

Vance/Vans Y-DNA Project – Analysis of Results

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Overview of Participants

The Vance/Vans Y-DNA Project currently has 26 participants. Of these 26 participants, results are in for 25. We have been able to determine that 6 of these 25 participants are probably not related to any of the other participants in the project. We have determined that another 5 may be related to others in the project, but we can't say for sure until we can compare them on more markers. We have divided the remaining 14 participants into three groups, based on the probability of them having a common descent. In the course of this report, I'll touch on all these participants in greater detail.

<u>Participant</u>	<u>Classification</u>	<u>Earliest Vance Ancestor</u>
• 39200	Group I	John Vaus of Barnbarroch (d.aft.1384)
• 39128	Group I	Rev. James Vance of Frederick Co., VA (d.aft.1829)
• 44884	Group I	James Vance of Orange Co., NY (d.aft.1799)
• 43864	Group I	Samuel Vance of Surry Co., NC (d.1789)
• 39459	Group I	Patrick Vance (d.1803, Knox Co., TN)
• 38105	Group II	Robert Vance of Roan Mt. (1784-1855)
• Sor1	Group II	Robert Vance of Roan Mt. (1784-1855)
• 45791	Group II	James Vance (d.1835, McDonough Co., IL)
• Sor2	Group II	James Vance (d.1835, McDonough Co., IL)
• Sor3	Group II	James Vance (d.1835, McDonough Co., IL)
• Sor5	Group II	James Vance (d.1835, McDonough Co., IL)
• 33023	Group III	James Cowan (b.1777, MD)
• 10000	Group III	James Williams (b.1787, Bowdoin, ME)
• 15403	Group III	James Williams (b.1787, Bowdoin, ME)
• 44166	Possibly Related	Maj. William Vance (d.1788, PA)
• N21545	Possibly Related	Thomas M. Vance (d.1862, Cannon. Co., TN)
• 48374	Possibly Related	Thomas Vance of Gallia Co., OH (b.c.1820)
• 47531	Possibly Related	John Vance (b.1773, Frederick Co., VA)
• N20182	Possibly Related	Robert Vance (b.c.1810, TN) m.Sina Brewer
• 39021	Ungrouped	David Vance (d.1880, Butler Co., PA)
• 47042	Ungrouped	Hugh Vance (d.1839, Knox Co., TN)
• N8118	Ungrouped	Patrick Vance (d.c.1805, Henderson Co., KY)
• 4828	Ungrouped	Jeptha Israel (?son of David Vance of Buncombe?)
• 44944	Ungrouped	John Vance (b.c.1760) m.Mary Allison
• 48973	Ungrouped	John Vance (d.1860/70, Washington Co., AR)
• 54198	Results Pending	William M. Vance (1826) m.Nancy Wortham

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WAMH R1b Participants

There is a certain group of 16 participants in the Vance/Vans Y-DNA Project who are within a genetic distance of 1 from each other on 12 markers. (This group includes the participants we've placed in Group I and Group II, as well as a handful of others whom we can't place in either group until we have seen their upgraded results.) All of these participants either have, or are 1 mutation off from, the most common haplotype yet observed, called the Western Atlantic Modal Haplotype (WAMH). They all know how extremely common WAMH is, because they've seen that they match hundreds of other individuals in FTDNA's database who have different surnames. This kind of mass matching doesn't happen in most cases. For instance, I personally didn't get any matches on 12 markers until two years after I tested, and when I did get a match it was with someone of the same surname – a distant cousin I never knew I had.

So what is this WAMH and why is it so common? WAMH is an acronym for Western Atlantic Modal Haplotype. It is so called because it is found in its highest concentrations on the Atlantic seaboard of Europe. Those who have this haplotype belong to haplogroup R1b, which is the most common haplogroup in Western Europe (you can think of a haplotype as a subsection of a haplogroup). The frequency of R1b in southern England is about 70%. In parts of Spain and Ireland, over 90% of the population is R1b. It is thought that R1b represents a lineage from the first modern humans to colonize Europe. The prevailing theory is that during the last ice age Europeans retreated to various refuges in the south of Europe. One particular area has been identified from archaeological and climatological evidence as a likely refuge for R1b – the Pyrenees of southern France and northern Spain, which happens to be precisely one of the regions where R1b is currently at its highest concentration. As the ice melted, (from 15,000 to 10,000 years ago) this group of humans spread northward and recolonized western Europe. As wave after wave of future invaders came into Europe from the east, the genetic scene in central and eastern Europe became more mixed, but less so in the far west where the invaders and migrants didn't penetrate as thickly. It is thought that this accounts for the high concentration of R1b in the more isolated areas of Western Europe, such as the Pyrenees and the British Isles. For an illustration of how common R1b is in Western Europe, see the diagram on page 2 of this web document (R1b is colored red):

<http://www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf>

As for WAMH's place in R1b, WAMH is simply the most common haplotype in western European R1b. In fact, WAMH may be the most common haplotype in the world. At the very least, it is the most common haplotype observed among those who have had their Y chromosome tested, whether for scientific or genealogical purposes. It has been suggested that about 1.5% of all western European males may share the identical WAMH 12 marker Y-DNA signature. If we include those who are a genetic distance of 1 from WAMH, the percentage is even higher. The simplest explanation for why WAMH is so common is that there once lived a man many thousands of years ago who had this particular DNA signature, and he had numerous children. His children in turn were very successful at spreading their genes, and their children in turn, and so on.

