What are Jews: interrogating genetic studies and the reification of race

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Summary - Scientific studies on the genetic proximity of Jews undertake to shed light on "who or what Jews really are". However, various scientists and scholars have warned that such studies reify racial thinking. This essay delineates and contextualizes the debate held between various geneticists and social scientists on the danger of reification within the Jewish context. This is mainly a debate about the impact of (traditional, religious, and Zionist) narratives on scientific research as well as on the ethical responsibility of scientists. The paper claims that such genetic studies test Jewish religious narratives against genetic research results and do not necessarily enforce old notions of distinctiveness.

Keywords - Genetic population studies, Jewish identity, Race, Racism, Genetic studies.

Introduction

Past and present genetic, anthropometric, and molecular studies of Jews often serve as examples for the impact of narratives on scientific research. In the 18th and 19th centuries, physical anthropology was concerned with categorizing humans into groups based on their appearance. Today, the field of human population studies focuses on patterns of genetic diversity with the goal of mapping population developments and migrations over time. The main purpose of researching population stratification is biomedical, to identify and predict genetic disorders. A relatively small part of the papers on human population studies, however, aims to reconstruct the history of one or more population groups. These papers belong to a field that resides within the realm of both history and biological research, and therefore invite a discussion on the scope of the impact of narratives on scientific hypotheses. To be sure, "Jewish genetics" is only one of many examples for the search of origins of today's population groups with the help of DNA analysis. Whether it is "the origin of modern Japanese populations" (Cooke et al. 2021), the "genetics of ancient Romans" (Antonio et al. 2019), or an analysis of the genomes from "Bronze Age Bulgaria" (Modi et al. 2019) to give only a few examples, ancient forefathers and -mothers are a fascinating topic for scientists as well as for the general public. In the case of "Jewish genetics", however, scientific work can get easily politicized, even when there is no "Jewishness" involved – as happened recently after the publication of a research paper on the genetic origin of the Philistines (Feldman et al. 2019), which prompted Israel's then-premier minister to project the scientific results onto the Palestinian question for making his political point – based on the wrong assumption that Palestinian equaled Philistine (Gannon 2019).

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But rather than dealing with politicians and their use of scientific papers for populistic ends, this essay highlights, delineates, and contextualizes the ongoing debate between various geneticists and social scientists on two main points. One is whether or how narratives impact the work of the researchers. In our case, it is the association of modern Jews as the (biological) descendants of the biblical Hebrews or today's Cohanim as descendants of the biblical priestly caste. As the debate on the Khazars exemplifies, genetic research can be politically loaded. Scientific theories or research results about the origin of Ashkenazi Jews are used for political purposes - but interest in the topic also places the researchers into a context of ideology and identity politics, which is closely linked to real or perceived national interests (Weitzman 2017). The other point is the discussion about the danger that genetic studies on population groups reify race. Neither of these questions applies only to genetic research on Jews, but for Jews they have a special meaning that is rooted in Jewish history and culture. A short introduction will highlight the historical context of Jews as a research subject in physical anthropology. The first part of this paper focuses then on some well-known genetic population studies on Jews and the criticism that was voiced against them by other geneticists. It weighs the arguments that are brought forward by various scientists and attempts to answer the question of whether the two much-discussed genome association studies on worldwide Jewry from 2010 (Atzmon et al. 2010; Behar et al. 2010) are biased and convey a biological view of Judaism.

The second part deals with the arguments of scientists and humanities scholars who evaluate the connection between genetic studies on Jews and racial thought in various ways. It covers the range from those who see the responsibility for misuse and racism in the work of the scientist, to those who emphasize the formation of group identity as the salient feature of such genetic studies, and to the scholar who considers genetics studies to be an antidote to racism, as they emphasize human diversity and universality. It is not the aim of the essay to point to singular arguments as being either right or wrong but to highlight the many facets of this complex subject which are derived from Jewish religion and history.

Historical background

The idea that Jews are the descendants of the biblical Hebrews, and are characterized by certain physical features, predated, and ultimately informed modern science (Mosse 1978). In the 19th century, physical anthropology compared population groups using anthropometric measurements to establish body features that differentiate between population groups. In its long

