PART I

Imaginations of Finnishness

CHAPTER 1

The Genetic Imagination

Imaging Populations and the Construction of Nationhood

Aaro Tupasela
University of Helsinki

Abstract

This chapter explores the ways in which genetics, particularly population genetics, generate representations of difference and similarity. Using examples drawn from both scientific literature, as well as popularizing texts, I show how visual representations of difference and similarity have come to provide compelling forms of evidence for constructing nationhood, as well as national identity. Using the case of Finnish genetics, as well as the study of rare diseases in Finland, I will describe how genetics and historical understandings of nationhood have come to complement other forms of national identity, such as culture. If the national romantic period in Finland from the late 19th to the early 20th centuries drew its legitimacy from literature and the arts, then the role of genetics in the construction of nationhood can be understood through the lens of what I have termed *genetic romanticism*. Much like the national romantic

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period, I consider genetic romanticism as a set of practices and processes through which national identity becomes defined and stabilized.

Keywords: nationhood, population genetics, genetic romanticism, visualization

Introduction

According to the British philosopher Kwame Anthony Appiah (2010: 151), "upholding differences among groups may entail imposing uniformity within them." Within the interdisciplinary field of science and technology studies (STS), research exploring the generation of similarity and difference has focused on the ways in which science and its related technologies become intertwined with these processes. The generation and maintenance of racial and ethnic differences/uniformity have in many ways rested on using the visual senses to understand physical differences between individuals. Whether we examine the history of phrenology or race classification under apartheid in South Africa (Bowker and Star 1999) or the ways in which artificial intelligence platforms come to perpetuate racial inequalities and discrimination (cf. Mitchell 2019), the role of the visual in upholding difference has always played an important role.

When it comes to nationhood and nationalism, the generation of difference draws on a far wider gamut of resources to generate difference. This includes culture (music, art and literature), symbols of nationhood (flags, statues), as well as science and technology (Adas 2015). The role of science and technology in constructing and mediating representations of difference and similarity has become a powerful tool, which is all too often understood as being neutral and unbiased. Recently, numerous authors have pointed to the myriad of ways in which bias and racial discrimination are built into technologies (Benjamin 2019; Eubanks 2018; Noble 2018). Unpacking the role of technology in generating perceptions of difference and similarity are, therefore, central concerns in better understanding how "whiteness" is being created today. "Whiteness," according to some commentators, has become the accepted norm and measuring stick against which other races are compared (Bonnet 1993; 1996).

During the past half century, discussions surrounding the genetics of difference have garnered a great deal of attention in relation to difference and uniformity between people and nations (Lipphardt 2014). Nadia Abu El-Haj (2012: 22) has pointed out how genetic markers have been understood as "'mere' indexes of ancestry and origin," whereby genetics is seen as a neutral representation and archive of human origin and ancestry. The role of early genetic studies of populations, such as the HapMap project and the Human Genome Diversity Project, sought to provide scientific explanations of genetic variation and difference, only to fall into the trap of *a priori* assumptions of what constitutes

meaningful genetic difference in the first place (M'charek 2005). Although these projects were rooted in the work and curiosity of Luca Cavalli-Sforza and his interest to understand the evolution of humans over time (Cavalli-Sforza 1990; Cavalli-Sforza et al. 1991), the project was nonetheless plagued by ethical, legal and social criticisms (Wasserloos 2001; Weiss 1998; Reardon 2009). Most significantly, a number of commentators accused the proponents of the project of being a "vampire project" and its organizers molecular colonialists for "'targeting' ethnic groups without consulting them" (Young Kreeger 1996).

The role that genetics has played, however, in constructing and solidifying scientifically derived differences among populations, particularly national populations, has been surprisingly significant, particularly within the Nordic context (Tupasela 2017; 2021). Genetics not only provides a technologically mediated basis for understanding similarity and difference (thus something that is perceived to be neutral and natural), but it has also provided surprisingly striking visual tools and representations of similarity and difference between various groups of individuals. "Whiteness," according to Richard Tutton (2007), has become a mainstay in many of today's genetic study designs and is used to uphold an asymmetry of power in relation to who deserves to be studied and for what reasons (Frankenberg 1993; see also Maldonado-Torres 2016). Within the Finnish context, whiteness has come to encompass more a nationalistic as well as a cultural delineation, whereby differences have been drawn between language groups (Finnish versus Finnish-Swedes and non-Finnish-speaking, especially Russian), as well as ethnic minorities, such as the Sámi and Roma populations.

Evelyn Ruppert (2011) has suggested that a population is not an object that awaits discovery, but rather enacted through specific devices and technologies. According to Nancy Krieger (2012: 634), "who and what makes a population has everything to do with whether population means are meaningful or meaningless, with profound implications for work on population health and health inequalities." In this sense, technologies of population visualization based on genetics enact particular types of relations between individuals and populations rather than represent an archive or index waiting to be discovered.

