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CONTEMPORARY JEWISH GENEALOGY

A MULTI-FACETED ACADEMIC ACTIVITY*

WSPÓŁCZESNA GENEALOGIA ŻYDOWSKA WIELOASPEKTOWA DZIAŁALNOŚĆ AKADEMICKA

Streszczenie

Genealogia przynależąca do nauk pomocniczych historii, a szczególnie genealogia żydowska, poddawana jest w ostatnich dwudziestu latach dużej transformacji. W jej obrębie podjęto rozległe, wieloaspektowe badania naukowe. Autorzy artykułu dokonują przeglądu tych osiągnięć oraz wskazują na nowe narzędzia badawcze przydatne w genealogii. Podając konkretne przykłady z rozmaitych jej poddziedzin, nawiązują wprost do współczesnej genealogii żydowskiej i wytyczają dalsze jej perspektywy jako dyscypliny akademickiej. Określają także przybliżony zakres jej obszaru badawczego, który zyskuje coraz większą aprobatę.

The preservation of memory is widespread among humans, regardless of their culture, and reasons for it are various. Acts of remembrance are significant, symbolically and practically, to each of us, most certainly because we are mortal. Collective memory has meaning for groups of individuals because it helps crystallize commonalities, concretizes their togetherness and brings them closer to each other. The Jewish people, Ashkenazi Jews in particular, have yet another reason for being actively involved in acts of memory: large portions of their families have altogether vanished in the Holocaust and often there is not even a single trace left of their very existence, of the concrete fact that they lived on earth – unless a search is actively performed to find such traces. To illustrate this with a concrete example, one of the authors of this article (HDW) has, over the last few years, reconstituted his family tree for the branch of his grandmother Ester Potaznik. Ester was born in Zdunska Wola, Poland, and had a large number of siblings. She and two of them survived the Holocaust

* Selected parts of this article have appeared in "Avotaynu" 22: 2006 no. 1, pp. 3-11, and are reproduced here with permission.

by hiding in Liege, Belgium, but all others and their spouses and children, whose existence had been altogether unknown until a genealogical search of the archives was performed, vanished –in the full sense of the term- in the Holocaust. The genealogical activity therefore permitted to reconstitute at the very least the *memory* of their existence.

Genealogy as a whole – and Jewish genealogy in particular – is at present undergoing a rapid transition. What used to be a pastime consisting mostly of recording names, dates and places of origin, with as sole purpose to transmit basic family information to succeeding generations, has become a field of far-reaching information and knowledge from which society benefits significantly, as recently described by Gary Mokotoff.[1] In the last 15-20 years, the character of genealogical research has increasingly become an intricate, multifaceted academic pursuit. Figure 1 shows the enormous increase in the number of peer-reviewed articles published in the field of genealogy. As seen, the number of publications in the exact sciences largely outgrows those in the fields more traditionally associated with genealogy. The examples presented below demonstrate that such a gap is rooted in recent major scientific advances.

I. BREAKTHROUGHS IN MODERN GENEALOGY

The emergence of a global computer network and the rapid developments of information technology and communication means in the last decade have radically transformed our world. Human activities and interactions have been deeply affected, as all forms of communication have become almost instantaneous, and an ever increasing amount of information has become widely available to every one of us almost anywhere on the planet. Equally importantly, as we demonstrate here, a number of scientific tools belonging to the "hard" sciences (biology, mathematics and even statistical physics) have led to fundamental breakthroughs in our understanding of the larger issues of genealogy as a whole and of Jewish genealogy in particular.

The consequences in the field of genealogy of those developments and scientific breakthroughs are many. At the personal level, it is now much easier and faster to document family histories using online databases that a short while ago did not exist or were unavailable to the public.

[1] G. Mokotoff, *The Role of Genealogy in the Jewish Community*, "Avotaynu" 21: 2005 no. 3, pp. 3-5.

At a higher level, the "para-documentation" (information or research emanating from the wider historical, geographical, anthropological, ethnological or sociological contexts) that accompanies and enriches our personal research often has become almost immediately available. It is undeniable that private individuals easily become highly knowledgeable in genealogy-related areas in ways that were impossible before the advent of the Internet.