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The extreme commonality of WAMH R1b poses some problems for us when it comes to interpreting DNA results. Quite simply, we can't get any truly reliable use out of WAMH results on anything less than 37 markers. A lot of WAMH R1b individuals will be close matches on 12 markers, and even close matches on 25 markers – but upon comparing them on 37 markers, it becomes apparent that they are not all related to each other in genealogical time. For this reason, if anyone's 12-marker, or even 25-marker, results come back as WAMH R1b, or very close to it, we simply don't feel we can use these results to determine anything in genealogical time. Unfortunately, for WAMH R1b the only really useful test in genealogy is the 37 marker test. We learned this firsthand in the Vance/Vans project. We started out with a group of four participants who were all very close matches on 12 markers. Since they were WAMH R1b, we encouraged them to upgrade to 25 markers so we could see if the match still held – and it did. Just to be safe we then upgraded them all to 37 markers. At that point we found that they actually constituted two distinct groups which were probably unrelated to each other – we've labeled them Group I and Group II.

Dividing the WAMH R1b Participants into Related Groups

The first thing we had to do when dividing the WAMH R1b participants was decide what constitutes a “match”. In other words, how closely do two people need to match before we place them in the same group as probably related?

Given the long time frame involved with the Vance/Vans surname (39200's lineage goes back to John Vaus of Barnbarroch, who lived in the 1300s), we have chosen to be more generous with interpreting genetic distance than one might normally be. It is probable that some lines branched off 500 years ago or more, and that when they branched off their surname was already established.

Our rule of thumb has been to include people in a group as possibly related if they are within a genetic distance of 6 on 37 markers. This is a large genetic distance, normally too large for us to comfortably say two people are related. But, again, given the timeframe involved, we are trying to err on the side of inclusiveness. On the results page of the website we've grouped together those participants whom we are comfortable saying are probably related and given them the same color. Any participants who are a little too distant for comfort, but whom we feel are probably still related, are marked with a different shade of the same color, to differentiate them but still point out that we're viewing them as part of the larger group.

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Group I (violet on the website)

This is our largest group of potentially related participants, with 5 individuals. A sixth individual matches them very closely on 25 markers, but we are waiting for upgraded 37 marker results before finally including him in this group. There are a few others who might belong in this group, but who only have 12 marker results. Until they upgrade we can't determine whether to place them in Group I, Group II, or in an entirely different group. Right now, we can only analyze the 5 who have upgraded to 37 markers.

Genetic Distance

There are two ways to look at the DNA results: in terms of genetic distance, and in terms of mutations. These may seem like the same thing, but they're not necessarily.

Here's the genetic distance report for the 5 participants we've grouped together and named Group I:

39200 – John Vaus of Barnbarroch (d.aft.1384)

Genetic distance of 6 from 39128, 39459, 43864, 44884

39128 – Rev. James Vance (b.Frederick Co., VA – d.aft.1829, Jefferson Co., KY)

Genetic distance of 4 from 43864, 44884

Genetic distance of 6 from 39200, 39459

39459 – Patrick Vance (b.c.1745, prob. Ireland – d.1803, Knox Co., TN)

Genetic distance of 4 from 44884

Genetic distance of 6 from 39128, 43864, 39200

43864 – Samuel Vance (d.1789, Surry Co., NC)

Genetic distance of 3 from 44884

Genetic distance of 4 from 39128

Genetic distance of 6 from 39200, 39459

44884 - James Vance (d.aft.1799; lived in Orange Co., NY) m.Martha

Genetic distance of 3 from 43864

Genetic distance of 4 from 39128, 39459

Genetic distance of 6 from 39200

Taking the genetic distance on its own, we can say with some confidence that 39128, 39459, 43864, and 44884 probably share a common ancestor. All of them are within 4 mutations of one of the others.

Here's what FTDNA has to say about a genetic distance of 4 on 37 markers:

“33/37 You share the same surname (or a variant) with another male and you mismatch by four 'points' --a 33/37 match. Because of the volatility within some of the markers this is about the same as being 11/12 and it's most likely that you matched 23/25 or 24/25 on previous Y-DNA tests [NOTE: this is true with our Group

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I participants]. If you matched exactly on previous tests you probably have a mismatch at DYS 576, 570, CDYa or CDYb in our newest panel of markers [NOTE: this is also true with our Group I participants]. If several or many generations have passed it is likely that these two lines are related through other family members. That would require that each line had passed a mutation and one person would have experienced at least 2 mutations. The only way to confirm is to test additional family lines and find where the mutations took place. Only by testing additional family members can you find the person in between each of you...this 'in betweener' becomes essential for you to find, and without him the possibility of a match exists, but further evidence must be pursued. If you test additional individuals you will most likely find that their DNA falls in-between the persons who are 4 apart demonstrating relatedness within this family cluster or haplotype.”

Therefore we are prepared to say that Reverend James Vance of Frederick County (d.1829, KY), Patrick Vance (d.1803, TN), Samuel Vance (d.1789, NC), and James Vance (d.aft.1799, NY) all probably descend from a common Vance/Vans ancestor in the direct male line.

39200's results indicate that he is more distantly related: he is a genetic distance of 6 from all the others in this group, which normally indicates a very low probability of a common descent in a genealogical timeframe. It is thought that the Irish Vances branched off from the Scottish Vans's in the 1500s or 1600s, yet a genetic distance of 6 tends to indicate a much earlier separation, several centuries before. Yet, we have seen firsthand that FTDNA's time estimates can sometimes be either too big or too small. For that reason, and because of the strong tradition held on both sides of the Atlantic that many American Vances descend from Irish Vances who were themselves descendants of the Barnbarroch Vans's – we have chosen to include 39200 in this group. It is possible (in fact, we think it likely) that a participant might join in the future whose results bridge the genetic distance between him and the others.

Group I – Phylogenetic Tree

Having established from genetic distance that these participants are probably related to each other, we decided to take a more detailed look at the genetic distance by examining the actual results and plotting out the mutations on a phylogenetic tree.

