Ewing Surname Y-DNA Project – Article 18

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This is the eighteenth in a series of articles about the Ewing Surname Y-DNA Project. The previous seventeen articles have appeared in the last seventeen issues of this journal, which until this year had been called the *Journal of Clan Ewing*. They are also available online through links at the project's web site (*www.EwingFamilyAssociation.org/DNA_Project/index_Y-DNA.html*).

Discussing the Y-DNA Project requires using some terms and abbreviations that will be unfamiliar to beginners. Definitions and explanations of these can be found in the early Y-DNA Articles and elsewhere on the project's web site. Extensively cross-linked results tables, project participant lineages, group relationship diagrams and network diagrams are also available on the project's web site.

Ewing Project Presented in Houston

I and Ewing Project co-administrator Larry Bryant attended the 5th International Conference on Genetic Genealogy for Y-DNA Surname Project Administrators in Houston, March 14-15, 2009. I was one of two group administrators invited to make presentations on their surname projects.[1] I reported on the results of the Ewing Project and showed some of the novel methods for presenting results that we have developed, but the main point of the talk was to illustrate the limitations of genetic distance in determining how closely related two men might be. This very problem has resulted in a considerable amount of confusion among Ewing Surname Y-DNA Project participants, and it seemed like a good subject for this issue's article.

I am sure you will be able to get something out of this article by simply reading it, but if you are ready to spend an hour and really move your understanding of genetic genealogy forward, I suggest that you go to your (or your grandchild's) computer and print out the following documents to refer to as you read:

1. Ewing Surname Y-DNA Project: Article 3, *J. Clan Ewing*, Vol. 11, No. 3, August 2005, pp. 15-22 (*tinyurl.com/cua4hg*)
2. Modal Haplotypes (*dl.getdropbox.com/u/431003/ModalHaplotypesDiscussion.pdf*)
3. Network Diagram: Overview *(dl.getdropbox.com/u/431003/NetworkDiagramOverview.pdf*)
4. Genetic Distance from Overall Ewing Modal (*dl.getdropbox.com/u/431003/GD-BarDiagram.pdf*)
5. Group 2 Results Table (*dl.getdropbox.com/u/431003/Group2_ResultsTable.pdf*)

Genetic Distance

If you are less than fully confident that you understand what is meant by the terms 'marker' and 'genetic distance,' it would be a good idea to get clear about that before reading further. There is a short discussion of these terms in *Ewing Surname Y-DNA Project: Article 3*, which is available in the August 2005 *Journal,*[2] and via the first link above. The excruciatingly short story is that genetic distance is a

[1] For brief synopses of the presentations at the conference, have a look at *stephendanko.com/blog/2009/03*.

[2] *J. Clan Ewing*, Vol. 11, No. 3, August 2005, pp. 15-22 (*tinyurl.com/cua4hg*).

coarse measure of the difference between the Y-DNA test results of two project participants. On average, we expect men related more closely to be separated by a smaller genetic distance than more distantly related men, but the words *on average* must not be skipped over lightly. It is tempting to think that genetic distance should be proportional to conventional genealogic relatedness, so that brothers or first cousins are always at a smaller genetic distance from one another than, say, tenth cousins. This is emphatically not the case.

Usually, father and son have identical Y-DNA test results, so they are at genetic distance 0 from one another. Indeed, we expect to find genetic distance 0 between father and son on the 37-marker panel nearly 93% of the time. But this means that we will find a genetic distance 1 or more in father-son pairs almost 7% of the time, and 0.006% of the time we will even find them to be at genetic distance 3. Tenth cousins are more likely to have slightly different Y-DNA test results; they will be at genetic distance 1 or 2 from each other 58% of the time. But almost 20% of the time they will be at genetic distance 0, and 0.65% of the time they will be at genetic distance of 6 or more. We commonly say that men who are at a genetic distance of more than 5 are not likely to be related to one another in a 'genealogic time frame,' but tenth cousins is a reasonable estimate of genealogic time frame and 0.65% is not zero. And if we double our estimate of mutation rate[3] and re-do these calculations, we would find that about 10% of tenth cousins are expected to be at genetic distance 6 or more.

