

# *A Lab of Their Own: Genomic sovereignty as postcolonial science policy*

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## Abstract

This paper analyzes the emergence of ‘genomic sovereignty’ policies as a newly popular way for postcolonial countries to frame their investment in genomics. It identifies three strands in the genealogy of this policy arena—the International Haplotype Mapping Project as a model and foil for postcolonial genomics; an emerging public health genomics field which stands in contrast to Western pursuits of personalized medicine; and North American drug companies increased focus on ethnic drug markets. I conceptualize postcolonial genomics as a nationalist project with contradictory tendencies—unifying *and* differentiating a diverse body politic, cultivating national scientific and commercial autonomy *and* dependence upon global knowledge networks and foreign capital. It argues that the ‘strategic calibration’ of socio-political versus biological taxonomies in postcolonial genomics creates two primary challenges for this arena, which I refer to heuristically as dilemmas of *mapping* and *marketing*.

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We believe that if we do not carry out studies to understand our genomic patrimony, well, no one else will because they will be interested in their own populations. Secondly, should the interest exist and they [other countries] come to get this information, they make us dependent on this information and then it will cost us. We have to develop our own genomic information.<sup>1</sup>

Researchers in a growing number of countries outside of North America and Europe are successfully lobbying their governments to exercise a kind of protective ownership over the DNA of their populations. They do so in response to the increasing implications of genetic variation for health outcomes and the growing economic value of genetic information in pharmaceutical development (Whitmarsh, 2008). They lay claim to new biopolitical entities, “Mexican DNA” and “Indian DNA” among others, strategically calibrating socio-political categories (i.e. nationality and race-ethnicity) with scientifically produced ones (i.e. genotypes). On the surface, this policy frame asserts a deeply nationalist sentiment of self-determination in a time of increasing globalization. It implicitly ‘brands’ national populations as biologically distinct from other populations, ‘naturalizing’ nation-state boundaries to ensure that less powerful countries receive the economic and medical benefits that may result from population genomics. However, the following analysis reveals the contradictory tendencies of genomic sovereignty policies—unifying *and* differentiating a diverse body politic, cultivating scientific and commercial autonomy *and* dependence upon global knowledge networks and foreign capital.

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<sup>1</sup> From an interview with Mexican Institute of Genomic Medicine official, cited from Séguin et al. (2008b).

Despite these contradictions, proponents of this field tend to celebrate its emergence as a form of empowerment without careful attention to the ways in which genomic sovereignty inherits the perils produced by the ‘geneticization of life’ more broadly. Of particular concern are the ways in which national and group identities once premised on a “history of comradeship and mutual alliance” are increasingly understood as genetic affiliations that can be made or unmade with blood tests (Johnston, 2003).<sup>2</sup> Anthropologist Margaret Lock (1997) refers to the “category fallacy” embedded in the Human Genome Diversity Project, arguing that “to make a selection of contemporary groups identified on the basis of a shared culture, and then to assume that their genetic make-up is also shared, is to conflate time and space in an entirely inappropriate way” (285). Much of this critique rightly warns against the negative implications of research initiatives based in North America and Europe which uses the non-Western world and indigenous peoples as genetic laboratories (Marks, 2005). But developments in postcolonial genomics, wherein non-Western researchers are building ‘labs of their own’ for liberatory and empowering ends, provides a new scientific context that is less amenable to such broad dismissal (pace Lock), even as it still requires careful analysis of the relationships between political rhetoric, scientific practice, and social effects.<sup>3</sup>

Drawing upon a political sociology of science framework, this paper examines how structures of power and inequality in the global distribution of scientific, technological, and economic resources impact the institutionalization of new genomic knowledge practices and policy framings. It engages work on the methods and rhetoric used to ‘align’ categories of human difference (Epstein, 2007; Foster & Sharpe, 2002; Kahn, 2006) with particular focus on the ‘resuscitation’ of racialized constructions of group identity (Benjamin, 2010; Fullwiley, 2008; Montoya, 2007; Reardon, 2004; Soo-Jin Lee et al., 2001). I identify three strands in the genealogy of this policy arena—the International Haplotype Mapping Project as a model and foil for postcolonial genomics; an emerging public health genomics field which stands in contrast to Western pursuits of ‘personalized medicine’; and North American pharmaceutical companies increased focus on ethnic drug markets.

