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The Avotaynu DNA Global Census of the Jewish People – March 2020 Update

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Megiddo, or Tel Megiddo, is the site of an ancient city in northern Israel's Jezreel valley. It is believed to be the place where the battle of Armageddon will be fought. The picture shows an aerial view of Tel Megiddo. Photo by Itamar Grinberg.

For three years the Avotaynu DNA Project has been spearheading a collaborative international DNA project that includes academics at leading institutions such as the Technion, New York University Winthrop Hospital, the University of Colorado, the

University of Haifa and others around the world, together with a local cadre of Jewish historians and community leaders. The project currently has DNA from more than 8,000 participants in its database. Our aim has been to describe the origins and migrations of the world's Jewish populations since the founding of the Jewish People approximately 3,000 years ago.

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During our study, we have actively tested Jewish men on six continents, from China to Chile. In doing so, we have been the first project to ever describe the enormous genetic diversity of Jewish males worldwide. Using statistical anal- ysis of Short Tandem Repeats (STRs) in the Y chromosome we have segregated our Jewish participants into separate lineages, each lineage representing the descendants of a specific man whose male direct descendants are (or were) Jewish during the past 1,000 years. During 2019 alone, the number of separate Jewish paternal lineages preliminarily identified by our project grew by 25 percent, from 518 to 640. Of these 640 lineages, it is worth noting that while 85 percent of the lineages are found almost exclusively in the non-Ashkenazi population, an overwhelming number of both Ashkenazi and non-Ashkenazi Y chromosomes draw from the same, general, pre-Jewish population living in the Middle East at the time of the Patriarchs during the Late Bronze Age.

In terms of Jewish Y-DNA diversity, this is the tip of the iceberg, as the number of currently identified Jewish lineages does not include the large number that became extinct over the centuries. As described in 1873 by the statistician Francis Galton, a substantial number of paternal lineages inevitably become extinct because of the Galton-Watson process, which describes the probabilistic tendencies by which a specific male lineage no longer has any sons on whom to pass its Y chromosome. These tendencies are particularly strong in small populations, such as those of the small, non-Ashkenazi, Jewish lineages that found safe harbor in various corners of the world, e.g., China, Portuguese India, Italy, and portions of North Africa.

Galton had a second insight that equally contributed to our understanding of the Y chromosome, the statistical concept known as "regression to the mean." This concept refers to the fact that in any sample of data where measurable outcomes diverge, those results will tend over time to return to the average (or mean) measure. Any student of baseball hitting streaks knows the concept. A hitter will have periods when he is hot, and periods when he suffers slumps, but ultimately, absent an external factor such as better eyeglasses or a new hitting coach, he will return to the average degree of hitting success that has described his career overall.

Low-level STR Testing Frequently is Misleading

Regression to the mean affects variables such as STR markers as well. Researchers who have used the distance between highly variable Y-DNA STR markers to identify genetic distances between men, have noticed STR markers have a strong tendency over time to mutate back toward their original positions. This tendency, called "convergence" by geneticists, causes relationships between two men to appear to be far closer than they truly are, leading to many misunderstandings of DNA results, especially when comparing men whose common ancestor lived more than 20 generations ago, only yesterday in terms of Jewish history.

Research also has identified an equal and opposite problem called genetic drift. This is the term for the situation whereby STRs in small populations, such as the Jewish people, randomly diverge over time to such an extent that they are no longer recognizable as sharing a common ancestor. Taken together, these two characteristics of STR testing have represented an enormous problem for those studying Jewish genetic history.

We are frequently contacted by Ashkenazim who find Spanish-language surnames among their Y12 and Y25 matches. “Experts” on social networking frequently encourage these participants to believe that our contacts descend from Sephardi exiles. Nothing could be further from the truth. At the Y12 and Y25 level, because of convergence and drift we cannot possibly tell whether those Span- ish-surnamed matches share a common ancestor with our Jewish participant within the last 2,000 years, let alone the mere 500 years since the Spanish Expulsion. What we can state reliably is that our participants share common ancestors with individuals who presently have Iberian identity. To go beyond that using low level STR tests alone is fantasy, not science.

Next Generation Sequencing to the Rescue

Although geneticists continue to use STR testing as a low-cost means of conducting extensive DNA sampling around the world, our researchers have begun retesting representative samples in our project using an advanced (and more expensive) Y-DNA testing technique called “Next Generation Sequencing” (NGS), commonly known in the genealogical world as Family Tree DNA’s “BigY” or “Y700” product. Instead of analyzing 37 STR markers as the project has done to date, the NGS product looks at approximately seven million locations on the Y chromosomes, offering a far more specific definition of an individual’s paternal lineage in the context of Jewish history. The test uses single nucleotide polymorphisms (SNPs), a measure of genetic variations between members of a species.

Fortunately, the SNP mutations uncovered by NGS do not “return to the mean” as do STRs. Of the more than 1,000,000 Y-DNA SNP variations discovered by NGS testing up to now, only one has been seen to mutate back to its original position. The occurrence of SNP variations is correlated to the number of births and will occur at a steady rate in stable populations. A careful study of the thousands of Y-DNA SNPs discovered by NGS to date has led to an estimated rate of new, measurable Y-DNA SNPs in a stable population of once in 84 years for the latest Y700 test offered by Family Tree DNA.