Since genetic distance cannot definitively distinguish tenth cousins from father-son pairs, is it completely useless? No, not completely. We cannot confidently reach conclusions about relationships on the basis of genetic distance 0 versus genetic distance 5, but we can be very confident that when we find differences in genetic distance of 15 or 50 between two men, there is no relationship between them in a genealogic time frame. Genetic distance can tell us that two men are 'related,' but it cannot tell us exactly how closely they are related or whether they both fall into the same branch of a family tree.

Large Genetic Distance

Genetic Distances from the Ewing Modal

The bar diagram on the following page shows how many participants are at given genetic distances from the Ewing modal haplotype. It will be easier to read and interpret this diagram if you print it out larger and in color by using the fourth link above.

Notice that the first bar on the left shows that there are five men[4] who exactly match the Ewing modal haplotype, so are at genetic distance 0 from it. Moving to the right, notice that there are twenty men at genetic distance 1 from the modal, seventeen at genetic distance 2, sixteen at genetic distance 3, and so on across the page. The vertical dotted lines show how we have divided the groups.[5] Groups one and two are thought to have the same common ancestor in a genealogic time frame, because all the men in these groups are within genetic distance 5 of the Ewing modal.

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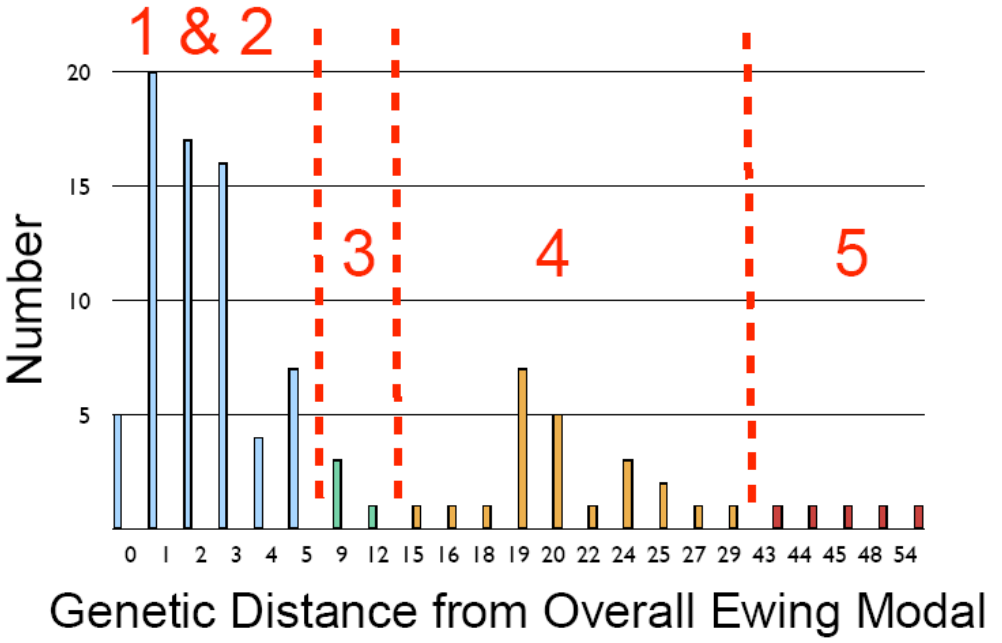
[3] In this paragraph, I have used the rate 0.002 per marker per generation.

[4] In fact, there are now six men in the project who exactly match the modal, but I have not added the most recent one to this diagram.

[5] The Groups are further subdivided on the basis of conventional genealogy. To read about our rationale and the composition of the groups, have a look at Results Introduction via the link in the Results Directory of the project's web site, and at *dl.getdropbox.com/u/431003/Results_Intro.pdf*).