My central claim is that in the context of national genomics initiatives the work of calibrating scientific and socio-political classifications is not haphazard conflation, but a deliberate interpretation of genomic data to match the socio-historical record and a re-imagining of historical and cultural narratives to make sense of genomic findings. This ‘strategic calibration’ is carried out in the service of often laudable public health and social justice aims. However, precisely because of this national empowerment framing, it is tempting for analysts to overlook the ways in which the geneticization of national populations impacts groups differently, enriching some and dispossessing others, solidifying and weakening group ties to the nation-state in unexpected, and potentially detrimental, ways. Thus, in the second part of the paper, I delineate two related challenges that grow out of postcolonial genomics, which I refer to heuristically as dilemmas of *mapping* and *marketing*.

To preview, the first set of dilemmas around *mapping* genetic diversity refers to the challenges involved in defining populations of interest in such a way that they are methodologically useful and politically unproblematic. For researchers, the first phase of mapping involves identifying common genetic patterns in a national population, based on shared haplotypes. A *haplotype* is the set of alleles found on a single chromosome, and careful identification of a minimum set of haplotypes is thought to ‘capture the signal of untyped markers’ on the genome, most importantly those associated with disease susceptibility (Terwilliger & Hiekkalinna, 2006) and drug metabolism (Nebert & Menon, 2001). Genotyping is the process of determining the allelic variation on a particular person’s DNA. While there is wide consensus following the completion of the Human Genome Mapping Project that human beings share 99.9% of their genes, such that researchers cannot point to clear, qualitative genetic breaks between one population and another, researchers are interested in the variation of shared haplotypes across populations. In the second phase of mapping, called genome-wide association studies, researchers focus on how these haplotype groupings are linked to disease risk. By comparing people who have a particular disease with people who do not, putative risk loci are identified which can be studied in more depth (Manolio, Brooks, & Collins, 2008).

<sup>2</sup> As the case of U.S. Black Seminoles (descended from freed slaves, not considered ‘pure’ or ‘blood’ Seminoles) illustrates, those who already hold a precarious or minority status within a group are more vulnerable to the exclusionary effects of genetic identity (Johnston, 2003).

<sup>3</sup> My use of the terms ‘developing’, ‘postcolonial’, and ‘non-Western’ mirrors the language of genomic sovereignty proponents. I use them interchangeably throughout the paper to signal that genomics research in these contexts is being strategically framed in relation to European and North American scientific and political dominance.

Haplotype mapping becomes politically problematic when, for example, researchers find that a given social group shares more genetic similarity with a rival social group than with their own in-group members, as was the case in the Kashmir region of India (Mudur, 2008). Or, controversy may arise when genome results contradict a widely held origin story of a group or nation, as was the case recently in Mexico when results seemed to indicate that the ‘younger’ Mestizo ethnic group may be ‘older’ than the indigenous groups thought to be its ethnoracial precursor (Schwartz, 2009). It is not that researchers do not expect or enjoy such ‘surprises’. Rather, the central role of national governments as the sponsor of these HapMap projects creates greater public scrutiny and less insulation for scientists to make sense of these developments as purely scientific curiosities. The biopolitical context in which postcolonial genomics occurs, transforms curiosities into controversies that compel proponents to *strategically calibrate* socio-political and biological taxonomies in ways that can simultaneously advance the science, foster public support, and produce health and economic goods.<sup>4</sup>

The second set of dilemmas around ‘marketing’ relates to the increased focus of North American pharmaceutical companies on ethnic drug markets in non-Western contexts, wherein ethnic groupings act as proxies for population genotypes to which drugs can eventually be tailored. In this part of the discussion, I focus on the ambiguous relationship of diasporic and indigenous populations vis-à-vis the creation of ethnic drug markets. These groups, in particular, highlight the existing social fault lines that make claims about discrete ‘national genomes’ untenable in the face of transnational migration and difficult to establish as a ‘universal good’ in the face of socio-economic inequities that severely limit access to such goods. A disjunction exists between these groups’ participation in genomics knowledge production as DNA donors and their marginal importance as genomic consumers. Genomic sovereignty claims are complicated by these two biopolitically rogue populations; neither ethnic proxies nor what we might call ethnic precursors—indigenous people who are thought to have contributed to the national genome lineage but are ethno-racially distinct and prior to it—are the target markets of pharmacogenomics. Their upstream inclusion and downstream exclusion requires sustained attention as a matter of science and health policy analysis.

