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Politics, Governance, and the Law

The Study of Human Genomic Diversity in Latin America: Nation and Population

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Genomic science values the genetic diversity revealed by advances in genetic sequencing that allow the detailed mapping of diversity at the level of the individual as well as the population group. This has reinforced the idea that humans share the vast majority of their DNA and that the diversity that does exist cannot be parceled into biological categories that align with older categories of race, which are deeply implicated in the practices and structures of racism. However, the practice of genomic science and medical genetics continues to make use of collective categories and populations. This paper argues that practices in genomic science in Latin America change but also reproduce and even reinforce (by biologizing) familiar and enduring categories of race at different levels in society—among scientists and among nonscientists. The Latin American cases are particular in showing that race is often parsed through ideas about the nation, seen as emerging from the mixture of three ancestral populations. Biologization effects can reinforce the racism (and nationalism) that depend on racialized categories. The paper ends by arguing that these effects are a result of the basic concept of population that has in the past organized and continues today to organize genetic diversity in science practice, despite the ability of genomic technologies to handle genetic diversity at the level of the individual. The grounding role of the population concept is accentuated by Latin American national identities being based on ideas of mixture, which entails a corresponding idea of original purities.

INTRODUCTION

The understanding and classification of human diversity has been a concern for thinkers from ancient times: why do humans look different from each other and act in varied ways? For many centuries, the main answer to this was the impact of environment, although this could include not only climate and other aspects of the physical surroundings, but also political systems. The questions of human physical appearance and of human behavior were not clearly distinguished in the way that Western thinkers separated "biology" from "culture" beginning in the late nineteenth century, when the idea began to take shape that human physical nature was shaped very strongly by a heritable essence (named germplasm at the time, later called genes) that was not susceptible to environmental change, at least in the short term. In the twentieth century, this biology/culture division was gradually hardened by anthropological theories, such as those of Franz Boas, that saw biology as a substrate that was separate from and explained little or nothing about culture. Such an approach underwrote feminist distinctions between sex and gender and antiracist ideas about race as "a social construction."[1]

Over this very long and varied trajectory, it is difficult to say if philosophers and scientists understood human diversity as people (in the West) tend to see it today, which is as a good thing, either in itself or as a means to an end (such as greater freedom or more productivity). What is clear is that many thinkers—from the ancient Chinese, to the ancient Greeks and Romans, to medieval Arabs and Westerners from the Renaissance onward —were concerned about locating their own type of people at or near the top of a hierarchy of value. In that sense, human diversity was generally viewed through the lens of ethnocentrism. From about 1800, biology emerged as a discipline in its own right in the West, and understandings of human diversity tilted toward

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1 For an extended discussion of—and a guide to the voluminous literature on—the history of understandings of human diversity, see Wade (2002, 43–66) and Wade (2015, 23–104). See also Hannaford (1996); Smedley (1993); (Stepan 1982); Stocking (1982).

comparative anatomy. As a result, ideas of race, which until then had rested on a mixture of concepts that we would now differentiate as biological versus cultural, became increasingly defined in terms of biology—with biology seen as determining moral and cultural attributes. Human diversity was organized into a small number of "races," seen as durable and ancient: even long-standing biblical tenets of the unity of humans descended from Adam and Eve now competed with theories of polygenesis (the idea that each race had separate ancient origins) (Hannaford 1996; Smedley 1993; Wade 2002, chap. 3; 2015, chap. 3). These races were located in a strict hierarchy in which whiteness and white people reigned supreme. Such biological theories helped reconcile the evident contradictions between Western political ideologies of liberalism, which promised equality and freedom, and the reality of the inequalities needed for capitalism to function. If inequalities could be rooted in biology, they were not amenable to political intervention.

During the twentieth century, this racial/racist science was gradually dismantled by studies that demonstrated that human biological diversity could not be meaningfully parceled into the racial categories that science had previously relied on. It was shown that biological differences within so-called "races" are often greater than differences between them. From the 1990s, these findings were reinforced by exponential increases in the power of DNA sequencing technology to reveal genetic diversity, ushering in the era of "genomics." This made it even clearer that biological races are not tenable categories because humans are too similar—famously with 99.9 percent of genetic similarity, according to Human Genome Project in 2001—although it should be recalled that the remaining 0.1 percent accounts for the entirety of human genetic variation.[2] Also, due to millennia of human movement and mixture, this 0.1 percent of genetic diversity is usually spread gradually, or "clinally," across geographic space, with no clear genetic boundaries. The dismantling of the idea of biological race was seen as a major plank in the battle against racism and racial inequality. Diversity was seen as a superficial "skin-deep" overlay onto an underlying sameness (especially of cognitive ability): this legitimated political ideologies of social equality.

Nevertheless, during the second half of the twentieth century, many life scientists did not easily abandon the idea of race as a meaningful and useful way of classifying human diversity on a purely biological level (Kaszycka, Štrkalj, and Strzałko 2009; Lieberman and Kirk 2002; Morning 2011; Reardon 2005; Wade 2015, 92–104), perhaps attesting to the tenacious cultural hold of the idea of race and what Jonathan Kahn (2012) calls its inertial power. Indeed, a handful of scientists used the increasing amount of data available from genomic research to argue that, in fact, the old racial categories did have biological relevance. In an interview, the geneticist David Reich said: "With the help of these tools [DNA sequencing technology], we are learning that while race may be a social construct, differences in genetic ancestry that happen to correlate to many of today's racial constructs are real" (Reich 2018a). In his book, he advances a more qualified view: while it is "now undeniable that there are nontrivial average genetic differences across populations in multiple traits," he adds that "the race vocabulary is too ill-defined and too loaded with historical baggage to be helpful," and he prefers to use the concept of ancestry (Reich 2018b, 253).

