Ewing Surname Y-DNA Project Article 7

This is the seventh in a series of articles about the Ewing surname Y-DNA project. The previous six articles have appeared in the last six issues of the *Journal of Clan Ewing*. They are also available on-line at www.ClanEwing.org/Y-DNA.html. Also, I have just found a website that explains Y-DNA testing more clearly than I think I have done. Have a look at it and see what you think: www.blairgenealogy.com/dna/dna101.html

New Results

We have new results on seven participants with 37-marker panels, results on one participant for an upgrade from 25 to 37 markers, results pending for four more new 37-marker panels, and one collection kit out that hasn't been returned. We now have a total of 43 men who have joined the project, including four whose names are variant spellings. We have results on 38 men, 34 of whom are Ewings. We should have reports on the pending results in time for analysis before the Gathering. We hope this will encourage many of you who have been on the sidelines to join the project!

The results we have received so far are posted on the website of Clan Ewing at
www.ClanEwing.org/Y-DNAprojectresults.html.
We have decided not to include results tables in the print version of the Journal because of the expense of making color copies. If you have no access to the web and would like for me to mail you a copy of the results tables, call me at the phone number shown at the end of this article and I will do it.

In this article, I am going to organize reporting the results slightly differently, by reporting the new results on each new participant, one at a time.

John Perry Ewing (JP) of Louisville, Kentucky, is our 10th participant descended from John Ewing of Carnashannagh, the 1st through his son, Samuel Ewing, b. 1718. JP is genetic distance two from the Ewing modal haplotype, and has a single two-step mutation, CDYa = 35 (the modal value is 37). Three men in the William?[1] sub-branch, WR, DG and JN, also have CDYa = 35, as does SL, a Ewing man unrelated to the large related group of Ewings. CDYa = 35 in SL is clearly a recurrent mutation—this means that the mutation occurred independently in different lines, and rather than demonstrating a relationship, the match is coincidental. This is not obviously the case with the three men in the William? group. The only difference between JP and WR is that WR also has DYS 391 = 10, which is the mutation we have been using to identify members of the William? group. If we did not have conventional genealogy on JP, we might speculate that JP was in this group, too, but that he had a "back mutation." This would mean that whereas the common ancestor of the entire large related group of Ewings had DYS 391 = 11, and this mutated to DYS 391 = 10 in the common ancestor of the William? group, that there was subsequently a mutation "back" to DYS 391 = 11 in the line within that group leading to JP. But we do have conventional genealogy on JP, so we are going to argue rather that in his case, CDYa = 35 is a recurrent mutation. Because he is the only project participant descended from John of Carnashannagh's son Samuel, we cannot know where in the seven generations between John of Carnashannagh and JP this mutation occurred. Indeed, there may have been two mutations, each a single step—so, first one of his ancestors lost one repeat from CDYa = 37 to CDYa = 36, and later another ancestor lost another repeat from CDYa = 36 to CDYa = 35. This is "possible," but the most parsimonious explanation is that there was a single, two step mutation. I'll let you puzzle out why I think that on your own.

Guy Raymond Ewing (GR) of Racine, Wisconsin, is descended from James Ewing of Inch Island. I have especially been looking forward to GR's results, because I (DN) have also traced my ancestry to James of Inch. What a surprise this has turned out to be! GR is genetic distance three from the Ewing modal haplotype. He has DYS 460 = 9, two steps from the modal DYS 460 = 11. This mutation is not shared by any other project participant, though RL has the intermediate value, DYS 460 = 10. The surprise is that GR also has DYS 391 = 10! This is the mutation that we have been using to identify (actually, to define) the William? group. Why the surprise? Well, my haplotype is identical to that of GW and RB, both known to be descended from John of Carnashannagh, who did not have DYS 391 = 10, but shared a different mutation with me, DYS 576 = 19. We have been trying to explain the similarity of my haplotype with the John of Carnashannagh group by adducing a close relationship between him and James of Inch. Now it looks like we need to begin looking for a relationship between William? and James of Inch, and I need to begin thinking about whether I am in fact descended from James of Inch at all. You can bet I will be watching closely for the results that are pending on new participant **Steven Robert Ewing (SR),** who is another descendant of James of Inch.[2] Now, the fact is, we know that all the Ewings in the large related group of Ewings have

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[1] In my 4th DNA article, which appeared in the November 2005 issue of the *Journal of Clan* Ewing and is also posted on the Clan Ewing WebSite (www.clanewing.org/DNA_Project/DNA_Articles/051023_CEJ_Y-DNA_WebSite.pdf), I introduced the "I believe his name was William" sub-group. We are abbreviating this as, "William?"

