Ewing Surname Y-DNA Project Article 9

This is the ninth in a series of articles about the Ewing Surname Y-DNA project. The previous eight articles have appeared in the last eight issues of the *Journal*. They are also available on-line at the *Clan Ewing* WebSite, *http://www.ClanEwing.org*.

Status of the Project

We now have results on fifty-two participants in the Ewing Surname Y-DNA project. This is over halfway to our initial goal of recruiting a hundred Ewing men to participate in the project! We have another two participants whose samples are in analysis at the lab, and two who have kits that they have not yet returned to FtDNA. Four of the men on whom we have results have "variant spellings" of the name, including one Ewin man who knows that he is descended from a Ewing in Donegal.

There are now enough results that trying to display them in a single table has become unwieldy, so we have decided to subdivide the results in a way to make them more manageable. We have created seven groups, which are defined and discussed below. Five of these groups (Groups 1, 3, 4, 5 and 7) consist of men who may be descended from a single Ewing man within a genealogical time frame; none of them is further than genetic distance 5 from the "Ewing modal haplotype." Please recall that we constructed the "Ewing modal haplotype" by listing at each marker the number of repeats most commonly found among the participants of the project at that marker, and that we believe this to be a good approximation of the haplotype of the common Ewing ancestor shared by most of the men in the project.[1]

The men in the five groups of Ewings that are genetically related to one another all have exactly the same values at 23 of the 37 markers for which we have tested.[2] The Result Tables on the *Clan Ewing* WebSite (*http://www.ClanEwing.org*) show all the 37-marker results, but for this article I have deleted the columns where there are no differences in order to emphasize the differences and to make the tables small enough to fit the *Journal* format. Result Tables on the other two groups could not be edited to a reasonable size in this way, because they differ from the Ewing modal at so many markers. For these groups (Groups 2 and 6), we have instead prepared charts of the 12-marker haplotypes, which amounted to just lopping off one end of the 37-marker results tables with no effort to concentrate on the markers where there are differences. Again, full 37-marker results tables for these two groups are also posted on the WebSite.

Group 1: Unclassified lineages. These men are close to the Ewing modal, but we do not know their conventional genealogic connection with the others.

	DYS 390	DYS 391	DYS 439	DYS 437	DYS 448	DYS 449	DYS 460	GATA H4	YCA IIb	DYS 456	DYS 576	DYS 570	CDY a	CDY b
Ewing	25	11	13	15	18	31	11	11	23	18	18	17	37	38
RA	24	11	13	15	18	31	11	11	23	18	19	17	37	38
FI	25	11	13	15	18	30	11	11	23	18	18	17	37	38
DL	26	11	13	15	18	31	11	11	23	18	18	18	38	38
WL	25	11	13	15	18	31	11	11	23	18	18	18	37	38
MT	25	11	13	15	18	31	11	12	23	18	18	17	36	38
Ewin	24	11	13	15	18	31	11	11	23	18	18	17	36	39
DC2	25	11	13	15	18	31	11	11	23	18	18	17	37	37

Group 1: Unclassified lineages. These seven men are close matches to the Ewing modal haplotype (all ≤ genetic distance 3), and though this establishes that they are significantly related to the other Ewing men, we do not know their conventional genealogic connection with the others. We could and perhaps should have also put seven of the men who appear in Group 5 into this group, because we also do not know their conventional genealogic connection with the others, but we wanted to highlight the DYS 391 = 10 connection among the men in Group 5, so we put them there instead.

[1] You can read more about the meaning and significance of "modal haplotype" in Y-DNA Article #3 in the August 2005 issue of the *Journal of Clan Ewing*. This article is available online at *http://www.ClanEwing.org*.
[2] Four men in the project have been tested at 67 markers; the three of them that are in the five groups of related Ewings have identical results at the additional 30 markers.

Group 2: Singletons. These men do not appear to be related to any others in the project.												
	DYS 393	**DYS 390**	**DYS 19**	**DYS 391**	**DYS 385a**	**DYS 385b**	**DYS 426**	**DYS 388**	**DYS 439**	**DYS 389-1**	**DYS 392**	**DYS 389-2**
Ewing	13	25	15	11	11	13	12	12	13	13	14	29
JMc	13	24	14	11	11	15	12	12	13	13	13	29
TD	13	25	14	11	11	13	12	12	12	13	14	29
MK	13	24	14	10	11	16	12	12	13	13	13	30
SL	13	24	14	10	11	14	12	12	12	13	13	29
Js	13	23	14	10	11	14	12	12	12	13	14	30
Ewen	13	24	14	10	11	15	12	12	12	14	13	30
WM	14	22	16	10	14	14	11	13	11	12	12	29
JD	14	26	15	11	13	16	11	13	11	12	11	28
Ewan	14	26	15	11	13	16	11	13	11	12	11	28
Note: This chart is like the chart for Group 6 and unlike the other charts in this article, because the column designations are different. These charts show 12-marker haplotypes.												