This chapter explores the ways in which genetics, particularly rare disease genetics and population genetics in Finland, generates representations of difference and similarity. Using examples drawn from both scientific literatures and popularizing texts, I will seek to show how visual representations of difference and similarity have come to provide compelling forms of evidence for constructing nationhood, as well as national identity. Using the case of Finnish genetics, and drawing on the study of rare diseases in Finland, I will trace how genetics and historical understandings of nationhood have come to complement other forms of national identity, such as culture. The development of the notion of Finnish Disease Heritage (FDH) among Finnish pediatricians and geneticists can be understood as a form of kinship study within the Finnish context (cf. Sommer 2015). Subsequently, population geneticists have

transposed and translated these findings into a broader interpretation of Finnish genetic heritage and origin.

If the national romantic period in Finland (late 19th and early 20th century) drew its legitimacy from literature and the arts, then the role of genetics in the construction of nationhood can be understood through the lens of what I have termed *genetic romanticism* (Tupasela 2016). Much like the national romantic period, I consider genetic romanticism to be a set of practices and processes through which national identity becomes defined and stabilized. As Venla Oikkonen (2018) has noted, however, population genetics is a set of evolving technological and material practices, which means that the relations constructed through genetics are also fluid and dynamic.

I locate this chapter within a broader academic discussion on ethnic and racial relations, with a particular focus on the Nordic countries (Keskinen 2019). I argue that genetics and its associated technologies of visualization play a crucial role in how scientists and the media enact and construct Finnishness. A significant narrative in this process has been the argument that Finns are a unique and homogenous entity. This narrative of uniqueness is, however, constantly being negotiated and aligned with a narrative of being European and Nordic as well (Tarkkala 2019; Tarkkala and Tupasela 2019). Modern genetics, with its long and troubled history and entanglements with eugenics, racial hygiene and discrimination (Kevles 1985), has sought to distance itself from this heavy historical weight. Following the work of Nelson Maldonado-Torres (2016: 10), however, Western genetics still carry with them remnants of coloniality and decoloniality, in that many of the logics of processes associated with generating genetic difference and similarity still rest on the "matrix of power" inherent in "Western civilization" (cf. Tutton 2007). In Finland, this is particularly salient in relation to the Sámi population. By this, I mean that within genetics the significance of the white, Western, male still remains a dominant benchmark against which others are compared. Furthermore, in relation to nationhood, Finland has sought to use genetics as a tool for recreating and perpetuating notions of genetic uniqueness (Tarkkala and Tupasela 2019). The fluidity and malleability of genetic identity is an ongoing process, where the analysis of new samples and their comparison to samples collected from other populations generate new ways of understanding identity and ancestry (Oikkonen 2015).

There are several reasons why I draw attention to the role of genetic technologies in generating difference and similarity between people and populations. *First*, technologies always entail choices as to what is analyzed and how. Although many of the underlying assumptions about these choices may seem clear and straightforward to the researchers using them, their consequences may not be as clear to people who are unfamiliar with the underlying assumptions that their use entails. *Second*, what one chooses to analyze genetically is by no means a self-evident process. Given the vastness of the human genome, the choices related to what one wants to study will inevitably have

an impact on the outcome. The study of different parts of the human genome (mitochondrial DNA, as opposed to a comparison of a whole exome sequence) will yield different results in terms of relationships between individuals and groups of people. *Third*, and perhaps most obvious, is the question of which individuals are included in the studies. Although this may seem self-evident, genetics has a long history of exclusion. In Finland, for example, Roma people have never been included in a single population genetic study. Similarly, Samí people have not been included in all studies conducted in Finland, which has contributed to the generation of different types of population differences in a number of studies. *Finally*, the study of genetic difference and similarity between individuals and groups of people always entails the question of who are we comparing and to what? Genetics is always relative. Despite the sequencing of the human genome at the beginning of the millennium, the use of that genome as a baseline to qualify differences and similarities is always questionable. As I will discuss below, the question of the role of different reference populations will always generate changes in the relations between those being studied.

In the following, I will first discuss scientific visualizations as a particular object of study within science and technology studies, as well as the humanities. Following this, I will describe the early historical roots and linkages between the study of rare diseases and how nationhood has come to be represented genetically. Finally, I will discuss these points with reference to specific studies, which Finnish researchers have conducted with samples from various segments of the Finnish population and point to some of the challenges they pose in relation to delineating and constructing genetic Finnishness.