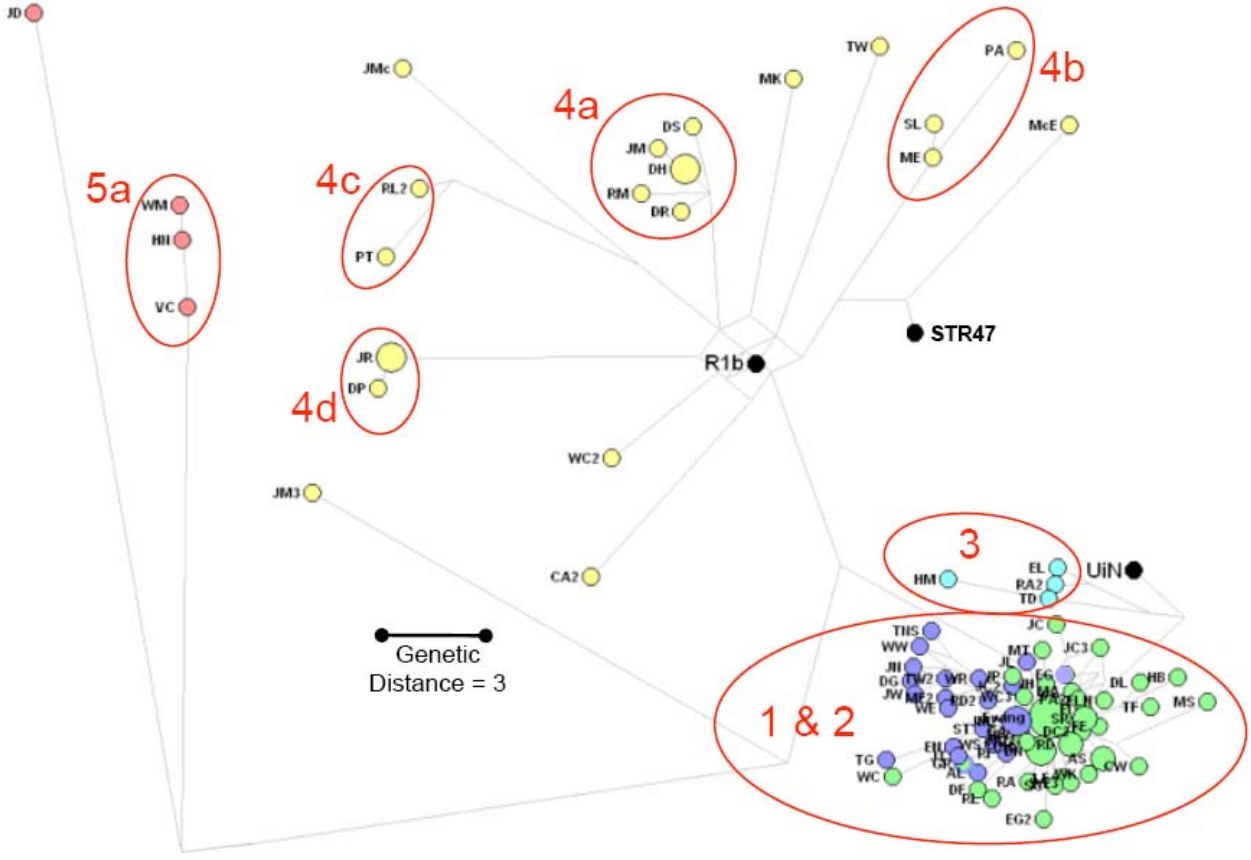
Network Diagram: Overview

The diagram on the following page displays genetic distances in the Ewing Project graphically. Have a look at this diagram. It will be much easier to read and interpret it if you print it out larger and in color by using the third link above.[6]

Genetic distance is proportional to the length of the light gray lines connecting project participants. The important things to notice here are how Groups 1 and 2 are practically piled up on top of one another, Group 3 is at a little distance from them, and Groups 4 and 5 are at considerable distance and rather spread out. The black node labeled R1b is genetic distance 15 from the Ewing modal, and the men in Group 4 are all at some additional distance further than that. Notice also that there are five clusters of men, labeled 4a, 4b, 4c, 4d and 5a, that are within genetic distance 4 or 5 of the others within the same cluster, but that each cluster is at a considerable distance from the others. I am just eyeballing it, here, but it looks like the Group 4 clusters are about genetic distance 15 from one another, and they are something like genetic distance 50 from Group 5a.