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history, the term race was never unambiguously defined, and it was not clear how many races existed. The difficulty in discussing race conceptually is precisely because there was no clearly defined, but different ones in different contexts (Hutton 2005; Goldberg 1993; Stepan 1982). Accordingly, there was no consensus about whether Jews constituted a race, and if so, if it was "pure" or made up of two or three "types" (Hart 2011; Efron 1994; Patai and Patai 1975). In the 17th and 18th centuries, human diversity was mainly explained by outside influences like climate, nourishment, and diseases (Niekerk 2019; Müller-Wille 2015). Human "varieties" or "races" were not understood as distinct groups, but as gradually changing, comparative to what today is called a clinal distribution (Marks 2007). But notions of inequality of human faculties entered these first attempts at taxonomy, most notably with German philosopher Immanuel Kant, who taught anthropology for several decades. There is an ongoing lively scholarly (and public) debate about the question "Was Kant a racist" (Kirkland 2017; Kleingeld 2007; Bernasconi 2001) which can only be pointed to here for lack of space. It has been shown that German physical anthropology of the 19th and early 20th century was, in stark contrast to Anglo-American and French physical anthropology, "a self-consciously liberal endeavor, guided by a broadly humanistic agenda and centered on efforts to document the plurality and historical specificity of cultures" (Glenn Penny and Bunzl 2003; Massin 1996). Racial ideologists were not among the professionals at research institutions. When towards the end of the 19th century the racist Gobineau Society was founded, it "aimed to racialize history and culture rather than biology and medicine" (Weindling 1989). After the death of the influential Rudolf Virchow in 1902, the liberal stance of physical anthropology changed gradually. Virchow had, among many other achievements, founded the Berlin Anthropological Society, founded several museums, was a liberal politician until he became Rector of the Berlin University, and dominated the field of physical anthropology in Germany (Glenn Penny 2008; Becker 2008). But mainly



under the influence of the First World War, German anthropology turned into a nationalistic and racist endeavor (Evans 2010). In the 20th century, physical anthropology understood race as referring to population groups that share anatomical features and heritage. This was in demarcation from "Volk", which denoted ethno-linguistic population groups (Hutton 2005). While racial anthropology could construct Jews as the racial "other", it could not explain what "European races" were, nor what racial mixture constituted the German Volk. Therefore, the uniqueness of the German Volk had to be explained with the help of linguistics (Hutton 2005). Long-existing stereotypes of the Jewish body fed into Nazi propaganda. In order to derive "justification" for persecution, Nazi propaganda portrayed Jews not only as physically - and therefore pathologically different but also as constituting a foreign body (Fremdkörper) within the body of the German people (Volkskörper) (Neumann 2009). Thus, race passed from categorization to evaluation. After the race ideology culminated in the Holocaust, the use of race as a taxonomy concept was called into question in many fields of science and the humanities. A study showed that unlike in English-speaking countries for example, in the years between 1946 and 2003, Israeli researchers in genetics, epidemiology, and medicine carefully avoided the term race in their scientific publications because of a "cultural-emotional barrier" (Gissis 2008). Still, in the post-war years, exploring human population history with the help of biological markers developed into an international research field. The molecularization of biology made possible a seemingly objective comparison between population groups. The human genome was perceived as storing the information on population history, which could be retrieved using advanced technology (Sommer 2008). In Israel, genetic population studies on Jews -based on self-identification - carried out almost as soon as the state was founded in 1948 and were strongly influenced by Zionist ideas (Kirsh 2003; Falk 2017).

Jews are instanced as the victims of race categories, but it is important to note that notions of inferiority of "the other" existed before and independently of scientific categorizations. Notions that we would call today racist entered the categorizations of various race theorists. That does not mean that racial categorization led to these notions, nor that "the race category" (as an abstraction of all possible racial categories) was intrinsically racist - this would disregard historical contingency. But learning from the way history developed, we know that racist misuse of science poses a danger also today. Anthropologists and human geneticists should be aware of the possible political implications of their studies. This, of course, applies to research in general, not only concerning Jews. Various factors play a role in the question of scientific responsibility, as we will see further down. For philosopher Hannah Arendt, it was the intention and practical implementation. She claimed that the responsibility for the misuse of science lies with the abuser and not with the scientist or even the pioneers of race thinking. She did not change her view when she made her essay Race-thinking before racism into a chapter of her book The Origins of totalitarianism more than a decade later. For her, "[r]acism sprang from experiences and political constellations which were still unknown and would have been utterly strange even to such devoted defenders of 'race' as Gobineau or Disraeli or Nietzsche. There is an abyss between the men of brilliant and facile conceptions and the men of brutal deeds and active bestiality, an abyss which no intellectual explanation is able to bridge." (Arendt 1944). Imperialism instrumentalized the race category, and racism constitutes a means to an end. Therefore, it was not the idea of race as a category that leads to racism. She suggests that the race category would eventually have been dropped had it not been a useful tool in the hand of imperialists. And even though the race category was used as a tool, she declares that "[...] it is unjust to make any particular science respon-sible for pseudoscientific superstition." (Arendt 1944). Racist scientists exist, of course, but their racism is not grounded in science, but in ideology as a political weapon: "[Ideologies'] scientific aspect is secondary and arises first, from the desire to provide for watertight arguments, and