Scientific Visualizations

A number of scholars have suggested that the emergence and ubiquity of digital technologies and the forms of new representation that they entail can be called a "visual turn" within contemporary culture (Carusi et al. 2015; Mitchell 1994; Rheingold 1992). The visual turn can be said to encompass and cover a number of interconnected perspectives, including concerns over perceptions and cognition of new visual technologies, new ways of understanding and interpreting scientific objectivity in relation to visual representations, as well as ontological questions about what count as scientific objects themselves (Carusi et al. 2015: 2).

The study of visualization as a technology is closely aligned with questions surrounding representation and objectivity. As discussed above, the study of representation as a scientific practice is by no means new (Coopmans et al. 2014). The use of visual representations within genetics research has helped to provide relief to compressing massive amounts of genetic information into images, which geneticists use to visualize relations. The translation of

mathematical and computational tools into visual representations, however, is not without its problems. Matei Candea (2019: 63), for example, has argued that diagrams do not provide "a clearer, simpler, or less deceptive" communication medium than textual arguments. One could even argue that visual representations of computational methods obfuscate and complicate our understanding of genetic relations and population migration through an oversimplification of those very processes.

The compression of large amounts of data in images masks many of the choices made by researchers in order to generate those visualizations. Visualizations, as well as genetic testing, all entail a large number of methodological choices, which will inevitably have a significant impact on the outcome of the results. Since there is no standard or commonly agreed upon measure within genetics to study difference, the result is a broad range of genetic studies, as well as visualizations through which relations and ancestry come to be represented. In this sense, I argue that the history of visualization goes hand in hand with the history of scientific observation (Daston and Lundbeck 2011; Lipphardt and Sommer 2015; Pauwels 2006).

What is interesting in a number of these studies that I will discuss below is how they form an extension of cartographic practices. Gunnar Olsson's (1998; 2010) critical work on cartography serves as an important entry point to examine visualizations generated by geneticists as attempts at generating new types of objects by drawing lines. The genetic maps, which geneticists generate, serve as powerful visual enactments, which help to stabilize, as well as destabilize, notions of identity in relation to genetic ancestry. Given that these visualizations draw on different collections of genetic material, collected using different criteria, as well as analyzed using different methods, the outcomes are equally different.

Visualizations and diagrams, such as population genetic trees and maps, are examples of such visualizations. As Marianne Sommer (2015: 108) has noted, "molecular tree diagrams freeze a hierarchical kinship system that is meant to represent a state before the great historical movements." On the one hand, these visualizations help to present a narrative and image of unity and similarity among those who are included within that visualization. At the same time, however, the visualizations are used as a form of exclusion, which seeks to draw its authority from empirical methods and computation.

Maps have always had an important role in the representation of power relations (Pickles 2004). With the combination of genetic analysis and mapping, medical professionals and geneticists inscribe biological traits on physical maps. These inscriptions serve as novel narratives of identity, ancestry and difference, which draw on scientific notions and claims of objectivity and neutrality. In the following, I will begin by discussing the role of the study of Finnish Disease Heritage (FDH), which has played an important role in creating an alignment between genetic analyses and historical narratives of identity and origin.

Finding Finnishness in Church Records

Although this chapter seeks to draw attention to the role that scientific visualization has played in constructing Finnishness, it would be a grave omission if I did not draw attention to the close relationship between medical (genetic) and historical research—in particular, the role that church records have played in helping to better understand how some genetic features came to be described as being particularly Finnish. To understand this relationship, I need to discuss the concept of Finnish Disease Heritage (FDH). FDH is a group of rare diseases that are overrepresented in the Finnish population (Norio 2000). First introduced as a concept in 1973, the term has come to cover some 30 typically recessive diseases in the Finnish population. The concept has represented a major research undertaking particularly within the Finnish pediatric profession initially, and later within the genetics research communities. The study of rare diseases helped to produce a historical account of population migrations in Finland as it relates to families who are carriers of the different mutations. The study of FDH has also been instrumental in elucidating the uniqueness of the rest of the population. This historical linkage was the result of researchers using church records to better understand how genetic inheritance between distant relatives may have given rise to the rare disease in question (Tupasela and Tamminen 2015).

The study of FDH over the years has also contributed to a stabilization and naturalization (though still contested) of the genetic uniqueness of Finns themselves. Despite FDH being a very heterogeneous group of diseases, it has served, in part, to formulate a specific vision of Finns as homogenous yet European during the past 50 years. The historical work conducted around FDH has had an important impact on later population genetic studies, as well as the narratives used to explain how Finns came to be unique since the studies showed how migration and intermarriage affected the prevalence of certain rare diseases in the population. Particular examples of this include the notions of isolation (such as in the case of Kuusamo and Kainuu), as well as bottlenecks, which feature heavily in some of the later explanations of Finnish homogeneity.