To that end, the remainder of the paper introduces the legal precedent of genomic sovereignty, juxtaposing the formal policy framing with social, economic, and political underpinnings which complicate the empowerment and protectionist rhetoric. Then I elaborate the three institutional strands of this policy arena, namely the International HapMap Project, the field of public health genomics, and ethnic drug marketing. I close with a discussion of two sets of dilemmas confronting this policy arena, which I have previewed above.

## 1. Background: National Genome, *Inc.*

In a recent analysis of ‘the global genome’, Thacker (2005) argues that globalization is a ‘biological phenomenon’ to the extent that the biotech industry crosscuts the traditional boundaries of nation-states in its pursuit of biovalue (xvii). As a response to what Thacker has identified, this discussion highlights a counter-emergence to the global genome—the assertion by countries left out of the Euro-American dominated International HapMap project of multiple national genomes. Proponents of genomic sovereignty policies strategically (re)biologize the nation-state by asserting that less powerful nations must protect the cumulative genetic heredity of its population from being pillaged by more powerful nations.

### 1.1. ‘Lab of Their Own’

In the most prominent assertion of genomic sovereignty to date, the Mexican Senate unanimously approved reforms to the General Health Law in 2008, which makes “the sampling of genetic material and its transport outside of Mexico without prior approval. . . illegal” (Séguin, Hardy, Singer, & Daar, 2008b: 6). The Genomic Sovereignty amendment

<sup>4</sup> Epstein (2007) refers to a similar process of ‘categorical alignment’ in which medical and political schemas are aligned or superimposed on one another. By contrast, my use of ‘strategic calibration’ aims to describe the process at an earlier stage when the work of matching up scientific and socio-political taxonomies is not aligned or invisible, as Epstein suggests. I prefer this nomenclature to the more common yet vague ‘co-production’, which does not account for the *iterative* dimension of strategically matching classificatory schemas, and to the more dystopic notion of ‘colliding’ (Kahn, 2006) which implies impending damage and chaos if taxonomies fail to match up.

states that Mexican-derived human genome data are the property of Mexico's government, and prohibits and penalizes its collection and utilization in research without prior government approval. It seeks to prevent other nations from analyzing Mexican genetic material, especially when results can be patented, and comes with a formidable bite in the form of prison time and lost wages. In addition to Mexico, countries such as India, Thailand, South Africa, China, and others have issued policy statements or passed legislation that seeks to develop genomics infrastructure explicitly to benefit their national populations (Séguin et al., 2008b). So while the term 'genomic sovereignty' is predominantly used only in Mexico, its conceptual underpinnings are emerging in other nations.

Unlike pan-indigenous advocacy groups that have asserted group sovereignty claims to opt-out of genomics research (Marks, 2005), these governmental policies set out proactive research agendas to stimulate health and economic gains. In this way, the biology of the population becomes a 'natural resource' and genomics serves as a nation-building project maximizing the potential of this resource. Unlike other nationalisms, the point of postcolonial genomics is not to posit the nation as 'pure' (as in the Iceland case, cf. Fortun, 2008), but as a unique genetic mixture (i.e. 'admixed') when compared to other nations.

Proponents of genomic sovereignty policies draw upon the empowerment idiom from the classic essay "A Room of My Own" by Virginia Woolf, asserting that if genomics research is a house then developing countries should "create a room of their own" (Séguin, Hardy, Singer, & Daar, 2008a). This discussion complicates the agenda to champion genomic sovereignty by examining the dilemmas that emerge out of this new research and policy domain. The title of this article draws upon one such illustration, wherein the actual labs in Mexico's genome institute were equipped by U.S. based biotech companies Affymetrix, Applied Biosystems, and Illumina. The labs are named after these commercial benefactors and not, as one might expect of an undertaking framed in terms of national sovereignty, after any of Mexico's historic scientific figures. The ways in which collaborating with North American commercial entities may shape the scientific agenda and political accountability of the institute are the focus of ongoing research. For the purposes of this discussion, we should note that the material and symbolic infrastructure of postcolonial genomics is comprised of a mixed genealogy that confounds the rhetoric of nationalist empowerment.