[6] You can read about how network diagrams are constructed and interpreted in greater detail at the current discussion of Network Diagrams (*www.EwingFamilyAssociation.org/DNA_Project/DNA_ProjectResults/AboutDiagrams.html - Network_Diagrams*).

Network Diagram: Overview



Limitations of Genetic Distance

The take-home lesson here is that large genetic distances (over 10 or so) rule out a paternal-line relationship in a genealogic time frame. Small genetic distances (5 or less) suggest that a paternal-line relationship could very well exist in a genealogic time frame, but one cannot conclude with any confidence that two men at genetic distance 0 are more closely related than two men at genetic distance 3.[7]

Off-Modal Markers

To follow this discussion, it is important to understand the concept of 'modal haplotype' and its implications. Refresh your understanding by reading the short discussion in *Modal Haplotypes*, which is available through a link in the Resources Directory on the project's web site, and through the second link above. Again, the excruciatingly short story is that the modal haplotype of a group of related men is almost certain to have been the haplotype of their common ancestor, and since mutations are rare events, all of the descendants of a common ancestor will match this haplotype at almost all of the markers. Each marker where a man does not match the modal haplotype is called an off-modal marker. In our Results Tables, these are highlighted to make them easier to see.

As you look at one of our Results Tables for groups of related men, you will see highlighted off-modal markers sprinkled here and there in the table. Some participants will have none because they exactly match the modal haplotype. Most will have one or two, and a very few will have three or more differences from the modal haplotype. This is because mutations occur at random and do not give us any particularly interesting genealogic information. We do not start to get excited until we see that two or more men match one another at one or more off-modal markers.

Matches at Off-Modal Markers

What follows here is really the central idea of this article and of genetic genealogy itself. Because mutations are rare and occur at random, we do not expect to see many instances of the *same* mutation, even in a good-sized kindred. I do not want to use too much math here, but consider that if the average mutation rate is 0.002 per marker, we expect to see a mutation at a specific marker only once in five hundred transmission events.[8] On the other hand, we expect to see a mutation at any of the 37 markers under consideration once in 500/37 = 13.5 transmission events, on average. This means that the odds are pretty good that tenth cousins, who are separated by twenty-two transmission events, will differ at a couple of random markers. But what are the odds that each of them will have exactly the same mutation; that is, they will match at an off-modal marker? Remember, if we are looking for just any mutation, we expect to wait 13.5 transmission events to see one, but if we are waiting for a mutation at

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[7] Keep in mind that we are and have been talking about genetic distance on the 37-marker panel.

[8] A 'transmission event' is an opportunity for a mutation to occur. A father and son are separated by one transmission event. Two brothers are separated by two transmission events, because there was a chance of a mutation when each of the sperm cells leading to them was made by the father. Tenth cousins are separated by twenty-two transmission events. This is eleven generations down from the ninth great-grandfather to each of the tenth cousins.

a specific marker, we would expect to wait five hundred transmission events.[9] Suppose that one of the tenth cousins has a specific mutation. The other cousin has only eleven transmission events in which to match it, and on average it would take five hundred transmission events to match it. So matches at off-modal markers are not so likely to occur by coincidence.

But mutations occur at random. What other way is there for matches to occur except 'by coincidence?' The other way is for the mutation that created the off-modal marker to have occurred a single time and for both cousins to have inherited it from a common ancestor. Now we have to let go of the tenth-cousin relationship and go back to the situation that we have more often: we have test results for two men, but we are not sure exactly how they are related. Based on genetic distance, we have concluded that they are in a related group and have a common ancestor with the others in the group, but that is all that genetic distance can tell us. But if they differ from the group modal and match at an off-modal marker, our first guess should be that they are descended from a common ancestor more recent than the common ancestor of the whole group. In other words, we should suspect that they are in the same sub-branch of the larger family.

I cannot emphasize this too strongly. Two men having markers that match the modal of their loosely defined 'closely related' group is nothing more than we would expect and follows from the definition of 'closely related group.' But two men matching at markers that do not match the modal (off-modal matches) may very well be more closely related to one another than they are to the whole comparison group.