[2] GR's lineage is James of Inch, Samuel, Samuel, Samuel, Samuel, John Otis, Guy Raymond Sr., GR; see Fife, p 304. SR's lineage is James of Inch, Alexander, Alexander, William, Alexander, Henry G., Albert C., Albert, Edmund, Edmund R., SR; see Fife, p 382, top of page. William Ewing m. Elizabeth Billingsley are his fifth great grandparents.

a common ancestor, and therefore that John of Carnashannagh, James of Inch and William? have a common ancestor. They all lived in virtually the same neighborhood in Donegal, and they may have been close kin. There are several possibilities. Their common ancestor could have had DYS 391 = 10, and this mutated to DYS 391 = 11 on the way to John of Carnashannagh, but we doubt this because we have so many participants that also have DYS 391 = 11, whose lineages have not been connected with any of these three lines. The common ancestor of all three men probably had DYS 391 = 11, and a common ancestor of James of Inch and William? mutated to DYS 391 = 10. But for me to be a descendant of James of Inch, I would have to adduce a back mutation (DYS 391 = 10 back to the modal 11) and a recurrent mutation, DYS 576 = 19, which coincidentally made it appear that I was in the John of Carnashannagh line. That's too much. I have to consider seriously that my genealogy may be wrong. Now, if SR turns out not to have DYS 391 = 10, maybe GR should start double checking his genealogy—goodness knows it would have been easy to get tangled up in all those Samuels! But to be really very confident about any of this, we will need another half-dozen descendants of James of Inch to participate in the project. I think it would be especially interesting to get one of **Ellsworth Samuel Ewing**'s descendants on board – he was the founder of Clan Ewing and is another descendant of James Ewing of Inch.[3]

John Craig Ewin (Ewin) of Brunswick, Maryland, knows from conventional genealogic research that his ancestor James Ewin, Sr., who was born about 1770 at Drumcliff, Co. Sligo, Ireland, changed his name from Ewing to Ewin at the urging of his son. Interestingly, John also tells me that a great grandson of the man that changed his name to Ewin changed the spelling to Ewan, so he has relatives with all three names, now. John thinks that the father of the James Ewing who became Ewin may have been named William. James Ewin, Sr. married Deborah Dickson (or Dixon) and they lived in Balloor, Tawley, Co. Leitrim, Ireland, near her parents until they immigrated in 1822. Leitrim and Sligo are the counties on the west coast of Ireland immediately south of Donegal. I'll begin referring to John Craig Ewin as "Ewin," now. Ewin's DNA results also place him at genetic distance three from the Ewing modal haplotype—close enough that he is certain to be a member of the large group of related Ewings, however he spells his name. He shares the mutation DYS 390 = 24 with RA, and he shares CDYa = 36 with MT and WE. He shares his third mutation, CDYb = 39, with EG. RA, MT, WE and EG all have other mutations that they do not share with him or with one another. This makes it impossible to say much about what sub-branch of the family Ewin may be in, except that DYS 390 seems to be a particularly slowly mutating marker, and therefore it is less likely than some to be subject to recurrent mutation, so we might consider that Ewin and RA constitute a sub-branch. Only more data will tell the tale on this.

Michael Thomas Ewing (MT) of Tulsa, Oklahoma, is the brother of Clan Ewing member Ardis Ewing McLeod, who enrolled him in the project. They are descended from Thomas and Mary Anderson Ewing, who seem to have lived on Inch Island, Donegal in the late 18th century. Their son, Samuel Alexander Ewing immigrated with his wife and seven children to Melbourne, Australia during the gold rush in 1853. Ten years later, two of his sons, including Ardis and MT's great grandfather immigrated to New York and ended up in Iowa. MT's DNA results reveal that he is genetic distance two from the Ewing modal haplotype, so clearly within the large group of related Ewings. This is proof certain that some members of our family remained behind in Ireland after many of our ancestors immigrated to America in the early 18th century, not that we ever doubted that this would be so. MT has two mutations; GATA-H4 = 12 is not shared by any of the other men in the large related group, but CDYa = 36 is shared by Ewin and WE. I may be making too much of the DYS 391 = 10 marker (which MT does not carry), but I think the fact that WE has this supports the idea that his CDYa = 36 is recurrent with respect to MT (that is, a coincidence). On the other hand, the fact that Ewin is also a "late" immigrant from Ireland makes me wonder whether Ewin and MT share this marker by inheritance from a common ancestor—perhaps one who had remained in Ireland after the pre-Revolutionary War immigrants to America had left. This is wild speculation at this point; we simply do not have enough data to say anything with confidence, yet.