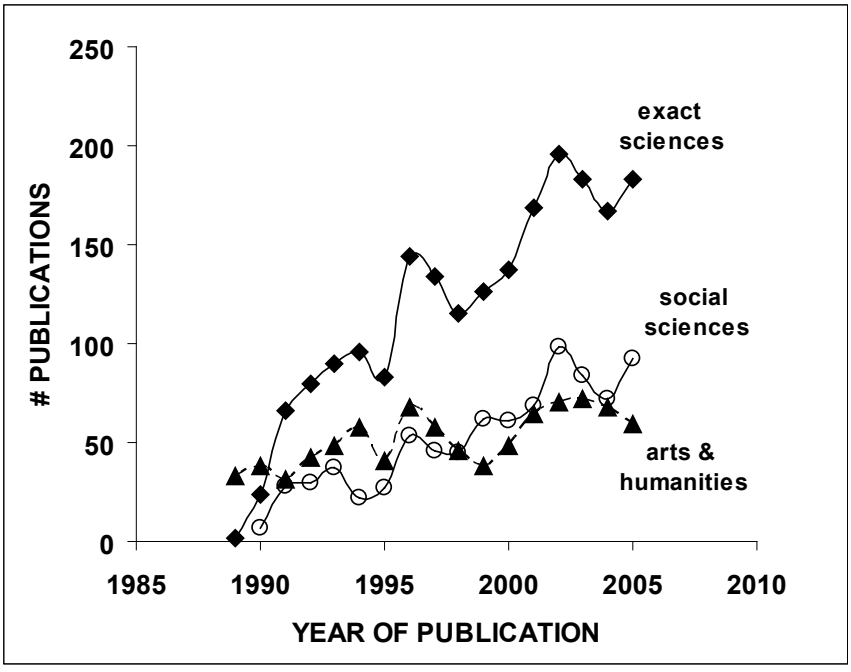

Fig. 1. Peer-reviewed genealogical publications, 1989-2005, generated by statistical analysis performed by the author on ISI Web of Science site using keyword "genealogy."

The various scientific and technological breakthroughs bear the promise of a much deeper understanding of phenomena that belong to areas of communal genealogy, to genealogy on a larger scale. In fact, as noted in the next section, results already have appeared in various fields that change the ways in which we look at human migrations, the meaning of races, the origins of specific subgroups of the human species – or the human species itself—the study of historical facts, study of names (onomastics), cure of specific diseases and much more. Step by step, geneal-

ogy is mutating into a major academic discipline, with a significant impact both at the theoretical and practical levels.

II. CURRENT RESEARCH AND FUTURE CHALLENGES

Genealogists routinely develop skills and tools to tackle issues belonging to a subfield of genealogy, here termed "microgenealogy," with which all genealogists become familiar in the early stages of family research. For example, to study a specific family name they learn to use a soundex system. By contrast a number of less familiar topics of investigation belong to so-called hard sciences; the source of the true transformation of genealogy into a modern academic discipline resides in the momentum arising from those areas. Those topics and tools help in solving problems belonging to the subfield of "macrogenealogy." This "dipolar" terminology (micro vs. macrogenealogy) is better defined and discussed elsewhere[2]. A succinct review is now presented of selected recent contributions to genealogy, and related research topics, emanating from the hard sciences.

1. Mathematics and statistics

Sometimes, when teaching rudiments of genealogy to schoolchildren, one asks the question: "Do you know the names of your eight great-grandparents? Your 16 great-great-grandparents?" Thus kids gain awareness of the chain of the living and, perhaps, of time and transience. Such questions lead to the following apparent paradox: Since every human has two parents, and, assuming that the length of a generation is about 25 years, it is easy to see that 750 years ago (thus, 30 generations ago, in the heart of the Middle Ages) everyone had more than a billion ancestors (2^{30} to be exact). The reader is welcome to perform the same exercise using 230 generations (=5750 years), thus going back to the creation of the Universe according to the Jewish calendar (as well as, interestingly, to the Mayan calendar!). The irrationality of such astronomical numbers of ancestors is obvious, especially if one remembers that the Jewish population (for example) on earth was never any larger than about 18 million souls (just prior to World War II).

The solution lies in the obvious fact that marriages between cousins or between uncle and niece, for example, took place frequently, especially

[2] H.D. Wagner, *Genealogy as an academic discipline*, "Avotaynu" 22: 2006 no. 1, pp. 3-11.

in such closed populations as the *shtetl*. Indeed, assume you belong to generation g = 0 and your parents to generation g = 1, your grandparents to generation g = 2, etc. If your parents happen to be first cousins, then two of your four grandparents are siblings, and all the ancestors of those two are thus identical: Your ancestor count has just been reduced by 25 percent! In algebraic terms, instead of having 2^g ancestors at generation g, as is the normal case, you will have only $2^g - 2^{g-2}$ ancestors (thus: six great-grandparents instead of eight, etc.), and the percentage of "disappeared ancestors" is thus indeed 25 percent, since $1 - [(2^g - 2^{g-2})/ 2^g] = 0.25$.

