

HAWKINS WORLDWIDE DNA Project

Newsletter 2008-03

31 March 2008



This Newsletter is addressed as a blind copy to protect individual identities.

Project site: <http://freepages.genealogy.rootsweb.com/~hawkinsdnaproject/>.

Family pages: http://freepages.genealogy.rootsweb.com/~hawkinsdnaproject/tree_g-1.html

Administrator: phil_hawkins@sbcglobal.net {phil_hawkins"at"sbc.... }.



We have established Hawkins Family Group #15. It is the first group started with no U. S. participants. One participant is in England and the other in Canada. I have a feeling that this group may have a common ancestor with our Hawkins Family Group # 03, but if that is so, it is a ways back. Additional participants will decide, in time, if 03 and 15 are the same family line (clade).

Participants from countries other than the U. S. are growing. Eight individuals are now participating; five in the UK, two in Australia, and two in Canada. We would like to see a lot more growth in this area.

The exchange rate between the British Sterling or the Euro and the US \$ is at its lowest point in a number of years. That means that there has never been a less expensive time to get your surname DNA on record. Reviewing some different testing companies, it is obvious that a test of about 25 markers (it takes this many to establish a relationship within the surname timeframe starting about 1400) is priced at less than \$ 150. Taking the calculator to that price and using rates from today's foreign-exchange quotations from Reuters, I come up with a conversion of £ 75.23, € 94.91, Australian \$ 163.48, and Canadian \$ 153.17.

Per Family Tree DNA: In 2007, they opened a European Office in Zurich, Switzerland, to better serve their European customers. This office provides support for our European customers in Spanish, French, Italian, German, and English, as well as providing local shipping and payment in European currencies. That site is at: <http://europe.familytreedna.com> or <http://www.familytreedna.com/europe.html>.

I have added a Search/Find function to the Family Pages at:

http://freepages.genealogy.rootsweb.com/~hawkinsdnaproject/tree_g-1.html



As I stated last month, I have been scanning clippings from one of my mother's scrapbooks (she had one going from the 1920s into the late 1990s), and I am again placing a couple in this newsletter. The gas coupons were probably unused when rationing ended. Note that it was almost two years after WW II ended before sugar rationing ended.

Washington, June 12.—(AP)—The last war-imposed coupon control over the American public vanished today, as sugar rationing for home, restaurant and hotel use ended at midnight.

After five years in which ration stamps meant more than money—when it came to meat, canned goods, shoes, tires, gasoline and a host of other things—individual Americans are free of coupon worries for the first time since April 28, 1942.

The last ration book can be thrown away. 1947

However, sugar price controls remain. So does rationing of industrial sugar. But these two curbs are scheduled to end October 31.

Preservation Tip of the Month by Becky Schipper: The polystyrene cases in which CD-ROMs & DVDs are sold are acceptable for long-term storage. Jackets made of paper (unless it is acid-free, archival paper), cardboard, PVC, and plasticized polymers are not recommended. Adhesive labels can cause long-term problems and affect the balance of the disk during reading. If you're planning on writing directly on the disk with a felt tip pen and expect to save that disk for a long time, consult the pen manufacturer to see if there are any potential problems with the ink interacting with the surface of the disk. In the event of degradation or if the media begins to become obsolete, the data should be transferred to new media. While there is some debate about how often this transfer really needs to be done, to be safe one should refresh one's storage media every thirty-six to sixty months.

Source: Genealogy Gems: News from the Fort Wayne Library No. 49, March 31, 2008.

Our Hawkins Project has 115 Y participants, and to date we have identified 50 different and unrelated Hawkins Y (male) lines. And I'll bet that you have noticed that your Hawkins ancestors are all named John or James, and of course, they all lived in England (or Virginia and/or the Carolinas at one time). Thank heaven for little door openers like DNA.

If you are a Hawkins male and have not yet joined our project, please - give it some serious consideration. The donation of your DNA for the benefit of your descendants might very well turn out to be one of the most generous things that you have ever done. Think 2099 A.D.

If you have a new address please advise me. Contact me if your are one of the following emails: "Due to extended inactivity new mail is not currently being accepted for these mailboxes:"

1stcav70@earthlink.net, ph52@earthlink.net, Berkfield2@aol.com, baxllo@aim.com.

I have included below a press release that publishes today. The blue are comments that I have added. There are some words that will be strange, but struggle through it, and I think that you will add a little more to your understanding of DNA.

Haplogroups are assigned letters of the alphabet, and refinements consist of additional number and letter combinations, Example: R1b1. So far, our Hawkins project has participants from six of the major haplogroups: E (E3b1), G, I (I1a and I1b), J (J2), K (K2), and R (R1A, R1b, R1b1, R1b1c, and R1b1c7). A haplogroup is a group of similar haplotypes that share a common ancestor. Think of your haplotype as your personal Hawkins family line.

PRESS RELEASE EMBARGOED: Not for release until 5:00 p.m. EDT (US time) on Tuesday, April 1, 2008.

Scientists reshape Y chromosome haplogroup tree gaining new insights into human ancestry,
Wednesday, April 2, 2008.