secondly, because their persuasive power got hold also of scientists, who no longer were interested in their research-results but left their laboratories and hurried off to preach to the multitude their new interpretations of life and world." (Arendt 1944). Not the race concept itself is dangerous, but its use as a political tool in the context of state power (Taylor 2011; Moruzzi 2000). Arendt's distinction between race as a category for thinkers (who did not understand it in national terms), and racism carried out by perpetrators might be too clear cut to be viable today when it comes to genomics – phenotyping is just one of the examples here. But, as will be discussed in more detail in the section on genetics and racial thought, does categorizing people necessarily imply a hierarchy? Or is it possible to forge a narrative that emphasizes the interconnectedness of populations, even in population genetic research?

Genetic population history and the Jews

Despite the difficulty in defining who is a Jew, the question of whether Jewish population groups are more related to each other than to non-Jewish population groups, and whether the differences between the two can be quantified, have fascinated geneticists for a long time. It was assumed that the more advanced the technology, the more precise the results, yielding clearer answers. In 2010 two genome-wide studies on the relationship between various worldwide Jewish populations were published almost simultaneously, but independently of one another, by international teams of researchers. They employed the most advanced technologies, represented the latest state of research, and received much attention. They will serve as examples for studies on the genetic relationship between Jewish communities (specific communities or worldwide). Since then, more than thirty genetic studies focusing on the genetic heritage of Jews in their historical context were published in international genetic research journals.

The first paper discussed here, authored by Gil Atzmon and his international research team, is titled Abraham's children in the genome era. The title highlights the commitment to the traditional belief that lews are descendants of the ancient Hebrews. In the introduction the team made it clear that their objective is to take up the old question of a biological definition of "the Jews". They (Atzmon et al. 2010) explicitly take on the notion of race: "For more than a century. Jews and non-Jews alike have tried to define the relatedness of contemporary Jewish people [...] whether the Jews constitute a race, a religious group, or something else." Atzmon and co-authors use race as a shorthand for a biologically definable entity, which might or might not be detected or verified by genetic research. Two years later one of the coauthors of the paper, claimed that the study had "demonstrated a biological basis for Jewishness." (Ostrer 2012). The wording in the scientific paper itself is more careful: "In this study, Jewish populations [...] formed a distinctive population cluster [...], albeit one that is closely related to European and Middle Eastern, non-Jewish populations." (Atzmon et al. 2010).

The second paper, titled The Genome-wide structure of the Jewish people, by Doron M. Behar and co-authors is published in the scientific journal Nature (Behar et al. 2010). This paper likewise aims to study the genetic relatedness of world Jewry. It assumes that contemporary Jewry consists of "ethno-religious communities whose worldwide members identify with each other through various shared religious, historical and cultural traditions." Like in older studies on questions of relatedness of Jewish groups, both studies aim to determine the scope of relatedness among Jews from the various communities, and between Jews and the non-Jews of their host populations. In addition, the goal of both studies is to verify, through genomic analysis, whether the communities share a common, ancient "source population" in the Middle East or the Levant. In broad terms, both studies find that most of the Jewish communities are interrelated to various degrees, are genetically closer to each other than to their non-Jewish hosts and have genetic ties to the

Middle East. In that respect, the results are not revolutionary, since from the 1950s onwards studies show that Jews from different geographic/ ethnic backgrounds were somewhat related. Just a year before the genome-wide studies, a research paper concluded that Jewish populations (represented by Ashkenazi, Moroccan, Tunisian, and Turkish Jews) are genetically closer to each other than to their host populations, share a Middle Eastern ancestry to a considerable extent and European ancestry to various degrees (Kopelman et al. 2009).