Data on human genetic diversity provide a useful tool in several areas: forensics (helping to identify the perpetrators of crimes and also sometimes their victims); evolutionary history (e.g., tracing prehistoric human migrations); and genealogical searching (finding lost relatives, identifying personal origins). But perhaps the area where such data are seen to be most productive is medical genomics. Genetic diversity is now seen as a resource to help scientists identify possible genetic dimensions of some of the most intractable and costly health disorders—such as hypertension, diabetes, obesity, and cancer—whether this be identifying causes, helping with diagnosis, or developing treatments.

But major debates are occurring in the field of genetic diversity and medicine. For example, there is disagreement on whether and how to use racial and ethnic categories in clinical and research practice: some say that it is necessary in order to monitor and hopefully correct racial disparities in health, whether globally or nationally; others counter that the use of such categories reinforces their legitimacy in the public realm, which may lead to reproducing disparities in health (Bliss 2012; Epstein 2007; Tutton et al. 2010). In this article, I focus on an issue that underlies the question about policies of category use. Whether or not individual scientists believe in the biology of race (and most claim they do not), it seems that some of their practices may reinforce the idea that racial categories have a biological reality and that their genetic data can be used to bolster familiar narratives about racialized nation formation (Bliss 2012; Krimsky and Sloan 2011; Morning 2011; Nash 2015).

This article draws on a project I directed that looked at how the practices in genomic science in Brazil, Colombia, and Mexico—which are mainly in the field of medical ge-

2 This figure has been subject to revision, and one study suggests that it is 99.5 percent (Levy et al. 2007).

nomics—relate to categories of race, ethnicity, and nation at different levels in society, among scientists and among nonscientists (Wade 2017b, 2017a; Wade, Deister, et al. 2014; Wade, López Beltrán, et al. 2014).[3]

I argue first that genomic research practices and the public dissemination of findings often reproduce and even reinforce familiar categories of race and dominant narratives about the nation. This effect can potentially reinforce the racism, ethnocentrism, and nationalism that depend on such categories and narratives. I explore the ways human diversity within Latin American nations is represented in genomic research in the region, shifting between an image of diversity as a huge multitude of different mixtures—with some versions locating this diversity at the level of the individual—and a more restricted image of diversity as a multiculturalist plurality of collectives. I then look at the broader issues around the concept of population that underlies these categories and argue that use of the concept tends to conflate social and genetic entities and thus biologize social categories. Latin American geneticists in particular, by highlighting the mixed quality of their national populations, tend to rely on an underlying and tacit notion of purity—and I show how this has been a long-standing trend from the mid-twentieth century.

THE REITERATION OF FAMILIAR CATEGORIES AND NARRATIVES IN A MOLECULAR REGISTER

In our research, we found that genomic scientists in Latin America, when looking at populations, very often had a deep interest in mapping degrees of mixture—what percentage of African, Amerindian, and European ancestry national, regional, and local populations had. This was an interest that stretched back to the 1940s, when the first techniques to assess such ancestral contributions were developed and deployed on Brazilian samples (Ottensooser 1944). Such calculations of ancestral contributions are very common nowadays in many areas of the world, and there is a commercial industry supplying such information to individual clients interested in their "ethnic" origins; there have also been critiques surrounding such procedures—their reliability, the variation in the results they produce depending on what databases and reference populations are used, and their tendency to reinforce the idea that there are "pure" examples of African, Amerindian, and European populations that can act as the reference points for calculations of mixed ancestries (Abel 2021; Bolnick 2008; Bolnick et al. 2007; Duster 2011; Fullwiley 2011).

There is also a medical rationale for mapping genetic ancestry in this way. This is complex to explain, but essentially, a medical genomics project that looks for a genetic variant associated with a specific disorder usually compares diseased cases with healthy controls. It is important to make sure that your cases and controls are matched in terms of ancestry: if you compare African cases to European controls, you will find lots of genetic differences, without being able to tell which are simple accidents of geographical ancestry and which are actually linked to the disorder in question (Fujimura and Rajagopalan 2011). Ancestry matching needs further refinement when dealing with people who have inherited genetic ancestries from diverse regions: because of a long history of mixture of this kind, a sample of Latin American people is likely to include individuals with very varied degrees of mixture of genetic ancestries. Genotyping individuals to quantify ancestries deriving from Amerindian, African, and European ancestors allows researchers to statistically control for mixture, so that matching of cases and controls can be fine-tuned (Choudhry et al. 2006; Tian, Gregersen, and Seldin 2008). A genetic trait that is linked to a given disorder will thus hopefully be evident, independent of other traits that happen to be associated with a given ancestry. (Evidence that a given genetic trait is linked to a disease may also allow researchers to infer that this trait is more prevalent among certain populations and ancestries than among others, thus predisposing such populations or people with such ancestry to the disease, which may be relevant information for clinicians and health policymakers.)

Such rationales were, in principle, behind the Mexican Genome Diversity Project developed by INMEGEN, Mexico's National Institute of Genomic Medicine (García Deister 2014; García Deister and López-Beltrán 2015). This state-funded and widely publicized enterprise sought to map the genomic diversity of Mexico's population with the overall objective of improving the health of the nation (perceived by the state and the medical establishment as undergoing a crisis due to skyrocketing rates of obesity and diabetes).

