	1290	1620	67	660		
2b2	1440	1800	1800	2010	2010	1440	1620	1440	1440	1440	1290	1800	1290	1620	2010	1440	1620	1620	1440	1110	1110	960	960	810	960	1110	960	960	1110	1290	1290	660	37		

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Which set of mutation rates is more trustworthy?

Clearly there is a great 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 mini-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 every instance more accurate. If they were to be used as a guide, we might have the most confidence in an estimate between the 50% and 95% mean estimates, with a frequent bias towards the 50% mean and some support for the overall estimate from the 50% range of the McDonald 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 FTDNA'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.

Again, if these four mini-studies are anything to go by, we might have the most confidence in an estimate between the mean 50% and mean 95% estimates given by FTDNA, and trending closer to the 50% mean. In terms of the relatedness of Groups 1 and 2, that means we might have the most confidence in a TMRCA estimate of between 1000 to 1440 years, with a bias towards 1000 years. This is also at the lower end of the range of the 50% estimates obtained using McDonald's rates. This happens to be supportive of a common ancestor in the era of the Norman Conquest or before, but not too much after.

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Analysis of DNA Evidence

Maybe it should suffice for our purposes to note that the probabilities are not enough to demolish the idea of a descent from someone who might have had the root surname of de Vaux or a variant. However, one thing to keep in mind is that all the participants in Group 2 bear the name Vance and that those in Group 2 who are able to trace back to Europe trace back to Ireland. The surname Vance is peculiar among Vaux-derived surnames in that it is supposed to be of relatively recent, Irish origin. The first man thought to have carried the surname was the Rev. John of Ireland, who lived there in the 1600s. According to the legend, all Vances are supposed to descend from him. One would think that if Group 2 split off from Group 1 farther back in time, they would carry some other version of the surname. Then again, it may also be possible that anyone with the name Vaus, Vausse, etc., upon moving to Ireland, might find the pronunciation of their name changed to Vance. Without further knowledge, it's hard to tell how much weight this Vance/Ireland factor should have. It would be interesting to gather more evidence on the morphology of Vaux-related surnames in early America and in Ireland. Spelling of the same family's name often varies from document to document and seems to have been very much dependent on local pronunciation. If an English (as opposed to Scottish) origin can be found for any of the participants in Group 2 prior to 1600, that might provide some support for the idea of a common de Vaux descent from the Conquest, which would not be incompatible with the DNA evidence.

It may also be that the two groups do not share a common genetic ancestor for several thousand years or more. One of our assumptions in the foregoing is that all shared marker values are inherited values. This assumption is necessary for the sake of the analysis, but it may be that this assumption is false and that several of these values are not inherited in common. In other words, it may be that the two lineages represented by Groups 1 and 2 underwent a series of mutations which have happened to make them appear more related than they are. If even one or two markers turn out to match by state (that is, an accidental match through the vagaries of mutation), and not by descent, that would skew all the age estimates considerably farther back in time and make a common genetic descent since 1000 AD unlikely. This interpretation is by no means unlikely, since both groups have the 12-marker Atlantic Modal Haplotype, the most common haplotype among males of western European descent and the one most prone to accidental matches. Further, there is not a lot of leeway in the TMRCA estimate, since 1000 years is as old as the surname is supposed to be in Britain. Even the slightest factor which might have the effect of skewing the estimates farther back in time would effectively serve to discount the possibility of a common genetic descent within the surname timeframe. One of these factors might be an assumption I have made in the above estimates that when there is a genetic distance of more than 1 between the groups on any single marker, that distance may be accounted for by just a single mutation. This is called the *infinite alleles* model of mutation. If we were to assume the *step-wise model*, in which each difference is accounted for by a mutation, then the estimates would certainly be skewed much farther back in time and would make a common descent unlikely. This is due to the three-step difference between Groups 1 and 2 on marker DYS456 and to two-step differences on two different markers in the 67 marker panel.

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Monogenesis of Vance and Related Surnames

For the purposes of determining the likelihood that the Vance surname had a single origin, it might be useful to look at a summary of the results of a study done of the Sykes surname, theorized by some to also be a surname with a single origin:

“A randomly ascertained sample of males with the surname “Sykes” was typed with four Y-chromosome microsatellites [i.e., STR markers]. Almost half the sample shared the same Y-chromosome haplotype, which has not been observed in control samples from the same geographic region or from the United Kingdom as a whole. This points to a single surname founder for extant Sykes males, even though written sources had predicted multiple origins. The distribution of other Sykes Y-chromosome haplotypes were not significantly different from those in controls and may be accounted for by the historical accumulation of non-paternity during the last 700 years, in which case the average rate estimate is 1.3% per generation. If this pattern is reproduced with other surnames, it may have important forensic and genealogical applications.”