As is usually the case in genetic population studies, group assignment is based on self-identification. Here, all four grandparents had to come from the same Jewish community for an individual to take part. This is an important point for studies that include Jews. Self-identification is seen by population geneticists as a convenient method, albeit with limitations (Shim et al. 2014). It was shown that individuals with four Jewish grandparents can be genetically differentiated from those without any Jewish grandparents (Need et al. 2009). At first glance, this might seem understandable, as according to traditional Jewish law, "Jewishness" is passed on biologically from mother to child. Especially after the Holocaust, the traditional view of Jewishness was challenged by some in their quest for meaning in their affiliation, who rejected a self-definition based on biology. On a greater scale, the traditional view of a biological basis for Jewishness through the mother-child relationship was challenged by intermarriage and the liberalization of religious law by the Reform movement, which in the early 1980s acknowledged patrilineal descent for determining "Jewishness" in addition to matrilineal decent (Falk 2015). This makes self-identification quite problematic in that its complexity is not reflected when samples are sorted binarily into "Jews" and "Non-Jews". An individual with only one Jewish grandparent would, according to tradition, be Jewish (if the grandparent is the maternal grandmother), or non-Jewish, if it is otherwise. The genetic "composition" of an individual is dependent on the level of liberality of the Jewish community from which the samples

are taken, and therefore, samples differ. This is important because the lay public might not be aware that genetic markers do not measure a biological feature but establish a correlation through comparison. The category "Jewishness" is ambiguous but in studies used in unambiguous terms and assigned to biological data.

The studies then subdivide "Jewish" into several Jewish ethnic subgroups. Clear-cut distinctions between Jews from different ethnic backgrounds are problematic, however, given for example the shifting borders within Europe, the history of Jewish migrations, and the largely unknown scope of conversions into Judaism in antiquity. Furthermore, these categorizations do not reflect affiliation with multiple ethnic groups.

Criticism from geneticists

Both genome-wide studies discussed above were published in high-impact journals and attracted much attention not only in the academic world. Even non-academic journals and newspapers reported on the studies at the international level. Therefore, it might have surprised some that in 2015, the Israeli geneticist Raphael Falk published an article titled Genetic markers cannot determine Jewish descent. Eran Elhaik (2017), another Israeli geneticist, commented that "Falk's perspective pulled the rug from under the field of Jewish genetics [...]." In his article, Falk reviews older scientific research papers on two different topics, both of interest for the Jewish, and especially the Israeli public. One is the relatedness of Cohanim, and the other is the so-called Khazar theory. According to traditional Jewish belief, all Cohanim are paternal descendants from the first priest, the biblical Aaron, Moses' brother, and are therefore themselves considered priests. As parts of Talmudic law are adopted by Israeli civil law, ritual marital restrictions prescribed only for Cohanim are, through Rabbinical Court's jurisdiction, binding in the State of Israel (Sinclair 2005). The Khazar theory claims that all or most of Ashkenazi Jewry originated from a Turkic, multi-ethnic population that is said to have lived in the Caucasus in the 8th century and converted to Judaism, rather than being descendants of

Jews who had settled along the Rhein and northern France and then spread eastwards. From the 19^{th} century onward, the Khazar theory has been invoked regarding the question whether Jews are a race, with or without antisemitic undertones, or in openly antisemitic contexts (Brittingham 2020; Kohler 2014; Shnirelman 2007). But the theory has been most clearly political in relation to Zionism – as for example in the last years of the British mandate in Palestine, when it was used "as a way to delink the victims of the humanitarian catastrophe in Europe from any ancestral links to Palestine as a way of preventing further Jewish immigration" (Miller 2020).

In academia, however, it is still debated whether a Khazar conversion to Judaism took place at all, and if so, to what extent. The theory gained much attention through a bestseller by Israeli historian Shlomo Sand (2009). His book challenges the notion, or as Sand calls it, the "historical myth" that present-day Jews are descendants of the ancient Hebrews and serves as a reference for some geneticists, e.g. Elhaik (2013).

The papers under review by Falk comprise studies on Y chromosome haplotypes whose frequency distinguishes Cohanim from other Jews (Falk 2015; Skorecki et al. 1997; Thomas et al. 1998, 2000). Falk remained skeptical about the interpretation of their results and finds that they are best explained only given the "assumptions and educated guesses and failing to take into account all other possible scenarios" (Falk 2015). He does not criticize specific scientific methods but stresses the interpretative bias created by wishful thinking that casts doubt on the scientific value of the study's results. Likewise, a group of researchers that re-analyzes the Cohen Modal Haplotype concludes in their article, edited by Elhaik, that their results show "its inadequacy for forensic or genealogical purposes" (Tofanelli et al. 2014). Lately, a research article confirms the genetic Cohen lineage as a subbranch of a certain haplogroup (Sahakyan et al. 2021).