The first thing we did was remove from consideration all those markers on which the group all had the same value. Since no mutations appear to have occurred on those markers, we don't need to factor them into our analysis. We then plotted out the remaining markers in a table, as follows:

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	390	458	459b	464c	607	576	570	CDYa	CDYb
39128	24	18	10	17	15	19	17	38	39
43864	24	19	9	15	15	18	17	38	39
39200	23	19	10	17	16	18	17	39	40
39459	24	19	10	17	15	17	18	38	41
44884	24	19	10	16	15	18	18	38	39

The first thing we were looking for was what value at each particular marker was the most common value. This is called the *modal value*. When we plot out the results on a tree, the modal will be like the hub of a wheel, and all the other participants will branch off from it like spokes. If this group shares a common ancestor, then the modal value is probably the value their Most Recent Common Ancestor (MRCA) had. Until we can determine exactly how these participants are related, we can't tell for sure that the modal value represents the MRCA's value – but that is the assumption.

After finding the modal values, we highlighted all the values that differed from the modal, as you can see in the above chart. It is presumed that these represent mutations from the modal value, and it is these differences which will make up the branches of the phylogenetic tree.

The next thing we looked for was whether any two or more individuals shared a value that the others didn't. We noticed one instance of this right away: 39459 and 44884 both have the value 18 at DYS570, whereas the others all have the value of 17. This is exactly the sort of pattern we look for when analyzing DNA results – it may be an indication that they constitute a distinct branch from the others, and that their common ancestor is more recent than the common ancestor of the whole group.

After taking a look at all the mutations in the above chart, the final step is to create a phylogenetic tree to represent all the mutations graphically. The tree is a good way of showing how mutations might have occurred. It allows us to visualize the genetic distance between the participants.

NOTE: The phylogenetic tree does not necessarily represent the way the mutations actually happened, it only represents a way they might have happened. Though it can't at this point be viewed as definitive, the phylogenetic tree is a very helpful tool when trying to get a better grasp of the situation. As more participants join who match this group the picture will become clearer.

I want to point out three things before presenting these trees.

1) at marker 576, participants 39459 and 44884 have the same value, implying that they might share a branch of the tree;

2) at marker 464c, participant 44884 has the value 16 and participant 43864 has the value of 15, suggesting that they might share a branch of the tree. (In other words, their ancestor experienced the mutation from 17 to 16, and then one of 43864's more recent ancestors experienced the mutation to 15);

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3) at marker CDYb, participant 39200 has the value of 40, and 39459 has the value 41, implying that they might be on their own branch. (In other words, their ancestor experienced the mutation from 39 to 40, and then one of 39459's more recent ancestors experienced the mutation to 41);

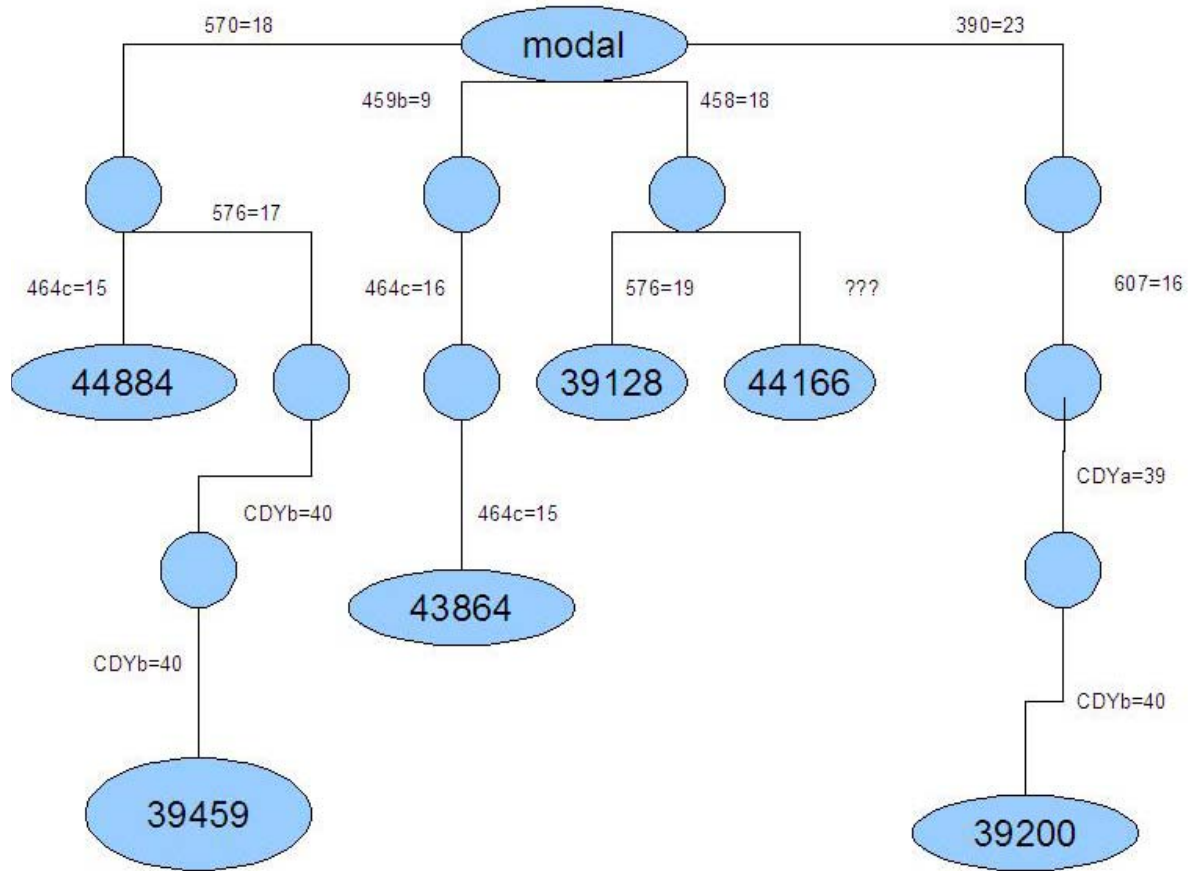
The problem with the above three scenarios is that they are not compatible with each other. If 44884 and 39459 are placed on their own branch due to the shared value at DYS 570, that means they both experienced independent mutations in their lineages at 464c. Likewise, it means that 39459 and 39200 would have experienced an independent mutation at CDYb. These kinds of mutations, where two people who descend from a common ancestor share the same mutation, but where the mutation happened separately in each of their lineages, are called *parallel mutations*. This phenomenon has been well documented in other projects.