Group 2: Singletons. This group includes the three men with "variant spellings" of the surname that are not known to be descended from a specific Ewing: one McEwan, one Ewan and one Ewen, as well as six Ewing men. These nine men are not related genetically to any of the others in the project. They are also not related to one another, except possibly for one Ewing man and the Ewan man, who match exactly on all 12 of the markers the Ewan man was tested for. This is suggestive, but it is not uncommon for 12 markers to match by coincidence in unrelated men with Scottish surnames. If we could persuade the Ewan man to upgrade to 37 markers and there was still a close match, then we could say with some confidence that these two men are related and that there must have been a change in the spelling of the name of one or the other of these two men somewhere along the line.

The Group 2 table included in this article has been edited to show only the 12-marker haplotypes, because displaying 37-marker results does not work well with the *Journal* format. Full results are available on the *Clan Ewing* WebSite. These men vary from the 37-marker Ewing modal haplotype by between 9 and 51 mutations, so some of the men vary by several steps at several of the markers. As you can see in the accompanying 12-marker chart, there are *lots* of differences, and even more so in the last three men in the chart. These three are in different haplogroups than all of the other men in the project.[3]

Perhaps I should take this opportunity to reiterate that although the Ewing men in Group 2 are not genetically related to the others in a genealogic time frame, they are by no means to be considered as "outsiders" to the Ewing Clan. In my view, a Ewing is a Ewing, and this doesn't depend on DNA. It is also important to remember that while sometimes anomalous DNA results (even if you could term these such) are due to "non-paternal events" like unreported adoptions, mistakes in paternity, or surname changes unrelated to paternity, this is by no means the only possible explanation. Surnames did not come into widespread use in the part of the world that the Ewings came from until relatively recently – maybe six or seven hundred years ago. When surnames were chosen, nobody was doing genetic testing. It is all but impossible that the first Ewing men would have had identical Y-DNA, even if they were closely related. Consider that early clans were not organized on strictly paternal lines, and the sons of sisters might have ended up with the same surname. They would be closely related, but might very well have had completely different Y-DNA. Some of those differences will have persisted to modern times.

[3] The concept of "haplogroup" has been discussed in previous *Journal* articles. The short story is that haplogroups separated from one another long ago, probably before the last ice age. Most of the Ewings, even the "unrelated" ones, are in haplogroup R1b1 (indeed, most of them are in the sub-haplogroup R1b1c7 – see the articles by John McEwan and myself in the August 2005 issue of the *Journal of Clan Ewing*). One of the three men at the bottom of this chart is in haplogroup G2, which is far more common in Central Asia than in Britain, and two of them are in haplogroup I, which is the second most common haplogroup in Britain, but is seen in greater proportions on the continent in Germany and Scandinavia.

Group 3: James of Inch. These men have conventional genealogies linking them with James of Inch.														
	DYS 390	**DYS 391**	**DYS 439**	**DYS 437**	**DYS 448**	**DYS 449**	**DYS 460**	**GATA H4**	**YCA IIb**	**DYS 456**	**DYS 576**	**DYS 570**	**CDY a**	**CDY b**
Ewing	25	11	13	15	18	31	11	11	23	18	18	17	37	38
DN	25	11	13	15	18	31	11	11	23	18	19	17	37	38
GR*	25	10	13	15	18	31	9	11	23	18	18	17	37	38
SR	25	11	13	15	18	31	11	11	23	18	18	18	37	38
JG	25	11	13	15	18	31	11	11	23	18	18	17	37	38
HW	25	12	13	15	18	31	11	11	23	18	18	17	37	38
*Note: GR appears here because his conventional genealogy links him with James of Inch, but he also appears in Group 5 because he has DYS391 = 10.														

