Comparing genomic narratives of human diversity in Latin American nations

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ABSTRACT

Human population genomics aims to improve health for all, trace human migration histories and refine forensic identification techniques. These aims transcend national borders: geneticists are part of a global community supported by transnational infrastructures. At this level, concerns have been raised that, in its intense focus on genetic difference, genomics re-inscribes “racial” differences. But global genomics is always enacted in specific contexts: although many projects are internationally collaborative, geneticists are embedded in national contexts and their data speak to questions of national identity and ethnic/“racial” diversity. In genomics in Brazil and Mexico “racial” difference is very clear – despite disavowals – because of the role of ideas about race mixture in national identity. Drawing on data collected in a comparative project, I show how genomic data figured in different ways in narratives about the Brazilian and Mexican nations. These national contexts show how “race” is reproduced in genomics more widely.

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Introduction

This article draws on a multi-sited project, “Race, genomics and mestizaje (mixture) in Latin America: a comparative approach”, which ran from 2010 until 2013, involving fieldwork in Brazil, Colombia and Mexico. The project traced how categories of race, ethnicity, nation operated in genomic science – in strongly gendered ways, as it turned out, although that is not the focus of this article (see Wade 2017, ch. 8). The project was comparative from the outset, aiming primarily to assess differences within Latin America, but also implicitly possible differences between “Latin America” – if this could be seen as a meaningful whole for these purposes – and other regions where the relation between race, ethnicity and genomics has been studied, such as the United States and Europe. In this paper, I argue that
human genomic science and ideas and practices around the idea of race are both global assemblages with a hierarchical order. Genomic human population science aims to provide tools to improve health for all, trace human migration histories across the globe, and refine forensic identification techniques. These aims transcend national borders: geneticists are part of a global scientific community with its attendant transnational infrastructures, which are centred on the United States and Europe, although China is an emerging player. At this level, concerns have been raised that, in its intense focus on genetic difference, genomics can re-inscribe the idea of “racial” difference that has long been part of a world history, despite a global turn towards anti-racism after the Second World War – again the form of these ideas about difference, and their denial, has been shaped powerfully by Euro-American concerns and knowledge production.

But, I argue that scientists are also embedded in national contexts and infrastructures, and the data they collect can speak to questions of national identity and human (ethnic/“racial”) diversity within the nation, whether it is the scientists themselves doing the speaking in technical and popular writings, or third parties who deploy their findings. This is the case for genomics in Brazil and Mexico. The key role of ideas about race mixture (mestizaje/mestiçagem) in national identity means “racial” difference is both very clear and also subject to persistent disavowals. While genomics routinely uses concepts of continental biogeographical ancestry that threaten to reinscribe familiar categories of race, this tendency is particularly noticeable in Latin American genomics, which necessarily invokes categories of white, black and indigenous, or European, African and Amerindian, when talking about mestizo majorities and about the past, present and future of the mestizo nation. On the other hand, it is precisely pervasive mixture that has been claimed by nation-builders to transcend racial difference and racism. Genomic data and discourses have been used to underwrite disavowals of racial difference, while also working to accentuate the presence of racial meanings. These contradictory effects are given added weight by the fact that, in Latin American mestizo nations, articulations of race and genomics do not just happen around racialized subordinate minorities or in unmarked ways around dominant groups, but around mainstream majority populations, which are (de-)racialized in new ways. Understanding how racialized meanings articulate with genomic data in these national contexts allows us to see how these meanings are reproduced and re-enacted in diverse ways to constitute genomic science as a heterogeneous and uneven whole.

**The rise of genomics**

The term genomics is recent, as opposed to genetics, which dates from the early twentieth century. Genomics emerged during a specific period from
about 1990, when the Human Genome Project started, to 2001–3 when its results were published. Key features of genomics include the greatly increased speed and cheapness of DNA sequencing, which allowed the possibility of “mapping” whole genomes; the rise of bioinformatics to process the vast amounts of data produced, with the emergence of visualization techniques to represent the data; the individuation of genetic data, with the promise of “personalized genomic medicine”; and the emergence of global studies of human genetic diversity, such as the Human Genome Diversity Project (initiated in 1991), the International HapMap Project (2002), the Genographic Project (2005) and the 1000 Genomes (2008), all of which were international collaborations. These were complemented by many national studies, such as the People of the British Isles project (2004), based at Oxford University, and the studies explored in this article – although such national studies might also involve international collaborations.