This simple counting exercise leads to much more intricate research by including progressively more realistic, but increasingly more complex, assumptions. One can study what happens to the above calculation (1) if pairs of cousins marry every two generations; or (2) if the probability of marriages between cousins is directly proportional to the size of the cousin population in a given generation; (3) if a tool is designed for a progressive stabilization (due to inter-cousin marriages, or more generally to inbreeding, epidemics, wars, etc.) in one's number of ancestors going back in time (such a tool would also explain the eventual global stabilization of the earth population at some point in the past). An example of a mathematical device designed to reduce significantly the increase in one's number of ancestors because of inbreeding is the principle of sibling interference proposed by S. Ohno.[3]

The next step in developing a realistic model of population backward growth dynamics could be the following: Instead of launching the ancestor count from a single individual, one could start with two or more individuals, which would lead to a variety of interesting questions. For example, if one picks two people at random in the present, how many generations back must one go to find their most recent common ancestor (MRCA)? How many generations back until *all* their ancestors are common? What happens to the MRCA if the population is restricted or inbreeding (such as in isolated tribes, island populations, specific human groups such as Ashkenazi Jews or royal families, etc,), instead of unrestricted? The merging of ancestor trees is termed coalescence; coalescence problems currently are the subject of a vast amount of academic research worldwide using sophisticated statistical models and mathematical simu-

[3] S. Ohno, *The Malthusian Parameter of Ascents: What Prevents the Exponential Increase of One's Ancestors?*, "Proceedings of the National Academy of Sciences" 93: 1996, pp. 15276-78.

lations.[4] Such mathematical models, combined with modern genetic research tools, recently have led to a number of significant breakthroughs, discussed below.

The paradox outlined above concerning one's unrealistically enormous amount of ancestors also arises when counting descendants, with additional complications and research directions. For example, if one picks a remote ancestor at generation g = 0, and – for simplicity's sake – one assumes a fixed number of children (N_D) for all subsequent generations, then the number of descendants at generation g is $(N_D)^g$. Starting 5750 years ago with Adam (or Eve), the theoretical number of descendants today (after g = 5750 divided by 25, thus 230 generations, assuming as before that the length of a generation is 25 years) would be N_D^{230} . For example, if every mating couple since Adam had on average given birth to four children, the number of present-day descendants would be 4^{230}, an astronomically large number indeed compared to the current world population of around 6 billion (about 4^{16}).

If one now assumes that a marriage between cousins occurred among Adam's grandchildren, say, thus at generation g = 2, the number of descendants at generation g would be reduced to $(N_D)^g - (N_D)^{g-2}$. Thus, the percentage of "disappeared descendants" would be $1 - [(N_D)^g - (N_D)^{g-2}/(N_D)^g] = 1/(N_D)^2$. If N_D (number of children per couple) is only 2, this simple result is identical to the number of "disappeared ancestors," thus 25 percent, and the result decreases rapidly as N_D increases. More such marriages between cousins reduce the population of subsequent generations. Early populations inevitably were small and therefore included much inbreeding, as did later tribal groups. Inbreeding also has favored genetic diseases, which further limits population growth. Other complicating factors include the effects of war and epidemics, multiple spouses, celibacy, etc. In the case of Jews, one also must include the effects of assimilation into other populations and of the mega-event that was the Holocaust.

[4] (a) B. Derrida, S. C. Manrubia, & D. H. Zanette, *Statistical Properties of Genealogical Trees*, "Physical Review Letters" 82: 1999 no. 9, pp. 1987-90. (b) J. T. Chang, *Recent Common Ancestors of All Present-Day Individuals*, "Advances in Applied Probability" 31: 1999, pp. 1002-38. (c) B. Derrida, S. C. Manrubia, D.H. Zanette, *Distribution of Repetitions of Ancestors in Genealogical Trees*, "Physica" A 281: 2000, pp. 1-16. (d) B. Derrida, S.C. Manrubia, D.H. Zanette, *On the Genealogy of a Population of Biparental Individuals*, "Journal of Theoretical Biology" 203: 2000, pp. 303-15. (e) D.L. T. Rohde, S. Olson, J.T. Chang, *Modelling the Recent Common Ancestry of All Living Humans*, "Nature" 431: 2004, pp. 562-66. (f) M. Mohle, *The Time Back to the Most Recent Common Ancestor in Exchangeable Population Models*, Advances in Applied Probability 36: 2004, pp. 78-97.