Alongside the medical rationale, there was also a representation of the nation. On the one hand, there was a tendency to talk in terms of "the Mexican genome" and to characterize the Mexican nation as genetically distinctive, as if it could be distinguished in genetic terms from other neighboring nations. Above all, the message of the project was that Mexico was genetically "mestizo" (roughly translatable as "mixed race"), thus underwriting the image of the mestizo nation that had been at the heart of nation-building imaginaries since the early twentieth century, when the Mexican political and intellectual elites elevated the mestizo to the position of prototypical citizen, thus carving out a specific national identity based on racial mixture and the

3 The project had two parts: "Race, genomics and mestizaje (mixture) in Latin America: a comparative approach" (2010–11, funded by the ESRC, ES/G036241/1) and "Public engagement with genomic research and race in Latin America" (2011-13, funded by The Leverhulme Trust, RPG-044). The project worked with a postdoctoral researcher and one or two research assistants in each country, guided by a local senior academic and the project director based in the United Kingdom. Methods included participant observation in the labs, interviews with geneticists, focus groups and interviews with members of the public (mostly university students), and reviews of the technical and non technical literature produced by the geneticists and their labs.

image of racial democracy that supposedly followed from that process and distinguished the country from its northern neighbor, seen as the home of racism (Miller 2004; Moreno Figueroa and Saldívar Tanaka 2016; Vasconcelos [1925] 1997).

On the other hand, diversity was explicitly part of the picture, and the project mapped different degrees of mixture in different states of the country. The state was chosen as a sampling frame, because it allowed the mobilization of state-level governance infrastructure to facilitate publicity and sampling: diversity was thus construed at this provincial level. But, going further, the genomic sequencing technologies employed meant that varying degrees of mixture could be mapped at the level of the individual. Indeed, one figure showed the ancestral proportions of the individual people sampled (Silva-Zolezzi et al. 2009, 8614; Fig 3A). Mexico was a mestizo nation, but made up of diverse mestizo individuals.

At the same time, however, diversity was established in yet another way that depended on the idea of pure, unmixed populations. (I will discuss in a later section how "population" is an underlying construct in all genomic research of this kind—and Indigenous people in particular are often reified as socially but also biologically different.) The geneticists employed statistical processes to visualize genetic diversity in particular ways (Silva-Zolezzi et al. 2009, 8613). A genetic scientist is well aware that each colored blob on the diagram reproduced here in figure 1 represents a sample taken from a present-day population in a specific place in the world; s/he is also conversant with the way the technique of PCA (principal component analysis) used to generate the chart purposely maximizes differences between samples. For the less specialized observer, the green blob becomes "African" (or *negro*, "black"), the yellow blob becomes "European" (or *blanco*, "white"), and the blue blob is "Amerindian" (or *indio/indigena*, Indian/Indigenous). Mexican mestizos are located on the chart as a range of mixtures between "pure" European and Indigenous parental populations, each of which appears to have a distinctive genetic profile.

Such technical depictions become simplified when presented for more public consumption. Figure 2 shows a map produced by a genetic scientist that was used on a website that recruited volunteers for a large-scale genetic science project (https://www.facebook.com/CandelaMx/). Here there is a straightforward translation made from a specific sample to a continental population. These apparently biological continental categories are, of course, very familiar to Latin Americans and others as the three component "races" that constitute national populations: *la raza negra*, *la raza indígena*, and *la raza blanca*—Black, Indigenous, and white. The concept of *raza* in Latin America is arguably a more biocultural than a simply biological concept—involving ideas of history, language, and cultural heritage, as well as "blood" and inherited phenotypical traits (Hartigan 2013; Wade 2015)—but this kind of depiction seems to give such categories an underlying biological reality.

In Brazil, a similar pattern was evident in the work of Sérgio Pena, a key figure in studies of population and medical genetics in the country. Interestingly, Pena was intent on using genetic science to debunk the concept of race, as being biologically meaningless and therefore also useless for medical purposes. His studies showed that the color categories used in the Brazilian census—white, brown, black, and "yellow" (i.e., of East Asian descent)—had no biological coherence. He insisted that for medical purposes, Brazilians had to be looked at individually: he argued that the population's diversity could not be corralled by pernicious ideas of race. However, in demonstrating this, he also used diagrams that suggested that such parental entities as Africa, Europe, and America did have (a simple and coherent) biological meaning (see fig. 3) (Pena et al. 2011).

In emphasizing the intense genetic diversity of the nation, Pena aligned DNA data to the dominant narrative of the Brazilian nation as—like Mexico—highly mixed. This narrative is not only dominant and familiar but also longstanding: scientists and intellectuals developed the idea during the twentieth century, using demographic and biological data (Loveman 2014; Santos, Kent, and Neto 2014; Skidmore 1974). The narrative has frequently been used to support the claim that Brazil is a "racial democracy," in contrast to the United States (Alberto and Hoffnung-Garskof 2018; Guimarães 2007). Now, while Pena did not make such a claim outright—doubtless because it has been systematically debunked by some fifty years of social science studies—he also used genetic evidence of diversity to lean in that direction, aligning himself with rearticulations of the idea of racial democracy that postpone it to the future, but still ground it on the idea of mixture (Da Costa 2016).