Using Group 2 as an Example

Have a look at the Ewing Group 2 Results Table on the following page. It will be much easier to read and interpret this table if you print it out larger and in color by using the fifth link above.

At the very bottom of the table you can see three men in Group 4c and one in 5b. I have included them in the Group 2 table because their conventional genealogies suggest that they are descended from the progenitor of Group 2a. But as you can see, the Y-DNA test results show this is impossible. These men are at a huge genetic distance from the men in Group 2. WD is at genetic distance 25 from the Ewing modal and each of the others is further than that.

Next, notice that all of the other men in this table share the off-modal marker DYS 391 = 10, where the Ewing modal is DYS 391 = 11. We have distinguished Group 2 from Group 1 not on the basis of genetic distance but rather on the basis of this off-modal marker.[10] Next, notice that there is a scattering of off-modal markers here and there, mostly at random. To the extent that these are random, they give us no genealogic information. Now, notice that all seven men in Group 2a have the off-modal marker CDYa =

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[9] Since markers can mutate either up or down at about the same frequency and we are looking for a mutation in the same direction, we would really have to wait for a thousand generations. The point I am trying to make is only that in a genealogic time frame, it is highly unlikely for two men to end up with the same mutation by chance.

[10] Even though GR also has DYS 391 = 10, we have put him into Group 1b rather than somewhere in Group 2, because we have not been able to find a mistake in his conventional genealogy showing his descent from James Ewing of Inch, the progenitor of Group 1b. You can be sure that this has driven us crazy, but we have finally decided that he must have had a parallel mutation at this marker. Parallel mutations are discussed briefly below.

Group 2 Results Table

Group	ID	DYS393	DYS390	DYS19	DYS391	DYS385a	DYS385b	DYS426	DYS388	DYS439	DYS389-1	DYS392	DYS389-2	DYS458	DYS459a	DYS459b	DYS455	DYS454	DYS447	DYS437	DYS448	DYS449	DYS464a	DYS464b	DYS464c	DYS464d	DYS460	GATA-H4	YCA-IIa	YCA-IIb	DYS456	DYS607	DYS576	DYS570	CDYa	CDYb	DYS442	DYS438
Ewing modal		13	25	15	11	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
2a	DG	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	17	16	18	17	35	37	11	12
	JN	13	25	15	10	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	35	37	11	12
	JW	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	35	36	11	12
	TW2	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	35	37	11	12
	WR	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	35	38	11	12
	TNS	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	16	16	16	17	11	11	19	23	18	16	18	17	35	38	12	12
	WW	13	25	15	10	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	35	38	12	12
2b	EG	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	10	19	23	18	16	18	17	37	39	11	12
	EN	13	25	15	10	11	13	12	12	12	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	17	17	37	38	11	12
	RC	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
2c	SA	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
	ST	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	32	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
2d	WE	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	33	15	16	16	17	11	11	19	23	18	16	18	17	36	38	11	12
	AL	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	19	31	15	16	16	17	11	11	19	23	18	16	19	17	37	38	11	12
2*	TG	13	24	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	32	16	16	16	17	11	11	19	23	18	16	17	17	37	38	11	12
	ME2	13	25	15	10	11	12	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	36	37	11	12
	RF	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	19	17	37	38	11	12
	JT	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	24	15	18	31	15	16	16	18	11	11	19	23	18	16	18	17	37	38	11	12
	JL	13	25	15	10	11	13	12	12	14	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	39	11	12
	RD2	12	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
	JC2	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	36	38	11	12
	WS	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	38	38	11	12
	JM2	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	11	11	19	23	18	16	18	17	37	38	11	12
1b	GR	13	25	15	10	11	13	12	12	13	13	14	29	17	9	10	11	11	25	15	18	31	15	16	16	17	9	11	19	23	18	16	18	17	37	38	11	12
4c	WD	13	24	14	11	10	15	12	12	12	13	13	29	18	9	10	11	11	25	15	19	29	15	15	17	18	11	11	19	23	16	13	17	17	35	36	12	12
	PT	13	24	14	11	10	15	12	12	12	13	13	29	18	8	9	11	11	25	15	19	28	15	15	17	18	11	11	19	23	16	13	17	17	35	36	12	12
	RL2	13	24	14	11	10	15	12	12	12	13	13	29	18	9	10	11	11	25	15	19	29	15	15	17	18	12	11	19	23	16	13	17	17	35	36	12	12
5b	JD	14	26	15	11	13	16	11	13	11	12	11	28	18	8	10	10	12	25	15	21	27	14	14	15	15	10	9	19	19	14	13	16	18	35	35	12	10