Group 3: James of Inch. These five men have conventional genealogies linking them to James Ewing of Inch Island in Lough Swilly, Donegal. All but one are within genetic distance 3 of the Ewing modal haplotype and one of them matches it exactly. Guy Raymond (GR) Ewing's conventional genealogy links him with this group, but since he has DYS 391 = 10, we have also put him into Group 5. He is the only man in the project who appears in two groups. GR is at genetic distance 4 (two steps at each of two markers) from his fourth cousin Harold Walter Ewing (HW), who is the brother of *Clan Ewing* founder, Ellsworth Ewing.[4] The likelihood of fourth cousins being at genetic distance 4 is only about 0.6%. Fourth cousins will have fewer than four differences 99.3% of the time. Less than a one percent chance of something happening does not make it impossible; however, a low likelihood event like this should make us take a closer look at our conventional genealogic evidence to make sure we haven't overlooked something. GR is only genetic distance 2 from the closest men to him in Group 5. Until you really think about the probabilities, it is tempting to argue that he just has to be more closely related to them. In fact, there is nearly a fifty percent chance that the most recent common ancestor of two men at genetic distance 2 lived more than eighteen generations ago.[5] James of Inch is only seven generations back from GR, so on purely DNA grounds, GR could easily be only distantly related to men in the other group. Notice that being dissimilar raises doubts, but being very similar doesn't really prove much. Always with DNA it is easier to disprove things than to prove them, but in this case we haven't proven anything.[6]

This point is worth emphasizing. In general, we expect men who are more closely related to have more similar DNA and men who are less closely related to have less similar DNA. A man will have an identical 37-marker Y-DNA haplotype with his father 93% of the time and with his brothers 86% of the time. So "most of the time" men will have identical haplotypes with their fathers and brothers, but not always: after all, this whole business depends on the fact that mutations do occur. And "most of the time" (85.4% of the time, to be precise) a man will have a different Y-DNA haplotype than his 12th cousins.[7] But this means he will have an identical haplotype with a 12th cousin 14.6% of the time. As we look at our results, sometimes we will find brothers at greater genetic distance from one another than 12th cousins!

Group 4: John of Carnashannagh. (The table for this Group appears on the next page.) These eleven men have conventional genealogies linking them to John Ewing of Carnashannagh, Parish of Fahan, Donegal. All of them are close to the Ewing modal haplotype (≤ genetic distance 3), and two of them match it exactly. This is still the largest and best-documented family group in the DNA project, and it best illustrates the potential value of DNA in genealogy. As you can see from the discussion about Group 3 above, absolute genetic distance does not give us terribly informative genealogic information. It would not be too surprising to find even men who have exact 37-marker matches to have a most recent common ancestor over twelve generations ago, which dates to before we have any decent conventional genealogy records. Consider that John of Carnashannagh is thought to have been born around 1648, he is only nine generations back from

[4] Lineages for Harold Walter Ewing, and his brother Ellsworth, appear in Chapter XXXIII of Margaret Ewing Fife's *EWING in Early America*, where Harold Walter Ewing's name is mistakenly given as "Harold *Walker* Ewing." Jill Ewing Spitler kindly checked with him personally before publication of this article to be certain of this; he assured her that his middle name is Walter, after his father, Walter Lee Ewing. A searchable electronic version of Mrs. Fife's book is available on our WebSite, *www.ClanEwing.org*.

[5] Or, if we assume a faster average mutation rate of .004, half this many, so nine generations. Calculations of this kind always depend on assumptions we make about how fast mutations are occurring.

[6] If we were talking about genetic distance 50 here, or even genetic distance 10, we could say we had "proven" there to be no relationship. Genetic distance 4 raises our eyebrows, but doesn't constitute proof.

[7] Remember, these calculations always depend on an assumption about mutation rate. Here, we have used .002. Had we used .004, we would have calculated that 12th cousins should have different haplotypes 98% of the time. Even so, there is a 2% chance of them matching perfectly.

his most distant descendant in the project, and he is only seven generations back from most of them. So (I hear your exasperated plea), how can DNA possibly give us information about more recent branchings in the family tree? Well, this is because of specific patterns of markers, not absolute genetic distance.

Have a look at the Group 4 table. You can see a scattering of mutations here and there, but two markers are of especial interest.

Group 4: John of Carnashannagh. These men have conventional genealogies linking them with John of Carnashannagh.