Subsequent genetics studies of the Finnish population have drawn heavily from the concept of FDH and its associated historical narratives. In particular, the relationship between genetics and historical explanations of population structure have become part-and-parcel of how many subsequent population genetic studies have been conducted in Finland. While the studies of FDH cases relied on more traditional visual representations of disease and relationships, such as maps showing the locations of where patients lived, the subsequent population genetic images and visualization represent far more persuasive tools for representing relationships between groups of people since they compress a massive amount of information into relatively easily

understandable images. Given that the study of rare diseases has involved special and unique communities, which were the result of isolation, as well as bottlenecks, it is surprising to see the degree to which these narratives have influenced more general population genetic studies. As Oikkonen (2015) has noted, however, population genetic studies draw on a multitude of technological and material practices, and the FDH-derived historical narrative represents only one theory of Finnish genetic origins and identity (cf. Sundell et al. 2010).

In the following section, I will discuss some of these images and related texts, as well as their significance for understanding how Finnishness has been visually represented in genetic studies.

Representing Nationhood (Population Structure) through Genetics

> The Finnish population in Northern Europe has been a target of extensive genetic studies during the last decades. The population is considered as a homogeneous isolate, well suited for gene mapping studies because of its reduced diversity and homogeneity. However, several studies have shown substantial differences between the eastern and western parts of the country, especially in the male-mediated Y chromosome. This divergence is evident in non-neutral genetic variation also and it is usually explained to stem from founder effects occurring in the settlement of eastern Finland as late as in the 16th century. Here, we have reassessed this population historical scenario using Y-chromosomal, mitochondrial and autosomal markers and geographical sampling covering entire Finland. (Palo et al. 2009)

Geneticists can study and represent genetic ancestry and relations in many ways. There is no one way, but rather a multitude of methodologies for sampling and analysis, which produce different results. Although this is self-evident to geneticists, methods, technologies and sampling decisions also have an impact on the ways in which nationhood and identity come to be represented and understood. The above excerpt from a study examining Y-chromosomal, mitochondrial and autosomal markers highlights how different methods and sampling strategies will generate different ways of understanding and representing identity and ancestry alike. Besides highlighting the different outcomes in interpretation of population structure, the article also highlights the significance of temporality in genetic studies of ancestry. Depending on the samples used, such as ancient DNA, different studies also open up different temporal vistas of ancestry (cf. Willerslev and Cooper 2005). During the past half-century, starting from studies on rare diseases and their causes, these studies have also contributed to an interesting and varied discussion regarding the origins and genetic relations of Finns.

As discussed above, Finnish genetic identity and the origins of Finns have traditionally been studied and understood through the medium of culture and cultural artifacts. Disciplines, such as archaeology and history, have contributed to the understanding of early settlement and origins of the Finnish populations. The national romantic period in Finland provided new material representations of national identity, including literature, art and architecture (Anttonen 2012). Alongside these approaches, genetics have provided new epistemological, as well as ontological, approaches to deriving identity "markers." Compared to culturally derived markers of identity and relatedness, genetics draws on the authority of natural science and calculation to derive its claims to scientific objectivity (cf. Daston and Galison 2007).

To highlight some of the challenges associated with the visualization of relations using genetics, I will begin by highlighting an article by Elina Salmela et al. (2008), which sought to study population structure by comparing samples collected from a number of populations within the Nordic countries and Europe. Figure 1.1 provides an example of the ways in which research groups use visualization to help present the results of an analysis comparing genetic samples taken from these 16 different population groups. Although the image itself is challenging to interpret given that it is in three dimensions, the colorful dots nonetheless provide us with a quick way of understanding how difference between samples taken from different people show up on an image. The first important point to make regarding the image is, despite it being in three dimensions, that it is able to compress a massive amount of information into a relatively simple color image that helps guide the reader into "seeing" genetic relations between individuals within these sample groups. Much like Nadia Abu El-Haj (2012) has noted, this serves as an indexical representation of relations, despite it being highly fluid.

Although I will not go into the specifics of the analysis, I would like to focus on an important insight, which the authors make in the article. They state:

> Interestingly, in the MDS plots the Finnish-Swedes stood out from the rest of Western Finland *only when* Sweden was included in the analysis, which highlights the importance of *relevant reference populations* also when detecting patterns of variation within a country. (Salmela et al. 2008) (emphasis added)

Despite having used a large number of samples from different populations, the authors noted that genetic difference among the samples collected from Western Finland only emerged when they added samples collected from Sweden to the analysis. This important observation points to the relational quality of genetic mapping. Geneticists can create difference by adding different reference populations to the comparison. In this sense, the process of drawing lines and mapping in genetics differs considerably from traditional cartographic practices in that differences and similarities are relative as opposed