Wilbur Earl "Buck" Ewing, Jr. (WE) of Pickerington, Ohio, has hit a brick wall back only a couple of generations, and hasn't been able to find his line in Fife or other standard sources. He is hoping that the DNA results will give him some leads about where to do further research. His haplotype is genetic distance four from the Ewing modal haplotype – close enough to place him within the large related group of Ewings. Further, he has the familiar DYS 391 = 10 mutation that characterizes the William? group. He also has CDYa = 36, which is shared by two men not in the William? group (MT and Ewin). Perhaps more interestingly, the three men known to be descended from William? all have CDYa = 35, and WE has the intermediate value between this and the modal CDYa = 37. (JP also has CDYa = 35, but we are discounting this as a recurrent mutation.) Finally, WE has his own unique two-step mutation, DYS 449 = 33, which may allow us to spot close relatives of his in the future. Our suggestion for now is that WE consider focusing on the descendants of Nathaniel (1693-1748, Fife Ch 24) and his half-brothers William (b. ca 1700; Fife Ch 27), Joshua (ca 1705-1758; Fife Ch 25), Samuel (ca 1705-1758; Fife Ch 26), James (b. ca 1712; Fife Ch 28) and George (d. 1798 in Spartanburg Co., SC; Fife Ch 29).

Stephen Lee Ewing (SL) of Minnetonka, Minnesota, is descended from James Ewing (ca 1787-1843, m. Elizabeth Morgan), who arrived in Illinois by 1818 and may have come from Scotland. SL (or rather, his wife Bev, who is the genealogist in the family) thought perhaps that this James was a grandson of Pocahontas James Ewing and his disputed second wife, Sarah Edwards, but the conventional genealogy was very iffy. The DNA results show convincingly that SL is not descended from

[3] He is a fourth cousin of GR, and they are sixth cousins twice removed of DN (if DN really belongs here) and sixth cousins three times removed of SR. SR and DN are seventh cousins of one another, both descended from James of Inch's eldest son, Alexander.

Pocahontas James. In fact, they show that SL is not related to any of the other men in the Ewing surname project! He is genetic distance 19 or 22 from the Ewing modal haplotype, depending on whether you count two-step differences as one or two mutations, but in either case, this is too far to consider there to have been a relationship in the period of genealogic interest. In my mind, this somewhat supports the idea that his ancestor came from Scotland rather than Ireland, but this is strictly speculation. The FtDNA[4] algorithm suggests that there is 50% likelihood that his most recent common ancestor with the modal Ewing haplotype is 103 generations – way before surnames were in use. On the other hand his haplotype is such that he is very likely to be in SNP haplogroup R1b1—the same as all but two of the rest of the Ewings and all but one of the variant spelling group.

Thomas Dale Ewing (TD) of Kansas, the father of Clan Ewing member Annie Ewing (and relative of Georgia Ewing Breen Morgan, another Clan Ewing member) is in a similar situation. We have the results of his upgrade from 25 to 37 markers. We had been interpreting his case as borderline and hoped that more markers would settle the issue, but we really didn't move forward too far. He is a genetic distance nine from the Ewing modal haplotype – so, half the distance of men who are clearly unrelated, like JMc, JM, DS and SL – but still too far to be considered part of the large genetically related group of Ewings. On the other hand, using the same assumptions as we did above to calculate the time to the most recent common ancestor, we come up with 43 generations opposed to 103 generations in the case of SL. So TD is more closely related to the large related group than SL, but we are still talking about a most recent common ancestor over 1000 years ago, probably. Like SL, though, TD is fairly clearly in the R1b1 haplogroup. Everyone in the R1b haplogroup shares a common ancestor among the Cro Magnon, who lived in Europe before the last ice age, something like 30,000 years ago, and the SNP mutation that characterizes R1b1 occurred sometime after that, so even the "unrelated" men in the project share a common ancestor who was probably living in western Europe sometime after the last ice age maybe 10,000 years ago or so, before agriculture came to Europe.