## 1.2. *Social cartographies*

In addition to its stated aims, genomic initiatives have the potential to naturalize social hierarchies and disparities. Debates surrounding genomics in Euro-American contexts—whether or not it naturalizes social inequalities as 'racial' (Duster, 2005; El-Haj, 2007; Fujimura, Duster, & Rajagopalan, 2008; Kahn, 2006; Montoya, 2007; Reardon, 2004; Soo-Jin Lee, Mountain, & Koenig, 2001) or fails to problematize the effects of capitalist accumulation on knowledge production (Etzkowitz, 1998)—still remain relevant to the arena of postcolonial genomics. But as a science policy born of global power inequality, postcolonial genomics can also be understood as having a mixed genealogy and trajectory that is at once innovative and retrograde in its assertions. While diversity maps serve as a 'naturalizing' cartography of the nation that aims to account for the accumulated genetic inheritance of a people, they also act as social maps for contemporary anxieties about social fragmentation and future cohesion.

As one example, the first major task of the Mexican HapMap Project was to investigate the common haplotypes distributed across six states. Schwartz (2008) explains that Mexican newspaper reports drawing upon the Mexican Institute for Genomic Medicine's public communications, stated that "due to the race, there is a pronounced difference between the populations of various states within the country. In Sonora they have the highest prevalence of European genes, 58%, while in Guerrero, their population presents a major index of African genes, 22%". While scientists at the Mexican Institute criticize the newspaper's use of 'race', preferring 'population' as a more scientifically valid substitute, the Institute's public statements and academic publications reveal their own use of race-ethnicity to describe Mexico as a predominantly 'mestizo' nation (Silva-Zolezzi et al., 2009; Contreras et al., 2009).

In its second phase of research and amidst controversy over the exclusion of indigenous populations from the first phase, the Mexican Institute broadened its demographic sample to ascertain the genetic relationship between indigenous communities and the dominant Mestizo population (Schwartz, 2008). The ethnoracial and geographic focus of the Mexican HapMap project mirrors ongoing disputes about disparities in the distribution of social and political resources across states and social groups, and in particular, the rights and relative marginality of indigenous communities within the country. Researchers at the Mexican Institute showed initial signs of relief and vindication at

the convergence of their HapMap findings with ‘what we already know’ about the existence of ethnic groups in the country.<sup>5</sup> One report indicates that “although there are some regional genetic differences between Mexican subpopulations, they are similar enough to be analyzed as a single group” (Jimenez-Sanchez et al., 2008: 1195). However, given that Mexico is comprised of over 65 indigenous ethnic groups in addition to the majority Mestizo population, the Institute is recently faced with the possibility that the tidy symmetry between social and genetic groupings may not entirely hold (Schwartz, 2009).

While in Mexico the indigenous–mestizo relationship anchors genomics research (Vergara-Silva, López-Beltrán, McManus, 2007), in India, caste-linguistic groupings infuse genome mapping (Reich, Thangaraj, Patterson, Price, and Singh, 2009). In all cases, there is a broader politics of difference at work in which genomics is being used to both unify and differentiate the population as part of a larger branding process—the nation as uniquely heterogeneous vis-à-vis other nations.

### 1.3. Biological brands

In promising economic stimulus through the development of a genetically-tailored national health sector that will cut costs and generate profitable treatments, postcolonial genomics also serves as a political lightning rod for growing anxieties over national economic development and population health crises. Proponents hail it as a way to carve out a biological and economic niche market from which the nation can profit. The director of the Indian Genomic Variation Consortium notes, for example, that “We’ve shown that [International] HapMap studies cannot always be applied to the Indian context.”<sup>6</sup> Like genomic sovereignty proponents elsewhere, the implication is that India’s exclusion from the International HapMap may lead to what Stefan Ecks (2005) has called ‘pharmaceutical marginalization’, caused by a lack of access to drug therapies that, in this case, will potentially be tailored to population genomes. Opponents of national genomics argue, in turn, that such investments threaten to gamble national resources on impractical approaches to public health (Ribeiro, 2005).