Because of these incompatibilities we had to create more than one tree, to reflect the different ways these mutations might have happened.

NOTE: 37 marker results are not yet in for participant 44166. However, given his exact match with participant 39128 on 25 markers, and the fact that they both share the value of 18 at 458, I'm provisionally placing him on these trees. As soon as the 37 marker results are in, I will adjust the trees accordingly.

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TREE I

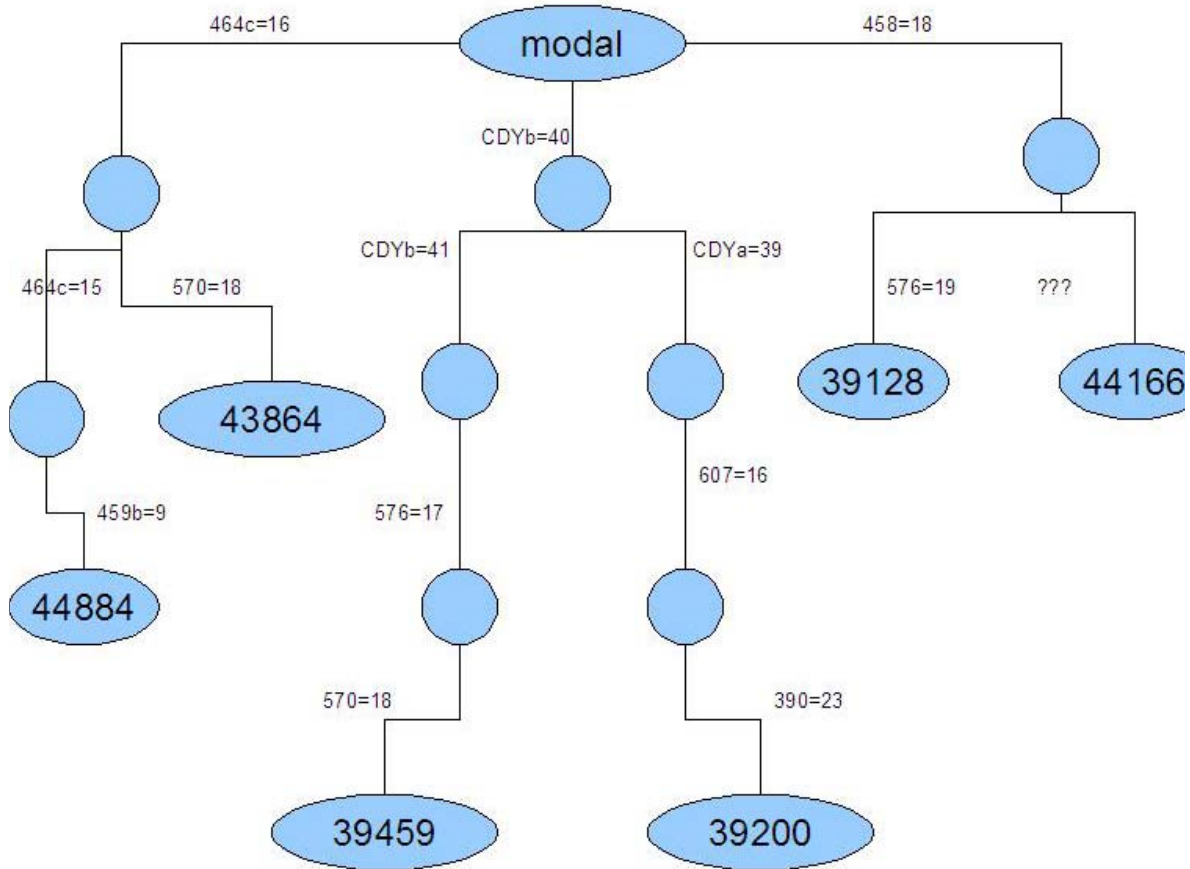


NOTE: the final segment leading up to 39459 should read CDYb=41, not CDYb=40

As you can see, in this tree we are assuming that both 44884 and 39459 experienced a mutation in common at DYS 570, from 17 to 18. Assuming this wasn't a parallel mutation, it means 44884 and 39459 may share a common ancestor more recent than the common ancestor of the whole group. Also, note that 39128 and 44166 share the mutation at DYS 458 from 19 to 18, implying that their most recent common ancestor (MRCA) is more recent than the common ancestor of the whole group. Again, we need to compare 44166 on 37 markers to be sure.

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TREE II



Tree II presents a different picture of the way these mutations might have occurred. The relationship of 39128 to 44166 is the same as in the first tree. But one big difference between the trees is that Tree II assumes that 44884 and 43864 share a common ancestor more recent than the common ancestor of the whole group due to a shared mutation at *DYS* 464c. Tree II also assumes that the mutation at *CDYb* from 39 to 40 was shared by 39459 and 39200, implying that they share a common ancestor more recent than the common ancestor of the whole group.

These trees illustrate that the picture we gained of this group by looking at the genetic distance alone was a bit misleading. In Tree I, 44884 and 43864 have a genetic distance of 5, whereas in Tree II they have a genetic distance of only 3. Also, in Tree I, 44884 and 39459 have a genetic distance of 4, whereas on Tree II they have a genetic distance of 6. It goes to show that it's always more revealing to look at a group as a whole, rather than compare participants on a one-on-one basis. Assuming the whole group is related, we have to take into account how they all relate to each other, not just how they relate individually.