William Myrl Ewing (WM) of Tulsa, Oklahoma, is an entirely different matter. He traces his line to a well known Ewing immigrant, William Ewing of Rockingham (1694-1796, m. Anne Shannon; Fife Ch 32), but his DNA is totally unlike any of the other project participants, and it will be very easy to distinguish his lineage from other Ewing lineages. So far we only have results on 25 of the 37 markers he ordered, so we can't give a genetic distance that is comparable to those we have been giving, but even considering just 25 markers, there is already a genetic distance of 28. Based on this haplotype, the best guess is that he is in SNP haplogroup G2. The common male ancestor of the G2 and R1b haplogroups lived about 45,000 years ago, probably in modern-day Iraq. He is the ancestor of virtually all of the people of Europe and of the Native Americans, and also has descendants throughout Asia. The founder of haplogroup G lived about 30,000 years ago somewhere along the eastern edge of the Middle East. Nowadays, G2 accounts for about 1 or 2% of Western Europeans, and maybe 30% of Georgians (not Georgia, USA, dufus – rather, the country of Georgia in Central Asia.) Some G2 members may have come into Britain when agriculture was introduced around 6000 years ago, and others during the Roman occupation 2000 years ago. Although members of G2 are in a distinct minority in SW Scotland, some of them have certainly been there for thousands of years.

Who is a "Real" Ewing?

I want to be excruciatingly careful that we don't allow anyone to get the idea that there are "real" Ewings and "not so real" Ewings, and I don't want any chance of creating an "in-group" and an "out-group." A Ewing is a Ewing – one family, one Clan. This DNA business is a barrel of laughs and it shows promise of helping us nail down some elusive paternal lines, but let's not give it more than it's due.

New Tests Available

In the last article I reported that Family Tree DNA had begun offering a 59-marker Y-DNA panel and "deep clade SNP testing." Now, they have announced that instead of 59 markers, they are in fact offering a 67-marker panel![5] And I was about to go bug-eyed trying to keep 37 markers straight. Let me explain what the deal is with these new tests.

Deep clade SNP testing

Warning: if you are allergic to technical talk or alphabet soup, you might want to skip this discussion, but you will need to understand some of it if you want to understand John McEwan's interesting article[6] in this issue of the Journal, and I promise to try to keep it light.[7]

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[4] "FtDNA" is Family Tree DNA, the lab our project uses.

[5] I hear someone asking: Where will this end? It looks like it will stop at something less than 200 useful STR markers on the Y-chromosome. If you want to risk learning more than you ever wanted to know about this subject, have a look at the June 2004 paper by Kayser, et al, available for free download at www.journals.uchicago.edu/AJHG/journal/issues/v74n6/41028/41028.web.pdf.

[6] J. McEwan. What can Y-DNA tell us about the Ewings? *J. Clan Ewing*, Vol. 12 No. 3 (August 2006). www.clanewing.org/DNA_Project/DNA_Articles/WhatCan.pdf

"Clade" means close enough to "branch" that I think I'll let it go at that. "Deep" just means "the smallest branches we know how to identify so far." SNP means "single nucleotide polymorphism." In the previous articles all of our discussion has been about STR (short tandem repeat) testing, which is a completely different thing than SNP testing. STRs are much more rapidly mutating than SNPs, and can be useful in genealogy. SNP mutations happen so rarely that once they do, for all practical purposes they create a permanent record. They are more useful in anthropological or population studies. There may be several hundred STRs we could use for our testing, a couple of hundred have been reported for use in forensic testing, and a little over a hundred are being used in genetic genealogy. The largest panel commercially available from one lab is FtDNA's 67-marker panel. There are potentially millions of SNPs that could be used for testing, but only a tiny fraction of these have been identified (36,259 as of July 2006, 200 of which are "well characterized," whatever that means), and of those, the only ones that are used are those that have been found to identify some population of interest.[8]