For example, in an article in a popular science magazine, he speculated: "If the many white Brazilians who have Amerindian or African mtDNA were to become aware of this, they would value more the exuberant genetic diversity of our people and, perhaps, would build in the 21st century a more just and harmonious society" (Pena et al. 2000). Mitochondrial DNA (mtDNA) is a tiny part of the genome, which does not code for visible physical characteristics and which is inherited in the maternal line alone. Historical patterns of sexual conquest by European men over Indigenous and African women mean that many Latin Americans today have genetic markers associated with Amerindian and African ancestry in their mtDNA. However, the idea of a white person having Amerindian or African mtDNA in their genome is not just a statement of a simple genetic fact: it resonates strongly with a well-known practice in Brazil's racial formation in which people who self-identify as white and who want to depict themselves as nonracist or want to claim solidarity with the darker-skinned majority (e.g., for populist political purposes) also claim nonwhite ancestry, using stock sayings such as having "a foot in the kitchen" (where Black domestic servants typically work and are often subjected to predatory sexual advances by the men of the household) or having a grandmother who was "caught by a lasso" (i.e., was an Indigenous woman who was trapped and forced into sexual relations by colonists).

These common and well-known claims gloss over the history of racist and sexist violence that underlies the for-

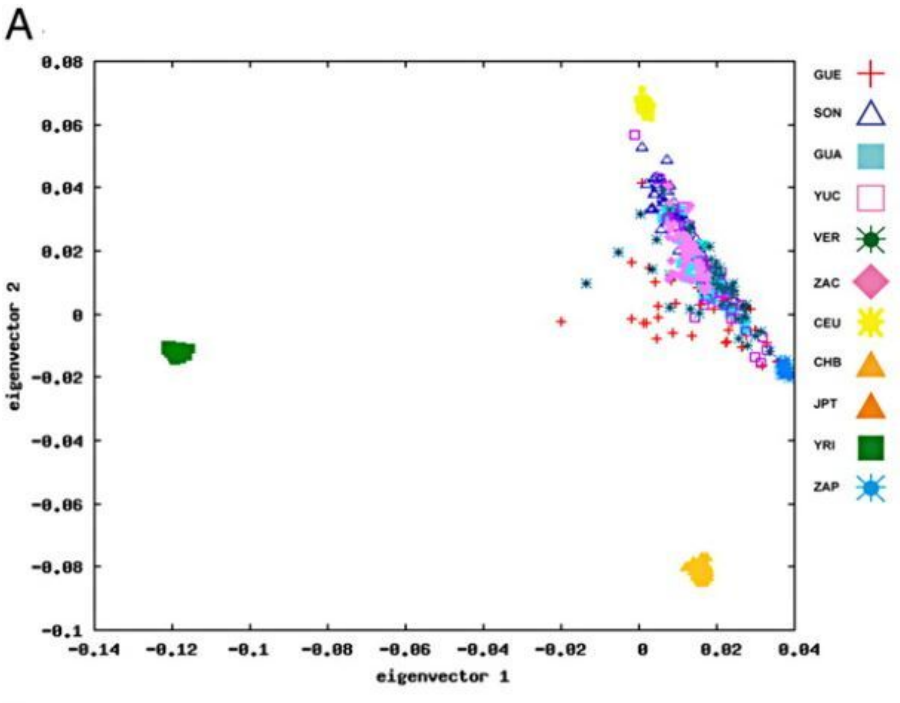


Figure 1. Color coding: Yellow = Utah (European); Orange = Tokyo-Beijing; Green = Yoruba; Blue = Zapotec; Others = Mexican mestizos from various states in Mexico

Source: Silva-Zolezzi et al. (2009).

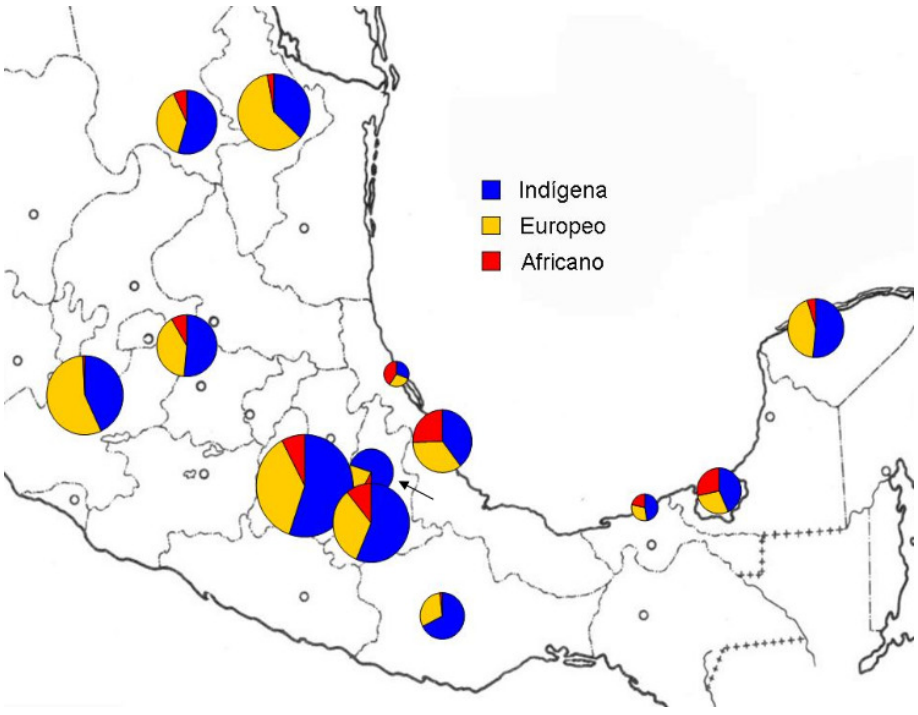
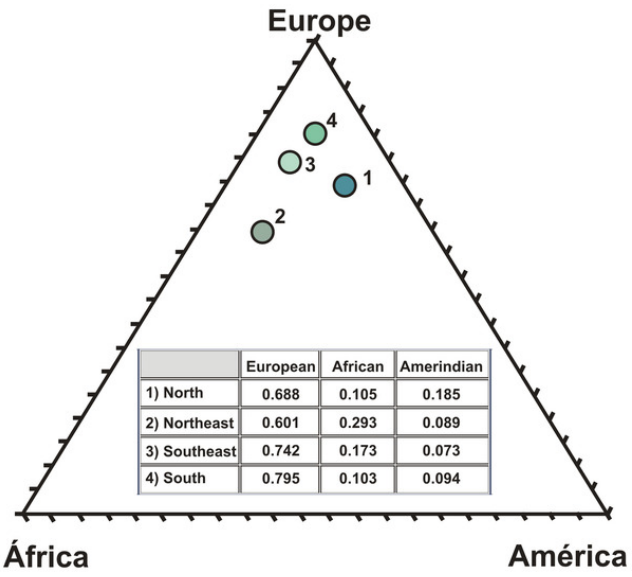


