DNA INSTALMENT FIVE

ANALYSIS OF THE GRIER, ETC. DNA CHART 1e

TOGETHER WITH COMMENTARY

GENERAL

In this report I address the revisions to the DNA Chart that have taken place this year. It should be noted that, as previously remarked, the science of DNA as applied to genealogy is advancing remarkably quickly. Indeed, by about November 2012, I expect that we will see some significant change in the general assumptions relating to the so-called "Niall" group - that is M222, and also to the L21 group, see below. With respect to M222, a new computer chip has established, so we are told, a series of SNPs below the M222 mutation. As that is a relatively young mutation, younger SNPs are likely to give some information about family grouping within the period of surnames, and if that happens, DNA genealogy will have reached one of the stated aims we set out to achieve 10 years ago.

You will note that there are several new haplogroups on this chart, each of which is carried by only one representative. Nothing in particular can be deduced from this information yet, and those men will have to wait for an expansion in the testing, hopefully by persons with paper trails going back a reasonable time.

There has been little advance within the Viking subgroup during this period.

There is additional information about some of the results shown here to be found at the Family Tree public website for Greer/Grierson, see:
http://www.familytreedna.com/public/GREER/defaultaspx?section=yresults

HAPLOGROUP R-M222

Continued testing in this haplogroup has served to confirm previous judgements. Of the Grierson/Greers shown, members 57611, 57917 and 139012 cannot be assumed to be part of the larger family. 57917 is clearly of Irish derivation, his haplotype almost exactly matching the M222 Irish modal. The others have insufficient markers tested to even be certain that they are M222, although it is probable in the case of 57611. All the remainder are certainly descendants of the founder of about 650 years ago, and their relative separation is made more obvious by the highlighted marker counts at 389-1, 576, and CDYb. I'm fairly sure that, if further testing in the 68-111 marker regions was carried out there would be similar differences evident. However, as stated below, I don't advise further STR testing at this time, pending further information about the young SNPs.

Of interest are the near and distant relatives shown in lines 55-62. In my judgement, Tucker, Stubblefield and Cool are direct descendants of the founder, the consequence of so-called NPEs, most likely adoption or extra-marital union. The two Millican models shown have been developed in the Amuligane study, and illustrate the

divergence that has occurred in the "Nith" cluster. Likewise, the Mosely and McKown comparisons, which indicate some relationship, but of a substantially older kind. Millican Modal 2 is clearly much closer to some of the Grierson results.

Mentioned above are the new M222 SNPs assumed to be younger than the M222 mutation which is, at the moment, assumed to be about 2000 years old. These have been discovered, as I understand it, during the progress of the Genographic Project being conducted by National Geographic, using what is called the Geno 2 Chip. This computer chip is capable of testing about 20,000 SNP,s, we are told, but their actual identity is not yet released. I have registered to be tested in this project in the hope that a "Nith" version of M222 becomes easier to identify. It is hoped that Family Tree DNA will eventually make available appropriate tests for the younger SNPs, and it is these types of test that I would prefer, from a research perspective, that members undertook.

Member 209737, at position 48 (DYS 425), has a zero count. This rather rare happening is known as a RecLOH event, which is short for "Recombinational Loss of Heterozygosity". Very briefly, during the course of a mutation at the point of recombination, in certain particular markers (so called duplicated markers) there may be an accidental overwriting of one marker by its twin. This results in no differentiation between them, hence the zero. It is important to understand that there is not a missing gene. I further understand that the frequency of occurrence of this type of event sits between those of the SNP mutation (rare) and the STR mutation (averaging perhaps one in five generations), so the possibility exists that it, too, might be of use in genealogical studies.

L21 now DF13

To illustrate the rate of change of knowledge in this business, let us consider the L21 haplogroup. Just a year or two ago, L21 was regarded as a significant haplogroup, with one or two known descendant groups such as M222. Indeed, the FT and ISOGG haplotrees still reflect this as is illustrated by the derivative labels of R1b1a2a1a1b4 (for SNP L21) and R1b1a2a1a1b4b (for SNP M222). But a look at the website of the L21 project will show how much this has changed:
http://tech.groups.yahoo.com/group/RL21Project/?v=1&t=directory&ch=web&pub=group&sec=dir&slk=420
There are now three known SNPs between L21 and M222, and the major SNP below L21, DF 13, is now known to have 10 younger SNPs, most off which themselves have significant numbers of descendants. Not all of these are available for testing as yet, but once they are they will provide significant information for those who wish to pursue family relationships.

Since the discovery of the DF13 and DF 63 SNPs, it has become obvious that only a small minority of those tested who were previously listed as L21 belong to DF63. That means that their contribution, as haplotypes, to the L21 modal calculation would be negligible, probably not even swaying one STR marker count. Therefore, it is more correct to refer to what was called the L21 modal as the DF13 modal, representing our best guess as to the haplotype of the DF13 founder. DF63 will support its own modal in due course.

Unfortunately, I have been unable to convince any member of this group to undertake further testing. Consequently, the genealogical knowledge they might have gained from DNA testing is not available to them. At this point, my advice is hold off from further testing until the "deep clade" tests begin to include the new, young, SNPs. I will, meanwhile, attempt to match their haplotypes with those of people identified in the newer haplogroups. Watch this space, and the FTDNA website shown in the introduction.

THE STANDARD APPEAL

The only way we will advance our knowledge about the interrelationships within the whole group of Grier(son)/Greer families is to convince males bearing these names who are interested in the truth in genealogy to undergo YDNA testing. Once again I challenge such men to "bite the bullet", and take the test, even though the outcomes might lead you to rethink those fables and myths about the Grierson ancestry.

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