

Journal: www.jogg.info

Originally Published: Volume 5, Number 2 (Fall 2009)

Reference Number: 52.003

INTERVIEW WITH BENNETT GREENSPAN OF FAMILY TREE DNA

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Interview

With Bennett Greenspan of Family Tree DNA

Interviews with people who play an important role in population genetics, forensic genetics, and genetic genealogy are presented in this feature. Suggestions for interview subjects are welcomed.

JoGG: The people who have attended the conferences for project administrators in Houston have heard you speak about the origin of Family Tree DNA (FTDNA), but many others in our community may not know how you got started. Could you repeat your origin story for JoGG readers?

BG: I was unemployed in 1999 and didn't have enough to keep me busy...my wife suggested that I take up my genealogy as a way to keep me out of her kitchen. In doing so I found not only long lost family members in the US, but I found a possible cousin in Argentina who I wasn't able to absolutely prove was related...I couldn't find the paper trail...I was at a dead end in the road. Fortunately I remembered articles on the Cohanim and the Jefferson study, both using the male inherited Y Chromosome and I reached out to the U of Arizona to help me. It turned out that they helped me right into new job, and an industry, Genetic Genealogy, was born.



Bennett Greenspan

JoGG: FTDNA recently announced that you had now processed over a half million samples for either Y tests or mtDNA tests, which is an amazing number. Can the rate of growth that you have experienced over the last few years continue? How long will it be before we hear about a million samples processed?

BG: I'm afraid that the 1,000,000-test mark is quite a ways away. I don't think the field is becoming less popular, but the curious have already tested...now it's going to be a little more difficult since the early adaptors have already tested--so the resistance level is going to be a bit higher in the future.

JoGG: You have recently put a lot of resources into automating the lab in Houston. Presumably that will speed up the processing of the type of non-standard orders that you carry out in the Houston lab, but will this automation also allow you to take on things that were not possible before, or were impractical?

BG: The Houston lab is one of the most advanced labs in the country. From an automation standpoint we are probably equal to the very best. In many of our processes, we operate in a humanless environment, which makes us faster and less prone to the types of errors that plague work where humans are involved. One example to this is the automated storage device, which retrieves our samples without human intervention. This automatic SHOULD allow us to turn around Deep Clade tests in two weeks (providing the sample is already in Houston).

JoGG: In regard to the "Walk Through the Y" or WTY project, you are sequencing about 100,000 bases of the Y chromosome for dozens of participants in many haplogroups in order to discover new SNPs that might be useful for phylogenetic purposes. How is that project coming along and what will it mean for our community?

BG: We have been talking about ways to 'bust' through the Y chromosome for a few years. We are offering to phylogenetically interesting people the opportunity to

run 100kB in an attempt to find new SNP's. The results range from none to three new SNP's discovered in a single sample. We have accepted about 110 orders and have completed about 20 of these so far (in July 2009).

JoGG: Full genome sequencing (FGS) for mtDNA is becoming a more common occurrence at FTDNA. About how many FGS orders have you filled at FTDNA?

BG: We have been offering the sequencing of the full mitochondrion molecule for about three years but in the past year it has really taken off. We have several hundred in process now and have completed over 5200, plus we regularly get requests from universities around the world to run these since we have created a pipeline especially designed to process large numbers of these in a relatively short period of time.

JoGG: Many of the FGS sequences have been uploaded to GenBank and are available for researchers to use. Does FTDNA do the uploading on request, or does the customer have to take care of that themselves? How many FGS sequences that were generated at FTDNA have been uploaded to GenBank?

BG: FTDNA feels that it's the customer's responsibility to upload his/her own data to Genbank, but we provide the FASTA file and others have created somewhat easy ways to do the uploading. We think that about 600 FTDNA samples are in Genbank already.

JoGG: I notice that some of the mtDNA research articles coming out now have mentioned that some of the FGS sequences they have used for their studies have come from FTDNA. While the FTDNA sequences are not coming from a controlled population, it would seem that phylogenetic studies would be quite willing to use such privately generated data. How do you see the FTDNA sequences being used?