Such population growth genealogy problems certainly could be examined with existing mathematical tools and growth models in the fields of ecology (spread of a given animal species, or of forest fires, for example, under various constraints) or epidemiology (spread of infectious diseases in isolated or open populations), in which predictions can be made ("is a species headed for extinction?"), and can indicate how the population will respond to external factors.[5]

2. Statistical physics

Genealogy deals with complex social phenomena, the of which have attracted the attention of physicists. Statistical physicists in particular rules use techniques that serve as an efficient tool to modeling phenomena in which intricate macroscopic behavior (for example: sand avalanches) emerges spontaneously on the basis of relatively simple microscopic dynamical rules (for example: the characteristics of individual sand grains). In particular, so-called scaling laws (or power laws) arise in virtually all areas of physics and have great importance because despite their apparent simplicity they often reflect the depth of the underlying physics. Scaling laws have been found also abound outside physics[6]: in such diverse areas as biology, distribution of incomes, insurance claims, city populations, family sizes and travel distances.

An intriguing example relevant to genealogical research is the distribution (and stability) of family names in a specific community or country, which also follows scaling laws. The study of the origins and evolution or transformation of surnames is a well-known aspect of genealogical research, but perhaps less well known to genealogists is the fact that information about surnames can be used in research on human population genetics,[7] if one notices that the transmission of surnames through the paternal line (such as in most current Western societies) fascinatingly resembles that of genetic information inherited from one of the parents (the exclusively paternal Y chromosome or the exclusively maternal mito-

[5] C.J. Rhodes, R.M. Anderson, *Power Laws Governing Epidemics in Isolated Populations*, "Nature" 381: 1996, pp. 600-602.

[6] (a) M.R. Schroeder, *Fractals, Chaos, Power Laws: Minutes from an Infinite Paradise*, (New York: W.H. Freeman, 1991). (b) G.K. Zipf, *Human Behavior and the Principle of Least-Effort. An Introduction to Human Ecology* (Cambridge, Mass.: Addison-Wesley, 1949).

[7] J.-M. Legay, M. Vernay, *The Distribution and Geographical Origin of Some French Surnames,* "Annals of Human Biology" 27: 2000 no. 6, pp. 587-605.

chondrial DNA). This approach has become important because information on surnames is readily available in civil registration (metrical) data, census lists, annual telephone directories, etc. Surnames research, then, can be used, for example, to estimate the probability that two individuals chosen at random carry genes inherited from a common ancestor and to estimate the size and geographical distribution of migratory movements in the past. Complications arise in such investigations from variations in the spelling of a particular surname. Research along those lines concerning French,[7] Japanese,[8] North-American,[9] German, [10] and Argentinian [10] surnames recently has been published; no such study apparently exists for the Jewish population of specific areas, even though ample metrical data are available.

3. Computer science

Computers (and software) offer a key tool to modern genealogy. They serve as an infinite repository for databases; they provide available information almost instantaneously; they serve as a simple and powerful family research tool, especially since the advent of Internet; and, combined with properly designed mathematical tools, they allow researchers to uncover hidden genealogical information (often of a scientific nature) as well as to create more meaningful databases by the exploration and merging of existing databases. Future academic research in areas related to genealogy-relevant computer software is likely to focus on a variety of diverse issues. As illustration, two examples of not-fully-resolved problems in the microgenealogical and macrogenealogical areas, respectively, are given here.

a. Soundexes

A significant software advance took place with the creation of soundexes. A soundex is a phonetic algorithm that deals with the problem of variations in name spellings that often appear in archival documents—sometimes in a single document! Surnames that sound the same but are

[8] S. Miyazima, Y. Lee, T. Nagamine, H. Miyajima, *Power-Law Distribution of Family Names in Japanese Societies*, "Physica" A 278: 2000, pp. 282-288.

[9] D. Zanette, S.C., Manrubia, *Vertical Transmission of Culture and the Distribution of Family Names*, "Physica" A 295: 2001, pp. 1-8.

[10] S. C. Manrubia, D.H. Zanette, *At the Boundary between Biological and Cultural Evolution: The Origin of Surname Distributions*, "Journal of Theoretical Biology" 216: 2002, pp. 461-477.

spelled differently (Baum, Bojm, Bohm) are assigned the same soundex code by the algorithm, so that a single lookup will find all occurrences in a set of records of a surname under its various spellings. Soundex development belongs to the subfield of microgenealogy, because soundexes must be adapted to families of surnames belonging to specific cultures or ethnicities. The concept of a soundex is old; it was invented and patented in 1918, well before the advent of computers, by M. O'Dell and R. C. Russell. The soundex was used to organize U.S. federal census data from 1880 to 1920. In 1985-86 two Jewish genealogists, Randy Daitch and Gary Mokotoff, developed a soundex system (Daitch-Mokotoff, or D-M, soundex) more suitable for Jewish genealogy than the traditional National Archives (or NARA) soundex. (For example, the latter soundex views Zilber and Silver as two different names, with codes Z416 and S416, respectively, whereas the D-M code is 487900 for both names.) The advantage of the D-M soundex is that variant spellings are all discovered, but many irrelevant "hits" inevitably are included (for example, Szlejfer also will appear when looking for Zilber). Future research may improve the efficiency of the system further.