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One large assumption behind these trees (an assumption which may turn out to be false) is what the ancestral values are. Again, the modal value is presumed to indicate the value their common ancestor had. However, this is not necessarily the case. For instance, the ancestral value at marker DYS 390 might have been 23, in which case all the other participants but 39200 would have experienced a mutation from 23 to 24 at that marker, while 39200's line did not. This change in the ancestral value would not affect the genetic distance between the participants, but it might affect the branching patterns and therefore it might affect how we interpret the Y-DNA results genealogically. For instance, if the ancestral value of 458 was 18 rather than 19, we could not conclude that 39128 and 44166 share a common ancestor more recent than the common ancestor of the whole group; though the genetic distance between them would be the same, they would instead be on separate branches of the tree. In most cases, however, the modal value is the value of the common ancestor.

Two more things about these trees:

If we were really to present a full picture of the different ways these mutations might have happened, we would need to include a tree in which all the participants are on separate branches – since it is entirely possible that all the shared mutations assumed in the trees above were actually parallel mutations. This would have the effect of making all the participants seem more distant. We don't actually believe this is the case, which is why I haven't included such a tree. Given the fact that they all have the same surname, we would expect that some, if not all, shared mutations indicate a shared descendant. Still, this possibility of parallel mutations is something to keep in mind.

Also – there should be an alternate version of each tree which takes into account the phenomenon of *multi-step mutations*. A *multi-step mutation* is when a marker mutates more than one step in a single mutational event. In other words, 39459's mutation to 41 at CDYb normally requires that we first include a mutation from 39 to 40. However, it has been observed that sometimes markers will mutate more than one step in a single event. In other words, in 39459's lineage the mutation from 39 to 41 might constitute a single mutation rather than two separate mutations. The same goes for 43864: at 464c there might have been just a single mutation from 17 to 15, rather than two. This would have the effect of shortening their true genetic distance. These kinds of mutations are rare, but they do happen. Because of their rarity, we haven't made any trees which take multi-step mutations into account. But any time you see a two-step mutation in one of these trees, you should be aware that even though the genetic distance is two, it may involve just a single mutation.

At this point, I realize a lot of you might be a bit confused by all the technical details I'm throwing at you, and frustrated by all the different possibilities of interpretation. Believe me, I know how you feel. I do wish this was less complicated. The bottom line is we believe from looking at the DNA evidence that Group I is most likely related. And these trees, and this detailed look at the DNA, is all part of our effort to try to figure out exactly *how* they might be related. That's what this project is all about – comparing as many Vances as possible until we can place them on different branches and start getting an idea of when certain Vances branched off from others, thereby getting closer to finding the common ancestor of the various branches. I'm confident that the more participants join the project, the more of them

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we'll be able to place in this group, and the clearer and more detailed the picture will become. It has already become a lot more detailed than it was in the beginning.

There is one further circumstance that leads us to believe this group is related. The vast majority of the genetic distance we observe in Group I can be accounted for on markers which have been observed to mutate at a faster rate than other markers. These markers are colored red on the results page of the website. When genetic distance is primarily due to differences on fast markers, it tends to strengthen the probability of a relationship. This is another reason why we're more tentative about placing 39200 in this group: his genetic distance includes markers which have been found to mutate more slowly.

Possible Conclusions Based on DNA Comparison

1) 44884 (James Vance, d.aft.1799; lived in Orange Co., NY) and 39459 (Patrick Vance, b.c.1745, Ireland, emigrated 1754 to PA, d.1803, Knox Co., TN) may share a common ancestor who is more recent than the common ancestor of the whole group. This would be due to a shared mutation to 18 at DYS 570. Accepting this possibility necessarily excludes the following possibility:

2) 44884 (James Vance, d.aft.1799; lived in Orange Co., NY) and 43864 (Samuel Vance, d.1789, Surry Co., NC) may share a common ancestor who is more recent than the common ancestor of the whole group. This would be due to their shared mutation at 464c from 17 to 16 for both, then from 16 to 15 for 43864. Again, if this interpretation is true, then interpretation 1 must be false.

3) 39200 (John Vaus of Barnbarroch) and 39459 (Patrick Vance, b.c.1745, Ireland, emigrated 1754 to PA, d.1803, Knox Co., TN) may share a common ancestor who is more recent than the common ancestor of the whole group. This would be due to their shared mutation at CDYb from 39 to 40 for both, then from 40 to 41 for 39200. This may indicate that his line branched off from the Barnbarroch Vans's earlier than the others. This interpretation necessarily excludes interpretation 1, but is compatible with interpretation 2.

4) Assuming 44166's 37 marker results support this conclusion, it appears very likely that he (Major William Vance, b.1718, Scotland - d.1788, PA) and 39128 (Rev. James Vance, b.c.1776, Frederick Co., VA - d.aft.1829, Jefferson Co., KY) share a common ancestor who is more recent than the common ancestor of the whole group. This would be due to their shared value of 18 at DYS 458.

Overall Conclusions

All the above participants except 39200 are American Vances, most of whom have a tradition of descent from Scotch-Irish Vances. 39200 represents the ancestral lineage of Barnbarroch, from whom many Scotch-Irish Vances are thought to descend. Therefore, we would expect him to be more distantly related to the American Vances than they are to each other. It turns out this is consistent with the DNA evidence as presented in Tree I. We believe the Y-DNA results indicate that Group I is most likely descended from the Barnbarroch line, going back to John Vaus of Barnbarroch (d.aft.1384).

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Still, 39200's genetic distance from the others is never less than 6. A genetic distance of 6 on 37 markers indicates about a 54% chance of sharing a common ancestor in the last 19 generations. Reckoning a generation at about 30 years, that means that the probabilities don't start to tip in favor of a common ancestor until we go back 570 years, to the 1400s. This is definitely a lot earlier than the Irish Vances are supposed to have branched off from the Scottish line. For this reason, we are presenting 39200's results along with this group, but shading his results differently to indicate that we're not completely comfortable saying they are related. We're simply trying to be cautious about our interpretations, so as not to lead ourselves or any of you astray. There are two reasons we're placing him in this group, even though the genetic distance between him and them is so great. First, there is the tradition of American Vance descent from the Barnbarroch Vans. Also, we have observed firsthand from looking at Group II's results that FTDNA's standard rate of mutation (which is generally reliable) can in specific cases be much slower than actual rates of mutation. (See our discussion of Group II for more on how we discovered this.)