The Y chromosome retains a remarkable record of human ancestry, since it is passed directly from father to son. In an article published online today in *Genome Research* (www.genome.org), scientists have utilized recently described genetic variations on the part of the Y chromosome that does not undergo recombination to significantly update and refine the Y chromosome haplogroup tree. The print version of this work will appear in the May issue of *Genome Research*, accompanied by a special poster of the new tree.

Human cells contain 23 pairs of chromosomes: 22 pairs of autosomes [22 from the father, and a like 22 from the mother], and one pair of sex chromosomes. Females carry a pair of X chromosomes that can swap, or recombine, similar regions of DNA during meiosis. However, males harbor one X chromosome and one Y

chromosome, and significant recombination between these dissimilar sex chromosomes does not occur. Therefore, the non-recombining region of the Y chromosome (NRY) remains largely unchanged over many generations, directly passed from father to son, son to grandson, and so on, along with genetic variations in the NRY that may be present. Scientists can use genetic variations, such as single nucleotide polymorphisms [polymorphism means having multiple alleles of a gene, or saying it differently it is a marker mutation] (SNPs), on the Y chromosome as markers of human ancestry and migration.

In 2002, the Y Chromosome Consortium (YCC) constructed a tree of 153 haplogroups based upon 243 unique genetic markers. In this report, researchers led by Dr. Michael Hammer of the University of Arizona [Mike Hammer is Family Tree DNA's Chief Scientist, and member of the Scientific Advisory Board] [see short bio and picture at <http://www.familytreedna.com/about.html>] recognized the need to revisit the Y chromosome haplogroup tree and incorporate the latest data. “The YCC effort in 2002 was a landmark in mapping the then known 300 or so Y-linked SNPs on a single tree, and getting the community to use the same nomenclature system,” explains Hammer. “The rate of SNP discovery has continued to increase over the last several years, as are publications on Y chromosome origins and affinities. While this new information is useful, ironically it also brings with it the danger of introducing more chaos into the field.”

Hammer’s group integrated more than 300 new markers into the tree, which allowed the resolution of many features that were not yet discernable, as well as the revision of previous arrangements. “The major lineages within the most common African haplogroup, E, are now all sorted out, with the topology providing new interpretations on the geographical origin of ancient sub-clades,” describes Hammer. “When one polymorphism formerly described as unique, but recently shown to have reversed was replaced by recently reported markers, a sub-haplogroup of haplogroup O, the most common in China, was considerably rearranged,” explains Fernando Mendez, a co-author of the study.

In addition to improving the resolution of branches, the latest reconstruction of the tree allows estimates of time to the most recent common ancestor of several haplogroups. “The age of [haplogroup] DE is about 65,000 years, just a bit younger than the other major lineage to leave Africa, which is assumed to be about 70,000 years old,” says Hammer, describing an example of the fine resolution of age that is now possible. “Haplogroup E is older than previously estimated, originating approximately 50,000 years ago.”

Furthermore, Hammer explains that this work has resulted in the addition of two new major haplogroups, S and T, with novel insights into the ancestry of both. “Haplogroup T, the clade [a family line from a single common ancestor] that Thomas Jefferson’s Y chromosome belongs to, has a Middle Eastern affinity, while haplogroup S is found in Indonesia and Oceania.”

More SNPs are being discovered, and we anticipate the rate to increase with the 1000 Genomes Project,” says Hammer, referring to the wealth of human genetic variation data that will soon be available. While this report represents a significant advance in mapping ancestry by Y chromosome polymorphisms, it is certain that future discoveries will necessitate continual revisions to the Y chromosome haplogroup tree, helping to further elucidate the mystery of our origins.

Scientists from the University of Arizona (Tucson, AZ) and Stanford University (Stanford, CA) contributed to this study. This work was supported by the Salus Mundi Foundation.

Media contacts:

- Michael Hammer, Ph.D., has agreed to be contacted by email for more information (mfh@u.arizona.edu).
- Interested reporters may obtain copies of the manuscript from Peggy Calicchia, Editorial Secretary, *Genome Research* (calicchi@cshl.org; +1-516-422-4012).

About the article: The manuscript will be published online ahead of print on April 2, 2008. Its full citation is as follows: Karafet, T.M., Mendez, F.L., Meilerman, M.B., Underhill, P.A., Zegura, S.L., and Hammer, M.F.

New binary polymorphisms reshape and increase resolution of the human Y-chromosomal haplogroup tree. *Genome Res.* doi:10.1101/gr.7172008.

About *Genome Research*: *Genome Research* (www.genome.org) is an international, continuously published, peer-reviewed journal published by Cold Spring Harbor Laboratory Press. Launched in 1995, it is one of the five most highly cited primary research journals in genetics and genomics.

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If you maintain a website that relates to any of our Hawkins DNA lines, please advise, and I'll list it on our site.

If you maintain a web site with Hawkins information, please add a link to our Hawkins DNA Project.

If you know someone that would like to be on the Hawkins project information mailing list, please send me their name and email and I'll add them. Anyone that desires not to be on the list should request removal.

Please advise us of any planned Hawkins reunions. We would like to list them indicating the patriarch, place, dates, and any other special information. Consider collecting donations to have some of the cousins in your group tested. Maybe you have the perfect paper records, but the mutations that occur in the separate lines need to be identified now for succeeding generations (and just maybe your paper records are not as solid as you assume).

If you have tested with someone other than Family Tree DNA please contact me about also participating in our Hawkins Project.

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