	DYS 390	DYS 391	DYS 439	DYS 437	DYS 448	DYS 449	DYS 460	GATA H4	YCA IIb	DYS 456	DYS 576	DYS 570	CDY a	CDY b
Ewing	25	11	13	15	18	31	11	11	23	18	18	17	37	38
GW	25	11	13	15	18	31	11	11	23	18	19	17	37	38
RB	25	11	13	15	18	31	11	11	23	18	19	17	37	38
RL	25	11	12	15	18	31	10	11	23	18	19	17	37	38
WK	25	11	13	15	18	31	11	11	22	18	18	17	37	38
BE	25	11	13	15	18	31	11	11	22	18	18	17	37	37
FE	25	11	13	15	18	31	11	10	22	18	18	17	37	38
RP	25	11	13	15	18	31	11	11	22	18	18	17	37	38
RD	25	11	13	15	18	31	11	11	22	18	18	17	37	38
EG2	25	11	14	14	18	31	11	11	23	18	17	17	37	38
JP	25	11	13	15	18	31	11	11	23	18	18	17	35	38
JE	25	11	13	15	18	31	11	11	23	18	18	17	37	38
TN	25	11	13	15	18	31	11	11	23	18	18	17	37	38

- Five men share YCA-IIb = 22, which is a relatively slowly mutating marker. Exactly these same five men are all of those in the project known to be descended from John Ewing of Carnashannagh's son, Pocahontas James Ewing. No other man anywhere in our project has this same marker. This is very strong evidence that YCA-IIb = 22 is a marker for the descendants of Pocahontas James Ewing. If we find a Ewing man with unknown ancestry who shares this marker, we can tell him there is a good likelihood that his ancestor is Pocahontas James Ewing.
- Three men share DYS 576 = 19, which is a more quickly mutating marker. Exactly these same three men are all of those in the project known to be descended from John Ewing of Carnashannagh's grandson, John m. Alice Caswell. We think we can use this as a marker for his branch of the family, notwithstanding that there are five other men in the project who also have DYS 576 = 19.[8]
- John McEwan (JMc) and Thomas Dale Ewing (TD) in Group 2 are far enough from the modal haplotype that we know that they are not related. Robert Allan Ewing (RA) in Group 1, David Neal Ewing (DN, that's me) in Group 3 and Albert Leon Ewing (AL) in Group 5 are not so easily excluded—especially DN, because he matches GW's haplotype exactly.
- DN (Group 3) has had another look at his conventional genealogy because of this finding, but remains convinced of his descent from James Ewing of Inch, so we have let that stand.
- RA (Group 1) doesn't know his genealogic connection with any of the other men in the large group of related Ewings, but he is only genetic distance 2 from the modal, so he is plainly in the group. He should certainly look again at his conventional genealogic data and consider whether he may be a descendant of John m. Alice Caswell, but his slowly mutating marker DYS 390 = 24 somewhat diminishes the likelihood.
- AL (Group 5) also shares the rapidly mutating DYS 576 = 19 with this sub-group, but he differs from them at two slowly mutating markers, our old friend DYS 391 = 10 and DYS 448 = 19. This much

[8] When two men have the same marker by coincidence rather than because they have a common ancestor, we say that there has been a "convergent" or "parallel" mutation. These are more likely to happen in more rapidly mutating markers and less likely to happen in slowly mutating markers. The jury is still out, but the range of mutation rates for different markers seems to run between .0001 and .006 or so. A commonly used average value is .002, but our actual experience in the John of Carnashannagh family is more like double that. In general, markers with higher repeat values tend to have higher mutation rates, but this is not a hard and fast rule.

reduces the likelihood that he is a descendant of John m. Alice Caswell. Furthermore, he has a pretty good handle on his conventional genealogy, which also excludes him from this group.

Group 5: DYS 391 = 10. These men all have DYS 391 = 10; but only WR, DG and JN have conventional genealogies linking them with "I think his name was William."