The phylogenetic trees we've presented are starting to reveal some potential branching patterns. In particular, we've seen that 44884 probably shares a branch with either 43864 or 39459. Also, 39128 and 44166 probably share a branch, as we're hoping 44166's 37 marker upgrade will reveal. As other Vances join the project who end up belonging in this group, and as more current participants upgrade who match the group on 12 marker, the picture will change again and resolve itself into greater detail. Another way to better resolve this picture is to try to find the *ancestral haplotype* held by each participant's earliest known ancestor.

A Word About Ancestral Haplotypes

Our Y-DNA signature is not necessarily the same as our ancestor's Y-DNA signature. In fact, the farther back in time that ancestor lived, the greater the chances of our own Y-DNA being different, due to mutations having occurred. It can be extremely useful in Y-DNA testing to figure out the exact Y-DNA signature of your ancestor, called the *ancestral haplotype*. This can often be done by testing someone who descends from a different son of your ancestor. If you both match exactly, then we know your DNA is the same as your ancestor's. If you are different, then we have two possibilities for what your ancestor's Y-DNA looked like. At that point, testing a third cousin descended from a different son would provide the answer, or we might be able to hazard a guess based on which value is closest to the others in your group. We realize that for many lineages it is not feasible to find the ancestral haplotype. Sometimes there is only one surviving male line. In other cases (as with 39200) the ancestor simply lived so long ago that tracking down descendants from other sons is pretty much impossible. Still, this is often something to aim for. The 4 participants in Group II who are descended from James Vance of McDonough Co., IL, provide an example of a deduced ancestral haplotype (see below).

If it is possible to do so, we would like to test results from other descendants of Group I's ancestors to find the ancestral haplotypes. In the meantime, even though this analysis has revealed nothing conclusive, those participants who find themselves sharing a branch on the phylogenetic tree might wish to begin using that as a clue in their research.

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Group II (blue on the website)

This group consists of 6 participants from two different lineages.

38105 and SOR1 - Robert Vance of Roan Mountain, TN (1784-1855)

45791, SOR2, SOR3, and SOR5 – James Vance of McDonough Co., IL (1764-1835)

It is not yet clear to us 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 our comfort. For this reason we have portrayed them on the website in different shades of blue. However, we have chosen to group them together for two reasons. First, right now our level of resolution between the lineages is low, since we can only compare 2 of them on 37 markers – 38105 and 45791. It may be that if we were to test all 6 on 37 markers, the genetic distance between them would diminish.

The 4 participants labeled SOR are not actually participants in the project. They are men who were tested by the Sorensen Molecular Genealogy Foundation (SMGF) and whose results we found in the SMGF database and incorporated into our project. Since SMGF does not test all the same markers as FTDNA, we can't make a full comparison on 37 markers. 45791 was formerly known as SOR4. We were able to get in touch with him and get him to join the project so that we could make a full comparison between him and 38105, which revealed the genetic distance of 7. We would really like to test the remaining SOR participants, to see if any of them might bridge the genetic distance.

The other reason we're including these two lineages in a single group is the values they have on marker DYS 456. We have been able to deduce that James Vance of McDonough had the value 19 at DYS 456, and that Robert of Roan Mountain had the value 20. These values are extremely rare in R1b. A gentleman by the name of Whit Athey conducted a study of marker values in R1b to determine their frequency and found that the values of 19 and 20 (the defining values for the two lineages in Group II) were not even present in his sample. This indicates an extreme level of rarity in both lineages. The rare values these lineages have at DYS 456 hint at the possibility of a common descent, in which one of the lineages experienced a one-step mutation at DYS 456.

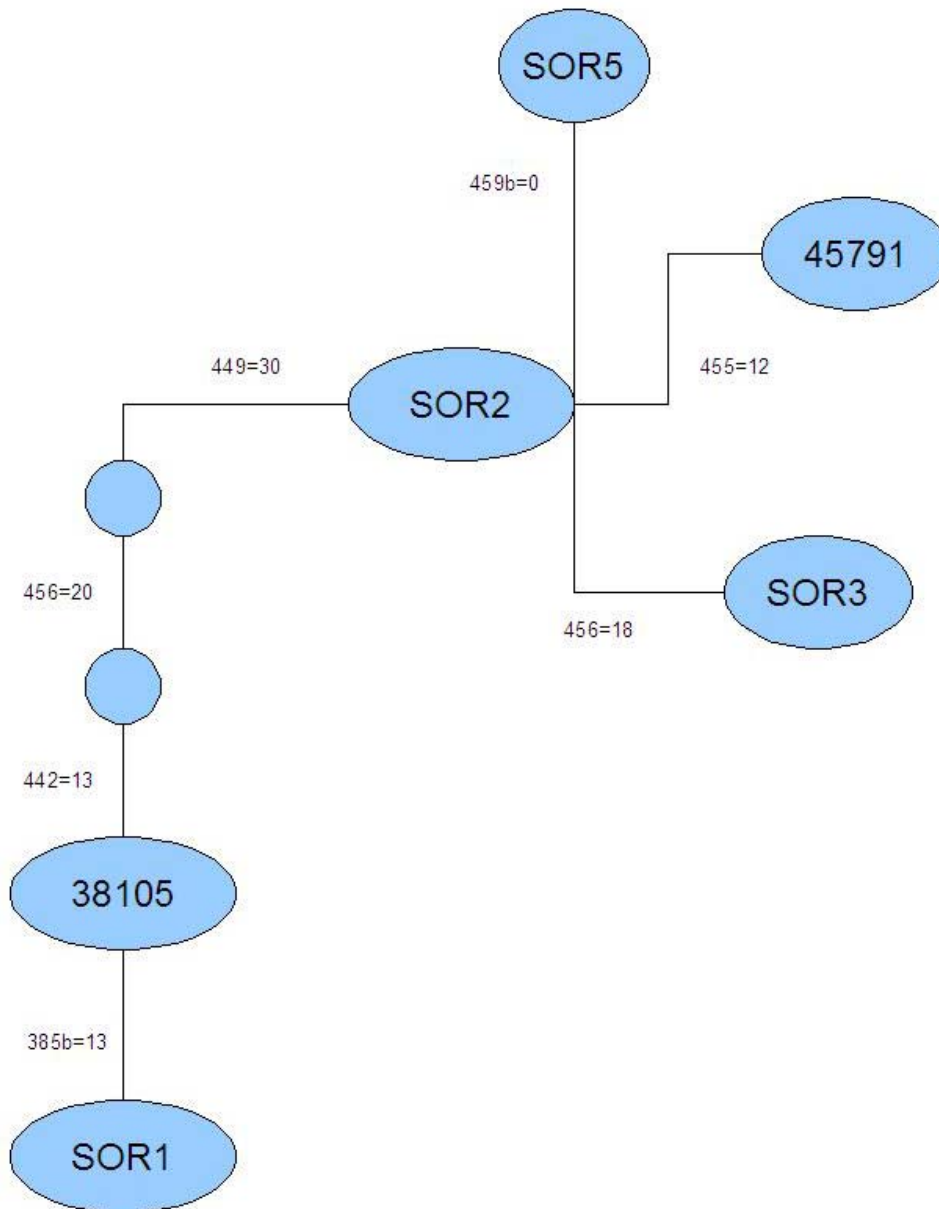
Moreover, marker DYS 456 has been observed to mutate very slowly, which is why we feel confident this group is not related to Group I, who all have the value of 16 at DYS 456. For a slow-moving marker to mutate from 16 all the way to 19 or 20, would take a very long time. Unless a multi-step mutation happened on that marker, the chance of a relationship between Group II and Group I is extremely slim. However, we are not discounting the possibility of a multi-step mutation occurring. If other evidence accumulates to hint at a genetic relationship between Group I and Group II we will alter our analysis.