BG: More universities are having FTDNA do the FGS for their studies, and in addition we have a policy of asking our FGS clients if they want their results placed into a repository that researchers can 'tap,' anonymously, to bulk up the FGS samples. In addition we are quite keen to help the semi-professional community with recruitment for projects that are important but haven't reached the eyes of the academic community yet. Just because the academics aren't interested, our clients's research should NOT suffer!

JoGG: Do you see some of the examples that we have discussed as a part of a growing partnership between the "amateur" and "professional" genetics communities?

BG: I think that anytime the academics will listen to what is actually being found by the semi-professionals that they have to reflect on just how active a customer

base we have. The academics are few in number and don't have the resources that the general community does, so it's not really surprising that the semi-professionals are in some areas taking a commanding lead in research and knowledge. FTDNA is pleased to be part of that effort, be it via the Walk The Y project or in our focus on the FGS mitochondria profiling.

JoGG: At the present time, Y-STR tests are available as "standard orders" for panels of 12, 25, 37, and 67 markers at FTDNA. But, you also can test about 50 additional markers under your "Advanced Orders." Can we expect to see new panels of "Standard Orders" forthcoming in the near future, and do you expect additions of new STR markers to the "Advanced Orders?"

BG: Yes and Yes.

JoGG: As you are aware, JoGG published an article by John Butler of NIST, and also published an editorial, in the Fall 2008 issue on the subject of standardization of Y-STR nomenclature. Since then ISOGG has called on every company to adopt the NIST recommendations. What does FTDNA plan to do on this matter?

BG: Since Family Tree DNA began this industry and featured matching from our inception we have the oldest database schema of any company in the business--translation: converting to a new database structure that incorporates all the items called for by Dr. Bulter isn't trivial. The adoption of the nomenclature is something our IT folks are working on now, but we will incorporate micro-alleles at that time as well. We have approximately 170 pages on the site that will be affected by these changes to our system, not to mention the total rewrite of FTDNATiP that will need to account for microalleles. Since most other testing companies don't offer these features their conversion is much more trivial. Our IT staff is budgeting 11 weeks for two programmers to complete this task; we have begun, but don't anticipate its completion until toward the early part of 2010.

JoGG: Will the reporting of microalleles be retroactive, or will they only be reported for tests completed after the change to your database structure?

BG: Glad you brought that up. We will obtain an entirely new refresh to the Y database for all samples ever sent to us from Arizona and also from our local lab in Houston so extra copies of various markers, microalleles and standardized nomenclature will become available all at one time.

JoGG: What else does the future hold for genetic genealogy? There has been a gradual downward trend in price for your standard orders. Will that continue? What kind of DNA processing technologies do you view

as having the biggest impact upon the field now and in the future? Is there some “game-changing” technology on the horizon?

BG: I just can’t answer this—it’s always problematic to announce possible future product developments, both for competitive reasons and the fact that the best laid plans don’t always work out.

JoGG: There seems to be an increasing call in some quarters for more regulation of the genetic genealogy field. Do you think any kind of regulation is needed? Do you see regulation as a threat to the way you do business?

BG: If the call is intended to stop people getting a peek at their DNA in the open way they can now, then I’m completely against the regulation. However, I have seen many interpretation errors on the part of some

people/companies and that bothers me. So, if the purpose of the regulation is to stop those that don’t know what they are talking about...then that is a good idea. It is our belief is that it’s YOUR DNA and therefore it’s YOUR right to know what it says, and the academics who sit in their Ivory towers and dream of YOU not seeing able to see what’s in your DNA need to go away. I respect whatever they do in THEIR lives but, so to speak, ‘stay out of my bedroom’!

JoGG: In addition to your “official” position at FTDNA, you are also the project administrator for several projects. How’s that going? Have you established any connections with any famous Greenspans?

BG: If I were a cobbler I’d have lots of holes in my shoes...the Greenspan project has not reflected the same level of success as most of our clients’s projects.