So lest the focus on genomic sovereignty as a policy ‘discourse’ overshadow its material implications, such assertions aim, in part, to biologically brand the nation in order to develop profitable pharmacogenomic markets. These are increasingly understood as ‘bioethnic’ markets (Montoya, 2007) developed through processes of ‘niche standardization’, whereby human bodies are classified as neither part of a universal or as individuals, but as biologically meaningful social groups (Epstein, 2007: 135). The need to map and protect national genetic diversity and regulate the ownership of genetic ‘biovalue’ (Waldby & Cooper, 2008), is motivated in part by the promise of health interventions that will save the country in healthcare expenditures and generate profits from ‘tailored’ drug development. The following section outlines three institutional strands in this broader political-economic and scientific nexus, followed by a discussion of the dilemmas posed by attempts to map and market national diversity.

## 2. Genealogies of genomic sovereignty

### 2.1. The International Haplotype Mapping Project

The first strand in the genealogy of genomic sovereignty policy is the International Haplotype Mapping project (hereafter “International HapMap”) and, in particular, the sense of exclusion expressed by researchers in countries that were not included in this initiative. During the first phase (2002–2005) of the International HapMap, DNA samples were collected from participants in Tokyo (Japan), Ibadan (Nigeria), and Beijing (China). These were added to an existing database of samples from U.S. residents of northern and western European ancestry. During the second phase (2005–2007), samples were collected from seven additional groups, among which were several diasporic populations including Mexicans in Los Angeles, California and Gujarati Indians in Houston, Texas.<sup>7</sup> Interestingly, both Mexico

<sup>5</sup> Personal communication. Meeting with INMEGEN researchers and bioethicists. Author’s Fieldwork Notes, March 6, 2009.

<sup>6</sup> To date, the ICVC has analyzed approximately 75 genes from 1871 individuals belonging to 55 caste, tribe, and religious groups over the last three years, constituting the largest cross-section of any single population (including the International HapMap), according to the Consortium.

<sup>7</sup> The complete list of samples as they are classified in the HapMap’s official database, Corriell, are as follows: Luhya in Webuye (Kenya), Maasai in Kinyawa (Kenya), Chinese in metropolitan Denver, Colorado, people of African ancestry in Southwest U.S., Mexican ancestry in Los Angeles, California, Toscana in Italy, and Gujarati Indians in Houston, Texas.

and India are at the forefront of postcolonial genomics, in part, because researchers in these regions do not consider the International HapMap's diasporic samples to be a satisfactory snapshot of the genetic diversity of their national populations. But from the point of view of the International HapMap Consortium, "As most common patterns of variation can be found in any population, no one population is essential for inclusion in the HapMap" (2003:791). So, technically, there is no need for a 'representative sampling' of the entire human population, because no one population is so genetically distinct as to justify representing a particular human 'kind'. Even so, the Consortium's original sample comprised of distinctly ethnoracial populations (i.e. Yoruba, Chinese, Japanese, and a White U.S. sample from Utah), fueling vigorous debate about whether and to what extent genetic ancestry and race-ethnicity correlate (Duster 2005; Burchard et al., 2003; Fujimura et al., 2008; Hamilton, 2008).