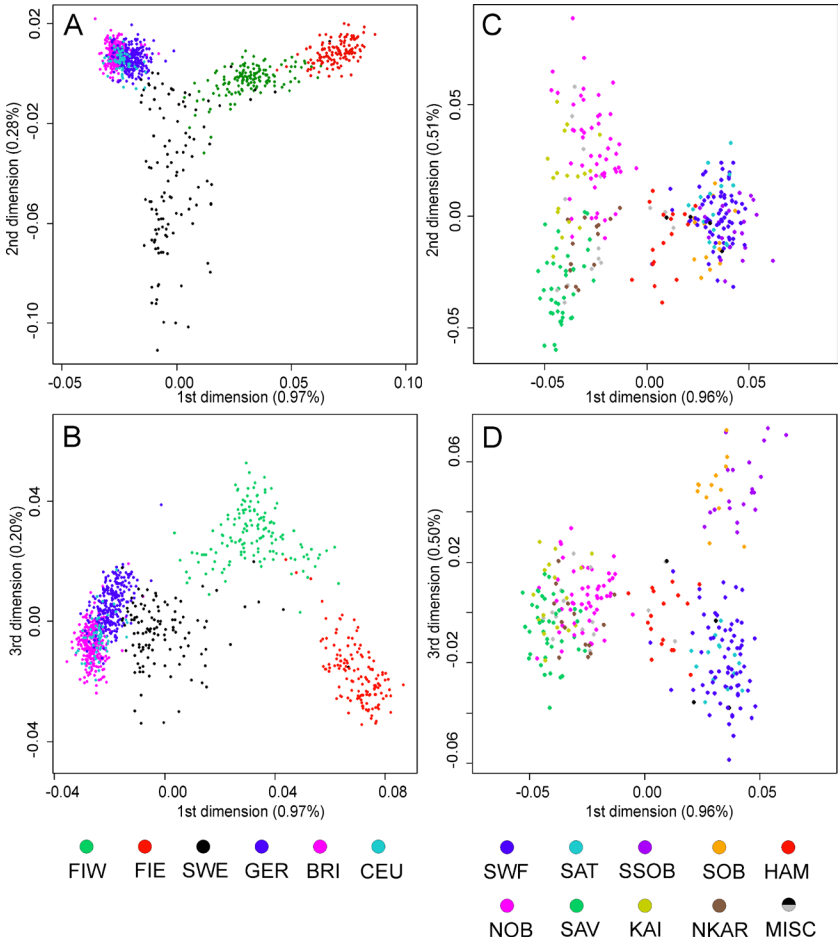

Figure 1.1: Mapping genetic relatedness. Source: Salmela et al. 2008. Published under CC BY 4.0.

to fixed physical entities. The point also highlights an even more important consideration when conducting these comparative analyses. Since genetic relations are always in relation to something (another sample or samples from a population), including different reference populations will either increase or decrease the location of the dots on the visualization. This will represent, therefore, closer or more distant relations. It is important to note, therefore, that in relation to Gunnar Olsson's (1998) notion of creating new objects by drawing lines, the comparisons that geneticists generate of populations are not stable, fixed objects, but rather always enacted through relations, which are materially and technologically mediated.

This important observation is significant for a number of reasons. *First*, the observation highlights the relational nature of many of the genetic studies, which provide visual representations of similarity and difference. *Second*, although geneticists understand this challenge, the images and studies that they create may cause confusion as to the fixed nature of relatedness. *Third*, there are no standards or accepted practices as to which reference populations ought to be included in such comparisons, rather, studies have tended to include samples based on which ones have been available for the researchers.

The study by Salmela et al. (2008) carries also many of the challenges, which I mentioned earlier in relation to methodological considerations. Much like the study by Jukka Palo et al. (2009), this study takes as its starting point a particular analysis methodology (MDS). Studies such as this have significant implications as to their epistemic authority. Although the researchers recognize the fluidity of genetic studies such as this, the visual objects that are generated have considerable significance in popular culture. The translation of scientific studies to popular media and culture is a significant element in the reproduction of Nordic coloniality, in that it reinforces notions of uniqueness and difference. I will discuss this point later on.

There is also an important temporal perspective raised by this type of study. As new studies are published using different samples from different populations, so changes the narrative of origin and genetic relatedness. In comparing the Palo et al. article to the Salmela et al. article, we can already discern the emergence of a competition between narratives of relatedness and origin, which are reliant on the materials and technologies available to the researchers.

The Salmela et al. (2008) study is representative of many similar studies which draw comparisons and contrasts between populations. It is, however, worth examining another significant study published in 2010 by the Finnish Institute for Molecular Medicine (FIMM). In a press release entitled "Finnish Genes Placed on the Genetic Atlas of Europe" (FIMM press release 2010), they describe a study conducted in the Netherlands (see Figure 1.2) in which genetic samples from Finns, among many others, had been analyzed to study differences and similarities between European populations (Lao et al. 2008). One of the figures in the article is comprised of two maps next to each other: the one on the left is an image where populations are compared based on their SNPs (single nucleotide polymorphisms), whereas the map on the right is a traditional cartographic map of Europe indicating where the samples have been collected.