b. Merging databases

One of the most important research issues in current genealogical research is the creation of sophisticated software dedicated to merging genealogical databases. Merging databases is a good example of a general research tool belonging to the subfield of macrogenealogy that can be applied to specific cases of microgenealogical research, as shown below. In the simplest case, two databases containing genealogical material that includes both overlapping (usually names of individuals) and nonoverlapping information are compared. An example is the merging of a town's metrical birth and death records. In addition to details regarding the newborn, birth records usually include also the names, ages and occupations of the parents and death records often include age at death and identify surviving family members. Merging databases obviously increases the amount of genealogical information in one place. The main problem, of course, is to ensure that the merging procedure links identical individuals, namely that the birth and death documents of John Smith, for example, are those of the same John Smith! In other words, merging criteria of "identicalness" must be defined as accurately as possible. Some commercially available family genealogy packages (for example, Family Tree Maker) prompt the user regarding a possible match between two individuals in a family tree when those two seem to possess identical data.

Complexity (as well as usefulness) grows when more than two databases are available for merging. As an example, consider the Polish town of Zdunska Wola, for which various types of databases exist for its pre-World War II Jewish population[11], including more than 30,000 metrical data (from three original databases: births, marriages, deaths) for the years 1808-1942, 3,000-plus burial records created from tombstone transcriptions in the Jewish cemetery, 2,300-plus necrology records from the Jewish Memory Book (*yizkor* book), 1,100-plus surnames from the 1929 Polish Business Directory data, and records from smaller databases, such as the names of Auschwitz survivors, surnames on the Zdunska Wola memorial monument erected in Tel Aviv by survivors, etc. Significant benefits may arise from merging some or all of these data sets.

In principle, merging could be applied to a large number of family trees existing in a given community (the "community forest") in an effort to create a single communal tree.

Clearly the development of sophisticated merging tools is a priority in macrogenealogical research; it certainly is so in Jewish genealogy, where a major objective of a large number of researchers is the virtual reconstruction of one's ancestral town or shtetl. A more detailed analysis of the complexities involved in automated database merging will be presented in a separate study.[12]

4. Molecular biology

Over the last decade genetic research has greatly expanded our understanding of the probable origins, evolutionary history, and geographical patterns of various human communities, including Jews. It also has provided news insights into the way in which humans are genetically related to each other. We begin with a brief overview of basic terms and concepts.

In every nucleus of human cells, tightly coiled threads of deoxyribonucleic acid (DNA) are organized into structures called chromosomes. Humans possess 23 pairs of chromosomes. In 22 pairs, both members are essentially identical, one deriving from the individual's mother, the other from the father. In females the 23rd pair has two similar chromosomes called X,

[11] K. Klauzinska, *A Modern Approach to the Genealogy of Polish Jews: Zdunska Wola as a Test Case*, Submitted (June 2006).

[12] K. Klauzinska, H.D. Wagner, *Database Merging: A Tool for the Virtual Reconstitution of Vanished Jewish Communities*, In Preparation (July 2006).

whereas in males that pair is composed of one X and one Y, two very dissimilar chromosomes. These chromosome differences determine a person's gender. Most of the Y chromosome is transmitted from father to sons as an integral unit, passed without alteration, unaffected by any influence of the X chromosome of the mother. The Y chromosome is the only nuclear chromosome that escapes the continual reshuffling of parental genes during the process of sex cell production. Such uniqueness makes the Y chromosome useful to genealogists. Most of the time a father passes an exact copy of his Y chromosome to his son. This means that the markers (definable segments along the DNA with known genetic characteristics) of the son are identical to those of his father. On rare occasions, however,a random mutation, or change in one of the markers, occurs. Thus it is possible for two distant cousins to match exactly on all markers, while two brothers might not match exactly. Because of the random nature of mutations, statistics and probability must be used to estimate the Time to the Most Recent Common Ancestor (TMRCA).[13] The complex mathematical calculations of TMRCA depend on knowing the rate of mutation and the true number of mutations. Various models and an online calculator for TMRCA are available.[14]

On the other hand, humans also inherit mitochondrial DNA (mtDNA) from their mother (and none from their father). Unlike chromosomal DNA, mtDNA is located outside the nucleus of the cell in the mitochondria (an organelle inside most cells). A person's maternal ancestry can be traced using his or her mtDNA, which is generally passed down unchanged by the mother. Test results are compared to another person's results to determine the time frame in which the two people shared a most recent common ancestor.

