

CHAPTER 5

Belonging:

Population Genetics, National Imaginaries, and the Making of European Genes

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Introduction

National narratives and imaginaries typically celebrate the roots of the nation: the moments that can be construed in retrospect as foundational to the emergence of the nation as a coherent historical entity. Since the eighteenth century in particular, national narratives have often drawn on the natural sciences – paleontology, geology, comparative anatomy, evolutionary theory – to promote the uniqueness and coherence of the national community. Ancient hominin remains have played a key role in attempts to establish ancient roots for the nation through science. Ancient remains have provided a means of ascribing great antiquity to the modern national population by connecting it to the imagined prehistoric landscape of the region (for examples, see Goulden; Oikkonen 73-129; or Sommer).

Since the 1990s, human population genetics – the study of genetic variation among human populations – has served increasingly as a rhetorical and imaginative resource for national narratives. For example, the various national genome initiatives that have appeared since the late 1990s generally operate on the premise that the national population is a

meaningful unit of genetic analysis. Helen Busby and Paul Martin have explored this dynamic in the context of the UK; Amy Hinterberger in the case of Quebec, Canada (“Investing”); and Aaro Tupasela in the context of Finland. Technological developments have also increasingly enabled the analysis of DNA retrieved from ancient human remains. By conjoining population genetic study of human genetic diversity and paleontological examination of ancient human remains, ancient DNA research has appealed to those wishing to establish a material trajectory between modern and ancient human populations.

In this chapter, I interrogate how human population genetics, and especially ancient DNA research, has shaped how the evolutionary roots of nations and national communities may be conceptualized. The central argument is that modern nations and prehistoric populations are not easily compatible. Yet, as I will show, population genetics and ancient DNA are repeatedly invoked to establish appealing narratives of national or ethnic belonging across the political continuum. These narratives have included, on the one hand, empowering personal accounts of ethnic roots produced through genetic ancestry tests, as Alondra Nelson has shown, and, on the other hand, populist nationalist accounts of “authentic” national communities, as Anne-Marie Fortier has demonstrated. I am interested in the ambiguity of communal origins produced through population genetics and ancient DNA: population genetics can be invoked and appropriated to support various kinds of local, global and national communities as well as a range of political positions. In what follows, I explore how the discrepancy between modern national and ancient human populations, and the ambiguity of population genetic belonging, challenge the evolutionary rootedness of national communities, and how such ambiguity affects how national belonging can be imagined through population genetics and ancient DNA. In particular, I focus on the tensions between national, continental, regional and personal genetic belonging.

I address these questions through the case of “Ötzi the Iceman,” the 5,300-year-old natural mummy discovered in Tyrol close to the Austrian-Italian border in 1991. The chapter explores the discursive and technological means through which Ötzi was variedly rendered Austrian, Italian, Tyrolean, and European as his bones, clothes, equipment and stomach contents underwent scientific analysis. The primary focus is on the impact of genetic analysis on Ötzi’s role as a prehistoric, geographically located individual. I use the public and scientific debates about Ötzi’s genetic place in human evolution and the peopling of Europe to examine the cultural appeal and conceptual limits of genetic knowledge. As my focus is on conceptual issues arising from the conjoiner of ancient DNA and national frameworks, the chapter does not engage in an in-depth analysis of these debates but uses selected examples to illustrate key questions that Ötzi’s discovery mobilized. Throughout the chapter, I approach ancient human DNA as an epistemically contested site through which ideas of local, national, continental and personal genetic belonging are debated and negotiated. The case of Ötzi sheds light on both the appeal and complications of crafting evolutionary national narratives through a past that precedes nation-states by millennia.

Human population genetics

Human population genetics studies genetic variation between and within human populations. Historically, population genetics has often focused on the analysis of noncoding DNA (DNA that does not control physiological or behavioral characteristics) and non-recombining DNA (DNA inherited from only one parent). Most important sources of such genetic material were the noncoding sections of mitochondria – tiny organelles located outside the cell nucleus and inherited from the mother – and the non-recombining section of the Y-chromosome inherited from the father. As changes in mitochondrial and non-recombining Y-chromosomal DNA result primarily from mutations, mitochondrial and Y-chromosome DNA were used as a so-

called *molecular clock*. The idea is that the more differences there are between two DNA sequences, the longer the evolutionary distance between the populations they represent. The approach has been used to build evolutionary trees to trace when particular species or populations diverged in evolutionary history.