Group II provides another illustration of how there are more ways to use DNA evidence than simply looking at genetic distance as reported by FTDNA. We have already seen how plotting out mutations on a phylogenetic tree can alter and complete the picture in ways not foreseen. Now we can also see that looking at the rarity of specific marker values can help

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distinguish groups from one another, and lead us to tentatively group together individuals whom we might otherwise have kept apart.

Here is a phylogenetic tree illustrating the genetic distance between the participants of Group II. This Tree takes into account a comparison of the whole group on the 23 markers which they have tested in common. Again, since we only have 37 marker results for 2 of the participants, we can't compare the whole group on 37 markers. If and when the SOR participants join the project, we will be able to compare the whole group on 37 markers, and this picture will become more detailed.



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I want to point out two things by taking a closer look at the descendants of James Vance of McDonough. First, from looking at the James Vance group, we are able to show that FTDNA can sometimes overestimate the number of generations to most recent common ancestor. Second, we have been able to deduce the ancestral haplotype of James Vance's descendants, effectively discovering what James Vance's actual Y-DNA signature was.

First, observe that SOR5, 45791, and SOR3 are all a genetic distance of 1 from SOR2 on 23 markers; yet they are all a genetic distance of 2 from each other. Now, we happen to know this group of participants all descend from James Vance of McDonough in either 6 or 7 generations. Yet, suppose we didn't know this, and suppose SOR2 wasn't in the picture. We would then have three participants who are all a genetic distance of 2 from each other. This is certainly enough for us to start considering them probably related, but according to the standard mutation rate, the probability of them sharing a common ancestor in 7 generations is only about 23%. For these descendants of James Vance of McDonough, we can clearly see that FTDNA's mutation rate is not fast enough to account for the genetic distance we can observe. This is another reason we have chosen to be more inclusive in general when grouping participants.

Here's the second thing I'd like to point out by using the James Vance of McDonough descendants as an example. Many people think that if they have tested themselves, then their ancestor is spoken for, that they can accurately represent their ancestor's DNA, and that when they compare their DNA with another participant, it's like comparing their ancestor's DNA with the DNA of that person's ancestor. Of course, that's not necessarily the case; both participants' Y chromosomes may have undergone mutations. However, by testing one or two cousins it is possible to discover what your common ancestor's DNA looked like. Then when one makes a comparison with another participant, it will be like you are comparing your ancestor's actual Y-DNA. Since we have results from 4 of James Vance of McDonough's descendants, through two different sons, we can actually say what James Vance's Y-DNA signature was, and can now use those values and compare them with participants from other lineages, knowing that we are comparing the actual Y-DNA signature of James Vance himself. It turns out that SOR2 represents the exact Y-DNA signature of James Vance of McDonough on 23 markers. No mutations have occurred in his line on those 23 markers.

We can almost deduce the ancestral haplotype of Robert Vance of Roan Mountain on 23 markers. We have descendants of his from two different sons, and one observed mutation between them. By testing a descendant of a third son we would be able to determine in which line that mutation occurred. Robert Vance either had the value of 13 or 14 at 385b. If he had the value of 14, which is James Vance of McDonough's value, then we could say for sure that James Vance and Robert Vance themselves were a genetic distance of 3 from each other on 23 markers. We would like to involve all the SOR participants in our project and test them on 37 markers, because a large portion of the genetic distance between 45791 and 38105 occurs in FTDNA's third panel of markers, which SMGF does not test. By testing the SORs on these markers, we might find we can bridge the gap between James Vance of McDonough and Robert Vance of Roan Mountain.

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Group III

Group III consists of the following three participants:

15403 and 10000 (27 markers) - James Williams (b.1787, Bowdoin, ME)

These participants, a father and son, do not have the surname Vance. They began the project with reason to suspect they may be ultimately descended from a John Vance, who was born about 1763 in Philadelphia. They do not have the surname Williams either. They were fairly confident that they were descended from a James Williams of Bowdoin, Maine. However, testing of one of James Williams's descendants revealed they were not related to him. They can't be sure of this until testing another descendant of James Williams from a different son.