Falk (2015) also places the studies that evaluate and ultimately reject a possible genetic contribution by the Khazars to Ashkenazi Jewry (Behar et al. 2003; Behar et al. 2004) into the ideological context of "clarifying the Jewish identity in the process of the Zionist project of 'ingathering of exiles' in Israel". He contrasts this with a study published by Elhaik in 2013, which was based on datasets from Behar et al. (2010), mentioned above. Even though using Behar's datasets, Elhaik (2013) concludes that his findings support the Khazar hypothesis. This led to a further research study by Behar et al. (2013), who published a rejection of Elhaik's conclusions. As representatives of the Khazars, Elhaik (2013) uses the samples of the contemporary populations from the central and southern Caucasus. Behar et al. (2013) added samples from the north of the Caucasus to their data. This is based on historical and archaeological findings by Khazar expert Peter Golden and others that support a Khazar presence in the northern Caucasus (Behar et al. 2013; Golden 2007).

Even if Falk's assumption of a political bias of the authors is true, it does not necessarily follow that the papers are not scientifically sound. Here, sampling is the obvious problem of a genetic approach to Khazar history. As Behar et al. (2013) point out, "no contemporary population is identified, either by self-identification or by historians, as Khazars or Khazar descendants."

It is obvious that in the case of the Khazar empire, too little is known about people and territory through historical and archaeological research. Under the given circumstances, Behar et al. (2013) take the most scientifically sound approach – they state the methodological problems, employ wide sampling based on prior historical knowledge, and interpret the results carefully. They are convinced that samples from the southern Caucasus area reflect the genetic proximity of its populations with Middle Eastern populations, rather than a Caucasus ancestry for Ashkenazy Jews.

In his critique, Falk (2015) makes an important point: In the case of the Jews, a shared religion, culture, and language resulted in kinship relations so that shared biology is the consequence of a (social) Jewishness rather than its origin. He thereby casts doubt on the notion that there exists some kind of distinct original gene pool of ancient Jews, although this was not explicitly claimed in the genetic studies discussed above (Atzmon et al. 2010; Behar et al. 2010). Whether such an original gene pool once existed cannot be dis/proven, but whatever the genetic proximity between Jewish groups may be, it reflects social phenomena - for cultural and religious reasons Jews married among each other. Therefore, Falk (2015) concludes that "in spite of considerable consanguinity, there is no Jewish genotype to identify." His concerns are of political or societal nature. He warns that DNA studies could turn "the evidence of DNA sequences into the *essence* of the characterization of Jewishness rather than its *consequence*." (Falk 2015. Italics in the original).

In a similar vein Elhaik ties the search for "Jewish biomarkers" to racial thought. He claims that today's geneticists who belong to what he calls the biological Jewishness school, are looking for practically the same biological essence -only on the molecular level- as the early anthropologists, one that would set Jews apart from the rest of humanity (Elhaik 2016). He refers explicitly only to two scientific papers but asserts that these geneticists work to substantiate the biblical narrative. Both studies (Behar et al. 2010; Chaubey et al. 2016) claim to have determined a middle Eastern ancestry among Jews, although Elhaik (2016) dismisses the results as "unsubstantiated by identifiable mutations and [which] are rather the products of ad hoc choices of data partitioning techniques followed by a creative interpretation of the results." His opinion is mainly based on the argument that the admixture components, which were supposed to denote the Middle Eastern origin in Ashkenazim, are not unique to the Middle East. To prove his point, he designed an analysis of his own and compared the genetic distance of the representatives of different Jewish groups from a simulated "Jewish archetype." He generated this "archetype" from four major admixture components, which he then compared with samples of around three hundred Jews from thirty Jewish communities. In his results, the genetic difference between his "Jewish archetype" and the sampled Jews roughly corresponds to the geographical distance from each of the Jewish

communities to Israel. He concludes that this result contradicts the traditionally held belief that Jews form one group with ancestry in the Middle East. Apart from the fact that his methodology is questionable (composing an archetype and then using it as proof), his argument is also formulated to the extreme, as none of the authors of genetic research papers claimed the existence of one single marker common to all Jews. He thus seems to be equally guilty of interpretative bias.

Do Atzmon and coll. and Behar and coll. promote a notion of a biological essence of Jewishness?

Atzmon and collegues aim to settle the question of what "constitutes" the Jews (Atzmon et al. 2010). However, they make it clear that there is no one genetic marker shared by all Jews. In fact, they conclude that their study "demonstrates that the studied populations represent a series of geographical isolates or clusters with genetic threads that weave them together. [...] Over the past 3000 years, both the flow of genes and the flow of religious and cultural ideas have contributed to Jewishness" (Atzmon et al. 2010). The publication by Behar and his team, which was singled out by Elhaik as deliberately substantiating the biblical narrative, explicitly assumes Jews to be a social group. It neither presupposes nor pre-empts the notion that today's Jews are the descendants of the ancient Hebrews. By presenting Jewish communities as social formations, and Jewish ethnic groups as interrelated to various degrees, both studies may as well have been taken for *de*constructing traditional notions of Jewishness. However, Falk and Elhaik share the concern voiced mainly by humanities scholars that studies on genetic proximities reify old notions of race.

