The Ewing Family Association Brick Wall Project: A New Chapter for the Ewing DNA Project

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This article introduces the Ewing Family Association Brick Wall Project (BWP), which will be far more effective in helping participants break through brick walls in their genealogy research than the Ewing Surname Y-DNA Project has been. The BWP will completely revolutionize and much expand upon the Ewing Surname Y-DNA Project. Because he has an extensive background in data analysis, DG Ewing volunteered to become a co-administrator of the Ewing Surname Y-DNA Project when he joined the project in 2016.

Recently genetic genealogy has been moving progressively toward SNP testing, both Y-SNP testing and the SNP testing of autosomal DNA. Y-SNP testing can give far more reliable information about the paternal line than is possible with the Y-STR testing that the project originally relied upon. And autosomal DNA testing can be used with both women and men participants and gives information about all family lines, not just the strictly paternal line as both Y-STR and Y-SNP testing do. But perhaps the main strength of the BWP will prove to be a system DG has devised to systematically correlate information from all three kinds of genetic testing with conventional genealogy. This is the Most Distant Known Ewing Ancestor Project (MKDEA).

DG has created a Brick Wall Project with three arms:

a. Y-DNA (yDNA) SNP testing and analysis, primarily using the FTDNA Big-Y test.
b. Autosomal DNA (atDNA) testing from any of the several labs and shared at Gedmatch.com
c. The Most Distant Known Ewing Ancestor (MDKEA) Project

We will discuss these arms of the BWP in more detail below. All of them require not only participation by members of the EFA and others interested in their Ewing ancestry by having their DNA tested, but also require a tremendous amount of work in data collection and analysis and maintaining a website and online database. David Neal Ewing is old and tired and pretty nearly at the limits of his energy and understanding dealing with the original STR testing. DG could really use some help with each of the other arms of the project. Analyzing Y-SNP data requires a fair amount of technical sophistication and detailed knowledge about the vagaries of this kind of testing, but anyone who knows or wants to learn how to do this would be welcome to participate. There is a bit of a learning curve involved in interpreting atDNA testing, but this involves mostly conventional genealogy research, logic and only a little technical and scientific detail. The MDKEA involves mainly understanding and tabulating conventional Ewing genealogic data on a new website dedicated to the task.

The Promise of SNP testing and the Big-Y[1]

[1] Various vendors test Y-SNPs, but our project has come to rely on Family Tree DNA and its product, the Big-Y, which tests millions of nucleotides and 700 different STRs. We have focused on the SNP results of the Big-Y.

In STR testing we test relatively few markers that have a relatively high rate of mutation. In SNP testing we test an enormous number of markers that have an extremely low rate of mutation. SNPs are several orders of magnitude less likely to mutate than STRs. The importance of this is that the likelihood of a specific SNP mutating is so excruciatingly small that there is a negligible possibility that a mutation will occur again by coincidence or that once mutated an SNP will revert to its previous state; that is, we do not have to worry about parallel or back mutations. When testing 37 STR markers, we expect to find one mutation every several generations.[2] But with the Big Y we test millions of nucleotides and even though the rate of mutation is very much slower, we expect to find a mutation or two pretty much every generation. Once a nucleotide mutates it will be passed to all subsequent generations with virtually 100% fidelity. If two men are found to have the same mutation, they can be sure that this is because they both inherited it from the same ancestor. So ALL men in Haplogroup R1b1 have the SNP R-M269. ALL men in the "NW Irish" branch of R1b1 have the SNP R-M222. So far we have found that ALL the men in the large group of closely related Ewings (LGCRE) have the SNP FGC19865, which we believe will serve as a definitive branch marker for the men in this group.

Though we can be sure that two men who have the same Y-SNP have a common paternal line ancestor, we cannot tell how many generations ago that may have been without more information. We can figure out the order in which SNPs occurred by correlating their appearance with conventional genealogy. Once we have enough participation, we should be able to identify specific SNPs that identify known genealogical branches of the family.[3]

Autosomal DNA testing and the atDNA Ancestor Project at GEDmatch.com

DNA testing is not confined to the Y-chromosome. Autosomal DNA (atDNA) testing is another example of SNP testing that has become very useful and popular for knocking

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[2] There is a detailed discussion of this issue in David Neal Ewing's Y-DNA Project Article 18, which can be downloaded from our website at https://www.ewingfamilyassociation.org/DNA_Project/DNA_Articles/DNA_Articles/090415%20CEJ%20Y-DNA_WebSite.pdf