The study is interesting and important in relation to our discussion of Finnishness for a number of reasons. As I discussed earlier, the question of what methods are used to study differences is a significant question. In this particular study, the researchers chose to compare slightly over 300,000 single nucleotide polymorphisms (SNP) using principal component analysis (PCA). What is important in the study is that they point out some of the shortcomings of earlier analysis techniques, one of which is characterizing population

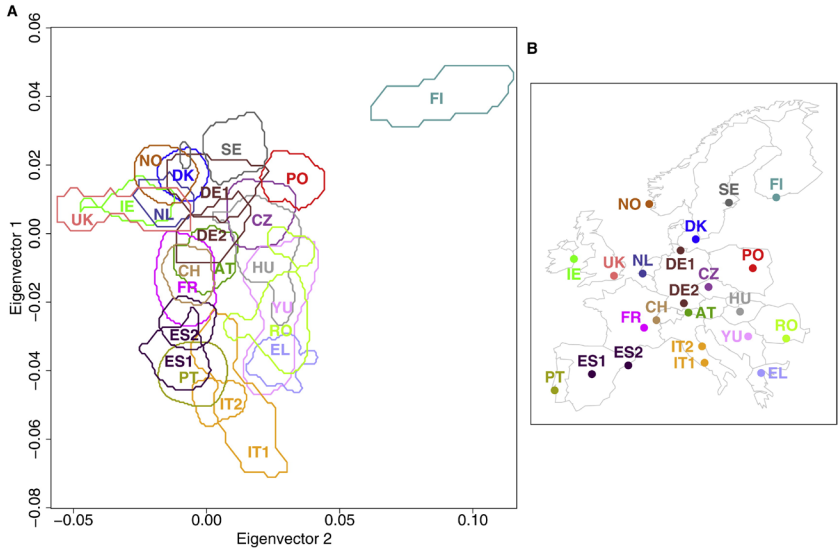

Figure 1.2: SNP-based PCA of 2,457 European individuals from 23 subpopulations. Source: Lao et al. 2008. Published with permission, all rights reserved.

structure and how it correlates to geography. Although it is not the purpose of this chapter to question the validity of these results, I do wish to point out that those differences and similarities can be studied using a multitude of methods, as well as technologies. Furthermore, depending on what part of the genome one studies, the results may provide different insights into similarity and difference. SNP studies, for example, do not provide insights that one might get from studying mitochondrial DNA. In terms of who is studied, it is unclear which individuals have been selected to serve as representatives of a national population. For Finland, 47 samples from Helsinki were included in the study. Following Noah Tamarkin's (2014) discussion of diaspora, the study raises a number of interesting questions. The Finnish samples chosen to represent Finns and Finnish genetic ancestry did not contain representations of ethnic minorities (e.g. Sámi or Roma). Such exclusions and *a priori* assumptions of Finnish history and representation lead to the question of what types of scientific representations of the population and belonging become stabilized in such studies.

Furthermore, the sampling criteria in the different countries also differs considerably. In Finnish sampling protocol, the requirement is usually that samples are taken only from people whose both grandparents were born in the same county. The same criteria, however, have not been applied to samples collected from other countries. This difference in sampling protocol helps to create differences in how homogeneity and reduced variability become expressed in the studies.

According to Lao and colleagues:

> Overall, our study showed that the autosomal gene pool in Europe is comparatively homogeneous but at the same time revealed that the small genetic differentiation that is present between subpopulations is characterized by a significant correlation between genetic and geographic distance. (Lao et al. 2008)

The notion of "comparative homogeneity" used in the text is interesting since what constitutes genetic homogeneity is not defined explicitly. In their article, Palo et al. note how Finns have reduced diversity and are genetically homogenous. As some authors have noted (Tarkkala and Tupasela 2020), genetic homogeneity can take on different meanings depending on what the researchers are referring to.

Much like the study of Finnish population structure, there are many questions which this study raises in terms of inclusion. Many of the countries in the study have significant immigrant populations who have lived in those countries for several generations. From a comparative genetic perspective, however, they are not included in the studies, since their presence would alter the ways in which the lines between national populations would end up being represented in the visualization.

The study also raises the question of what interpretive limitations are built into the study from a broader comparative perspective. What would happen to the conclusions and relations between populations if samples from other populations, such as the Baltic countries or Russia, were included in the study? Would European homogeneity and genetic relations change, and in what ways if the geographic scope of the study were broader?