The genetics of Jews and racial thought

For the social scientists and geneticists discussed here, genetic studies on population history are connected to several, interrelated social phenomena such as racism, nationalism, or ethnic identity construction. Increasingly, historians and anthropologists warn that genetic population stratification, even with its professedly nonracial language and outlook would still convey or manifest either the same old notions of race or a slightly different version of the old concept(s) (Duster 2015; Fujimura et al. 2008; M'Charek 2008; Gannett 2004, 2001). This applies to genetic ancestry testing, and even to categorizations for medical purposes, mainly because ancestral groups are (claimed to be) characterized by a heritable difference or distinctiveness.

The Jews as a biological group

The concern that racism might be an inevitable consequence of categorizing humans into population groups is reflected in the one question which keeps re-appearing: after having experienced persecution from the Nazi regime for allegedly constituting a "Jewish race"- even though their concept was pseudoscientific - why would geneticists claim a genetic distinctiveness of the Jews? Anthropologist Roselle Tekiner (1991) points out that "[C]onsidering that the concept of a Jewish race was the basis of the anti-Semitic campaigns of the Third Reich, it may seem strange that some Israeli scientists, a half-century after the Holocaust, are engaged in research that is claimed by a participating researcher to support the significant genetic distinctiveness of Jews and that the Israeli and foreign Jewish press react positively to the news. To a biologist, findings of significant genetic distinctiveness can only mean that Jews constitute a race."

The extent to which today's human population genetics are compared to past theories of race varies greatly, and thus the emphasis on an inherent danger of racism. In the Jewish context, the genetic studies on collective Jewish ancestry are mainly criticized as being designed or interpreted in the framework of a "Zionist narrative", as essentializing biology, or both (Egorova 2014; Abu El-Haj 2014; Prainsack and Hashiloni-Dolev 2009; Gibel Azoulay 2003; Brodwin 2002).

Taxonomy and hierarchy

An interdisciplinary workshop group of Stanford University researchers addresses the problem of a possible reification of race in genetic (biomedical) research in an open letter with several statements. They make clear "that there is no scientific basis for any claim that the pattern of human genetic variation supports hierarchically organized categories of race and ethnicity", and that the difference in human variation is a result of geographical distance. The team then recommends several appropriate measures to counter a possible reification of race in genetic research, and one of them is, for example, to take into account that genetic clusters cannot be equated with sociopolitical ethnic categories (Lee et al. 2008).

The genetic studies by Behar et al. (2010) and Atzmon et al. (2010) point out, on the one hand, that Jewish communities are social structures, but they use genetic proximity as a means of measuring identity. However, discussions of possible dangers of such studies began decades ago. In her essay quoted above, Tekiner (1991) criticizes as politically motivated the research articles by Israeli geneticist Batsheva Bonné-Tamir. These research papers were published in the late 1970s and 1980s and claim to show a Jewish genetic distinctiveness. Tekiner (1991) argues that even if researchers themselves do not believe in racial inequality, it is enough to think of population groups as being of distinct common heritage, because "it is not a belief in racial inequality that makes the promotion of a population as a race a racist action, but rather the contribution of the promotion to further discriminatory policies". In her opinion group distinction is synonymous with inequality. Therefore, scientists are responsible for the misuse of the category, as they - even unintentionally - promoted it. In the same vein, Falk (2015) argued that "[the race category provides] socio-cultural justifications for discrimination on the basis of presumed and irrelevant biological properties".

For historian Veronika Lipphardt the way human diversity is researched today, putatively in a scientific and objective way, resembles nevertheless pre-World War II notions of race in certain ways (as in population isolates and population admixture). According to her (2012), Jews became an object of scientific study because they were at first perceived as a population isolate in the Darwinian sense, and later as a mixed-race, and so, "Jewish history was told in biological terms - ...a myth's scientification." Therefore, she warns (2012) that the danger for contemporary research lies in understanding human evolution as Darwinian, because it could lead to "biohistorical narratives."