	DYS 390	DYS 391	DYS 439	DYS 437	DYS 448	DYS 449	DYS 460	GATA H4	YCA IIb	DYS 456	DYS 576	DYS 570	CDY a	CDY b
Ewing	25	11	13	15	18	31	11	11	23	18	18	17	37	38
RC	25	10	13	15	18	31	11	11	23	18	18	17	37	38
JM2	25	10	13	15	18	31	11	11	23	18	18	17	37	38
GR*	25	10	13	15	18	31	9	11	23	18	18	17	37	38
EN	25	10	12	15	18	31	11	11	23	18	17	17	37	38
WR	25	10	13	15	18	31	11	11	23	18	18	17	35	38
DG	25	10	13	15	18	31	11	11	23	17	18	17	35	37
JN	25	10	12	15	18	31	11	11	23	18	18	17	35	37
JW	25	10	13	15	18	31	11	11	23	18	18	17	35	36
WE	25	10	13	15	18	33	11	11	23	18	18	17	36	38
EG	25	10	13	15	18	31	11	10	23	18	18	17	37	39
AL	25	10	13	15	19	31	11	11	23	18	19	17	37	38

*Note: GR has conventional genealogy linking him to James of Inch and so also appears in Group 3.

Group 5: DYS 391 = 10. These men all have DYS 391 = 10; but only WR, DG and JN have conventional genealogies linking them to “I believe his name was William" ("William?"). [9] Another, Albert Leon Ewing (AL), is a man we met at the 2004 Cecil County, Maryland gathering where he still lives near to where his ancestor, William Ewing b. 1762, immigrated in 1783/4 (this is not the same man as “William?", who did not immigrate). The line for William Ewing b. 1762 is covered in Fife, Chapter XXI, pg. 158, where Ms. Fife reports that E.W.R. Ewing thought this William Ewing might have been a distant relative of Nathaniel Ewing (the ancestor of JN).[10] All of the men in Group 5 are at least somewhat close to the Ewing modal haplotype (≤ genetic distance 5), and two differ only at DYS 391 itself. Genetic distance 5 is getting into borderline territory for adducing a relationship in a genealogic time frame. Even assuming the relatively fast mutation rate of .004, half the time the most recent common ancestor (MRCA) for men at genetic distance 5 will have lived over 20 generations ago. If we use the more commonly assumed .002 mutation rate that I have been using elsewhere in this article, half the time the MRCA will have lived over 42 generations ago, long before the era of surnames in Scotland. So why do I think the relationship is closer than this?

Well, we have conventional genealogic evidence of the relationship among WR, DG and JN. DG and JN are genetic distance 2 from one another, and each is genetic distance 5 from the modal. Both are known relatives of WR and are at genetic distance 2 from him, and although he is at distance 3 from the modal, 2 of these steps are at CDYa, which is a notoriously quickly mutating marker. This means that the genetic evidence is that WR is in the closely related Ewing group, and since JN and DG are related to him and at reasonably close genetic distance to him, we can conclude that they must also be in the same large group.

It is also worth noticing that in addition to DYS 391 = 10, all three of the men we know to be descended from “William?” share CDYa = 35, as does participant JW, who does not know of a conventional genealogic connection with the others. This is evidence that there may very well be a connection for JW, and we have encouraged him to look for this, though the evidence would be a little stronger if there were a similar pattern with a more slowly mutating marker. As with DYS 576 discussed above, though, there are some examples of CDYa = 35 among project participants who are not thought to be in this lineage and to have resulted from convergent mutation.

[9] For discussion of this family, have a look at DNA Article #4 from the November 2005 issue of the *Journal of Clan Ewing*.

[10] The DNA results do not entirely rule this idea out, at least, but AL only vaguely resembles the three men who are known to be descended from “William?”.

Group 6: DS/RM/JM. These men form a genetic cluster suggesting a relationship among them, but they are unrelated to the other project participants.

	DYS 393	DYS 390	DYS 19	DYS 391	DYS 385a	DYS 385b	DYS 426	DYS 388	DYS 439	DYS 389-1	DYS 392	DYS 389-2
Ewing	13	25	15	11	11	13	12	12	13	13	14	29
Grp 6	13	24	15	11	11	15	12	12	12	12	13	28
WE2	13	24	15	11	11	15	12	12	12	12	13	28
DH	13	24	15	11	11	15	12	12	12	12	13	28
DS	13	24	15	11	12	15	12	12	12	12	13	28
RM	14	24	15	11	11	15	12	12	12	12	13	28
JM	13	24	15	11	11	15	12	12	12	12	13	28

Note: This chart has different column designations than the others in this article, and a different highlighting strategy, so cannot be compared directly with them. "Modal" here is the 12-marker modal for this group only. See text for more discussion.