Figure 2. Ancestral contributions of Mexican populations, estimates from a tri-hybrid model based on autosomal markers (Víctor Acuña, Laboratorio de Genética Molecular ENAH/INAH)

mation of the Brazilian population; and, although the speaker seeks to claim Black or Indigenous ancestry, these statements do not in themselves undermine racial inequalities or racist attitudes. Therefore Pena's implication that the internal diversity of white genomes (at least in the mtDNA) somehow reflects the overall diversity of the nation—together with his hope that publicizing this would help build a "more just and harmonious society"—works to translate these familiar narratives of race and sex to a mol-



	European	African	Amerindian
1) North	0.688	0.105	0.185
2) Northeast	0.601	0.293	0.089
3) Southeast	0.742	0.173	0.073
4) South	0.795	0.103	0.094

Figure 3. Triangular plot and table of the genomic proportions of African, European, and Amerindian ancestry in four different regions of Brazil, independent of color category. Each point represents a separate region, as follows: (1) North (Pará), (2) Northeast (Bahia), (3) Southeast (Rio de Janeiro), and (4) South (Rio Grande do Sul).

Source: Pena et al. (2011). Creative Commons Attribution (CC BY) license

ecular level, but, like them, to gloss over their racism and sexism.

Pena also deployed genomic evidence of diversity in a rather different way. He used his research to argue against the use of racial categories as a basis for the affirmative action programs that were emerging in Brazil from the early 2000s as part of a belated admission by the state that the evident racial inequality that existed needed to be addressed as a sui generis problem (Cicalo 2012; Htun 2004; Lehmann 2018). The programs generated heated controversy in Brazil and were challenged in the Supreme Court by opponents who alleged they were unconstitutional. Pena testified to the court that the racial categories used by such programs had no basis in biology, and he wrote essays promoting the idea that "scientific fact of the nonexistence of 'races' must be assimilated by society," adding: "Awareness of this [fact] meets the utopian wish of a nonracialist, 'colour-blind' society, where the singularity of the individual is valued and celebrated" (Pena and Birchal 2006, 13, 20). That is, Pena argued that racial categories had no meaning in biology and should not be used as a basis for medical decision-making and added further that the ultimate aim was a society in which diversity was construed on an individual basis. *Therefore*, he said, such categories should not be used for social policy either—even when this policy was seeking to repair harms suffered by people on the basis of their classification by such categories and to recognize and value diversity construed on a collective basis.

A study commissioned from Pena by BBC Brazil of the genetic ancestry of nine Afro-Brazilian celebrities found that one of them, Neguinho da Beija-Flor, an iconic Black musician and dancer, had ancestry that was 67 percent European. Neguinho brushed the finding aside, saying he had been Black all his life (from his own point of view and that of others) and would continue to be so, but the well-publicized finding was widely used by opponents of the whole program of affirmative action to undermine its legitimacy on the basis that the programs targeted categories of people that had no basis in "reality"—that is, biological reality (Kent, Santos, and Wade 2014). An editorial in *O Globo* national newspaper made an explicit link between science and policy, asserting that "Now it is science that proves the nonexistence of the 'Afro-Brazilian'"—as well as the white and the Indigenous person. The columnist concluded that any social policy based on color could not be justified (O Globo 2011b).

In the end, Pena's work depended in the first instance on using ancestral populations that could be easily assimilated to the familiar "races" he was so intent on debunking as biologically meaningless. In addition, his genetic message, which appeared to be on the side of greater equity by denying the meaningfulness of racial categories and celebrating a diversity of individuals, was in fact deployed to undermine reparative measures that sought to correct inequity that affects people classified into collective categories. Pena's view was that social policy needs to follow scientific understandings that race has no biological validity—but this ignores the fact that it is the social force attached to racial categories that obliges us to include such categories in social policy. Again, then, Pena aligned himself with a narrative of the Brazilian nation as one in which racial categories have, or should have, little relevance.

GENETIC DIVERSITY, MESTIZO NATIONAL IDENTITY, AND MULTICULTURALISM

As I have shown, in Mexico and Brazil, as in Colombia and other countries in Latin America, the genetic message was overwhelmingly that "we are all mestizos." This refrain is familiar across the continent as part of twentieth-century nation-building projects that sought to project an image of national homogeneity and to—at least in part—challenge northern European and North American eugenic ideas of racial mixture as deleterious and degenerative, while also promoting an image of racial democracy that contrasted favorably with US racial segregation. I say "in part" because the valorization of the mestizo and the claims to racial democracy went alongside a belief in and the promotion of the superior value of whiteness, evident in the existence of immigration policies favoring Europeans, personal marital strategies that attributed high value to lighter-skinned children and sought to "whiten" the family by seeking light-skinned partners, and aesthetic hierarchies that prized European phenotypes as the most beautiful (FitzGerald and Cook-Martín 2014; Hordge-Freeman 2015).