35 and no one else in Group 2 has this.[11] We put the members of Group 2a into this group on the basis of their conventional genealogy, and we know who their common ancestor was (though we do not know his name for sure). The fact that all of the men in this branch of the family match at an off-modal marker is an excellent illustration of the potential usefulness of off-modal matches. If you look at the Group 2a Relationship Diagram, you will also be able to figure out where the DYS 442 = 12 mutation shared by TNS and WW must have happened,[12] why they both have it, and how it now serves as a branch marker for the descendants of the man who appears in this diagram as 'Samuel Jr.'[13]

Those of you who are really on your toes will be wondering: How about the fact that there are some other pairs of men who share an off-modal marker?

- EN and WW share the off-modal marker DYS 439 = 12
- ST and TG share the off-modal marker DYS 449 = 32
- TNS and TG share the off-modal marker DYS 464a = 16
- AL and RF share the off-modal marker DYS 576 = 19
- WE, ME2 and JC2 share the off-modal marker CDYa = 36
- EG and JL share the off-modal marker CDYb = 39
- Three men in Group 2a and ME2 share the off-modal marker CDYb = 37

Precisely. This is where the action is. The fact that RC, SA and JM2 are at genetic distance 0 from one another and the Group 2 modal makes us very confident that they are all in Group 2, but it tells us almost nothing about which sub-branch they belong to.[14] Establishing a closer relationship and choosing a sub-branch requires us to look for off-modal matches. We are especially interested when we see that someone in Group 2* (which consists of those men who do not know their conventional genealogic connection with any of the others in Group 2) matches one of the men in another of the Group 2 subgroups at an off-modal marker, because this can give us a lead about what branch of the family he may belong to.

It is beyond the scope of this article to go through a detailed analysis of each of these off-modal matches, but I would be happy to do this for any or all of these cases privately with any of you who may be interested. Suffice it to say here that I do not think that EN and WW are in the same branch notwithstanding the fact that they both have DYS 439 = 12 for these reasons: We have good conventional genealogy that RC and EN are third cousins, both descended from John Ewing (born 1775). We have established that WW and TNS both descended from Samuel Ewing Jr., were born about the same time, and TNS does not have DYS 439 = 12, so the mutation at this marker that WW inherited must have occurred somewhere between him and his great-grandfather. Furthermore, EN does not have the CDYa = 35 marker shared by all the men in Group 2a. We are forced to conclude

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[11] The fact that the four men outside of Group 2 at the bottom of the chart also have this is due to coincidence. They are at such a large genetic distance from the men in Group 2 that we cannot make anything of this.

[12] It had to have happened as Samuel (born ~1740) was fathering Samuel Jr. because if it happened before that, WR would also be expected to have this mutation. If it happened afterwards we would not expect both WW and TNS to have it.

[13] Group 2a Results Table (*dl.getdropbox.com/u/431003/Group2aRelationshipDiagram.pdf*).

[14] I say 'almost nothing' because if they were in Group 2a, we would expect them to have CDYa = 35, and they do not, so they probably do not belong there.

that the off-modal match at DYS 439 = 12 must be coincidental, and that EN and WW did not inherit it from a common ancestor.

Dad-burned Complications

If I could teach my children and grandchildren just one thing, it would be this: There ain't no always. Nothing is certain, nothing lasts forever, and there is always an exception to the rule. And this is certainly true about genetic genealogy. This discussion would not be complete if I did not at least mention two sorts of exception to the rule.