The growing availability of high-throughput sequencing technologies since about 2005 has also increasingly enabled genome-wide approaches. While genome-wide approaches vary, they often identify and compare SNPs (single nucleotide polymorphisms, that is, molecular sites where people vary)—especially markers associated with particular populations—across a person’s overall genetic make-up. Whereas mitochondrial and Y-chromosome analyses have produced evolutionary trees that rely, respectively, on exclusively matrilineal and patrilineal genealogies, genome-wide techniques engender evolutionary histories that seek to encompass the reshuffling of genetic material within populations.

Population genetics has provided a culturally powerful means of reimagining the relationships between modern human populations and the place of each population in human evolution. Many of these projects have centered on the idea of national community and national belonging as rooted in evolutionary history, as is evident in the plentitude of national genome projects and biobank initiatives that seek to capture the genetic nature of the national population (for examples, see Kent et al.; Mitchell and Waldby; or Nash 101-135). Yet this national framing is awkward for several reasons.

First, there is a discrepancy between national and evolutionary frameworks in terms of their temporal and spatial investments. Evolutionary history involves the migrations of human populations across continents over millennia, and the gradual divergence of populations, a process that does not typically involve clear temporal breaks or geographical boundaries. The slow view of change characteristic of the evolutionary framework seldom coincides with the considerably shorter time frame of national narratives. Likewise, populations studied in

population genetics do not generally follow neat national borders, since national borders are mostly of modern origin. This underscores that the national population is not a naturally existing entity and may not be meaningful in an evolutionary context. National communities emerge as evolutionary communities only *within a particular temporal and spatial framing*. If the temporal or spatial parameters are changed, different kinds of communities—regional, transnational, continental, global—emerge as primary to the national community.

Second, population genetics is not a fixed approach but a dynamic set of techniques and materials that is used to tease out various sets of differences and similarities depending on the kinds of questions that scientists are trying to answer. Amy Hinterberger (“Investing”) and Amade M’charek have both shown how the very concept of population remains unfixed in order to operate as a methodological tool. Through the example of forensic genetics, M’charek demonstrates that the concept of population undergoes various technological and methodological adjustments in order to connect a DNA sample from a crime scene to an ethnic population (21-55). As for the use of population genetics to narrate national origins, a seemingly minor change in the methodological and technological setting of such analysis may engender forms of genetic belonging that contradict the idea of the national community as a coherent entity. What counts as *sameness* in one research setting emerges as *difference* when the setting is changed, as difference and sameness are tied to the choice of technology and computer software, availability of samples, and access to existing genetic databases. My discussion of Ötzi highlights the consequences of these issues for genetically grounded belonging.

In the analysis that follows, I use the case of Ötzi to demonstrate how this ambiguity of genetic population haunts the coherence of national narratives of belonging. I show how population genetics nevertheless remains an appealing rhetorical and affective resource for national imaginaries due to the epistemic power assigned to DNA in contemporary culture.

While with population genetics, the practices of marking differences and similarities are relative – that is, differences are always situated and technologically bound – in popular discourse DNA is made to stand for permanence, indisputability, and precision. DNA thus tends to appear as the ultimate proof of origins, boundaries, and belonging. Through this cultural appeal of genetic discourse, the ambiguity of evolutionary populations and belonging often becomes erased and domesticated.

Ancient DNA

In the 1980s, many researchers turned toward mummified remains and museum specimens to retrieve DNA. The first two important cases were Higushi et al.'s extraction of mitochondrial DNA from a 140 year-old quagga, an extinct species related to zebra, and Svante Pääbo's analysis of mitochondrial DNA from an Egyptian mummy. With the development of a technique for DNA amplification known as polymerase chain reaction (PCR), genetic material retrieved from old remains emerged as a highly interesting object of study in the early 1990s. Many of the early studies – such as a claimed analysis of dinosaur DNA – were later shown to be products of contamination by modern DNA left by archeologists, museum workers, or geneticists themselves. Nevertheless, toward the end of the 1990s several significant studies of ancient DNA had been published, including Handt et al.'s analysis of Ötzi's mitochondrial DNA in 1994, and Krings et al.'s analysis of a mitochondrial sequence from Neanderthal remains in Germany in 1997. With the increasingly routine use of high-throughput sequencing technologies in the past decade, ancient DNA studies have proliferated (see Hofreiter et al.; Perry and Orlando; or Rizzi et al.). A large number of genetic studies of considerably old remains, such as Rasmussen et al.'s analysis of the 9,000-year-old human remains known as Kennewick Man (The Ancient One) in Washington State, have been

