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‘SATIABLE CURIOSITY: RESEARCH NEEDS OF THE GENETIC GENEALOGY COMMUNITY AND PROPOSED PROJECTS THAT COULD ADDRESS THESE NEEDS

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'SATIABLE CURIOSITY

Genealogists will readily admit to an insatiable curiosity about their ancestors. Fitting one new ancestor onto a pedigree chart provides only a temporary moment of triumph. It immediately raises two more questions – who were the father and mother?

The same applies to tracing DNA patterns. We rejoice when we find a DNA cousin in one ancestral line, but our curiosity will not be completely satisfied until the complete genome of everyone on earth has been linked into one gigantic network, showing how we are all cousins many times over.

Yet if we take Rudyard Kipling's phrase, 'satiated curiosity, in a literal way, there are many questions that might be addressed with small-scale projects, perhaps even by students taking a class on DNA analysis techniques. The genetic genealogy community could provide samples that have already been analyzed to some extent, and the students could end up with a publishable paper.

For example, the Y-chromosome phylogenetic tree has been cobbled together using markers developed at different laboratories (see http://ycc.biosci.arizona.edu/nomenclature_system/frontpage.html). Some branches of the tree have two or even more markers, which are "phylogenetically equivalent" – that is, no cases have yet been found where one marker is positive and the other marker is negative. Yet not all papers actually report on both markers, and the number of samples may be quite small.

Take the fragment of the tree shown in Figure 1. We see that the markers P36, M242, and MEH2 appear on the main branch point

leading to Haplogroup Q. The researchers could put out a call to the genetic genealogy community for people who have been proven, or even predicted, to belong to Haplogroup Q. These could all be typed for both markers to see whether they all still hang together, or if they actually define two distinct branches. Similar experiments could be performed at other points on the phylogenetic tree.

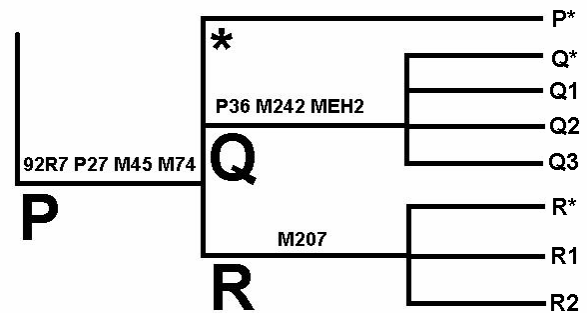


Figure 1 Fragment of the Y-Chromosome Phylogenetic Tree

The genetic genealogy community is an untapped resource of willing volunteers who have been prescreened by commercially available testing procedures. Future editions of this column will include requests from researchers looking for subjects as well as questions posed by genealogists. Please send submissions to Ann Turner at the address below, with the subject line "Satiated Curiosity."

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