An important exception to the calculation of mutation rates, however, results from the effects of rapid population expansion. A man with ten sons will have ten times the probability of having a son with a new SNP than a man with one son, resulting in a separate Y-DNA branch for the son who possesses the mutation not shared by his brothers. Over just a few generations of such expansion, this will lead to dozens of new SNPs, some of which could be expected to survive the Galton-Watson process by which Y- DNA variations are culled from small populations.

As we, and our colleagues in the field have begun using NGS more broadly, we have discovered discrete periods of simultaneous emergence of new SNPs and branches in an identifiable portion of the Y chromosome lineages found in the Jewish population. The first major expansion in Y-DNA SNP proliferation appears to have occurred 1,200 years ago, the second, 600 years ago. In our opinion, this represents the unmistakable settlement, economic success and population expansion of the proto-Ashkenazi population in France at the invitation of Charlemagne in the 9th century, and a similar experience among the Jews who settled in 14th- century Poland at the invitation of Casimir the Great.

Jewish Religious Practice and Surnames Often Are Unrelated to Place of Origin

These two expansion events are never seen among our known self-identified Sephardi or Mizrahi participants, except among those whose recent ancestors lived in areas where there was known interchange between Ashkenazi and non-Ashkenazi populations, such as northern Italy, Turkey and the Balkans. In these places, it is likely that an Ashkenazi ancestor migrated to a non-Ashkenazi land and adopted the local Jewish practice, surnames, and ethnic identity. We are now confident that in nearly all cases, we can quite easily distinguish between Ashkenazi lineages and non-Ashkenazi lineages based on the presence or absence of these Ashkenazi expansion events on any Y-DNA genetic tree.

NGS testing also has helped us interpret the unusual results among men with Ashkenazi genealogies who nonetheless match men with Spanish surnames living in Iberia or remote former Spanish colonies. In earlier years, we inferred that these results indicated a lineage that had left Spain at some time after the decline in Iberian Jewry commenced in 1391 and settled among the Ashkenazim in Central or Eastern Europe. NGS testing, however, has told a far more interesting story about the deep ancestry of some of the Ashkenazi lineages. In general, the Jewish branches of these lineages show the Ashkenazi branching events of 800 CE and 1400 CE, plus an additional major branching event in Iberia at approximately 500 CE (long before Sephardi and Ashkenazi identities had been established).

We now believe that we are seeing a split between descendants of a common Iberian ancestor in Roman times, some of whom entered the Jewish population and others who did not. Ample evidence shows a good deal of religious fluidity in the late Roman Empire, with evidence of individuals throughout the Empire "who worshipped the God of Israel as well as their own deities." (Paula Frederick- son, "Jewish Romans, Christian Romans and the Post-Roman West: The Social Correlates of the Contra Judaeos Tradition," https://www.bu.edu/religion/files/2010/03/ Jewish- Romans-PF-6-14.pdf accessed 12–24–2019). The vestiges of pagan conversion to Judaism in Iberia is a matter that the historians and geneticists on our team plan to investigate in further detail as we continue our NGS investigation.

NGS also has given us the power to prove connections between ancient Jewish communities. Discoveries such as the origins of the Jews of Kaifeng, China, or of communities of forgotten Jewish descent in mountain communities in the Americas, Eastern Europe, and Middle East now are a common occurrence as the results continue to come in from our worldwide DNA survey. All results will be described in peer-reviewed professional journals and summarized in the pages of AVOTAYNU.

Every genetic result from every individual who has been tested is vital to us, as it statistically sharpens our results. We encourage AVOTAYNU's readers to join their genetic library of YDNA results to our study— Sephardi, Mizrahi or Ashkenazi, whether male or female, STR or NGS, mitochondrial, or autosomal—by logging in at www.JewishDNA.org and pressing "join." Anyone with questions about our project, or their own DNA results is welcome to contact me at **Adam. Brown@AvotaynuDNA.org**.

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About Adam Brown

Adam Brown has researched his family's Jewish origins for over three decades. His groundbreaking articles "Interactive Web Site Brings Our Family Tree to Life" and "The Coming Big Bang in Genealogical Research" were presented at IAJGS conferences and on the pages of our sister publication, AVOTAYNU. He is Co-Chair of the planned 2017 Annual Conference of the International Association of Jewish Genealogical Societies (IAJGS) in Orlando.

He is the volunteer founder/coordinator of Jewish DNA database at FamilyTreeDNA with over 5,000 participants. Adam has worked extensively in all major online genealogical platforms - including Ancestry, MyHeritage, Geni, and WikiTree - and as a volunteer Geni Curator has helped countless users develop their own collaborative online projects focused on Ashkenazi and Sephardi families and their communities.

By profession, Adam is a lawyer and strategic planner, is a graduate of the University of Michigan and the University of Chicago Law School, and serves on numerous municipal, scientific research, and academic non-profit boards and commissions. In his home community of Englewood, NJ, he serves on the City's Budget Commission, Planning Board, and is Chair of its Economic Development Corporation.

In recent years, he has worked two seasons as an IT/telecommunications specialist at a remote field camp deep in the interior of Antarctica. and returned to the region during March-April 2016 as part of a multi-national scientific expedition that travelled 5,800 miles by sea to and from ice-covered yet volcanic Heard Island, a rarely visited pristine habitat in the stormy Southern Indian Ocean half way between Australia and South Africa.