The aims of human genomic science are primarily medical – the search for genetic variants that hopefully will lead to treatments for pressing health issues, such as diabetes, heart disease and cancer. Other aims include the use of genetic data on human diversity to trace patterns of human evolution and migration; and the development of forensic tools that will assist identification of individuals. An offshoot is “recreational” DNA testing, which allows individuals to gain some knowledge about their distant ancestry for personal reasons. We are still in the genomic era, but some people increasingly refer to a post-genomic era, in which the realization of the early promise attached to medical genomics is seen as progressively more distant as the science itself uncovers the huge complexity of genetic processes and their interweaving with the environmental factors that regulate gene expression through epigenetic and developmental processes (Hartigan 2013a; Richardson and Stevens 2015).

Genomics and race in the study of human diversity

From early on, we can identify two trends at work in the way genomics have been perceived to relate to ideas about race (Koenig, Lee, and Richardson 2008; Krimsky and Sloan 2011; Schramm, Skinner, and Rottenburg 2012). First, genomic data have been hailed as the final nail in the coffin of the concept of biological race – a coffin the lid of which, in this view, has been in the process of being closed for several decades by successive cohorts of life scientists. Second, there are concerns that genomic science in fact reinscribes biological race – again continuing a trend evident in the genetics and physical anthropology of the decades following the Second World War (Reardon 2005). This re-inscription often occurs without using the term race, although racialized categories, such as European, African, Asian and Amerindian are often used to classify “biogeographical ancestry”. In some contexts,
a more explicit language of race (or “ethnicity”) and racial (or “ethnic”) categories is used – for example in the United States and Britain – when genomic and medical data are collected using official categories of race and ethnicity for the avowedly anti-racist purpose of monitoring racial health disparities and hopefully contributing to their elimination (Bliss 2012; Reardon 2012; Smart et al. 2008).

In this second trend, critics have identified a key problem in the use of social-cultural categories (of ethnicity, nation, race or community) as a way to organize the collection of samples for genomic analysis: this leads to the creation of a genetic profile or “map” for these social categories, which then tends to create isomorphism between the two, implying that social and genetic boundaries coincide. Even if everyone knows that this is not strictly speaking the case, because genetic variation is clinal, the implication remains as an approximation or short-hand (Chakravarti 2014; Pálsson 2007). A second issue is that the genomic study of human diversity tends by definition to intensify differences: for legitimate reasons, the bioinformatics techniques used to process the data are designed to highlight the differences that the scientists are interested in. This is understandable but it also tends to background the fact – much heralded by genomics itself – that all humans share the vast majority of their DNA. For example, personal DNA ancestry testing can hide the fact that the autosomal genetic markers (inherited in recombined or “shuffled” form from both parents) that give clues to the geographic origins of one’s ancestors are usually not exclusive to certain regions, just more and less frequent. When such tests use the more specific markers in the mitochondrial DNA (mtDNA, inherited unchanged and unilineally down the maternal line) and non-recombinant Y-chromosome DNA (inherited unchanged and unilineally down the paternal line), the results can hide the fact that the deep lineages traced by the test only pick out a tiny number of a person’s myriad genetic ancestors, those with whom the person can trace a connection that, by chance, forms an unbroken matri- or patri-lineage (Duster 2011).

In any case, these contradictory trends indicate the wider fact that the way race appears in genomics is not univalent or simple. In some ways, race is reinscribed and re-enacted in quite a simple, fixed way – for example, when a heart drug is marketed to African American men (Kahn 2013), or when racialized categories specific to certain cultural contexts are used to organize forensic identification processes (Duster 2015; Kahn 2012; M’charek 2000, 2008, 2013). In other ways, complexity and uncertainty appear and race as an idea becomes destabilized. For example, a person’s genetic ancestral origins can vary enormously depending on which bit of the genome is being analysed. This is connected to the fact that everyone has genetic ancestries tied to multiple geographical origins and the markers that indicate them are often non-coding DNA, which means there is a complete disconnect between these
markers and (racialized) phenotype (Abu El-Haj 2012). This also allows people to highlight particular ancestries according to the personal narrative of belonging they wish to create and the hopes they invest in the process of buying DNA tests and interpreting the results (Nelson 2016). There has also been a shift away from simple determinism towards a language of probability and risk (Abu El-Haj 2007).