In summary, a person's DNA contains specific genetic information transmitted down with few changes from generation to generation. Two avenues of DNA research are of particular significance: (1) A man's paternal ancestry can be traced using the Y- DNA, and (2) a person's maternal ancestry can be traced using his or her mtDNA. These two avenues have limitations, however; each traces only a single ancestral line (the all-male and the all-female lines). Therefore at 10 generations back, where everyone typically has 1,024 ancestors, the Y-DNA and the mtDNA are used to study only 1 of those 1,024 ancestors.

[13] B. Walsh, *Estimating the Time to the MRCA for the Y Chromosome or mtDNA for a Pair of Individuals*, "Genetics" 158: 2001, pp. 897-912.

[14] http://nitro.biosci.arizona.edu/ftdna/TMRCA.html

Genetic studies, supported by mathematical and statistical tools, recently have yielded considerable insight into the origins of certain human groups, transmission of genetic diseases, and important historical debates, and are helping to solve problems of a forensic nature. The study of human genetics also directly fosters the development of new research avenues in paleontology, archeology, linguistics, migration patterns and history. The following examples focus on genealogy exclusively.

a. Origins of homo sapiens

Early studies have demonstrated how mtDNA might be used to track the ways in which humans are genetically related to each other. Substantial fossil evidence exists for the hypothesis of a common African origin of modern humans[15]: The common ancestor of all surviving mtDNA types existed 140,000-290,000 years ago, and subsequently spread throughout the world. Two other models exist as well: The multiregional model (no single geographical origin for modern humans) and the assimilation (or hybridization) model (some gene flow existed between modern humans who emigrated from Africa and archaic populations such as the Neanderthals). Future research undoubtedly will shed additional light on this macrogenealogical issue.

b. Origins of specific human groups

DNA studies are revealing unexpected common origins of populations previously presumed to be different. For example, a common ancestry has been found recently between African groups (Berbers, Fulbe from Senegal) and groups from the far Northern Hemisphere (Saami of northern Scandinavia, Yakut from northeastern Siberia)—populations living as far as 15,000 km apart and whose anthropological affinities are not at all obvious.[16]

The origins and migrations of Jewish populations are examined below.

[15] (a) R.L. Cann, M., Stoneking, A.C. Wilson, *Mitochondrial DNA and Human Evolution*, "Nature" 325: 1987, pp. 31-36. (b) S.A. Tishkoff, S.M. Williams, *Genetic Analysis of African Populations: Human Evolution and Complex Disease*, "Nature Reviews Genetics" 3: 2002, pp. 611-621.

[16] A. Achilli [et al.], *Saami and Berbers: An Unexpected Mitochondrial DNA Link*, "American Journal of Human Genetics" 76: 2005, pp. 883-886.

c. Genealogy and genetic diseases

Molecular genetics tools now permit study of a wide range of hereditary diseases. For example, Leber hereditary optic neuropathy (LHON), characterized by a maternally inherited loss of central vision mostly in males, was recently investigated in Italian families using both genetic (mtDNA) and genealogical approaches. This powerful combined approach allowed the reconnection into extended pedigrees of Italian and Brazilian families that were not known to be related. [17]

Another example is β-thalassemia, or Cooley's anemia, which affects a person's ability to produce hemoglobin, the protein in red blood cells that delivers oxygen to all parts of the body.[18] For years the disease was thought to affect only Greek, Italian, Asian and Sephardic Jewish families. In recent years, it has become clear that Ashkenazi Jews also carry the trait and could be at risk for the fatal disease.[19] In this case, too, the combination of genealogical searches with molecular genetics led to the discovery of previously unknown family and to six other Diaspora Ashkenazi families that carry the trait. The importance of this combined approach is in the possibility to alert extended unsuspecting families who may be at risk, and to warn them about the potential dangers to future generations.

Subtle DNA abnormalities (mutations) are responsible for many inherited diseases, such as cystic fibrosis, or may predispose an individual to cancer, major mental illnesses, and other complex diseases. For example, genealogical investigations and genetic studies recently were used to diagnose attention deficit hyperactivity disorder (ADHD) in an isolated Dutch population, of which 15 of 26 children were linked to a common ancestor within 10 generations, and 81 percent of the patients derived of consanguineous marriages (thus, marriages between close relatives).[20] Another example concerns a recent genealogical/genetic study of Tay-

[17] (a) D.C. Wallace [et al.], *Mitochondrial DNA Mutation Associated with Lebers Hereditary Optic Neuropathy*, "Science" 242: 1988, pp. 1427-1430. (b) V. Carelli, *Haplogroup Effects and Recombination of Mitochondrial DNA: Novel Clues from the Analysis of Leber Hereditary Optic Neuropathy Pedigrees,* "The American Journal of Human Genetics" 78: 2006, electronically published January 27, 2006.