Besides excluding individuals or groups from studies, geneticists will also "clean" their data before analyzing it. This means that samples whose data do not fit within certain parameters of the analysis will be excluded from the analysis. According to Sini Kerminen et al. (2019), for example, samples with heterozygosity over specific thresholds are removed from studies. The removal of outliers and samples, which skew the results, will have an impact on the results themselves. The act of cleaning data should also be seen as a way in which difference and similarity is reinforced within genetic studies.

One example of the different interpretations that exists regarding the historical development of the Finnish population is between the so-called "two-wave" versus "trickle theory." The two-wave theory of the development of Finnish genetic structure is perhaps best exemplified by a study in which the authors state: "The vast majority of Finns descend from two immigration waves occurring about 4,000 and 2,000 years ago" (Peltonen, Palotie and Lange 2000; see also Kittles et al. 1998). According to this theory, the majority of the Finnish population and its genetic composition can be explained by two major waves of population expansion. In contrast to this theory, another Finnish research

group used computer-modeling methods to try to explain the current genetic population structure of Finland. According to the study: "Immigration from neighboring populations, even if very limited but constant over prolonged time periods, can have drastic effects on a population's genetic composition" (Sundell et al. 2010). What these two studies suggest is that interpretations of population history, as it is in relation to genetic studies, are very fluid and flexible. Origin and relationships can be interpreted in drastically different ways depending on the approach one uses to conduct a study.

Revising Population History Time and Again

The studies I have discussed above, as well as numerous other population genetic studies which seek to describe the genetic origins of Finns, the population structure of Finns and/or their genetic relations to neighboring populations all share a common thread. The studies continually revise and rewrite population histories and relations based on the materials and technologies that are available to them. In this sense, genetics is no different from history or archaeology, which also rewrite migration history continually. These genetic narratives and origin stories play an important role in constructing nationhood and national identity.

Derek Fewster (2006; 2017) has examined the relationship between nationalism and history in Finland, noting how general myths of descent that the elite drew on were strongly drawn from cultural artifacts like the national epic poem, the *Kalevala*. The work of Finnish pediatricians and geneticists can be seen to perform similar activities in constructing narratives of a national genetic heritage through FDH and population genetic studies. Although the genetic studies seek to base their interpretations on computational technologies, methods and samples, there remains an uneasy question regarding the epistemic authority with which these studies are able to lay claim to their findings.

As one recent article noted: "Our work provides a general framework for using haplotype sharing to reconstruct an integrative view of recent population history and gain insight into the evolutionary origins of rare variants contributing to disease" (Martin et al. 2018). The rewriting of "recent population history" is not a stable process and does not produce a stable cartographic object. Although many of the studies make similar findings regarding population structure, there is always a revision involved regarding the historical origins and roots of populations. Concomitantly, this historical revision also entails revisions to our relations to neighboring or even distant populations. Given that the notion of Finnish population becomes so closely tied to national identity, belonging and otherness are also constructed along nationality. What makes the issue of salience in relation to whiteness is how being Finnish is attached or "tethered" (Hinterberger and Porter 2015) to a frozen moment in Finnish history which pre-dates larger population migrations.

Of course, it is important to note that geneticists are aware of this problem. In fact, several Finnish geneticists have written about the problem over the years. In a blog post from 2019, a Finnish forensic geneticist, Jukka Palo (2019), notes how the notion of genetic Finnishness is problematic for a number of reasons. In responding to an ongoing discussion regarding the notion of genetic Finnishness and its use by "ethnonationalists," Palo points out a number of challenges in making claims of homogeneity. He points out that definitions regarding similarity, as well as time as a context for analysis, has a significant impact on the results of interpreting Finnishness from a genetic standpoint. In this sense, Finnish geneticists are involved in the generation of both coloniality and decoloniality within the context of genetic studies. The significance of these studies can be perhaps best exemplified in the ways in which they become translated in the popular media. In the next section, I will briefly discuss this feature of Finnishness as it relates to recent media representations.

Population Genetics in the Media

Although the researchers who conduct and publish these studies are well aware of the limitations of their studies, as well as the contingent nature of comparisons and reference populations, the studies that I have discussed above have had a significant impact on discussion in the popular media. The process of translation into common narratives surrounding national identity and genetics is significant, since it often glosses over the small, yet significant, nuances surrounding genetic analyses.

Perhaps the most significant discussion surrounding Finnish identity in relation to genetics was in Finland's largest newspaper the *Helsingin Sanomat*. Published in their monthly publication, in July 2010, the article "Kaksi kansaa" (two people) sets out to explain how Finland's East–West genetic division can be explained by such common differences as how people mow their lawns (Malmberg 2010). The article draws its insight from the recently published genetic atlas of Finland and points out how Finns from the East of Finland are as genetically different from those in the West, as Italians and Swedes are from each other (FIMM 2010). The article spurred a plethora of discussions in the newspaper's online comment section, which highlights the way in which scientific studies of relatedness and origin translate into everyday discussions and conceptions of identity and belongingness. These discussions, however, rarely reflect the methodological and technical questions which are related to the analytic output in the first place.