Note that 700 years (the time the Sykes surname is supposed to have been around) is about the age of the Barnbarroch Vaus line. As the name Vance is supposed to come purely from the Barnbarroch line, Sykes’ study might provide a good benchmark for judging whether or not the DNA project supports the idea that all Vances come from a single source.

We have Y-DNA results for 67 individuals. Four of these men are not Vances, but joined the project because they believed they might be descended from a Vance due to a non-paternity event. We can remove them from consideration. We can also remove from consideration the 3 participants of Group 7, who are almost certainly descended from a German Wentz line. (In this sense, we already know that Vance is a multiple-origin surname, because some portion of American Vances will turn out to be descended from Germans whose names were Anglicized.) Removing the non-Vances and the known Germans from consideration leaves 60 individuals. We also have four participants who have only tested to 12 markers, but who might prove to match one of our big groups when they have more markers tested. We should also remove them from consideration so as not to bias the study. That leaves 56 participants. Out of these 56 participants, 38 of them may be placed in two large groups of related Vances – Groups 1 and 2. Group 3 consists of four participants, and groups 4, 5, and 6 consist of two each. The rest are non-matching individuals. So we have 2 very large groups, 1 small-to-medium-sized group, 3 pairs, and 8 non-matching individuals. Each of the pairs traces back to a single ancestor who lived in the 1700s; if we lump them together with the non-matching individuals we get a big/medium/small ratio of 2/1/11 or a big/small ratio of 2/12. This is exactly the sort of ratio one might expect to see in a single-source surname study that goes back roughly 10 to 15 generations. The reason for this has to do with the accumulation of non-paternity events, which are simply events that cause a descendant’s Y DNA to differ from his surname father’s Y-DNA.

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Non-paternity

Like mutation rates, non-paternity rates vary from study to study. The most generally accepted rates seem to be in the 1.3% to 2.5% range. Since it simplifies the calculations involved, let us assume a 2% non-paternity rate. A rate of 2% means there ought to be 2 non-paternity events out of every 100 transmission events. Let us also assume 2 transmission events per person per generation (i.e., the progenitor has two sons, his sons each have two sons, and so on). After 7 generations, there will have been 96 transmission events and about two of these should have been non-paternity events. Given that there are 64 descendants in the 7th generation, and continuing to assume 2 transmission events per person, there should therefore be at least 100 transmission events in the 8th generation alone, and theoretically two of these would be non-paternity events. In other words, there should be as many non-paternity events in the 8th generation alone as there were in all 7 previous generations. Regardless of the specific assumptions of the model (i.e., the precise non-paternity rate, the number of transmission events per generation, etc.) the pattern should be the same. That is, in terms of a sample of living men with a single-origin surname, we should expect to see just one or a few large groups (the genetic descendants of the original progenitor plus those non-paternity branches that arose in the first several generations), and a much greater number of small groups or non-matching individuals who have arisen in more recent generations. That is, in fact, the general pattern observed in the Vance project.

Let us assume the project has a representative sample of Vances and that the surname has a single origin. If all but the Group 1 participants are the heirs of a non-paternity lineage, that would mean that the majority of descendants today (66%) are descended from non-paternity events. That percentage of non-paternity participants is much greater than we'd expect to see with a single origin surname according to the data from the Sykes project, in which about half the men tested had the same unique haplotype. However, one of our assumptions is probably not true and highlights a large difference between the Vance and Sykes studies. That is, the Sykes study selected men at random, whereas the Vance project has not. As a result, certain lineages are not necessarily represented proportional to their share of the total Vance population. This is probably the case with Group 2.