There are four "letters" in the genetic code, which are more properly called "nucleotides." An SNP mutation occurs when a mistake is made in copying DNA and one nucleotide is stuck in where a different one should have gone. Since the purpose of the nucleotides is to spell out directions for making our bodies, mistakes of this kind can be fatal, and DNA copying is astonishingly accurate. Now, in the sort of genetic testing we are doing (whether SNP or STR), we are looking at regions of the DNA that are often called "junk DNA," because they do not code for the proteins that make up our body and have no known biological purpose. Even though these regions don't make any difference to our survival, they are still copied just as faithfully as the important areas. It's just that mistakes in the "junk" don't kill anybody, so they can accumulate and be passed on indefinitely. Fatal mistakes in the important areas don't get passed on, so far fewer mutations accumulate in these areas. A commonly used estimate of the SNP mutation rate is 0.00000002 per generation.[9] This means that at any specific nucleotide, we can expect a copying mistake to be made once every 50,000,000 generations.

What?! There haven't been anywhere near 50,000,000 generations since human beings first stood up on their hind legs. How could there be *any* of these mutations? Well, keep in mind that there are *lots* of nucleotides—like maybe 60,000,000 in the Y-chromosome alone. So even though there is only one mistake in 50 million nucleotides copied, we shouldn't be surprised to find a mistake if we copy 60 million, as we do in each generation. If you are following me, you should be saying, "Now, wait a minute. If there is one SNP mutation every generation, this should be terrific for doing genealogy." You would be right, except for the fact that when we check for SNPs, we need to know where in the chromosome we are looking—checking all 60 million places with current technology would cost about a bazillion dollars.[10]

When SNP testing is done, we go looking for some specific mutations that we already know about, which we think will tell us where the person being tested falls in the big anthropological family tree. The Y-DNA haplogroups you may have read about are defined on the basis of SNPs. Almost all the Ewing men tested so far[11] are in haplogroup R1b1—a branch of the R1b haplogroup that includes about 80% of all western Europeans, and nearly 100% of Irishmen on the west coast of Ireland in places never much frequented by invaders. Now, Family Tree DNA is testing some additional SNPs that allow us to subdivide R1b1 into "subclades." I got this test done on myself. Here are the results: M173 + M207 + M222 + M269 + M343 + P25 + M126 - M153 - M160 - M18 - M37 - M65 - M73 - P66 - SRY2627 -.12. These results place me in the R1b1c7 subclade. Have a look at John McEwan's article[13] in this issue of the Journal to see what the implications of this are.

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[7] If this discussion just whets your appetite for more information, then visit www.isogg.org/tree/index.html, which can serve as a portal to an inexhaustible supply of detailed information on SNP haplotypes, much of it through links to other interesting websites, but also through links to papers in the scholarly literature.

[8] www.isogg.org/tree/ISOGG_YDNA_SNP_Index.html will take you to a list of all the SNPs that have been published by those doing anthropological research—my count reveals that there are nearly five hundred. There would be no point in testing any single individual for all of them, because only a few of them distinguish the major branches and all the others are for sub-branches. Once you know a subject's main branch, you only need to test for sub-branches of that branch and can forget about the sub-branch markers for all the other branches.

[9] For a more detailed discussion of these matters, have a look at Charles Kerchner's website at www.kerchner.com/dnamutationrates.htm

[10] It cost me $79 to have 15 places checked—do the math. Actually, I am exaggerating. The mitochondrial DNA test of HVR 1 & 2 involves checking 1143 potential SNP loci, costs only $189 at FtDNA, and can be found elsewhere for about $100. FtDNA also offers to check the entire 16,569 nucleotide length of the mitochondrial chromosome for $895, so maybe we could check all 60,000,000 places for $3,240,000 or so, though no commercial lab offers this service, as far as I know. Prices are coming down all the time as testing technology improves, though, and pretty much all of the SNP loci of interest so far are concentrated in a couple of relatively small stretches of the Y-chromosome. If you want to see where, there is an exceedingly cool website at www.ensembl.org/Homo_sapiens/mapview?chr=Y. Maybe SNP testing for genealogy will eventually become feasible.