In these genetic studies, however, the idea of national homogeneity based on being mestizo was, with the power of individuation lent by recent genomic sequencing technologies, parsed as an intensely diverse range of mixture.

Everyone was homogeneously mestizo, but a potentially infinite diversity was constituted by the endless production of individual genetic profiles. At the same time, being mestizo and measuring degrees of mixture depended on the existence of populations, samples of which acted as proxies for the "original" pre-Conquest continental populations that had produced the mestizos. An infinite diversity of mestizos was based on a much reduced diversity of three original populations—on which more, below. Moreover, present-day Indigenous peoples in the nation were seen as directly biologically linked to ancestral Amerindian populations. This was explicitly the case in Mexico, where a local Zapotec population was sampled to provide the reference point for Amerindian ancestry (Silva-Zolezzi et al. 2009). It was less clear in Pena's work, which used international databases for European, African, and Amerindian reference points (Pena et al. 2011).[4]

The promotion of a message of national mixedness, alongside the reification of parental populations, needs to be seen in the context of some thirty years of multicultural reform in Latin America. Beginning in the late 1980s, governments across the region began to make political reforms that recognized Indigenous and, to a lesser extent, Black populations as having distinct identities, and accorded them certain rights—to land most often and also in some cases to representation in the institutions of governance. In many countries, antidiscrimination legislation was passed and educational curricula were adopted promoting the learning of Indigenous and Black histories and cultures.

So, after thirty years of attention—albeit limited and conditional—to racialized subaltern groups, the genetic message that, in the end, "we are still all mestizos" had a potent significance as a rearticulation, now in individualized form, of a national imaginary that had been more or less uncontested from the late nineteenth century until the 1980s, sustained also by early genetic studies (see below). Yet, at the same time, the post-2000 genetic studies reinforced the multiculturalist version of diversity that recognized the existence of Indigenous and Black peoples, seen as minorities in the mestizo nation.

In the case of Brazil, particularly notable was that Pena's work, while emphasizing that all Brazilians are very diverse and mixed, also highlighted the finding that not only was "the genomic ancestry of individuals from different geographical regions of Brazil more uniform than expected" but also that "in all regions studied, the European ancestry was predominant, with proportions ranging from 60.6% in the Northeast to 77.7% in the South" (Pena et al. 2011). An *O Globo* report on the research bore the headline "A More European Country" and coined the term *brasipeus* (a combination of *brasileiros* and *europeus*) to describe Brazilians (O Globo 2011a). A blogger associated with the national weekly magazine *Veja* declared, "It's nothing to do with Mama Africa! It's Mama Europe, in fact!" (Azevedo 2011).

So although Brazil was above all a mixed nation, it was also on the lighter, more European end of the spectrum. This was just as nation-building elites had planned and had asserted early in the twentieth century, when sociologists such as Oliveira Vianna claimed that the "Nordic-European type" had been influential in the colonization of Brazil and set it on the path to a whitened national profile (Loveman 2014, 137–38; Skidmore 1974, 200–202). By proving the dominant position of European genetic ancestry, Pena also implicitly reinforced the social value attached to lightness/whiteness.

BROADER ISSUES WITH THE CATEGORY OF POPULATION

The issues described above are in some ways particular to Latin America—for example, in the importance of the (mixed) nation as a way to frame and imply discussions of race without being explicit about it, and in the emphasis on mixture as a source of diversity—but they have also been explored in depth for other contexts (Duster 2015; Fujimura and Rajagopalan 2011; Fullwiley 2014; Krimsky and Sloan 2011; TallBear 2013; Wailoo, Nelson, and Lee 2012). A common problem underlying all these contexts is the use of social categories or socially defined "populations" (whether broad and continental or specific and local) to define sampling strategies and to label samples in genomic research—as we saw, for example, in the PCA diagrams of Mexican genetic diversity, cited above.

This seems an obvious and perhaps unavoidable way to manage diversity in the sense that it is precisely socially defined groups that are usually of interest to genomic scientists, social scientists, and the general public. But the key point is that the tactic inevitably creates a basic symmetry between social identity, locality, and genetics: it presents "populations" as distinguishable entities not just socially but also genetically. This is despite geneticists' simultaneous recognition that human genetic diversity is mostly clinal in form—that is, varying continuously over space, rather than showing clear boundaries. Alongside this recognition, there is a deep-seated tendency to think in terms of groups and populations, creating an "island model" of insular populations (Pálsson 2007, 179–81), which treats "culturally defined human groups as genetic units" (Nash 2015, 80–81). While an explicit language of purity is avoided nowadays, the social significance of culturally defined groups—for thinking about society, the nation, values, social and health policies, etc.—is powerful enough to brush under the carpet the problem that the concept of population is "not epistemologically tidy" (Zack 2002, 69), in terms of its boundaries and temporal continuity. It is strong enough to gloss over the fact that putting forward a genetic description of a population (for example, in terms of frequencies of certain gene variants) entails

4 Some Colombia studies also used local Indigenous populations as reference points to measure Amerindian genetic ancestry contributions (Rojas et al. 2010).

the very questionable assumption that this population has "discernible boundaries and determinate parts" (Gannett 2003, 998).