Making comparisons

We can learn something about how genomics and race articulate together by making comparisons. The obvious frames for comparison are often national or regional, but we need to be aware that the choice of comparative frame is epistemologically and politically loaded (Stoler 2001) and that an uncritical use of national and regional frames can hide relational connections and differences that work to constitute the “cases” being analysed (Seigel 2005). In this sense, it is important to see that genomics and the concept of race have global, transnational connections and circulations as well as national ones: they are both assemblages, the elements and connections of which can be viewed perspectivally and relationally as global and/or national at the same time.

Genomics is a global science: projects frequently involve transnational collaborations and the databases they create are often open-access (e.g. the International HapMap and the 1,000 Genomes projects). However, such projects and databases may be driven by key science centres (United States, Europe, China). For example, the 1000 Genomes Project involved many countries including China, Italy, Japan, Kenya, Nigeria, Peru, the United Kingdom, and the United States; however, it was funded principally by British, US and Chinese money. As such, this global science entrains some familiar politics of knowledge production, as it is structured by predictable hierarchies of knowledge and funding – thus there have been protests about Northern science exploiting or objectifying Southern populations and scientists (Reardon 2005); and calls for the greater representation of Southern populations in global databases seen as biased towards Europe or the global North (Bustamante, De La Vega, and Burchard 2011).

The way race appears (and disappears) in genomics is entwined with these global, transnational processes, not least because racialized concepts themselves historically have global dimensions, linked in part to science but also to global markets in production and consumption. For example, since the Second World War (and, in fact, a bit before) there has been a globalizing anti-racist agenda at work, driven by science and politics, and this agenda pervades genomics. As noted above, this tends to make race disappear, but may make it appear again in anti-racist mode (as a tool for monitoring racial health disparities), in which case it is not unusual to find certain influential categories
(e.g. US racial ones) migrating into (or colonizing) other regions, in general and in genomic science, as many international projects and key journals are based in the United States. Participation and publication in these scientific endeavours may result in the translation of complex local categories into simpler US racial schemas – a slippage which may occur almost unremarked (Olarte-Sierra and Díaz del Castillo H 2014). Certainly, key categories such as African, European, Asian and Amerindian are in common genomic usage worldwide to classify genetic ancestries and this could be seen as a result of a global system of scientific knowledge production dominated by Europe and the United States, although this view risks being reductive and glossing over the productive work that such categories do for scientists in other regions.

At the same time, these processes and enactments of genomic science can be perspectively (re)-cast in national, sometimes nationalistic, frames. For example, there is frequently a concern about national “genomic sovereignty”, in which a government seeks control over the human and non-human genetic material that is located within its borders and perceived as (potential) bio-capital because it may have useful features that are scarce on the global market; the idea that particular countries have genetic material that is “unique” to their territories obviously enhances its potential commercial value (Benjamin 2009; Schwartz-Marín and Restrepo 2013). Also, national governments often fund national science to address national priorities; this may involve genomics projects with primarily medical aims, but which also generate data that address or can be used to address national histories and imaginaries. For example, as I discuss below, in Mexico, the state invested directly in medical genomics to tackle what was seen as a national health crisis of obesity and diabetes. In Brazil, the state took a more hands-off approach, supporting genomics through standard channels of research funding. This less centralized approach perhaps influenced the fact that some of the resulting DNA data was used to challenge the anti-racist policies that the state was keen on promoting.