Parallel Mutations

I mentioned that any single specific marker is likely to mutate only once every five hundred generations on average. So when we see that two men have the same mutation (for instance, they match at an off-modal marker), we should have a high degree of suspicion that they inherited it from a common ancestor. The fact is, though, mutations can and do arise independently and coincidentally. We speak of 'parallel mutations' when this happens. Two men are said to have inherited parallel mutations when they both have the same off-modal marker, but they did not get it from a common ancestor. What is more, though it may be true that, on average, markers only mutate once in five hundred generations, some markers have much faster than average mutation rates. In particular, the CDY markers are thought to mutate nearly twenty times as fast as this average.[15] And while I have not tallied or estimated the total number of transmission events in the Ewing Surname Y-DNA Project and done the math, my impression is that we have found way more parallel mutations than the mutation rate estimates might suggest that we should find.

Back Mutations

We expect all descendants of a man in whom a mutation occurred to inherit the same mutation. This is to say that the descendants will match the mutated value and not the ancestral value. So if your father had a mutation at some marker, you would match him rather than your grandfather at that marker. Of course, eventually there could be another mutation at the same marker. Markers are more or less equally likely to mutate in either direction; that is, they are about equally likely to add a repeat or lose one (the number is as likely to increase or decrease). Suppose your grandfather had CDYb = 37, and your father had a mutation to CDYb = 38. We would expect you and your offspring also to have CDYb = 38. Of course, your son could have another mutation to CDYb = 39, in which case he would be one step different at that marker from you and your father, and two steps different from your grandfather. But your son could as well have a mutation from CDYb = 38 back down to CDYb = 37. In this case, your son would match not you and your father; he would match your grandfather. When a mutation occurs that results in matching an ancestral value, we say that a 'back mutation' has occurred. This makes it appear that a line has not had a mutation, when in fact it has had two, but in opposite directions so that the second 'cancels' the first and both become invisible.

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[15] If you want to see one take on per-marker mutation rate estimates, they are shown at the top of the Modal Comparison Table available at the Modals comparison chart (*dl.getdropbox.com/u/431003/ModalComparisonTable.pdf*).

This is what appears to have happened in Group 2a at CDYb. To follow this, you should look at the Group 2 Results Table and Group 2a Relationship Diagram. Notice that the Ewing modal at CDYb is 38, but that JN, DG and TW2 all have CDYb = 37. This makes us think that William? must also have had CDYb = 37. If so, his son Joshua should also have had CDYb = 37. But Joshua's three descendants through his son Samuel (born c1740) — WR, WW and TNS — all have CDYb = 38, and his descendant through his son Nathaniel (born c1741) — JW — has CDYb = 36. What is going on here? There must have been a back mutation in Samuel (born c1740) to CDYb = 38 and so all of his descendants match the ancestral Ewing modal notwithstanding that they have a couple of common ancestors (Joshua and William?) who had CDYb = 37. And JW has CDYb = 36 because there was another mutation (from CDYb = 37 to CDYb = 36) somewhere along the line between Nathaniel, born c1741, and JW.

To Join or Get More Information

If you are ready to join the project, go to *www.familytreedna.com/surname_join.aspx?code=M44915*. Participation by Ewing women is welcome; they can get valuable genealogic information by persuading a male relative to submit a specimen. For more information, visit the project's web site[16] and the FTDNA web site.[17] If you want to ask questions, call me at +1 505.764.8704 in the evening, or EMail me at *davidewing93 at gmail dot com*.

David Neal Ewing has been a member of Ewing Family Association *since 1996 and has served as its Chancellor since 2006. He previously served as Chair of its Board of Directors from 2004-2006. He is also Administrator of the Ewing Surname Y-DNA Project, which he founded in 2004, and he is a regular contributor to the* Ewing Family Journal*. Dr. Ewing has a private practice in clinical geriatric neuropsychiatry in Albuquerque, New Mexico. He received his M.D. degree from the University of New Mexico and did his residency training at the University of Michigan Hospital in Ann Arbor, Michigan.*

"You don't look anything like the long haired, skinny kid I married 25 years ago. I need a DNA sample to make sure it's still you."

[16] *www.EwingFamilyAssociation.org/DNA_Project/index_Y-DNA.html* .

[17] *www.FamilyTreeDNA.com/public/Ewing*