published. Instead of relying on mitochondrial DNA, these technologically advanced studies have employed genome-wide techniques.

Apart from providing new knowledge on extinct species and past populations, ancient DNA promised to complicate the evolutionary trees produced by population genetics. Population genetics had largely operated on DNA collected from living people. Variations within modern samples have been used to construct evolutionary histories that show when particular populations or species diverged. The appeal of ancient DNA lay in its promise of material concreteness. Instead of having to rely on extrapolation from modern samples, scientists could see what ancient sequences looked like. One advantage was that ancient samples could point to now extinct variations that could not be detected through modern samples. The idea of a direct material connection between modern populations and a prehistoric ancestor had obvious cultural appeal. By conjoining the materiality of ancient bones with the imagined material precision of DNA, the study of ancient remains appears as establishing a firm and indisputable link between us and our genetic roots. Without ancient DNA, those roots would remain largely theoretical and statistical. However, the assumed concreteness of the connection between modern and ancient samples is somewhat misleading, as the connection relies on methodological choices, statistical software, availability of samples, and selection of SNPs for analysis (see Oikkonen 73-129 for further discussion).

Biological material discovered in melting permafrost has provided an important source of ancient DNA, as ice can preserve DNA without significant degradation. The discovery of Ötzi in the Alps in 1991 was a key event in the scientific use of naturally frozen remains in the study of human evolutionary history. Ötzi's body was remarkably well preserved under the ice and therefore a unique source of information. However, advanced sequencing technologies of the past decade have enabled scientists to retrieve DNA from astonishingly small samples. In 2010, Rasmussen et al. analyzed DNA from human hair discovered in

permafrost in Greenland to construct the genome of a 5,000-year-old man (“Extinct Palaeo-Eskimo”). Also, in 2010, Krause et al. and Reich et al. constructed the evolutionary history of a previously unknown hominin population – the Denisovan – based on DNA retrieved from a finger bone and tooth discovered in a cave in Siberia. Crucially, discoveries like Ötzi or the Denisovan appear to challenge the sense of temporal distance that organizes the cultural view of prehistory as a far-gone realm. In his discussion of Ötzi, David Turnbull argues that *cryopreservation*—the preservation of biological material, such as DNA, in ice—unsettles prevalent assumptions of temporality and spatiality in foundational ways. Turnbull shows how the discovery of hominin remains in melting ice engenders unexpected constellations of time and space, and how a range of technological maneuvers, such as different types of scientific analysis and narrative framings, are brought together to produce a coherent account of human evolutionary history.

The Discovery of Ötzi

In September 1991, two German hikers came across a frozen corpse protruding from the ice close to the Austrian–Italian border in the Ötztal Alps. The body was initially thought to be a deceased hiker, but a closer examination a few days later revealed that the body was much older. Subsequent radiocarbon dating established the age of the remains, dubbed “Ötzi” or “the Tyrolean Iceman,” at about 5,300 years. What made the discovery so remarkable was the well-preserved state of the body: to date, Ötzi is the oldest known natural mummy discovered in Europe. He even had red blood cells still in his body.