The way race appears and disappears in these frames depends in important ways on national racial formations – which never operate independently of more global general and scientific ideas about race, such as the conviction that racism is wrong and that race is biologically meaningless, but also that aspects of human biological diversity are, for certain purposes, usefully classifiable into broad continental categories, which are held to reflect patterns of human evolution. Thus in the United States, we encounter the Bidil phenomenon, noted above, in which a heart-disease medicine was patented and marketed as particularly effective for African American men, implying that all men in this social category shared some significant genetic trait (Kahn 2013). This clearly reflects a specifically US racial formation with it foundational black–white divide. Or in Britain, the People of the British Isles project organized
its sampling and analysis in such a way that, while the results represented British as a “mixed people”, it was mainly intra-European mixture that was foregrounded, while colonial mixture was backgrounded and post–Second World War mixtures were not considered (Nash 2015). This is intimately linked to a specifically British racial formation, based on notions of imperial whiteness and a history of post-war non-white colonial migration to the metropolis, which together tend to define even British-born non-whites as not fully British. Or, to go further afield, in India, genetic data may be increasingly used as evidence in the definition of scheduled castes and other groups for legislative purposes linked to affirmative action (Kapila 2007). Although it is not clear that this is actually about “race” in any simple sense, it surely reflects a specifically Indian concern with caste.

In Latin America, the way race (dis)appears is shaped by regional and national ideas of bio-cultural mixture. In ways that vary from one nation to another across the region, mestizaje acts as a founding myth that conjugates three primordial origins – African, Amerindian and European, even if in some cases one origin (usually the African) may be almost completely disavowed (Walsh 2015). The issues surrounding varying processes of mixtures between indigenous, African and European people, located in powerfully hierarchical structures of power, status and wealth, has been an obsessive concern in different ways from the colonial period onwards. Colonial authorities generally sought to regulate and control mixture and its human products – mestizos – rather than ban it outright or deny the new social categories that arose from it. But they also saw it as problematic overall (Martínez 2008; Twinam 2015). From the mid-late nineteenth century, the idea of mixture began in some nations to be used self-consciously by nation-builders and intellectuals as a defining feature of the nation in contradictory ways. Some continued to see African and indigenous heritage as a problem, blocking the desired national progress towards modernity, defined in Eurocentric terms, while others heralded mestizaje as a positive force that, by transcending racial difference, would enhance a modern democracy and stand as a lesson to the world. The latter vision – most comprehensively elaborated in Brazil and Mexico – led in some cases to a partial valorization of African and indigenous heritages, although this did not entail full acceptance of contemporary black and indigenous minorities (Appelbaum, Macpherson, and Rosemblatt 2003; Graham 1990).

In genetics, the concern with mestizaje was reflected in explorations of the biological dimensions of mixture, with a burgeoning interest in measuring degrees of mixture. The mathematical methods that permitted a calculation of the proportions of parental population ancestry in admixed populations were developed in the 1930s by a German mathematician, Felix Bernstein, and were first used in Latin America by the Brazilian geneticist, Friedrich Ottensooser in the early 1940s and later in Mexico, for example by the
geneticist Rubén Lisker in the 1950s (Souza and Santos 2014; Suárez-Díaz 2014; Wade 2017). Nowadays, genomic science nearly always measures degrees of mixture – with much greater precision and at an individual as well as population level – and the stated aim is usually to contribute to medical genomics. But the data produced also generate a genetic portrait of the nation, even in the technical papers. The data are used by scientists themselves in non-technical publications and by non-scientists in press reports and other outlets to address questions about the character and make-up of the nation in the past, present and future.

Thus, while it may be disavowed by geneticists and others, the idea of race constantly re-appears, because mixture/mestizaje is an inherently racialized concept: “bastard and mixed-blood are the true names of race” (Deleuze and Guattari, A Thousand Plateaus, cited in Young 1995, 180). Mixture does not transcend origins, because it depends on them for its very existence (Wade 2004). The centrality of mestizaje as a set of ideas and practices in Latin American genomics highlights the vital role played by the nation in constituting a scientific space in which race can be made present, usually without naming it directly as such and, instead, referring to the concept of mestizaje which, while often hailed as having the power to transcend race, is itself inherently racialized (Wade et al. 2014). In this scenario, the nation does not sit alone, but exists as a particular, quite durable way of assembling certain elements and relations that can also be seen, from a different perspective, as transnational.