[11] Five of the men in our project have paid extra to have their haplogroup confirmed by SNP testing. The others have not had any SNP testing, but most of their STR haplotypes are characteristic of R1b1, so there is essentially little doubt that they are also R1b1. I am the only Ewing man who has had the "Deep clade SNP test," which tests for more SNPs, but all of the Ewing men in the large related sub-group of Ewings have STR haplotypes so similar to mine that they are certain also to be in the R1b1c7 subclade of R1b1. It is possible that this is not so for three of the four Ewing men tested so far who are "unrelated" to me—specifically Js, JM2 and DS. Js is probably in R1b. JM2 and DS have both had SNP testing confirming that they are in R1b1, but they could be in a different subclade. On the other hand, of all the Ewings, TD's haplotype is the most similar to the Ui Neill STR haplotype, and even though his is different enough from mine to say that we are probably not related in genealogic time, he is almost certainly also in the R1b1c7 subclade. Of course, since WM is in the G2 haplogroup, he cannot be in a subclade of R1b1

[12] Hooboy. When we report on STR mutations, we give a number that corresponds to how may repeats there are at the locus in question. When we report on SNP mutations, we give the name of the SNP locus in question, followed by a "+" or a "-." The "+" after a mutation name

The 67-marker panel

The "markers" we have been talking about in the Ewing Surname Y-DNA project are STRs. They are also called "microsatellites;" the two terms are synonymous. They refer to sections of the non-coding region of the Y-chromosome where a series of between two and eight nucleotides is repeated several times, generally on the order of 10 to 30 times. When the DNA is being copied in preparation for making sperm, sometimes an error is made and an extra repeat or two is stuck in or left out. Such errors are also called "mutations."

So the difference between SNPs and STRs is that when there is a SNP mutation, just one "letter" is changed. In a STR mutation, a series of several "letters" is added or left out when copying a sequence of letters where the same series is repeated a number of times. The value reported for a STR marker is just the number of repeats that is found at that locus on testing. Any mutation will then be faithfully passed on to all male offspring of the man who has it until such time as there is another mutation at the same marker.[14] An issue currently under active discussion is how often these mutations occur. The most often quoted estimate is that, on average, any one STR marker can be expected to undergo a mutation once every 500 generations, for an average mutation rate of .002 or 0.2%. This is 100,000 times faster than the SNP mutation rate. Recently, a lot of folks are finding that the average mutation rate of the markers we have been using is a fair amount faster than that, maybe even two or three times faster.[15]

Let's talk about what this means. For the sake of discussion, let's assume that the average STR mutation rate is 0.4% in our family. At any one marker locus, we would expect to see a mutation in 250 generations. But if we test 37 markers, we would expect a mutation in 250/37 = 6.76 generations. Now, 6th cousins have the same 5th great grandfather, who is seven generations removed from each of them following different lines. This means that 6th cousins are separated by 14 generations, and that on average, we should expect to see their 37-marker profiles differing at two markers. If we increase the number of markers tested to 67, we have to redo the math: 250/67 = 3.73. So if a 67-marker panel is tested, on average we should expect to see a difference at two markers in the 67-marker profiles of 3rd cousins, who are separated by 8 generations.

So far, only two Ewing men have been tested on all 67 markers. They are Chancellor George Ewing and me. To our surprise, we still match on all 67 markers. So what does this mean? George believes himself to be the 6th great grandson of John Ewing of Carnashannagh. I believe myself to be the 6th great grandson of James Ewing of Inch. We have no documentation of a relationship between these two men, but they were close neighbors in Donegal and were almost certainly related. The difference in their ages suggests that they probably weren't brothers, but let's suppose they were. This would mean that George and I have a 6th great grandfather in common, so are separated by 16 generations. Based on "averages," we would expect to find differences at four markers in the 67-marker panel. The key word here is *average*. FtDNA calculates that there is