Since the discovery, Ötzi has undergone extensive scientific study including, for example, an analysis of the contents of his stomach, indicating when and what he ate before his death (Dickson et al.; Oeggl et al.; Rollo et al., “Last Meals”); analysis of the pollen present in the food, locating his death in the spring (Oeggl); analysis of the isotopic

composition of his tooth enamel, indicating where he grew up and where he lived in the surrounding regions (Müller et al.); and an analysis of so-called Beau's lines on his nail, suggesting several bouts of sickness during the last six months of his life. Aspöck et al. showed that Ötzi had an intestinal parasite—a whipworm—whilst Maixner et al. identified the strain of *Helicobacter pylori* in his gastrointestinal track. Scientists have also presented a number of theories on how Ötzi died, including hypothermia, loss of blood from an arrow wound, a blow to the head, and ritual killing, and why he was undertaking the arduous trip across the mountains: was he hunting, or herding, or perhaps fleeing? His sophisticated clothing and equipment, which included a prestigious copper axe and medicinal supplies, have given rise to various theories on his social role and rank. Who was Ötzi, where did he come from, and where did he belong in human evolutionary history?

Genetics played a key role in addressing these questions. The first genetic studies examined Ötzi's mitochondrial DNA, a focus that reflected the technological state of ancient DNA research at the time. Handt et al.'s 1994 study was able to locate and amplify one section of noncoding mitochondrial DNA that was not too badly degraded or contaminated by other DNA. The paper concluded that Ötzi's mitochondrial sequence "seems to fit within the European gene pool" while being "closest . . . to the individuals from the Alpine region" (1994). Furthermore, the paper states that Ötzi's sequence has "been found in 7 of 155 individuals from northern Germany, Denmark, and Iceland and twice among 100 British Caucasoids" (1994). In the wake of advances in sequencing technologies in the mid-2000s, this initial study was complemented by several new studies including Rollo et al.'s more detailed analysis of Ötzi's mitochondrial DNA in 2006 based on new samples retrieved from his intestines ("Fine Characterization"), and Ermini et al.'s sequencing of his whole mitochondrial genome in 2008. These analyses showed that Ötzi belonged to a previously

unknown branch of the mitochondrial subclade K1, a result that was confirmed by Endicott et al.'s 2009 study.

In 2012, almost twenty years after Handt and colleagues' initial mitochondrial analysis, Keller et al. were able to sequence Ötzi's nuclear genome. The new study traced a number of SNPs associated with physiological characteristics, such as eye color, blood group, lactose intolerance, and susceptibility to coronary heart disease. While the mitochondrial analyses had suggested that Ötzi was connected to populations around the Alps, the sequencing of his nuclear genome pointed to recent common ancestry between him and present-day populations of the Mediterranean islands of Sardinia and Corsica. The study also identified Ötzi's Y-chromosome haplogroup as G2a4-L91, a haplogroup that is particularly common in southern Corsica and northern Sardinia. Sikora et al.'s 2014 population genomic analysis of Ötzi along with several other European ancient remains and additional samples from modern European populations provided further details and corroboration.

National, Regional, or Continental Belonging?

Although the genetic studies of Ötzi's mitochondrial and nuclear DNA deployed the technical language of populations, haplogroups, and SNPs, such studies were engaged in conceptualizing Ötzi's prehistoric existence in terms of ethnic, racial, and regional affiliations. This becomes clear already in Handt and colleagues 1994 paper, which suggested that "[c]omparisons of DNA sequences from the body with contemporary populations may reveal aspects of his ethnic affiliation" (1775). This is in line with the discourses and framings of population genetics and ancient DNA studies at the time (Oikkonen 73-129). As we saw above, the genetic studies that emerged after 2005 provided increasing detail and specificity about Ötzi's genetic origins. Yet, as I will argue next, pinning Ötzi down to a national or

regional identity is a complicated issue, and genetics can engender only a specific, epistemically situated view into Ötzi's national, regional, and ethnic belonging.

First of all, the question of Ötzi's national affiliation is closely tied to the shape of modern nations. What is interesting about Ötzi's case is that his body was found on the section of the Austrian-Italian border where the precise location of the border was unmarked due to the long-standing presence of thick ice. Consequently, Ötzi was first assumed to be found on the Austrian side and was sent to Innsbruck, but was soon deemed to have been discovered in Italy, and arrangements were made to move his body eventually to the South Tyrol Museum of Archaeology in Bolzano. Turnbull observes that “[t]he question of Ötzi's retrospective nationalization was so intense that it led to an official surveying and marking of the border. It was determined that Ötzi was spatially located 92 meters on the Italian side of the border. After intense negotiations he was rechristened with an Italian identity” (160; see also Spindler, 66-69). Ötzi's ambiguous national identity was reflected in media accounts. For example, *The Guardian* described Ötzi as “the 5,000-year-old Austrian iceman” in 1995, while an article in the British paper *The Observer* published in 1994 called him “an Italian Iceman” (McKie, “Italian Iceman” 5). In addition to national identities, Ötzi has also been given regional identities such as the “oldest of Tyroleans” (Anastas A108). My point here is not to suggest that one assignment of identity is right and the others wrong—that is, whether Ötzi was Italian or Austrian or simply Tyrolean. Rather, I want to highlight that national categories of belonging simply do not make sense in the context of prehistoric events 5,000 years ago.