Interestingly, these two reveal a case of a mutation happening between father and son.

33023 (37 markers) - James Cowan b. 1777, MD

This participant is a genetic distance of 3 on 27 markers from participant 10000, the father of 15403. Interestingly, 33023's middle name is Vance. His great-grandmother Mary Ann "Mollie" Vance was the daughter of a John A. Vance and married William Thomas Cowan. This John A. Vance was born around 1715-1720 and died (probably killed by Indians) in 1759 in Bedford Co., VA. His wife was Martha (surname unknown). John and Martha Vance left two orphan boys: John Vance Jr. (b.c.1752 - d.bef.Sept.1794, Sullivan Co., TN) and Jacob Vance (b.c.1754 – d.1814, Giles Co., TN). As yet, it is unknown whether the genetic relationship between 33023 and the other two is a coincidence or whether they share a common descent. Obviously, since they match no other Vances in the project, it is also unclear yet whether their common descent (if they have it) is from a Vance.

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Possibly Related Participants

These participants may be related to either Group I or Group II. Until they have tested on the full 37 markers, we do not feel comfortable including them in either group.

44166 (25 markers, 37 pending) - Major William Vance (b.1718, Scotland - d.1788, PA)

This participant is an exact match on 25 markers with 39128. We are expecting 37 marker results for him in a few months. We believe that he will end up being related to Group I, and that his upgraded results will show him to be on a distinct branch along with 39128.

48374 (12 markers) - Thomas Vance (b.c.1820, prob. Gallia Co., OH)

This participant is a genetic distance of 1 from both Group I and Group II. He is probably a member of either Group I or II, yet we can not know where to place him unless we can compare his 37 marker results. Unfortunately, this participant became very angry when I tried to explain to him why he would need to upgrade. He suspected the whole DNA thing to be a hoax, and asked never to be contacted again. My impression is that, being WAMH R1b, he saw the enormous amount of matches he had on 12 markers with other surnames, and figured all DNA would end up proving was that he is ultimately related to everyone else, just like the Bible says. He's right, of course, we are all related to each other – but some of us are more closely related than others. And by comparing people of the same surname on as many markers as we can, it becomes possible to start distinguishing relationships.

47531 (12 markers) - John Vance (b.1773, Frederick Co., VA) m.Lydia Reese

This participant is a genetic distance of 2 from 48374, and a genetic distance of 3 from Groups I and II. While a genetic distance of 2 on 12 markers is not close enough to comfortably say he is related to either Group I or Group II, it is not so far away that we can say he is definitely unrelated. In another project, I have personally observed a genetic distance of 3 on 12 markers turn into a genetic distance of 4 on 37 markers – that participant went from looking probably not related, to looking probably related. Participant 47531 was disappointed in his 12 marker results, and has chosen not to upgrade.

N20182 (12 markers, 37 pending) - Robert Vance (b.c.1810, TN) m.Sina Brewer

This participant, who joined the Vance project from the National Geographic Project, is an exact match on 12 markers with Groups I and II. Thankfully, he has agreed to upgrade to 37 markers, and we're looking forward to seeing whether he belongs to either Group I or Group II. We're expecting his results to come in around the beginning of April 2006.

N21545 (12 markers, 37 pending) – Thomas M. Vance (d.1862, Cannon. Co., TN)

This participant is an exact match on 12 markers with Groups I and II. He just joined the project from the National Geographic Project. We are waiting on his 37 marker upgrade before placing him in a group of related participants.

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Ungrouped Participants

The following participants are probably not related to any other participants in the project. We have explained why we think this for each of them.

39021 (25 markers) - David Vance, b.1815, Ireland; immigrated to Baltimore, 1831

This participant's closest match on 12 markers is 10/12 with 15403, a member of Group I. While a genetic distance of 2 on 12 markers does not absolutely rule out a relationship, 25 marker results have further revealed a genetic distance of 10 between 39021 and 15403, too distant to be considered related.

47042 (37 markers) – Hugh Vance (1807-1839) of Knox Co., TN

This participant's closest match on 12 markers is 8/12, a genetic distance of 4. At this distance we can be pretty confident he does not share a common direct male ancestor with any of the other participants.

N8118 (37 markers) – Patrick Vance, d.1805, Henderson Co., KY

This participant's closest match on 12 markers is 8/12, a genetic distance of 4. This is so distant that we were fairly confident he does not share a common direct male ancestor with any of the other participants. This unrelatedness has been borne out by his 25 and 37 marker upgrades, in which his closest match in the project is a genetic distance of 8 on 25 markers and 12 on 37 markers, revealing only a 5% chance or less of a common ancestor in the last 24 generations. However, he does have numerous 25 and 37 marker matches with people of other surnames in FTDNA's database.

4828 (25 markers) – [??] Col. David Vance of Buncombe Co., NC (d.1844)

This participant, who does not have the surname Vance, has reason to suspect that his ancestor was an illegitimate child of David Vance of Buncombe Co., NC. Thus far, his closest match on 12 markers is 8/12, a genetic distance of 4. At this distance, we can be confident he does not share a common direct male ancestor with any of the other participants. We do not yet have a direct male descendant of Col. David Vance in the project, so we have yet to test his theory of descent; all we can say is that he is very probably not related to any of the current participants.

44944 (12 markers) - John Vance (b.c.1760, prob. in Ireland)

This participant's closest match on 12 markers is 8/12, a genetic distance of 4. At this distance we can be confident he does not share a common direct male ancestor with any of the other participants.

48973 (25 pending) – John Vance (b.1796, TN - d.1860/70, AR)

This participant's closest match on 12 markers is 8/12, a genetic distance of 4. At this distance we can be confident he does not share a common direct male ancestor with any of the other participants.