Group 6: DS/RM/JM. This group forms a genetic cluster with one another that is unrelated to the project participants in the other groups. As with Group 2, the chart I have included with this article displays only 12-marker haplotypes. Heads up, though! I have constructed a new modal haplotype for just this group, which appears under the Ewing modal haplotype in the chart, and I have used a different highlighting strategy. The bold boxes around markers in the "Grp 6" haplotype show where they differ from the Ewing modal. The participant haplotypes are highlighted at markers where they differ from the Group 6 modal, not where they differ from the Ewing modal. I did this to allow you to see how closely related the members of this group are to one another, but if you don't pay attention, you will not see how very different they are from the larger Ewing group.

The Group 6 12-marker modal haplotype is genetic distance 7 from the Ewing 12-marker modal,[11] but the 37-marker modal is genetic distance 20 from the Ewing modal. The 37-marker haplotypes appear in the results tables on the WebSite. Each of the Group 6 participants is within genetic distance 3 of their own Group 6 37-marker modal. WE2 exactly matches the Group 6 modal, and JM is at genetic distance 1. Donald H. Ewing (DH), has results so far on only 25 markers, but matches the modal exactly on these. RM and DS are each at genetic distance 3 from the Group 6 37-marker modal, but genetic distance 4 from one another and from JM.

James Morgan Ewing (JM) and William Earl Ewing (WE2) are known on conventional genealogic grounds to be fifth cousins, once removed; both are descended from William (d. ca 1774) m. Eleanor Thompson, who lived in Cumberland (now Franklin) County, Pennsylvania and later moved to Indiana County, Pennsylvania. The other three men are close enough genetically to these two to suggest that they all have a common ancestor, but we do not know who this may be.

Group 7: James Ewing b. c1720/25. These men all have conventional genealogies linking them with James Ewing b. c1720/25.

	DYS 390	DYS 391	DYS 439	DYS 437	DYS 448	DYS 449	DYS 460	GATA H4	YCA IIb	DYS 456	DYS 576	DYS 570	CDY a	CDY b
Ewing	25	11	13	15	18	31	11	11	23	18	18	17	37	38
DL2	25	11	13	15	18	31	11	11	23	18	18	17	37	38
WC	25	11	12	14	18	31	11	11	23	18	17	17	37	38
SC	25	11	11	15	18	31	11	11	23	18	18	17	37	38
DC	25	11	11											

Group 7: James Ewing b. c1720/25. These four men all have conventional genealogies linking them with James Ewing b. c1720/25. All of them are close to the Ewing modal haplotype (≤ genetic distance 2), and one of them matches it exactly. SC and DC are father and son; though DC has only a 12-marker profile, he is very likely to have exactly the same haplotype as SC. There are too few men in this group so far to begin speculating about sub-branches, but it is interesting to note that Daryl Leon Ewing (DL2) is at genetic distance zero from the Ewing modal haplotype. This is true also of James Gilbert Ewing (JG) in Group 3, and of Thomas Newell Ewing (TN, *Clan Ewing* Chair Mary Gosline's dad) and James Earl Ewing (JE) in Group 4. We have four men who match the Ewing modal at all 37 markers, yet we have put them into three different groups. What gives? I will try to answer that question in the next section.

[11] Count 2 steps at DYS 385b.

Genealogically Useful Markers

By correlating Y-DNA data with the conventional genealogies of the fifty Ewing Surname Y-DNA Project participants, we have made several interesting discoveries that have implications for genealogy research. We expect more such discoveries as more participants join the project.

One of the most interesting and robust findings of the Ewing Surname Y-DNA Project so far is that the majority of Ewing men are quite remarkably close to the Ewing modal haplotype. We don't ordinarily speak of a modal haplotype as a "marker," but in a way, matching this haplotype closely is a "marker" of descent from a common ancestor. Four of our participants match the modal exactly; twelve are at genetic distance 1, seven at genetic distance 2, and ten at genetic distance 3 from the modal. This has allowed us to identify with confidence one major branch of the Ewing family.

The DNA evidence is also fully adequate to distinguish Group 6 from other project participants, and it will be easy to determine whether future project participants belong in this branch. If we should be so lucky as to find a participant matching this group who has his genealogy worked out a few generations beyond the men presently in the group, they may be able to identify their common ancestor. In any case, the Group 6 modal haplotype has allowed us to identify this as a distinct and clearly identifiable unrelated branch of the Ewing family.