The relationship between the visual aspects of genomics and national identity are well laid out in the article since it contains the genetic map that was published by FIMM. The visual cues provided by the map serve as an important form of evidence to support the genetic differences between Finns. The genetic differences are then concomitantly translated by the article into cultural

(language) differences between Finns living in the East versus those living in the West of Finland. While language, art and literature served as vehicles through which national identity was constructed during the national romantic period, the use and circulation of the genetic maps of the Finnish population does the same, except through the medium of genetics. What is interesting in this process relates to the ways in which genetics integrates the traditional symbols of nationhood and identity as allies and evidence.

The *Helsingin Sanomat* article was by no means the only article to circulate the discussions surrounding the genetic origins and development of the Finnish population. Another article popularizing the FIMM study in the media, also published in 2010, was in the Finnish science magazine *Tiede* (Kaaro 2010). According to the article, the human genome is a type of history book. In many ways that is correct, but it should also be noted that the genome can be read and interpreted in many different ways. Furthermore, just like archaeology, it is a "text" that is continually revised and rewritten. In this sense, the book comparison is also problematic since it suggests something that is stable and fixed. As we have discussed, however, the study of the human genome and inheritance always entails interpretations and choices as to how to read the genome itself.

The translation of scientific studies into popular media is always a challenge, in that once they are publicized and published, there is always the chance that they are interpreted in ways that they were not originally intended. This is something that geneticists are also aware of. The problem, however, is that regardless of whether researchers understand this, the images become part of debates and discussions among Finns. As such, they continue to perpetuate common notions of Finns as genetically unique. This process can be seen as a perpetuation of Nordic coloniality, whereby Finns maintain a genetically unique, exclusive and separate history from other Nordic countries and Europe, as well as the rest of the world. In this sense, the images can be seen to contribute to an ongoing logic whereby Finnishness is not just a cultural identity represented through language, for example, but more importantly a genetic quality, which seeks to exclude those people whom geneticists have systematically sought to exclude from their studies.

Discussion

Suvi Keskinen (2019: 165) has called for more studies which explore Nordic differences within the postcolonial period. Since the late 1960s, Finnish genetics have followed a strong path of studying the Finnish population from a genetic perspective, more so than in the other Nordic countries, with perhaps the exception of Iceland. With the case of FDH, the goal has been to help families who are carriers of rare diseases. These studies have helped set the foundation for a particular narrative of Finnish genetic history as being unique and homogenous in comparison to other Nordic countries. These studies can be said to practice a form of "white innocence" (Wekker 2016). They help to

strengthen ideas of the Finnish nation as genetically unique despite the knowledge that the methods and sampling techniques that researchers use always entail decisions regarding inclusion and exclusion. Although many researchers are very aware of this issue and even regularly write about the problems of Finnishness as a genetic quality, these conceptions nonetheless become regularly translated into the popular media and thus everyday understandings of what Finnishness entails.

The studies that I have discussed above also have a concrete impact on current policies and strategies regarding precision medicine in the Nordic countries (Njølstad et al. 2019; Tarkkala, Helén and Snell 2019). For example, Danish researchers recently sequenced 150 "Danish" genomes in order to construct a national reference genome (Maretty et al. 2017). The people selected to represent the Danish population required a significant amount of discrimination and exclusion within the general population. Geneticists are, therefore, constantly involved in generating interpretations of the historical origins and naturalness of the nation-state. Depending on who is included as a "natural" or "real" representative of a nation will have impact on the way in which medical technologies and treatments are developed. For Finland, this would most certainly entail discrimination against the Samí and Roma populations, as well as the exclusion of more recent immigrants such as the Somalis. It would also entail the exclusion of most people whose family histories involved any member of the family moving around. In this sense, Finnish genetic history is closely tied to the lack of mobility.

Oikkonen (2018: 6) has suggested that genetic technologies, such as population genetics, contribute to a narrative of nostalgia where continuity plays an important role. The exclusion of individuals and populations, the cleaning of data of statistical outliers and the visual representations of relations through various technologies helps to contribute to the writing of national narratives. In this sense, genetic romanticism represents a continuation of efforts to maintain national identity and stabilize relations among those whom researchers consider to be Finns. Colonialism has been traditionally understood as a process by which authority is exerted over other people or territories. As Maldonado-Torres suggests, we need to extend this understanding to notions of coloniality and decoloniality. I have sought to use the case of Finnish genetics to show the way in which colonialism and coloniality, as well as decoloniality, operate within the context of genetics. The visual technologies I have described in this chapter should be seen as part of a broader context in which Finnish identity is reproduced through the medium of genetics.

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