

THE Y-DNA PROJECT

January 2013

Quarterly report from Elizabeth O'Donoghue/Ross, the Society's Group Administrator

Happy New Year to everyone!

A great deal has been accomplished in the genetic genealogy community over 2012, much of it quite technical and beyond the scope of this Y-DNA Project. But, for those who are interested, there is a blog report of 2012 Top 10 Genetic Genealogy Happenings at <http://dna-explained.com/2012/12/28/2012-top-10-genetic-genealogy-happenings/> which may be of interest to some of you. This is a website maintained by Roberta Estes, a respected member of the citizen scientist genetic genealogy community.

Last quarter I reported that the society funded an upgrade for one of the original participants recruited by Prof Tom – Florence O'Donoghue, a member of the Glens tribe and the Crothur Ógs of Inch – from 25 to 37 markers. At that level, he was found to be closest to the group of Roger, Jerry and John. After the disappointment of the group last year that Michael O'Donoghue, who owns the farm which is most likely their old family home, was not related to them at all, they were intrigued by this news. As it happens, Flurry lives just across the road from Michael's farm. This instigated Clarke Glennon (Jerry's cousin) to encourage the group to fund a further upgrade to the full 111 markers to see if the connection might be close enough to consider Flurry a relative in genealogical times. The upgrade was ordered and the results came in, and Flurry is closest to John Joseph Donohue at 111 markers, but closer yet to Nic (Bertolero, adopted name of father) Donahue at 67 markers.

Nic has previously been in touch with John Joseph's daughter, and they haven't yet been able to find the paper evidence their common ancestor, though they are comfortable that they have one, since she has the same reoccurring family names in her family as Nic. But the situation of Nic, Roger, Jerry and John is clearer, since they know that they have common ancestors in Florence and Hanora Donahue – cousins to some degree and both Donoghues themselves. Nic is descended from Florence, and the rest of the group are descendants of Hanora's male siblings or cousins that lived in the Northfield, Vermont area.

Since Florence and Hanora are also related, it would be expected that the genetics of both sides of that family would be relatively close in haplotype, and there are some common off modal marker matches between them all. However, it appears that Nic is possibly more directly related to Flurry of Inch than any of them. Further upgrades to 111 markers for the remaining members of the group may shed more light on the relationships.

I've rearranged the order of the Glens group in the spreadsheets to add John Joseph and Flurry to the cluster of Roger, Jerry, John and Nic.

It has been a quiet quarter for new results, but in addition to Flurry's upgrade in the Glens tribe, we have another SNP result in the Mór group.

You may recall in the April 2012 report I discussed the enigma of the SNPs found in the different subgroups of the Mór lineages. Prof. Tom's cluster are positive for DF21 along with Tighe, while Rod is negative for DF21. In addition, Tighe is also positive for DF5 and

Z248, while Merle Thornton in Prof Tom's group tested negative for these additional two SNPs. There is another SNP, DF25, which lies between DF21 and DF5 in the hierarchy of SNPs, which Tighe is presumed positive by virtue of the fact that he is positive for the downstream DF5. Merle hadn't tested for DF25 either, but the DF21 project administrator suggested that Merle test for DF25, and he did. His results show he is positive for DF25, which as a result places him closer to Tighe than previously thought.

The appearance of a back mutation for Rod and his cluster (as detailed in the April Report) still seems the only explanation for their not being positive for DF21. To imagine that Tighe and Rod's cluster are not related since the estimated time of the first mutation to DF21 (several thousand years) is just not plausible, considering their sharing the same name, the very uncommon value of 12 at DYS392, the proximity of their places of origin (some within 25 miles or less), even similar physical characteristics. Hopefully, further research and discovery of SNPs will help clarify this anomalous situation.

You may remember the National Geographic's Genographic Project was launched in 2005. The number of participants is around 500,000 by now. A number of our participants started with the Genographic's 12 marker STR test, then joined us; and most have upgraded since then. Recently, National Geographic has expanded to include the Geno 2.0 Project (<https://genographic.nationalgeographic.com/>) which is focusing on testing for nearly 150,000 SNPs. Family Tree still has a Deep Clade test for \$139, but for many haplotypes, particularly in the R1b1a2 haplogroup, the Deep Clade test is no longer useful since so many new SNPs that have been discovered over the last few years through Walk-the-Y tests (<http://www.familytreedna.com/faq/answers/default.aspx?faqid=27>) the 1000 Genome project (<http://www.1000genomes.org>) and other independent research projects are not included in the current Deep Clade test.

The main shortcoming of the Geno 2.0 project is that not all the most recently discovered SNPs are included in this test, and there was no indication that it would be useful in any particular way to those in our project, so I hadn't mentioned it earlier, thinking that if any new SNP would be discovered that might relate to anyone in our project, that SNP would be offered by Family Tree at some point for the \$29 charge for an individual test.

As it happens, a South Irish participant of our Munster Irish DNA Project ordered the test and his results have shown two SNPs identified in one of the previously mentioned projects but not assigned to any haplotype yet - CTS4466 and CTS5714. We can't be sure, but we are hopeful that these SNPs will be found to identify the South Irish cluster – we will then be able to call it a true subclade.

When the CTS4466 and CTS5714 SNPs are available for individual testing, I will send a bulk email to all project participants to advise them. At this point, there is no indication when Family Tree will offer them. In the meantime, if anyone is interested, they can always join the Geno 2.0 project and get the complete test. Joining the Geno 2.0 costs \$199.95, and you must participate through National Geographic rather than Family Tree, but you can have the results transferred to your Family Tree account. Let me know if you have any questions about the Geno 2.0 or any other subject related to our project.

If you find inaccuracies in this report or on the website, please let me know. The spreadsheets should be updated shortly and Rod will let you know when they are available.