In Latin America, where mixture has been such a powerful narrative in nation-building and as an object of interest for the life sciences, the concept of the population assumes a particularly important role as a counterpoint that gives meaning to the process of mixture—and this has a substantial history. During the twentieth century, life scientists were deeply involved in exploring biological mixture, often with an eye to medical matters, and in the process they regularly constructed populations in relation to which mixture existed, frequently parsing these in terms of "purity," which is an extreme form of the island model.

In Brazil, for example, as part of his studies on sickle-cell anemia in the 1940s, the hematologist Ernani Martins da Silva sought to "identify 'pure' white, black, or indigenous groups as well as mixed groups" (Cavalcanti and Maio 2011, 388). Early studies on degrees of racial mixture by Friedrich Ottensooser in the 1940s and by Pedro Henrique Saldanha in the 1950s and '60s all used "parental populations" of Africans, Indigenous Brazilians, and Europeans or "white" Brazilians to act as reference points to measure mixture. In Mexico, there was a greater focus on the Indigenous population, assumed to be straightforwardly distinguishable from mestizos. The physical anthropologist Juan Comas, in "establishing a racial classification of man," sought samples of Indigenous groups that were the "purest possible" (Comas 1942, 70, 73), and, while he rejected the racial hierarchies of scientific racism, he accepted race as a valid biological category (Vergara Silva 2013). Later, the Mexican geneticist Rubén Lisker also sampled Indigenous populations on the basis of cultural traits and perceived phenotype by choosing people who "lived in Indian villages, could speak the particular dialect and had the physical appearance of Indians" (Cordova, Lisker, and Loria 1967, 58).[5]

In recent genomic projects in Latin America, we found that this established pattern of creating symmetry between social identity, locality, and genetics was reinforced by certain sampling practices. There was even a sense in which these projects sought out genetic purity. For example, in the INMEGEN project to study Mexican genomic diversity, as noted above, scientists created a "Zapotec" sample, which they used to represent Amerindian genetic ancestry. They did this by going to a "Zapotec village," which they—like Lisker in the 1960s—identified using social and cultural criteria of identification by the local residents and by others, including the state. There, they sampled only people whose four grandparents had all been born in the locality and also spoke Zapotec. In addition, some people sampled as "Indigenous" were excluded from the sample if they were genetically close to those sampled as "mestizos," on the grounds that extraneous "noise" needed to be removed (García Deister 2014).

Now this is a reasonable and justifiable practice if you want your sample to represent "pure" native American ancestry (compared to African or European ancestries) in a population that historically derives from the mixture of populations from these three continental origins. But the practice also inevitably reproduces a congruence between social and biological categories and implies a genetic dimension to social diversity, conceived here in terms of a plurality of collectives, rather than an infinity of individuals. The practices of the 1940s, '50s, and '60s clearly persist in more recent genomic projects, despite the ability of recent genomic science to work at the level of the individual person or to map particular genetic variants, independent of the person or population they occur in.

Some geneticists recognize that "admixture approaches … take as an assumption the reality of parental populations; that is, it is assumed that there are, or were, such 'pure' human populations." Weiss and Lambert object to what they call the "selective de facto typological sampling and the assumption of statistically homogeneous source populations" involved in the measurement of admixed ancestries (Weiss and Lambert 2014, 17, 24).

Going further, the geneticist Aravinda Chakravarti says: "Yes, there are differences in genetic variation at the continental level and one may refer to them as races. But why are continents the arbiter? … If humans have had this single continuous journey disobeying continental residence—and as evidence we have the continuous distribution of genetic variation across the globe, not discrete boundaries like political borders—where do we divide humanity and why?" (Chakravarti 2014, 9). He goes on: "Human evolution has always been studied with respect to such populations defined by language, geography, or cultural and physical features. Consider instead what we could decipher if we could sample a million humans (say), without regard to who they were, across a virtual grid across the world … These types of global surveys of diversity have been performed for other species and may provide the first objective description of ours, bereft of race and other labels" (Chakravarti 2014, 11).

Such a grid sampling approach would avoid reproducing a congruence between social and biological categories. But it would also mean that the kinds of categories that are socially meaningful to people would not figure in genomic research. For this reason, I believe, the practice of using social categories—and not grids—as the basis for creating samples will continue.

For example, when talking about possible genetic components in the medical "crisis" of obesity and diabetes in Mexico, scientists, science writers, journalists, and policymakers are inevitably drawn to using categories such as "Indigenous" and "mestizo" because they are historically familiar, apparently easy to manage, and make sense to all concerned when thinking about the diversity of Mexican society. The categories allow easy-to-grasp statements like the following, taken from INMEGEN's public news bulletin:

5 See also Suárez-Díaz (2014).

"there is evidence that the indigenous population is more susceptible to diabetes and in Mexico 10% of the population is indigenous, which is why … INMEGEN is identifying the genetic risk factors for diabetes among indigenous people." The bulletin also notes that a genetic variant of interest (one involved in the metabolism of triglycerides) is "very frequent in the indigenous and Mexican mestizo population" and observes that it is "common among other Latin American populations, but infrequent or absent in European and African populations" (INMEGEN 2014).

Statements such as these may seem unexceptional and straightforward—and they have precursors in Mexican genetics going back to the 1940s. As I explained earlier on, it is also medically relevant to have information on genetic ancestry to help control for confounding factors in the search for genetic variants that may be connected to health disorders. But when this information is packaged into familiar social categories—and especially racialized ones—problems emerge, because the process attributes biological characteristics to the categories, reifying and essentializing them.