[18] T. Martino, F. Kaplan, S. Diamond, A. Oppenheim, C.R. Scriver, *Probable Identity by Descent and Discovery of Familial Relationships by Means of a Rare* β-*Thalassemia Haplotype*, "Human Mutation" 9: 1997, pp. 86-87.

[19] www.geocities.com/heartland/pointe/1439

[20] E.A. Croes [et al.], *Phenotypic Subtypes in Attention Deficit Hyperactivity Disorder in an Isolated Population*, "European Journal of Epidemiology" 20: 2005, pp. 789-94.

Sachs disease (TSD),[21] which is relatively frequently encountered among Ashkenazi Jews (1 in 29) and much less so among Moroccan Jews (1 in110) and Iraqi Jews (1 in140). The relevant mutations were found to have occurred in the years 626 C.E. and 442 B.C.E., respectively (but with relatively large error margins).

d. DNA analysis and historical events

The following is a classical example of the role played by DNA analysis to solve historical and genealogical puzzles. In 1991, nine sets of skeletal remains were excavated from a mass grave near Yekaterinburg, Russia. It was unclear whether the remains were those of the tsar's family (the Romanov), namely Tsar Nicholas II, Tsarina Alexandra, and their daughters. Nuclear DNA testing [22] of the remains verified such a family group (additional bodies were those of three servants and a doctor), and mtDNA sequences of the presumed tsarina matched a known maternal relative, Prince Philip, Duke of Edinburgh.

e. Origins of the Jews

A number of important molecular genetic studies have been published over the last decade concerning the origins of various Jewish populations and communities, including genetic profiles of contemporary Jews,[23] that show that, despite migrations and physical separation, Jews have retained their genetic identity over thousands of years.[24] Some studies have focused on the role of genetic contributions to Ashkenazi DNA from European and Central Asian peoples, including the Khazars who lived in Southern Russia during the 8th through the 12th centuries C.E.[25]

Two recent studies have yielded interesting conclusions regarding what is known as the "founding event," A founder event occurs when a new

[21] M. Karpati [et al.], *Specific Mutations in the HEXA Gene among Iraqi Jewish Tay-Sachs Disease Carriers: Dating of Founder Ancestor*, "Neurogenetics" 5: 2004), pp. 35-40.

[22] P.L. Ivanov [et al.], *Mitochondrial DNA Sequence Heteroplasmy in the Grand Duke of Russia Georgij Romanov Establishes the Authenticity of the Remains of Tsar Nicholas II*, "Nature Genetics" 12: 1996, pp. 417-420.

[23] H. Ostrer, "Nature Reviews Genetics" 2: 2001, pp. 891-898. ???

[24] M.F. Hammer [et al.], *Jewish and Middle Eastern Non-Jewish Populations Share a Common Pool of Y-Chromosome Biallelic Haplotypes*, "Proceedings of the National Academy of Sciences" 97: 2000, no. 12, pp. 6769-6774.

[25] E. Levy-Coffman, *A Mosaic of People: The Jewish Story and a Reassessment of the DNA Evidence*, "Journal of Genetic Genealogy" 1: 2005, pp. 12-33.

community is started by a few members of the original population. This small population size means that the community may have reduced genetic variation from the original population, and a non-random sample of the genes in the original population (for example, the Afrikaner population of Dutch settlers in South Africa is descended mainly from a few colonists). The genetic significance of this may be that today's descendants of such population may carry an unusually high frequency of a gene that causes a given disease, because those original colony members happened to carry that gene with unusually high frequency. Thomas et al. demonstrate that most Jewish communities were founded by relatively few women and that subsequent genetic input on the female side from surrounding populations was limited.[26] The paternally inherited Y chromosome, on the other hand, shows diversity similar to that of neighboring populations and shows no evidence of founder effects. Interestingly, the same researchers find little evidence of a strong founder event on the female side of Ashkenazi Jews. These findings seem to contrast with the results of another, more recent, study that demonstrates that close to one-half of Ashkenazi Jews can be traced back to only four female ancestors, likely of Near Eastern ancestry, carrying distinct mtDNAs that are virtually absent in other populations, with the important exception of low frequencies among non-Ashkenazi Jews.[27] Future research should clarify this further.

f. Specific Jewish subgroups

Researchers have conducted Y-chromosomal studies of two subsets of the Jewish people, male Jews comprising the priesthood (Kohanim, the plural of Kohen, the Hebrew word for priest) and the Levites.[28] According to Jewish tradition, the male descendants of Aaron (Moses' brother) were selected to serve as priests. Levites are the male descendants of Levi (the third son of the patriarch Jacob and paternal ancestor of Aaron) who are not Kohanim. Both the Kohanim and Levites were assigned special

[26] M.G. Thomas, [et al.], *Founding Mothers of Jewish Communities: Geographically Separated Jewish Groups were Independently Founded by Very Few Female Ancestors*, "American Journal of Human Genetics" 70: 2002, pp. 1411-1420.