Genetics, race and nation in Brazil and Mexico

Mexican and Brazilian nation-builders have historically made much of the mestizo character of their respective countries, although the Mexican mestizo is perceived as primarily an indigenous-European mix, while the Brazilian one is predominantly African-European (Kent et al. 2015).

Mexico

The research in Mexico focused primarily on the National Institute of Genomic Medicine (INMEGEN, founded in 2004) and its flagship project, the Map of the Mexicans’ Genome (2004–9), also known as the Mexican Genome Diversity Project (MGDP) (Silva-Zolezzi et al. 2009); attention was also paid to some subsequent projects involving INMEGEN and others on indigenous genetic ancestry and diabetes. This work was all tied directly to a national public health agenda: obesity and diabetes rates in Mexico have been increasing dramatically and the government has characterized this as a national emergency and a threat to Mexico’s ability to compete effectively in the global economy (García Deister and López-Beltrán 2015). Early on, INMEGEN was
also tied to discourse about “genomic sovereignty” and the supposed particularity of Mexicans’ genetic profile, produced by the specific historical mix of indigenous peoples and Europeans (and some Africans, although these received minimal attention). This ostensible specificity made it necessary to characterize the national population in genetic terms in order to tailor health interventions accordingly.

Although the discourse of genomic sovereignty served to legitimate the creation of INMEGEN, some geneticists were uncomfortable with the implication that Mexicans had a genetic profile that made them biologically distinctive as a national population (Schwartz Marín 2011). Although references to la raza mexicana are not unusual in Mexico, this refers to a bio-cultural entity, defined as much by history and culture as by biology, and most geneticists would deny that this entity could be defined in genetic terms. In addition, the MGDP was only very occasionally linked to the language of race: for example, an early English-language press report published in a US journal referred to a “bold race-based genome project” (Guerrero Mothelet and Herrera 2005). Generally, however, INMEGEN scientists disavowed the biological concept of race (Hartigan 2013b).

On the other hand, following standard genomic practice (Ruiz Linares 2014), they routinely referred to African, European and Amerindian ancestries as the component parts of the genomic profile of Mexican mestizos (García Deister 2014; Wade 2017, ch. 6). The presence of these ancestries was measured by using standard international reference samples representing African and European populations, while the standard samples commonly used to represent Amerindian ancestry were replaced in the MGDP by a rural Mexican Zapotec group, especially sampled for the project to represent the Amerindian “ancestral population”. The data were visualized using pie and bar charts to show the proportions of these ancestries in particular samples of mestizos, which suggests that a person’s genome is easily separable into three genetically distinctive components. Also used were statistical techniques that maximized the genetic distance between sample populations, giving the impression of clear biological differences between them and masking the fact that all these populations share over 99 per cent of their genetic material (Silva-Zolezzi et al. 2009). Mexican geneticists – in common with other scientists who study Latin American populations (Wang et al. 2008) – also routinely used racialized categories, such as mestizo, indígena (indigenous person), Native American or Amerindian. The conceptual distinction between mestizo and indígena, which is foundational to the idea of the Mexican nation (Lomnitz-Adler 1992; López Beltrán, Deister, and Sandoval 2014), pervaded the practices of the MGDP, from sample design, storage and analysis, through to data interpretation and presentation. For example, samples were labelled as either mestizo or one of a small number of indigenous ethnonyms (e.g. “Maya”) and kept in separate places in the laboratory freezer (García...
Deister 2014). This follows the common practice, noted above, of defining sample populations using cultural categories and then describing them in genetic terms, conflating the two.

This tendency to re-inscribe racial difference through genomic analysis was strengthened by projects in which geneticists identified genetic variants, possibly associated with obesity and diabetes, which were “found exclusively in Amerindian and Amerindian-derived populations such as Mexican Mestizos” (Villarreal-Molina et al. 2007) or were “exclusive to Native American and descent populations” (Acuña-Alonzo et al. 2010). Post-MGDP, collaborations between INMEGEN, the [Carlos] Slim Initiative in Genomic Medicine for the Americas (SIGMA) and the Broad Institute of MIT and Harvard were reportedly based on “evidence that the indigenous population is more susceptible to diabetes … which is why … INMEGEN is identifying the genetic risk factors for diabetes among indigenous people” and tracing these factors in mestizo populations with Amerindian genetic ancestry (INMEGEN 2014; see also SIGMA Type 2 Diabetes Consortium 2014). A scientist directing a project along these lines in the Yucatán peninsula was described in a university press release as saying that:

a Mayan mestizo, or a person from the city, has a genome that is half Mayan and half mestizo. In this sense, the research carried out in [rural] Mayan communities explains 50 per cent of the genes of [mestizo] people in this region. (Coordinación de Medios de Comunicación Universidad Autónoma de Yucatán 2015)