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means that mutation was found; the "-" after a mutation name means that mutation was not found. Because SNP mutations are unique and persistent, each of those we use has a conclusive meaning. All men in the large R haplogroup have M207+. In fact, having M207+ is the definition of being in the R haplogroup. M173+ places one in the R1 subgroup, M343+ in the R1b sub-subgroup, and P25+ in the R1b1 sub-sub-subgroup. So everyone in R1b1 has all three of these mutations. So far, at least five different subtypes of R1b1 have been identified. Four of them are distinguished by four different additional mutations and the fifth by the fact it doesn't have any of the four. M269+ defines the R1b1c sub-sub-sub-subgroup. So far, eleven different subtypes of R1b1c have been identified (one of which itself has three subtypes). Ten of these are distinguished by ten different additional mutations and the eleventh by the fact it has none of these. M222+ defines the R1b1c7 sub-sub-sub-sub-subgroup (and I think maybe you are beginning to understand why I defined "deep clade" as I did above). So my deep clade SNP testing results include M207+, M173+, M343+, P25+, M269+ and M222+, and this puts me in the R1b1c7 subclade. The remainder of the SNPs tested did not have a mutation. Two of these distinguish R1b1a and R1b1b, and the others distinguish R1b1c1 through R1b1c6 and R1b1c8. The mutations distinguishing R1b1d, R1b1c9, its two subtypes, and R1b1c10 were not tested, not that this matters too much. The fact is that if a man tests for M222+, you can be pretty doggone sure that he is in subclade R1b1c7 without any additional results. The reason that all of these SNPs are tested is a matter of economy and efficiency. If we know a man is in the R haplogroup and we want to pin down his deep clade, we can set our machine up to look at 19 SNPs and be sure of getting an answer. We could save a little time and money by just testing for one SNP, but only if we were lucky and chose the right one to test for on the first try. If we checked only for M222 and didn't find it, we still wouldn't know what his deep clade was, and we would have to test more SNPs. It would be prohibitively time consuming, confusing and expensive to check 60 million SNPs all at once, but checking 19 all at once is easier than checking for fewer several times.

[13] J. McEwan. What can Y-DNA tell us about the Ewings? *J. Clan Ewing*, Vol. 12 No. 3 (August 2006). www.clanewing.org/DNA_Project/DNA_Articles/WhatCan.pdf

[14] One would think it is vanishingly unlikely for a given SNP locus to mutate twice independently, because the rate is 1 mutation in 50 million generations, which would take on the order of a billion years. But nowadays there are approaching 10 billion human beings, half of them men. Do the math: 1 in 50 million times 5 billion equals 100. Now, I can't tell you what fraction of men will have sons each generation or how many they will have, but the fact that the population of the world keeps going up makes me think that it averages something more than one apiece overall. This suggests that we should expect 100 recurrent SNP mutations at each base pair locus somewhere in the world each generation. But since we are only testing a few thousand men each year for SNPs, and we only check in some specific places on the chromosome, we are never going to find these, no? So how did we find the ones we have found, for goodness sake? Well, the interesting ones happened a long time ago, and by now they have been passed on to lots and lots of men. Really old mutations are either long gone or "relatively" common. On the other hand, STR mutations happen so frequently that it is quite common to find an STR locus where there have been several mutations, and sometimes even "back mutations," which is what we call it when a marker mutates and sometime later mutates back to the same number of repeats it had originally.

[15] Our data in the known descendants of John Ewing of Carnashannagh reveals a difference at two markers separating 6th cousins (on average), suggesting that the average mutation rate in this family is about 0.04%.

a 50% likelihood that two men who have a perfect 67-marker match have a common male ancestor within the last three generations (so, six generations of separation—second cousins or closer), and 90% likelihood that their common male ancestor was within the last five generations. If we are right about our conventional genealogies, George and I have a common male ancestor no more recently than eight generations ago. It is unlikely (something less than 5% probability) that we should have an exact 67-marker match, but it is not impossible. By itself, the perfect match between George and me is not enough to raise serious questions about our conventional genealogies.

There is another factor in this case that really has me scratching my head, though. This is that George and both of the other descendants of John Ewing m. Alice Caswell in our project have the mutation DYS 576 = 19, and so do I. The only other man in what I have been calling “the large group of related Ewings” who has this mutation is RA, whose immigrant ancestor is not known. The fact that George and his cousins share a mutation from the ancestral haplotype of the whole group with me, when added to the perfect 67-marker match between George and me, has me beginning to wonder if my conventional genealogy is correct. Maybe I am a closer relative of George than I thought. Furthermore, in the New Results section above, we found out that GR, another descendant of James of Inch, has DYS 391 = 10, none of the other descendants of John of Carnashannagh have that. This has me beginning to think I may have hung my hat on the wrong branch of the tree

A project participant can upgrade from 37 markers to 67 markers for another $99, but at the present stage of development of the project, we won’t be able to tell you any more with a 67-marker panel than we can with a 37-marker panel. We do not recommend the 67-marker panel for most purposes, though it may be useful for fine tuning some branches of the family once we have the basic structure worked out.

To Join or Get More Information

If you are ready to join the project, go to 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, genetic distances and time to the most recent ancestor estimates expressed as number of generations on the website of Clan Ewing. There are also links on the FamilyTreeDNA website 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.