[27] D.M. Behar [et al.], *The Matrilinear Ancestry of Ashkenazy Jewry: Portrait of a Recent Founder Event*, "American Journal of Human Genetics" 78: 2006, Advance online publication.

[28] (a) K. Skorecki [et al.], *Y Chromosomes of Jewish Priests*, "Nature" 385: 1997, p. 32. (b) M.G. Thomas [et al.], *Origins of Old Testament Priests*, "Nature" 394: 1998. pp. 138-140.

religious responsibilities, but particular restrictions were placed on the Kohanim (for example, they were not permitted to come in contact with the bodies of the dead, even of parents; they were not permitted to marry a divorcee, etc). Significant differences were found between the Y chromosomes of Kohanim and those of other Jews. Moreover, Kohen chromosomes are homogeneous, and their origin was traced back about 3,000 years, early during the Temple period. The presence of the same genetic signature among Kohanim of several Ashkenazi and Sephardic communities strongly suggests common origin.[28] However, unlike the Kohanim, the Levites' Y chromosomes were found to have heterogeneous origins, indicating that contemporary Levites are, therefore, not direct patrilineal descendants of a paternally related tribal group. The Ashkenazi Levites, however, form a tightly clustered group whose origins are probably not in Near Eastern countries,[29] with an inferred common ancestor within the past 2,000 years. When compared in terms of genetic similarity, Ashkenazi Levites cluster more with Slavonic populations than with other Jewish populations, including Sephardi Levites.[29]

g. Populations of Jewish descent

Several communities around the world may descend from a Jewish ancestral population. Such claims often are made on the basis of oral tradition only, and DNA studies may help shed light on such issues. The Lemba tribe in Southern Africa and the Abayudaya in Uganda, for example, claim descent from Jews from Africa. Interestingly, one of the Lemba clans carries, at a very high frequency, the Y-chromosome type assigned to Kohanim,[30] and a Semitic genetic contribution. Other populations found by DNA analysis (using either the Y chromosome or the mtDNA approach) to possess common ancestry with Jewish populations include the Samaritans [31] (who may be traced back to a Jewish Kohen ancestor), and the Chueta, who are the Catholic descendants of Jewish

[29] D.M. Behar [et al.], *Multiple Origins of Ashkenazi Levites: Y Chromosome Evidence for Both Near Eastern and European Ancestries*, "American Journal of Human Genetics" 73: 2003, pp. 768-779.

[30] M.G. Thomas [et al.], *Y Chromosomes Traveling South: The Cohen Modal Haplotype and the Origins of the Lembas—the 'Black Jews of Southern Africa'*, "American Journal of Human Genetics" 66: 2003, pp. 674-686.

[31] S. Peidong [et al.], *Reconstruction of Patrilineages and Matrilineages of Samaritans and Other Israeli Populations from Y Chromosome and Mitochondrial DNA Sequence Variation*, "Human Mutation" 24: 2004, pp. 248-260.

victims of the last Spanish Inquisition (in the late 17th century) on Majorca Island.[32]

This capsule summary of recent accomplishments with applications for genealogy in a host of fields using a wide variety of scientific tools details only the beginning of a succession of research achievements that most certainly will appear in the near future. Mathematical and biological methods and models, combined with the ever-increasing power of computers, serve as the basis of the future discoveries.

CONCLUDING COMMENTS

The type of academic research described here is indispensable to yield significant breakthroughs in genealogy. An obvious challenge to such research is the fact that genealogy continues to develop as an increasingly multidisciplinary activity. University training and academic research, therefore, are faced with rather complex challenges. Clearly, the development of a suitable high-level curriculum initially will encounter a number of difficulties: Teaching genealogy is a difficult venture (and Jewish genealogy even more so). And testimony, no genealogy textbook currently exists and genealogy is not taught anywhere in a formal, academic setting.

Jews in particular have a specific reason to pursue the burgeoning field of genealogy: The tragedy of the Holocaust has created an enormous vacuum in practically all European families, a vacuum that begs to be filled. Possibly the best way to put it, for many of us who lost relatives, is to state: "At home we never had an attic"[33], simply because our parents emerged from the Holocaust without most of their family, without documents and photo albums. Without a past.

[32] C. Crespi [et al.], *HLA Polymorphism in a Majorcan Population of Jewish Descent: Comparison with Majorca, Minorca, Ibiza (Balearic Islands) and Other Jewish Communities*, "Tissue Antigens" 60: 2002, pp. 282-291.

[33] G. Krajzman, personal communication, January 2006.