This formulation repeats the time-worn stereotype that opposes rural indigenous communities to urban mestizos, while also reifying Mayans and mestizos as biologically distinct (despite the fact that mestizos are by definition a mixture of European and indigenous ancestries), the combination of which produces the sui generis “Mayan mestizo”, who is doubly mixed. The project sampled Maya-speaking adults in rural communities with the aim of tracing associations between ten genetic variants and diabetes. As usual, the diseases seen as creating a national emergency were being associated with indigenous ancestry, depicting this as a dangerous and risky burden for Mexican mestizos and pathologizing indigenous peoples.

In short, these genomic projects depicted Mexico as a basically mestizo nation with a significant indigenous minority population, tied to rural areas, linked to the past by figuring as an ancestral population and pathologized as the bearer of risky genetic variants. African ancestry was routinely measured, but little interest was shown in this component. Overall, race was disavowed as an appropriate language and concept, while racialized categories were multiply re-inscribed through scientific practice. Although INMEGEN and other laboratories were involved in many international collaborations – given that diabetes and obesity are hardly just a Mexican concern and genomics has long seen indigenous populations worldwide as objects of
scientific interest – the space of the nation was taken for granted as a relevant frame of analysis to the point that the idea of the “genomic sovereignty” of Mexico and the implied genetic distinctiveness of Mexicans could figure as legitimating tropes in political lobbying for the establishment of INMEGEN.

**Brazil**

The research in Brazil included an intensive focus on the work of geneticist Sergio Pena and his colleagues. In 2000, Pena first-authored an article, “Molecular Portrait of Brazil”, published in a popular science magazine. This presented to a general audience the key results of several genomic projects. A main finding was that people who identified as white in Brazil usually had significant amounts of Amerindian and/or African genetic markers in their mtDNA. The article concluded by speculating that, if these people were to become aware of their genetic heritage, “they would value more the exuberant genetic diversity of our people and, perhaps, would build in the twenty-first century a more just and harmonious society” (Pena et al. 2000, 25). This marked Pena’s conviction that genetic realities could and should guide social attitudes and even government policy. His work was taking place in a social context in which the Brazilian state had responded to decades of academic and social movement lobbying around the idea that, far from being a “racial democracy” as had been claimed by the state around the mid-twentieth century, Brazil had a significant problem with racism. In 1995, this was publicly acknowledged by President Fernando Cardoso, ushering in a period of legislative reform that involved the implementation of affirmative action, including race-based quotas for admissions in some public universities, and some race-based differentialist approaches in health policy (Wade 2017, ch. 5). The university quotas in particular caused great controversy, with opinions across the political spectrum opposing them, usually on the grounds that they would exacerbate racialized division.

Pena et al. weighed in with genetic data showing that the social race/colour categories that had long operated in Brazil (e.g. in the census), and which were being used in the affirmative action policies, had no genetic reality – like all racial categories they were biologically meaningless (Kent, Santos, and Wade 2014). He argued that “science could contribute to a prescriptive position in favour of a nonracialist society” and that the “scientific fact of the nonexistence of ‘races’ must be assimilated by society” in order to realize “the utopian wish of a nonracialist, ‘colour-blind’ society” (Pena and Birchal 2006, 20). While not claiming that Brazil was free from racism, such anti-quota arguments resonated strongly with widespread views that saw Brazil as a mixed society in which racialized differences were secondary to class and that proposed colour-blind, class-based policies to correct social inequality. In the 2010 Supreme Court hearings on the constitutionality
of race-based quotas in universities, Pena testified “On the nonexistence of races and the consequences for Brazilian society” (Wade 2017, 132) and his data consistently emphasized the mixed genetic ancestry of all Brazilians, who therefore could not be divided into biological racial categories.