Human population genetics beyond race

Nadia Abu El-Haj, an anthropologist, sets out to analyze the "construction of genomic pasts" of the Jews in her book The genealogical science not least in order to answer the question - "why it is that individuals who identify as members of social groups who suffered dearly the violence of race science and eugenics in such recent memory seem so willing to embrace and even to promote a biological self-definition today" (Abu El-Haj 2014). In her discussion of genetic research papers from Israeli geneticists from the 1950s and 1960s, she concludes that "[...] Israeli population genetics was a biopolitical project of relevance to - even if not seamlessly directed by - the interests of a newly founded state and the struggle of its various elites (political, military, scientific) to produce a Jewish nation that it presumed already to exist." While the technological sophistication has advanced at great pace, she finds that the "politics of epistemology" have changed only to a limited degree. Both Tekiner (1991) and Abu El-Haj (2014) point out that genetic evidence is used as a means to an end, which is ultimately political, and in this specific case, Zionist. This interpretation corresponds to the above-mentioned view by geneticists Elhaik and Falk. Abu El-Haj (2014) argues that while racial thought in the 19th and early 20th century linked the political to the biological struggle for existence, this is no longer the case today: "In contrast to race science and racist thought, genetic history embraces a liberal commitment to human agency and choice in its epistemological and commercial presumptions, practices, and norms." But this, she points out (2014), still has a determining authority, because it "reveals to us in actual fact our true (biologico-historical) selves".

However, as will be shown, racial thought in the 19th century was not understood as "a biological struggle for existence" - the use of the race category then was also, like today, a parameter for self-analysis or self-inspection.

In his anthology "Jews and Race," historian Mitchell B. Hart collects texts written by Jewish scholars before 1940 about whether there was a "Jewish race" or how it manifests itself. He points out and demonstrates that Jewish race thought before the Holocaust can be viewed as an integral part of general Jewish thought, and specifically as part of a discussion among Jews of their own "Jewish racial identity" (Hart 2011). This puts Jewish racial thinking into the realm of Jewish studies or Jewish philosophy as opposed to biology. The explanation for the contemporary understanding of Jewishness based on common ancestry, Hart agrees with historian Susan Glenn, is to be found in what she called "blood logic", as "a way of defining and maintaining group identity" (Hart 2011; Glenn 2002). Jews made the race category, or "blood logic" part of the scholarly examination of their history and religion, and thus of themselves as citizens of their respective nation-states.

The modern scholarly discussion of their identity began with the establishment of "Wissenschaft des Judentums" (Jewish Studies) and reached its peak in the late 19th century. The idea of the Jewish people as a people in the national sense long predated Zionism (a point which Abu El-Haj disregards). In 1822, the first edition of the journal "Zeitschrift für die Wissenschaft des Judenthums" printed an essay titled "On the concept of a Wissenschaft des Judentums", as a founding document. The author Immanuel Wolf traces the history of the Jews as one people (Volk) from the time of their statehood, through the diaspora, until his time and argues that there is an inner need for the Jews to focus scientific research on their own self. He states that "the Jews preserved their identity as a people [Volksthümlichkeit] and remained Jews wherever they were." In the same text, Wolf - not apologetic in any way - states that "[t]he history of the European Jews in the Middle Ages contains for the most part a series of deeds with which the enemies of this unfortunate

people [dieses unglücklichen Volkes] intended to suppress and destroy it. Only the history of European greed in America and Africa surpasses these crimes." (Wolff 1822, my translation). For Lipphardt (and others) however, Jews were victims of a "biologization" which was established and defined by non-Jews. When Jews themselves used the concept, it was allegedly because of their will to assimilate (Lipphardt 2008; Efron 1994,18; Stepan and Gilman, 1993). But the race category offered more than that, it was a way to reassure and shape Jewish identity. Not unlike in the late 19th and early 20th century, research into genetic ancestry today can be viewed as a means to explore history and the embedded religious thought (Efron 2013, Weitzman and Rosenberg 2013). Because in Jewish tradition genetic lineage is an important part of religious and cultural belief (a Jewish mother has Jewish children, a Cohen or Levite father Cohen or Levite sons) thought along the lines of biological distinctness is greatly supported. To answer the question of why there are Jews who do not shrink away from a biological self-definition even after the Nazi crimes, there might be room to argue that in Jewish religious thought and tradition "biological" categories exist (Cohen or Levite, for example) without an inherent intention to discriminate against other groups. The fact that the State of Israel linked "Jewishness" (by descent, not necessarily by religion) with citizenship further enforces the biological interpretation of Jewishness - especially as conversions to Judaism are discouraged (Kohler 2021; Devir 2020; Egorova 2014). Yet, genetic ancestry testing is not considered valid evidence of "Jewishness", especially not for citizenship applications. "Jewishness" is determined by rabbis according to religious law and based on traditional documentation. While scientific findings of genetic proximity can potentially support the belief in biological connectedness of Jews, it must be emphasized that common ancestry is firmly implanted in the Jewish religious narrative.