[3] Ewing Group 1k consists of three men who are descended from three different sons of John Ewing (c1760–1803) and Margaret Townsley. They all have FGC19863. They also all have four other SNPs that have not been found in any other man (whether Ewing or otherwise) who has had Big-Y testing. We cannot tell whether these occurred in John Ewing or in one or more of his ancestors, or in what order, except that they must have occurred in generations after the Ewing man who first had FGC19863. We know that they did not occur in generations after John Ewing, because he is the most recent common ancestor of the three men in Group 1k and all of them have all four of these. **DN** (David Neal Ewing) also has a "private variant" 10142074. (We use the term "private variant" to refer to mutations that have been found in only one man. Once the same mutation is found in another man, we call it a SNP. Go figure.) Because the two other men in Group 1k do not have this, we know that John Ewing did not have it, and therefore that it occurred either in his son John Ewing of Xenia, or his grandson William Ewing, or his great grandson Fred Ewing, or in his great great grandson Stan Ewing, or in his 3rd great grandson David Ewing, who is **DN**, himself. We could find out whether it occurred in **DN** by testing his brother for it, because if he has it, it must have occurred in their father, Stan Ewing, or before. In any case, if Big-Y testing turns up another man with 10142074, **DN** will know he is a close relative--probably descended from his great grandfather's brother, Silas R. Ewing (1836-1910), because as far as he knows he is the only man in this line who had sons. **RB2**, another man in Group 1k, has two private variants that have not been found in any other man who has had Big-Y testing. The same logic can be applied to this result as was outlined for **DN**. No private variants were found in the third man in Group 1k (**DE**).

down brick walls. The term “autosomal” refers to all of the chromosomes that are *not* sex chromosomes; that is, to the 22 pairs of human chromosomes that are neither X nor Y chromosomes (though the laboratories doing atDNA testing also do some testing on the X chromosome). This has two main benefits for genetic genealogy. One is that this kind of DNA testing can be done on both women and men. The other is that atDNA contains genealogic information for essentially *all* of a participant’s family lines--not just the strict paternal line that is passed down through the Y-chromosome. What’s not to love about that? The challenge for genetic genealogy with atDNA testing is that when sperm and egg are formed a phenomenon called “recombination” or “crossing over” takes place. Each of our cells (except gametes--the sperm and egg) contains two copies of each autosomal chromosome, one that we received from our father and one that we received from our mother. As gametes are formed, a process known as “crossing over” or “recombination” takes place. In this process each chromosome pair undergoes a random exchange of genetic material, such that the resulting gamete contains a mixture of the genetic material from the members of each chromosome pair. As a result none of the chromosomes in gametes is identical to any of the chromosomes in the person that produced them. Each of your parents contributes what will become one member of each pair of your autosomal chromosomes, but what they contribute is itself a mixture of the genetic material they received from their parents. Each sperm and egg that is produced is unique. When a unique sperm cell and a unique egg join, they form a unique individual. This is why we do not look exactly like either of our parents, any of our siblings or any other human being on earth.

Though we receive 50% of our DNA from our father and 50% from our mother, none of our chromosomes is exactly like any of those of either parent.[4] And none of the chromosomes of either of our parents is exactly like any of those of either of their parents. Our atDNA ends up being a mixture of fragments of atDNA from several of our ancestors, and though it can be possible, it is not so easy to determine which specific ancestor contributed which specific bit of DNA.

It is not so easy, but it is not entirely impossible to determine which specific ancestor contributed which specific bit of DNA. By comparing atDNA tests of several relatives in different family lines (such as cousins on our mother’s side with cousins on our father’s side, or more distant relations for whom we know the conventional genealogy) and using a process called “triangulation” we can sometimes identify the source of a specific fragment of atDNA a few generations back. Successful triangulation requires a rigorously systematic approach and creating a “chromosome map” to keep track of where specific fragments of atDNA on specific chromosomes have come from. As you might expect, this becomes more difficult the further back in time one tries to go, but it is possible to go far enough back to break through genealogic brick walls that we have encountered five or six generations back. DG Ewing has been able to move his paternal line brick wall back four generations by using this method, and he believes it will be possible to identify the source of atDNA fragments even several generations beyond that.