A key genomic fact in this debate was the discovery, in a 2007 BBC Brazil project on Afro-Brazilian Roots which commissioned Pena to do ancestry tests on nine Afro-Brazilian celebrities, that a well-known black cultural icon, Neguinho da Beija Flor, had 67 per cent European ancestry. If even Neguinho’s DNA was mostly European, then who was “really” black and who could be a legitimate beneficiary of racial quota places? Black activists reported that they frequently encountered this argument from anti-quota critics and that this was often the way they first became aware of genetic data (Kent, Santos, and Wade 2014). Their response was that racism was based on cultural categories and that, because “black” was a social not a genetic fact, the arguments based on DNA data were irrelevant. As it turned out, the Supreme Court and state agreed with them: affirmative actions were consolidated in a 2012 law and extended to some areas of federal employment in 2014.

In Brazil, genomics was implicated in a debate about the very character of the nation: What place should be accorded to racial difference? Was Brazil basically a mixed nation, or a nation divided between “blacks” and “whites”? Genomics was used to reiterate the mixedness of the population, but of course, such claims also reiterated the three ancestral lines of European, African and Amerindian genetic heritage. In contrast to Mexico, the language of race was explicit (racial quotas), but, like Mexico, was also explicitly denied as valid by scientists (race was genetically meaningless).

**Conclusion**

This material indicates that, as has long been the case for science generally, genomic science operates in an assemblage that encompasses transnational nodes and relations and national ones, seen not as separate levels or domains but as different perspectival framings of the same networks. In Latin America, given the role of ideas of race mixture, national frames act as a key arena for articulating racialized meanings, which also articulate with more global framings. For example, Mexico’s concerns with indigenous genetics and with obesity and diabetes are both specifically Mexican and also transnational; the search for genetic variants linked to diabetes is a global one, and the interest of genomic science in “indigenous” populations lay at the heart of the controversies surrounding the Human Genome Diversity Project (M’charek 2005; Reardon 2005). In the same way, Brazil’s struggles with the ethics and politics of affirmative action and multiculturalism are not confined to that country.

In Mexico and Brazil, genomics resonated with the long-standing absent presence of race – on the one hand denied (“we are all mixed”), and on the
other constantly reiterated (“we are a mixture of black, white and indigenous”). The particular role of ideas about mixture in the Latin American national frames turns them into a lens that magnifies the absent presence of race in genomics viewed from a globalizing perspective. Whether genomic data are used to privilege the fact of mixture or the fact of difference – again a perspectival issue – racialized meanings are reiterated in quite overt ways that embrace entire national populations, not just minorities.

The comparison between Mexico and Brazil indicates that this reiteration happens in multiple ways: the overall re-inscription of race by genomic science is constituted through heterogeneous instances. In both countries, genomic data were deployed to address issues of health and public policy through the lens of mixture, but in rather different ways: in Mexico, mixture was basically a problem; in Brazil it was a solution, at least for some. (This ambivalence about mixture is not new: it has been around in discussions of the nation for at least 100 years, as noted earlier on.) In Mexico, there was a basic consensus around the importance of public health; the state and science agreed that genomics was an important tool to address this concern and the state funded genomics directly. Race and racism were not seen as important and were left tacit, as had long been the case in Mexico; nevertheless, racial difference was made absently present through genomic discourse about indigenous ancestry as a health risk for mestizos. In Brazil, there was more basic disagreement about the role of race in the nation; although, unlike Mexico, race (or “colour”) had long been more explicit (e.g. in the national census), when it came to acknowledging and addressing racism, the state leaned one way (towards naming racism and legislating for affirmative action for “blacks”), while science – funded in a more decentralized way by the state – leaned in another direction (towards proposing that non-existence of biological race should be a guide for a social policy that acknowledged Brazil’s history of mixture and built on it to realize a future of racial harmony, already prefigured in existing relations).