Furthermore, even modern borders are not clear and unambiguous. Borders are multiple. For example, different forms of surveillance and border control, or disparate personal, communal and institutional practices of border crossing define borders differently, as Sarah Green as well as M'charek at al. have shown. In the case of Ötzi, his renaming as

“Italian” did not simply correct an error, but rather made visible the multiplicity and ambiguity of borders. Although Ötzi’s discovery site turned out to be located on the Italian side of the unmarked border, the melting waters from the discovery site drained to the Austrian side suggesting that the site was in fact part of Austrian Tyrol, and that the current border was a miscalculation made possible by the ice cover. Turnbull argues that this resulted in “a topographic reality incompatible with a political reality in which Ötzi resides in an Italian museum” (160). To complicate issues further, borders have histories: in Ötzi’s case, South Tyrol had been annexed by Italy after World War I—before that it had belonged to the Austrian-Hungarian Empire. Crucially, feelings of resentment still lived in parts of Tyrol, registered, for example, by a 1998 account in *The Washington Post* noting that “[t]he date of the transfer [from Innsbruck to Bolzano] was kept secret, partly because of threats from Austrian nationalists who have never recognized the South Tyrol annexation” (Haller A19). This shows that in debates about genetics and national identity, it is pivotal to recognize that nations are historical entities with their own intertwined and often complicated histories. The power of population genetics to engender national belonging is thus challenged not only by the discrepancy between the modernity of nation-states compared to the antiquity of evolutionary landscapes. It is also complicated by the tension between the temporality of the nation—the emergence of a nation as a process that takes shape in relation to other nations—and the temporality of species-level evolutionary processes, such as human evolution. These national and evolutionary temporalities become entangled in problematic ways when scientists use historically evolved cultural concepts or administrative terms relating to ethnicity, kinship arrangements, or societal identity, to define scientific or technical terms such as population, as Amy Hinterberger (“Categorization”), Nina Kohli-Laven, and Tutton et al. have shown.

Second, there is a clear tension between national and continental frameworks of genetic belonging. For example, while the media liked to frame Ötzi as “Italian” or “Austrian,” they also portrayed him as “European.” For example, the British newspaper *The Guardian* suggested in 1995 that based on Ötzi’s genetic likeness with modern European samples, “he was, above all, a European” (*The Guardian* 26); a 2003 article in the British paper *The Observer* referred to Ötzi as a “Stone Age European” (McKie, “Secrets” 7); and a recent article in the *New York Times* maintains that Ötzi “has provided a trove of information about the life of Europeans at that time” (Wade). I suggest that the simultaneous presence of European, national, and regional frameworks in public discourses about Ötzi arise, to a considerable extent, from technological and material practices. Depending on the kind of population genetic analysis deployed, Ötzi’s identity as a prehistoric individual shifts. One crucial factor is the temporal scope: the further back we zoom in evolutionary history—say, 10,000 to 5,000 years ago—the more likely we are to focus on events that led to the larger patterns of migration within the European continent, a temporal focus that encourages framing prehistoric identities as continental rather than national. Conversely, working within a temporal frame closer to the present—say, what happened between 5,000 and 2,000 years ago—often encourages emphasis on movements around local boundaries such as rivers or mountain ranges, many of which became enmeshed in the project of constructing national borders during the past centuries.