Group 1 and Group 2 have an equal number of participants – 19. Yet Group 1 has about 10 distinct lineages that go back to 1750 without encountering a common ancestor. In Group 2, on the other hand, there are just 2 or 3 distinct lineages that go back that far. Moreover, six of the Group 2 participants (about a third of the total) descend from Matthew Vance of Pittsylvania; and the five participants in Group 2b (about a quarter of the total) seem to consist entirely of the descendants of Samuel Vance/Agnes Penquite. In other words, 59% of Group 2 can probably be traced back to just two individuals who lived in the mid-1700s. There are good reasons for this. In the case of Matthew of Pittsylvania, there happens to be a very passionate and engaged group of genealogists among his descendants. In the case of Samuel Vance/Agnes Penquite, three of the participants were selected for testing by the Sorensen Molecular Genealogy Foundation - they are more heavily represented essentially because James Vance of McDonough was an early

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immigrant to Utah. So the sample we have in the Vance project is not random and in fact there is every indication that a truly random sample would result in more people in Group 1 and less people in Group 2. If that were the case, Group 1's size may approach or exceed the 50% mark seen in the Sykes study and would then support the theory of a single origin for the surname. In either case, the ratio of large groups to small groups/individuals in the Vance Y-DNA Project seems basically consistent with a single origin.

Age of Group 2 and Its Effect on Relatedness Between Groups 1 and 2 and Descent of Group 2

On the topic of whether Groups 1 and 2 have a common genetic Vaux descent, there is another factor to consider. An analysis of Groups 2a and 2b indicates that those two subgroups probably don't share a common ancestor before 600 years ago, at a minimum. It would therefore be extremely unlikely that the non-paternity event happened within the Vance timeframe of 500 years. That would mean that the group got the name Vance or a variation of it prior to the time when the Vance surname was supposed to have arisen. In that case, it would mean there was a stronger likelihood that the Vance surname did not arise from one man in the 1500s, but that the Vance spelling or pronunciation might have happened independently in other Vaus lines that made it to Ireland. Since the MRCA of Group 2 may have lived around 1300-1400, it could be that Group 2 was the result of a non-paternity event in the Barnbarroch line or before and adopted the surname independently (whether once or twice), or it may be that they are true genetic and surname relatives from the Conquest and that the reason the group is so relatively small is because we are only seeing the Vance tip of the English Vaux iceberg, so to speak. The difficulty with the genetic distance between Groups 1 and 2 is that it is just close enough to make a common Vaux descent possible, but not close enough to inspire much confidence. This issue of the age of Group 2 also has a bearing on my conclusion that its two subgroups share a common origin within the surname. There is a possibility that the genetic ancestor of both subgroups had a surname other than Vance/Vans/Vaus, yet two of whose descendants happened to be involved in two different non-paternity events within the Vance surname. I won't venture to say whether this is more or less likely than the other scenarios. It is enough to admit the possibility, since there are as yet no clear answers.

To summarize, according to the estimates presented above a common genetic descent between Groups 1 and 2 from the original John Vaus of Barnbarroch (1300s) is extremely unlikely. A common genetic descent from the Conquest-era is possible only if several assumptions are correct, namely that shared values are inherited values and that certain markers have undergone multi-step mutations. If we accept a common surname descent for Groups 2a and 2b, then a common surname (as opposed to genetic) descent for Groups 1 and 2 is unlikely in the period after 1300, though it is possible at the beginning of the Barnbarroch line and becomes more plausible farther back in time. However the fact that a common Vance surname descent is so unlikely should give us pause when considering the conclusion that Groups 2a and 2b share a common genetic *and* surname ancestor.

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Three Plausible Scenarios

Given the above, three main scenarios present themselves as plausible interpretations of the evidence.

Scenario 1: Group 1 represents the genetic descendants of the progenitor of the Vans-Vance line, perhaps Sir Patrick Vans (d.1597). Group 2 arose from a Vaus line (whether Scottish or English) by a non-paternity event that occurred in the 1400s or earlier and adopted the surname Vance independently of Group 1. Or it may also be that the two branches of Group 2 represent two non-paternity events in the Vance line and that the genetic fathers in both cases happened to share a relatively recent genetic ancestor. As for the rest in the project, Group 3 probably arose from a non-paternity event prior to the mid 1700s, Groups 4 through 6 from non-paternity events in the mid-to-late 1700s or before, and the other non-matching participants may have arisen from more recent non-paternity events. It is also possible that some of the non-matching groups or participants are descended from German Wentz.

Scenario 2: Another plausible interpretation is the same as the first in all respects but one, namely that Group 2 did not arise from a non-paternity event, but rather represents a line of English Vaux who share a genetic descent with Group 1 going back to the Norman Conquest.

Scenario 3: It is possible that one or more of the Vance lineages in the project who don't match Group 1 did not arise from non-paternity events, but that the surname arose independently of the Barnbarroch or older lineages for reasons we can't discern. For instance, I have seen at least one source describe the origin of the surnames Vance and Vann as being tied to the old English word "fenn," indicating that the ancestor who first adopted the surname might have lived near a swamp. According to another source, in Middle English "vance" meant a "dweller at the windmill." It is enough to admit these as possibilities. I won't venture to gauge their likelihood.