Statements like the ones made by INMEGEN depend on social categories such as "Indigenous" and "mestizo," which are not now, and have never been, straightforward. Like all social categories, they are relational and situational, but their location in a Latin American racial formation shaped by histories and ideologies of mixture makes them particularly malleable. The figure of 10 percent cited by INMEGEN is a government statistic derived from census and survey data in which people identify as Indigenous in the context of that official encounter. But we know that measurements of the number of Indigenous people in Mexico have varied dramatically over time, from about 5 percent to about 15 percent between censuses in 2000 and 2010, and change substantially according to the criterion by which indigeneity is reckoned—self-identification, ancestry, language use, etc. (Telles and Project on Ethnicity and Race in Latin America 2014, 50–51).

If the categories are not clearly bounded socially, they are even less so biologically: two Mexican scientists, a geneticist and a physical anthropologist, based at Stanford, writing in a Mexican journal of anthropology and history, say: "How can we distinguish between an indigenous individual from Oaxaca [a region in southern Mexico with a substantial Indigenous population] with a certain amount of European ancestry and a Oaxacan mestizo with high levels of indigenous ancestry? . . . Genetically they are indistinguishable" (Moreno and Sandoval 2013, 270).

In the 1950s, Mexican geneticists encountered these same issues. One study published in the US-based *Annals of Eugenics*, which aimed to contribute to the understanding of "human races," sampled groups of people who were "carefully chosen for purity of breed," but the researchers noted that they were "not convinced of having studied in all cases [Indigenous] populations without some degree of European mixture," and indeed one group near Mexico City taken as "Indian" constituted "a very heterogeneous lot, in which pure white people, pure Indians and mixed individuals must be included" (Arteaga et al. 1951, 351). The language is different (for example, in 1954 *Annals of Eugenics* was renamed *Annals of Human Genetics*), but the issues are the same—in 1951, however, there was little critical reflection on the implications of using such social categories for genetic research. Today, there is more reflexivity—and not only among social scientists: some geneticists are conscious of the issues involved (Bliss 2012; Olarte-Sierra and del Castillo H. 2014).

In sum, messages from genomics about the intense genetic diversity of the mestizo nation depend on the use of concepts of population that produce a different version of diversity, based on collective categories—which are often reified in genetic terms.

CONCLUSION

As long as racial categories continue to have force in the everyday social world, they will continue to shape genomic science, as the latter is not completely insulated from the former, but coexists with it in a complex relationship characterized by a double dynamic of what Latour (1993) calls purification and hybridization, in which science is always seeking to purify itself of "contamination" by the social world, while constantly mixing with it.

I have shown how genomic science in Latin America reinforces the idea of a mestizo nation, now taking advantage of the power of DNA sequencing to individualize and diversify the notion of mestizo. At the same time, however, it reinforces and biologizes the notion of racial difference, producing a parallel version of diversity that is in tune with multiculturalist visions of the mestizo nation with Indigenous and Black minority populations. However it is rearticulated, the dominant narrative is that of the mestizo nation, which has been in play, in various forms, since the late nineteenth century. Despite the dramatic change in technology brought by genomics, I have shown that there are underlying continuities in the uses of racialized categories and concepts of population.

The encounter of Latin American scientists with human genetic diversity follows in many respects the trajectories of genomic science worldwide in the debates that have emerged around race, genetics, and medicine. The difference is that in Latin America, diversity has been construed primarily in terms of mixture, and this demonstrates the power of existing narratives about race and nation to shape science and especially the way science enters the public domain. Highlighting mixedness has been a favored tactic used since the late nineteenth century by nation-building elites to claim exceptional status for their countries as racial democracies, and, indeed, historical mixture and nationalist ideologies of mixedness have shaped racial formations in which racial categories are more situationally malleable than in places such as the United States or Europe. Latin American genetics has an ambivalent effect in this respect. On the one hand, it reaffirms the fundamentally mestizo character of the nation. On the other, the malleability of racial categories that mixture entails does not seem to have been an obstacle for long-standing processes of genetic reification, not just for Indigenous and Afro-de-

scendant peoples but also for mestizos, whose degrees of genetic mixedness are now measurable on an individual basis.

As a coda, it is interesting to ask: if racial formations shape the way genomic science works and engages with the wider society, to what extent does the reverse process take place? Does the reiteration of racial, ethnic, and national categories in a molecular idiom work to geneticize or biologize everyday understandings? The evidence on this point is ambivalent. Some people have identified a trend toward "geneticization," with people increasingly using genetic data and concepts to think about being and belonging. This may also mean that people increasingly think in biologically deterministic ways, linked to the status of genetics as a producer of reliable truth (Brodwin 2002; Byrd and Hughey 2015; Lippman 1991; Lynch et al. 2008). But other evidence, including data we collected in Latin America (Wade et al. 2015), indicates that people find genetic knowledge ambiguous or hard to interpret and that, in any case, they deploy it in selective and strategic ways, which fit in with the narratives they want to weave about themselves (Condit et al. 2004; Nelson 2008; Roth and Ivemark 2018; Schramm, Skinner, and Rottenburg 2012; Wade et al. 2015; Wailoo, Nelson, and Lee 2012).

In short, the ways in which genetic knowledge gets drawn into social life and in which social life shapes the production of genetic knowledge remain an area of debate, in which we have to examine specific cases. The use of genetic data to undermine race-conscious social policies—as happened with Brazil's affirmative actions in higher education—is a case in point, where the false leap from genetic fact to social value is blatant. But the wider point is that the congruence that genomic science produces between social identity, locality, and genetics may legitimate or facilitate processes of biologization, reification, and essentialization in the wider society—and this is a real danger that needs to be addressed by critical perspectives on the categories that genomic science creates, uses, and reiterates.

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COMPETING INTERESTS

None.

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