As with all testing for genetic genealogy, the value of test results depends on being able to

[4] What is more, though the chromosomes we receive from each parent are a combination only of bits they received from their parents, testing laboratories do not report results on each pair of chromosomes separately and rather report all of the SNPs found on both of them. This is called “unphased” DNA reporting.

correlate them with conventional genealogy. We recommend doing atDNA testing with Ancestry.com because it has the largest database of people who have taken the test. And we recommend that regardless of what vendor has done the test, participants upload their results to GEDmatch.com, which they can do at no charge.[5] DG has a paid subscription to GEDmatch that allows him to use sophisticated analytical tools to compare results for everyone who is participating in the Ewing project there. We tripled the number of participants in our atDNA Ancestor Project at GEDmatch.com within the first week of launching the project and we expect over 200 participants by the time this article is published.

The Most Distant Known Ewing Ancestor (MDKEA) Project

This arm of the EFT Brick Wall Project has grown out of the personal research of DG Ewing. He was applying the triangulation method mentioned above to the atDNA test results of members of his own family lines. Doing this successfully requires one to know and keep track of exactly which ancestors he has in common with the relatives for whom he has atDNA results. Five generations back we have 32 3rd great grandparents, so this can quickly get pretty confusing. What's more the fact that given names are so often repeated in succeeding generations of families makes it hard to know and remember who in the dickens we are talking about when we say, "William Ewing."

DG's first step was to assign every individual in his database a unique personal ID number. This is not a new idea; most genealogy programs allow one to assign personal ID numbers in a systematic way. DG's new idea is to create a database of Ewing ancestors for the BWP and assign standardized ID numbers that everyone doing research in the project will use to minimize confusion.

He has begun collecting and entering data in a database on "Most Distant Known Ewing Ancestors." One source of this has been the lineages provided by about 200 of the participants in the Ewing Surname Y-DNA Project. Another is his personal research. So far, he has identified over 350 persons with the surname Ewing for whom no parents have been identified–he calls these "terminal" or "orphaned" Ewings, which just means that their parents are so far unknown–and he has created a detailed database that will serve as a standard repository for MDKEAs. Each individual will be identified with a unique personal ID number. This is "phase 1" of the MDKEA project. The database will be posted online in a format that will permit participants to edit information there.[6] Their contributions will constitute "phase 2" of the project and the number of MDKEAs will gradually grow.

Further, the dedicated Ewing website will provide a forum to vet and exchange genealogic information that can also be coupled with DNA results and evidence. A formal launch of the website will be announced in all of our social media outlets. He expects that the website will "go live" before Valentine's day 2022 and a beta version will go live in 8-10 weeks. He is looking for beta users to flush out any issues before going live. If you are interested please contact him.

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[5] MyHeritage is another atDNA testing vendor which has a growing database and some unique analytic tools. Ones results can also be uploaded to this database for a small charge, which will allow comparison of results with people who have tested at MyHeritage and have not uploaded their results to GEDmatch.

[6] Note that because atDNA also derives from female ancestors, a MDEKA with two wives will create two MDKEA records.

Summary Recommendations

1. We recommend Big-Y testing for obtaining maximal information about ones paternal Ewing line. The Big-Y has the potential for providing information about specific family lines; however,
2. Ewings that are *not* in the LGCRE (ask if you are not sure about this) may not immediately get genealogically useful information until enough men in this group have had Big-Y testing to provide a sufficient basis for comparison. Ewings *not* in the LGCRE should consult with one of the Ewing project administrators before ordering the Big-Y.
3. Anyone interested in genealogy should get atDNA testing on themselves, and
    a. Get atDNA testing on as many of their parents and grandparents as possible, and the siblings of their parents and grandparents, and their cousins in lines of especial interest. The results for each of these relatives will have different mixtures of fragments of DNA from ones ancestral lines, and these will provide clues about where they originated.
    b. Upload all of these results to GEDmatch.com.
    c. Begin making a chromosome map to keep track of where specific chromosome fragments have come from.
4. All Ewings (through both paternal and maternal lines) should provide well-documented information as to the identity of their most distant known Ewing ancestor to the MDKEA Project. A website is being developed to facilitate this effort.
5. Volunteer to become a Brick Wall Envoy by becoming:
    a. A Beta User
    b. atDNA admin
    c. yDNA admin
    d. MDKEA admin
    e. Website admin
    f. All of the above