In order to better tell which of these scenarios is more likely, we will need to test more Vaux, Vaus, &c men who claim descent from the English de Vaux. Currently we have just a single Vaus in the project, representative of a lineage that claims descent from the same Norman source as the Barnbarroch line. His DNA (which doesn't match any of the other participants) can't carry the weight of the entire English branch. If even one English Vaus line comes back as a match of some kind with Groups 1 or 2, the picture will change. Other surnames with a tradition of descent from the English de Vaux are Fox and Strickland, both of which happen to have associated DNA projects. I will save a comparison of those projects with the Vance project for a future report.

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Appendix: Other Matching Surnames:

Although I didn't incorporate it in the report, I thought it would be of interest to include the following information on men of different surnames who are close matches with Groups 1 and 2 on 25 or more markers. These matches may provide a clue as to the deeper origins of the surname. I don't want to assign too much importance to these matches, since they are not quantifiable and since the information on the origin of the surname is not necessarily accurate or reliable. However, they ought to be included as part of the larger picture. The information on the surname origin was obtained from heraldry websites and other online sources.

Group 1 Matches: 25-Marker

Trenor/Traynor	Ireland, Co. Clare
Edwards	Wales, Denbigshire
Burt	England, Norfolk (Conquest)
Egan	Ireland, Tipperary
Hooks	England, Devonshire
Durgin	Scotland, Dumfreeshire
Polhemus	German, Swiss, Dutch
Pena	Spain, Castille
McPhillips	Wales
Wynn	Wales
Davidson	English/Scottish/Welsh
McGregor	Scotland, Argyllshire
Glover	Eng., Norfolk; Scot., Perthshire
Wilson	English/Scottish/Irish

Group 1 Matches: 37-Marker

Francoeur	France
Davidson	Welsh, Scot, English – Yorkshire
Henderson	English, Scottish
Horne	England, Durham
Young	England, Somersetshire; Scot Borders
Hindmarch	England, Northumberland
Kelly	SW Ireland
Moffitt	Scot., Dumfreeshire
Hamilton	Scot., Renfrewshire
Glenn	Peebleshire
McKnight	Scotland, Kirkcudbright
Curtis	England, Warwickshire

Group 1 Matches: 67-Marker

McClain/McLean	first in western Isles	Glendenning/Clendennen/Clendaniel	England, Roxburgshire
Batten	England, Somerset (Conquest)	Pryor	England, Derbyshire (Conquest)
Dugger	Germany, Westphalia	Ferguson	Scotland, Galloway
McIntyre	Scotland, Argyllshire	Thomson	Scotland, Ayrshire
Curry	Scotland, Midlothian	Robertson	Scotland, Perthshire
Elliot	Scotland/Ireland	Drew	England, Gloucestershire

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On both 25 and 37 markers, Group 1 has an even split between English and Scottish surname matches. However, on 67 markers the Scot matches outnumber the English by a factor of 7 to 3.

Group 2 Matches: 25-Marker

Iszard	England, Gloucestershire (Conquest)	Neubert	England, Wiltshire
Pierce	England, Somerset	Allen	England, Shropshire (Conquest)
Hudgens	England, Northumberland	Barnaby	England, Yorkshire
Pidcoe	England, Somerset	Hopper	England, Durham
Coberly	England, Buckinghamshire	Howard	England, Cumberland
Lake	England, Oxfordshire (Conquest)	McVitty	Scotland, Ayrshire and Galloway
Ingram	England, Northumberland	Adams	Scotland, Annandale
Payne	England, Sussex (Conquest)	Owen	Wales, Montgomery
Freeman	England, Essex; Ireland, Cork	Powell	Wales
Culver	England, Herefordshire	Henry	French/Irish?
Wilson	English/Scottish/Irish	Poteet	France, Berry
Earp	England, Lincolnshire	Huebner	Bavaria

Group 2 Matches: 37-Marker

Whalen	Ireland
Hutson	England, Yorkshire

Group 2 has overwhelmingly English matches, several with surnames that were supposed to have arrived with the Conqueror. There are surprisingly few Scottish matches. In fact, the English names outnumber the Scottish by 17 to 3. The one Irish match of Whalen is actually so close that I wouldn't be surprised if it turned out to be the result of a non-paternity event involving a Group 2 ancestor in Ireland.