Likewise, the point of comparison employed in population genetic analyses matters. Comparisons with modern, geographically localized samples are likely to foreground an ancient sample’s geographic locatedness in terms that resonate with national frameworks of belonging, while comparisons with other ancient samples often highlight much broader geographic scope thereby resonating with a continental framing. Furthermore, SNPs chosen for analysis play a significant role. Some SNPs are associated with broad areas—Africa, for

example—while others are considered to be more regionally specific. All in all, the line between continental, national, and regional frameworks is not clear-cut. Instead, these alternative forms of belonging appear or disappear through relatively minor revisions of the analytical apparatus. This reflects M'charek's carefully documented observations that population genetic practices are a matter of situated and pragmatic negotiations.

Enacting Personal Genetic Ties

Ötzi has become connected to modern and ancient populations in multiple and changing ways that are more than a matter of technologies becoming increasingly accurate over time. While technological innovation certainly has played a role, Ötzi's multiple and shifting genetic connections also reflect specific approaches within population genetics. For example, as we saw above, mitochondrial analyses suggested a genetic connection to the Alpine region and Y-chromosome analysis pointed to a genetic connection to Corsica and Sardinia because they examined different genetic material—mitochondrial DNA inherited through a maternal lineage and Y-chromosome DNA inherited through a paternal lineage. Crucially, mitochondrial and Y-chromosome analyses are culturally appealing because they seem to suggest a direct and irrefutable material connection between modern populations and an ancient individual.

The idea of an irrefutable and unique material connection between modern and ancient people gained particular momentum with the increasing interest in the genetic roots of specific modern DNA sequences at the turn of the twenty-first century. In the case of Ötzi, researchers and commentators have attempted to connect the iceman to modern individuals. These attempts reflect a larger cultural trend of seeking to root people within the patterns of prehistoric human migrations on *the level of the individual*. For example, commercial genetic ancestry tests have been marketed online directly to consumers since about 2000. Such tests

promise to engender concrete material ties by comparing the customer's DNA sample (retrieved with the help of a test kit sent through mail) to a database of DNA samples and established mitochondrial and Y-chromosome haplogroups. As scholars like Henry Greely, Jennifer Wagner, and Lee et al. have shown, the sense of concrete material ties that the tests promise is misleading, as the tests typically focus only on a small percentage of a person's genetic make-up and the results are products of particular situated methods and available databases.

The interest in creating specific connections between prehistoric and modern individuals was present in the discourses surrounding Ötzi. In his popular book *The Seven Daughters of Eve* (2001), geneticist Bryan Sykes, who was part of the team that authored the 1994 mitochondrial paper, tells the story of how he connected Ötzi's mitochondrial DNA to a living person, an Irish woman (and friend of Sykes) called Marie Moseley, who lived in Dorset in the United Kingdom. (Sykes is also the director of one of the first commercial genetic ancestry testing companies, Oxford Ancestors, launched right before *The Seven Daughters of Eve* was published.) Intriguingly, Sykes maintains that Moseley experienced the connection between her and Ötzi as emotionally charged, and that such emotional investments arose from the understanding that the connection between them was material and thus irrefutable (7-8). For my analysis, the important point is not whether Moseley actually felt this way, but that Sykes's account of the event represents the connection between modern and prehistoric individuals as a source of intimate emotions and belonging. This suggests that population genetics, when applied on the level of the individual, resonates strongly with cultural ideas of personal belonging.

This move toward belonging as personal also underlies a 2013 study of the Y-chromosome haplogroup G in Tyrol by Burkhard Berger and colleagues. The study used blood samples from 3,7000 men, along with self-reported genealogical information, to

evaluate the presence of various G subgroups in Austrian Tyrol. While only a small section of the article focused on Ötzi's haplogroup, it was this part of the results that interested the media. For example, the *Discover Magazine* website sported the headline: "Living Relatives of Ötzi the Iceman Mummy Found in Austria" (Draxler). Echoing the language of mainstream news outlets such as NBC News (Boyle) or the BBC, the text referred to the 19 Austrian men with Ötzi's haplogroup as "newly-found living relatives," "family members," "long-lost relatives," and "descendants of the Ötzi family" (Draxler). Such use of familial language rendered the connection between Ötzi and each of the 19 modern Austrian men private and potentially affectively invested, while insisting that the kinship relationship embodied a material reality that could not be refuted. This celebrated material connection is made even more special through the foregrounding of the specific type of genetic material—Y-chromosome DNA inherited from the father—used in the study. (The specificity of genetic material—mitochondrial DNA—was also central to the affective politics of Sykes's account of Marie Moseley.) Interestingly, the case of the modern Tyrolean men differed from the case of Marie Moseley in a crucial way: the men were not named, nor were they apparently informed about the results. Yet the very idea of a personal (rather than communal) genetic connection to the prehistoric past appears to carry such strong cultural resonance that the anonymity of the men seemed trivial in cultural discourses around the study.