Membership in Groups 2, 5 and 6 was assigned on the basis of DNA clustering. We can't say much about the men in Group 2, because all have unique haplotypes, but when we find a new participant that matches any of them, we will have discovered a new Ewing family group. Group 5 may be a distinct, genetically distinguishable family branch of the large group of related Ewings, but we do not as yet have adequate conventional genealogic evidence to fully support this. We need such evidence for Group 5 and not for Group 6 because Group 5 is so similar to Groups 1, 3, 4 and 7, whereas Group 6 is entirely distinct.

We have used DYS 391 to define membership in Group 5 because it is a slowly mutating marker that is shared by eleven of our participants. Three of them are descendants of "I believe his name was William," and all three of them also have CDYa = 35, which we believe can serve as a marker for their line. If we find a Ewing man with unknown ancestry who closely matches the Ewing modal haplotype and has both DYS 391 = 10 and CDYa = 35, we can tell him there is a good likelihood that his ancestor is "I believe his name was William." Indeed, a fourth member of Group 5 does have CDYa = 35, and though he doesn't have conventional genealogic proof of a connection with "I believe his name was William," we consider that this is likely. We have to be cautious, though, because CDYa is a rather rapidly mutating marker, and we can expect to find convergent mutation, as appears to be the case with JP in Group 4, who has CDYa = 35, but not DYS 391 = 10. As with DYS 576 = 19 discussed below, this will make CDYa = 35 a less reliable and persistent branch marker, but it is still interesting and potentially very useful.

Since DYS 391 = 10 appears in quite a number of men in the project who do not share CDYa = 35, the DYS 391 = 10 mutation probably occurred in an ancestor some indeterminate number of generations before "I believe his name was William," and it is probably a marker for a deeper branch of the family.

We have assigned group membership in four of our seven groups (Groups 1, 3, 4 and 7) on the basis of conventional genealogy rather than DNA clustering. We have not found markers specific to these groups. Another way of saying the same thing is to say that we have determined that John Ewing of Carnashannagh, James Ewing of Inch, James Ewing b. ca.1720/25, and whoever the ancestors of the men in Group 1 may have been had identical 37-marker Y-DNA haplotypes, and so were themselves closely related. On the other hand, we have found some genealogically useful markers that appear to distinguish some sub-branches within Group 4, and we expect to find future such markers distinguishing additional sub-branches as more men join the project.

The markers identifying sub-branches of Group 4 are:

- YCA-IIb = 22. If we find a Ewing man with unknown ancestry who closely matches the Ewing modal haplotype and shares this marker, we can tell him there is a good likelihood that his ancestor is Pocahontas James Ewing, youngest son of John Ewing of Carnashannagh. Of the genealogically useful markers that we have discovered, this one has the best conventional documentation and most robust theoretical support.
- DYS 576 = 19. All project participants known to be descended from John Ewing of Carnashannagh's grandson, John m. Alice Caswell, have this marker, so others in this branch will be expected to have the marker, too. However, DYS 576 is a rapidly mutating marker and will be more subject to convergent mutation. Finding it in a man with unknown ancestry who closely matches the Ewing modal haplotype will suggest that he should consider whether he is descended

from this line. We must exercise caution though, because individuals who are not in this line also may have DYS 576 due to convergent mutation. A convergent mutation creating DYS 576 = 19 will cause no confusion when a participant who has it has many other markers that differ from the men in the branch in question, because it will be clear that no close relationship exists. On the other hand, uncertainty will arise when a participant closely matches the haplotypes of others in the branch and also has this mutation, as is the case with two project participants (DN and RA).

Feedback Requested

Writing these articles is difficult because I can't see the looks on your faces when you read them, and I don't know whether I'm boring you by telling you things you already know, or by not making any sense at all. It would be enormously helpful to me to get questions from any of you who have them. I will be happy to answer these individually as they come in, and they will also give me a better idea what to say about the project in future articles.

To Join or Get More Information

If you are ready to join the project, go to *http://www.FamilyTreeDNA.com/public/ewing* and click on "Join this group" at the top of the blue section on the left of the page. Participation by Ewing women is also welcome; they can get valuable genealogic information by persuading a male relative to submit a specimen. You can see results tables showing participant haplotypes on the *Clan Ewing* WebSite, *http://www.ClanEwing.org*. There are also links on the FamilyTreeDNA WebSite (*http://www.FamilyTreeDNA.com)* to articles and FAQs. If you want to ask questions, call me at 505.764.8704 in the evening, or e-mail me at *DavidEwing93 at gmail.com*.