Human diversity and universalism

The possible liberal and universal character of human genetic population history is stressed by

geneticist David Reich. In his book Who we are and how we got here he takes on the discussion of racism and responsibility in scientific research. He criticizes, in an overly polarizing manner, that it is not the geneticists, but rather some social scientists who encourage the rise of pseudoscience (Reich 2018). While he dismisses the category race as too fraught with old misconceptions and, moreover, inadequate for reflecting genetic variation, he is convinced of the need to research populations with shared ancestry, or even researching "genetic predictors of behavioral traits" within populations (Reich 2018). Reich was widely criticized for that, most prominently in an open letter signed by a group of sixty-seven scientists and scholars stating that "such variation is not consistent with biological definitions of race. Nor does that variation map precisely onto ever changing socially defined racial groups" (Kahn et al. 2018). The claim that racial groups vary in intelligence has been made repeatedly in the past and has sparked controversies, in which the danger of scientific racism and eugenic thought were pointed out (Panofsky 2014; Sternberg et al. 2005). The dispute over the book by Reich shows once again how researchers with opposing views are convinced to fight against the old notion of race. The "ever changing socially defined racial groups" however, exist independently of "biological definitions of race". The stereotypes are not grounded in biological definitions of population groups, and negative connotations of group membership can be broken down. Scholarly research can contribute to a reimagination of human diversity. For example, a growing body of scholarship addresses Jewish experiences of "Whiteness "or "conditional Whiteness" and being "Black" (Schraub 2019; Haynes 2018; Goldstein 2006). Such research helps to dissolve the perceived group boundaries. In parallel, research on taxonomy in biomedicine shows that researchers are aware or can be made aware of the socioethical implications of their research and adjust their research design accordingly. For example, sociologist Catherine Bliss (2011) came to that conclusion in her work on racial taxonomy in genomics (in an article unrelated to our topic of genetic studies on Jews). She (2011) describes

taxonomic practice "as a reflexive form of biosociality, a conscious shaping of social notions about biology and race to produce a future that researchers themselves want to live in."

In his approach, Reich (2018) combines group identity with universalism. Starting from the idea of "the people of Israel" as in the story from the Exodus from Egypt, he explains "The story [of the Exodus] allows Jews to think of those millions of coreligionists as direct relations: [...] For me, the multitude of interconnected populations that have contributed to each of our genomes provide a similar narrative that helps me to understand my own place in the world [...]. This narrative of connection allows me to feel Jewish even if I may not be descended from the matriarchs and patriarchs of the Bible." Even though Reich as a geneticist is working with categories of difference, for him, the "centrality of mixture" does not signal an underlying concept of unmixed groups, but on the contrary the ongoing interconnection among human populations. Highlighting the connectedness of humanity serves as the antithesis to racist particularism: "The genome revolution provides us with a shared history that [...] should give us an alternative to the evils of racism and nationalism and make us realize that we are all entitled equally to our human heritage" (Reich, 2018). Likewise, one can observe that the previously mentioned genomic studies on Jews show an "admixture" genetic connectedness to non-Jewish population groups - that does not, or hardly, appear in the religious narrative (at least since the early middle ages) and that is difficult to estimate in historical research. To interpret genomic studies on Jews solely as a new way of narrating the old Zionist idea of shared biology does not do justice to their significance for the Jewish identity discourse.

Conclusion

The question that underlies the debate between scientists and scholars is whether studies that analyze statistically significant genetic differences between human population groups pose a problem to the ethical principle of the equality of all humans. This question is particularly pressing in human population studies that only indirectly serve a medical aim - population stratification plays an important role in Mendelian diseases – but that are popular among laypersons and/or are inevitably embedded in cultural, national, or religious narratives. It has been pointed out that categorizing humans biologically runs the risk to reify race. Bearing in mind scientific racism and Nazi atrocities, scientists and scholars emphasize the danger of the use of a race category as a tool, even when the term race itself is not used. However, genetic human population studies have a variety of functions, biomedical mainly, but also as a means of identity building and -fashioning. As such, they have the potential to shape a new understanding of biologically defined human groups and to shift the focus from the old, static, and deterministic notion of race towards a more complex and universal aspect of ancestry. It is important to trace and describe the ways in which race might be reified in (all kinds of) genomic studies, in order to stay aware of possible unwanted perceptions. The above discussed papers exemplify the awareness in academia. The genetic research on Jews shows that it is possible to underline connectedness and diversity, and to highlight the social aspect of Judaism. Even in genetic research Jews can be understood as part of social communities when consanguinity, as Falk pointed out, is understood as a result of cultural practice.

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