The reiteration of racialized difference in genomics is not, as noted already, a simple or univalent picture, in which genomics simply takes us back to the era of eugenics and scientific racism. Racial difference is both fixed and unfixed (Abu El-Haj 2007; Wade 2014). It is reiterated in quite simple ways (e.g. in the conflation of social and genetic profiles) and such ways are particularly evident in Latin American genomics in the constant repetition of tri-racial origins. But, it is also made more complicated: for example, genomics highlights the multiple ways ancestry can be assessed, using autosomal DNA, mtDNA and Y-chromosome DNA (not to mention X-chromosome DNA), each of which gives different proportions of continental ancestry. There is also a sense of the endless proliferation of differences: genomics makes it very clear that each individual has a different combination of ancestries, which counter-balances the simple categories of African, European and
Amerindian ancestries. Again, the Latin American context highlights these effects too in the genomic display of almost infinite degrees of mixture.

This argument relates to ideas about a post–Second World War global shift away from “biological” towards “cultural” versions of racial difference, with attendant fears about tendencies towards the “biologization” or “geneticization” of race that are seen to accompany genomics. Race has always been a bio-cultural construct: culture and “biology” (understood broadly as ideas about nature, blood and bodies) have articulated in varying ways over the long durée of racial thinking (Hartigan 2013a; Wade 2002). So the way genomics has been making racial difference absent present over the last two decades needs to be seen as a variation on a biological theme that never disappeared, even after the Second World War, as can be seen in studies of the way ideas about heredity and racial difference figure in practices of assisted reproduction and transracial adoption (Wade 2015, 122–126). This should not of course allay our concerns about genomics and the reiteration of race, but it should relativize them and nuance our understanding of cultural change. Latin America again gives an interesting variation of this problem.

The role of culture (language, dress, residence, and behaviour) in defining racial belonging has always been very significant in the region, especially for creating the boundary between “indigenous” and “mestizo”. In this context, genomics appears to stand out as a force re-biologizing what was generally avowed to be a cultural difference (between indigenous and mestizo). However, biology has been a powerful interest not only in the eugenic period, but also thereafter, in the shape of a concern with heredity, blood and bodies (Wade 2015, 126–130). Attentiveness to the subtle ways that ideas about biology, broadly understood, have inflected concepts of indigenous-mestizo difference show that genomics is not directing cultural change as radically as it appears.

In making comparisons of genomic narratives my aim has not been to claim exceptional status for Latin America – exceptionalism is the ghost that haunts comparative endeavours. Rather I have drawn on a relational, perspectival approach that sees “cases” – nations, regions – as interconnected parts of assemblages, the elements of which can be framed in varying ways. Latin America is an interesting site for seeing how “the nation” frames the way racial difference figures in genomics. While the intersections of race and nation and the intersections of race and genomics are both familiar scholarly fare, Latin America invites us to explore the way race, nation and genomics can be assembled together.

Notes

1. The project was actually two sub-projects: “Race, genomics and mestizaje (mixture) in Latin America: a comparative approach” funded by the ESRC
grant RES-062-23-1914) and “Public engagement with genomic research and race in Latin America” funded by The Leverhulme Trust (grant RPG-044). The projects were directed by Peter Wade, with teams in Mexico (Carlos López Beltrán, Vivette García Deister, Mariana Rios Sandoval, Abigail Nieves Delgado and Sandra P. González Santos), in Colombia (Eduardo Restrepo, María Fernanda Olarte Sierra, Adriana Díaz del Castillo, Ernesto Schwartz Marin and Roosbelinda Cárdenas González), and in Brazil (Ricardo Ventura Santos, Michael Kent, Verlan Valle Gaspar Neto). The ideas expressed here are indebted to the conversations with project team members but do not necessarily represent their views. I am grateful for writing-up time allowed by a British Academy Wolfson Research Fellowship.

2. Knowing what proportion of the ancestry of a person or a group derives from particular continental regions is useful in medical genomics projects that need to match the background ancestry of samples of people with a given disorder to a control sample, in order to reduce confounding effects. Measuring degrees of mixture is also useful in the search for interesting variants using techniques of admixture mapping.

3. These sections draw on research carried out by the Mexico and Brazil teams respectively.

4. For reasons of space, I focus on Brazil and Mexico. The project included Colombia, where genomics also measured degrees of mixture, without DNA data entering so clearly into realms of public policy.

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