All in all, this turn to personal ancestry complicates evocations of national genetic belonging. While both the Irish mitochondrial descendant and the Austrian (Tyrolean) Y-chromosomal descendants emerge as ethnically and geographically located individuals, they are not related to Ötzi through their national identity: most Irish people and most Austrians (or Tyroleans) are not genetically connected to Ötzi in any meaningful way. While personal genetic belonging and national genetic belonging may sometimes coincide and reinforce one another, Ötzi's case shows that this is not necessarily the case, and in fact, national and

personal frameworks often contradict each another. Moreover, the various forms of genetic belonging are all tied to specific technologies, such as mitochondrial, Y-chromosome, or genome-wide techniques of analysis. Interestingly, this multiplicity of technologies is most clearly visible in personal belonging, as the connection between a prehistoric and a modern individual is typically conceived through mitochondrial or Y-chromosome analysis. At the same time, the claims to material specificity in personal belonging suggest that national belonging, too, relies on specific situated technologies.

Conclusion

The chapter has shown that a prehistoric human like Ötzi can be construed alternatively within the frameworks of continental, national, regional, and personal genetic belonging. In the discourses surrounding Ötzi's discovery and genetic study, he appears as an early European who represents the role of Neolithic people in establishing the foundations of European societies and a European way of life. Ötzi also emerges as an early "Austrian" and an early "Italian" to whom modern national populations can arguably be traced. He is also constructed as an "authentic" Tyrolean, who tread the same laborious paths across the Alps as modern Tyroleans 5,300 years later. Finally, he is the ancestor of geographically located modern individuals whose private family histories are represented as arising from the intimate life of Ötzi. All these forms of belonging are potentially emotionally charged, resonating strongly with cultural discourses that seek to root communities and individuals in the distant past.

This multiplicity of continental, national, regional and personal belonging suggests that it might be very hard for one version of belonging—such as national belonging—to take precedence over the others. Or, to put it slightly differently, such precedence is always situated and temporary rather than arising from the biological qualities of Ötzi's remains. I

have argued that Ötzi is rendered continental, national or regional through technological and material practices as well as through cultural narratives and imaginaries. Seen from this viewpoint, Ötzi is a sociotechnical and material *assemblage* that has come into existence through an evolving range of scientific practices, transnational collaboration between research teams, legal definitions (such as national borders and national autonomy) and circulating cultural narratives.

The case of Ötzi shows that population genetics can be invoked to engender culturally powerful narratives of belonging because ancient DNA is perceived widely as a concrete material point in the past where modern belonging can be anchored (see Oikkonen 73-129, for further discussion). At the same time, accounts of national, continental or regional evolutionary roots rely on constant epistemic and rhetorical work to downplay and erase the alternative levels of genetic analysis and alternative narratives of belonging that Ötzi also enables. While population genetic knowledge and ancient DNA can produce trajectories that appear as material and irrefutable, it is important to remember that genetic analysis of SNPs or geographical distribution of haplogroups cannot tell us anything about emotional attachments, societal or political affinities, or the complicated and intertwined processes through which national and regional communities have emerged and transformed over time.

In fact, the ways in which Ötzi became a source of imagining roots in multiple narrative frameworks raise more questions than settle them. What counts as roots in an evolutionary genetic framework? What is belonging when conceived through genes and prehistoric migration patterns? What is the relationship between national community and land, or national community and time in an evolutionary framework? How should the temporal and spatial borders of communities be defined if communities are examined as evolutionary entities? Crucially, the ultimate ambiguity of these issues is precisely what makes possible the multiple frameworks of genetic belonging that surround ancient human

DNA. The ambiguity enables national genetic belonging to emerge and coexist simultaneously with continental, regional, or personal genetic belonging in sociotechnical practices and cultural imaginaries.

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