To understand genomics' researchers explicit rejection and implicit acceptance of racial-ethnic classifications, social scientists have begun focusing on the bioinformatic programmes used in genome-wide association studies (Fujimura, 1999; Suarez-Diaz & Anaya-Muñoz, 2008). In particular, the need for researchers to input a designated number of clusters by which to stratify the population, means that they tend to have some idea of how many genetically discernible groups they think exist in the broader population, if not also, what groups. A fundamental critique of genomics is that it employs under-analyzed starting assumptions about the association between ancestry, geography, 'folk' ethnoracial categories, and disease risk (Barnholtz-Sloan, McEvoy, Shriver, & Rebbeck, 2008; Bliss, 2009; Fujimura et al., 2008; Terwilliger & Hiekkalinna, 2006). In reference to the complex methods of producing genomics knowledge, anthropologist Kaushik Sundar Rajan (2006) explains, "the more things get reduced to their molecular components. . . the more one needs to rely on statistical, population-based data to 'individualize' therapy. This means that one can individualize therapy only on the basis of population classifications" (163). So paradoxically, while the International HapMap serves as a foil for many national genome projects because they do not consider their populations to have been fully represented, the former also provides a problematic methodological template according to which national initiatives are modeled.

## 2.2. *Public health genomics*

The field's most influential proponent, the University of Toronto's McLaughlin-Rotman Centre for Global Health, is comprised of a multidisciplinary research team of over 35 members who have been instrumental in institutionalizing public health genomics as a field. The Centre embarked on a set of high profile research and policy initiatives that is primarily focused on bringing public health genomics to developing countries (Séguin et al., 2008b). Through tremendous visibility and strategic collaboration, this relatively small group of health policy entrepreneurs is playing a principal role in the growing political will among governments to sponsor genomic initiatives and implement genomic sovereignty legislation. The Toronto group was instrumental in Mexico, for example, testifying before the Mexican legislature on behalf of the Mexican Institute for Genomic Medicine. Lamenting the possibility of a global 'genomics divide' between poorer and richer countries, Toronto Centre co-directors Singer and Daar (2001) warn of a future when "the unfolding [scientific] revolution resulted in designer pharmacogenomics in rich countries and lost opportunities for advancing the health of those in Africa, Asia, and Latin America" (87).<sup>8</sup> The second strand in the genealogy of genomic sovereignty policy is the field of 'public health genomics', which health policy entrepreneurs frame in direct contrast to genomics practiced in wealthier Western countries. For example, Wilmot James, dubbed 'father of African genomics', contends that,

It may be, in the North, that one result will be the emergence of personalized medicine, of having drugs and interventions designed specifically for the unique modality of one person's disease profile. . . We in the [Global] South, as elsewhere, need to work hard at figuring out how to make genomics relevant to clinical practice in private and public medicine, so that it does not remain with the privileged elite few.<sup>9</sup>

Within the field of public health genomics, 'withholding' genomic information from and failing to develop pharmacogenomic interventions for individuals and communities in poorer countries is conceived of as a "new form of discrimination" (Brand, Brand, & Schulte in den Bäumen, 2007: 11). Researchers in the vanguard of public health

<sup>8</sup> Singer, P. A., & Daar, A. S. (2001). Harnessing genomics and biotechnology to improve global health equity. *Science*, 294(5540), 87–89.

<sup>9</sup> James, W. (2004). *Africa in the age of biology* (p. 8). Human Sciences Research Council Publishers.

genomics report, for example, that “Only 16 of the 1,393 new drugs that were marketed between 1975 and 1999 were registered for diseases that predominantly effect people in developing countries. . .In the future, pharmaceutical companies in the developed world will have to pay more attention to developing countries” (Daar & Singer, 2005: 245). They argue that rather than focusing solely on the development of ‘personalized medicine’, genomics researchers should seek to ‘carefully define’ population differences with the stated goal of being able to tailor drugs to specific ethn racial groups in developing countries who are most in need of efficient treatment options (241).

Proponents of public health genomics draw, in part, upon international policy statements, most notably the World Health Organization’s *Genomics and World Health* (2002), a report that grew out of world-wide consultations with physicians, scientists, and health policy makers working in poorer countries. While attentive to both the possibilities and perils that characterize this new biomedical terrain, the report is decidedly optimistic that genomics can be ‘harnessed to advance human development’ and address local and regional health needs. Even while emphasizing that infectious disease comprises the majority of the current disease burden of developing nations, the report suggests that in some countries there is a shift underway towards more chronic diseases, for which genomics therapies may prove beneficial. One of the refrains characteristic of this new field, then, is translating genomic findings “from lab to village” so that knowledge production has a real impact on public health.<sup>10</sup>

In response to the danger of an increasing scientific and health divide, the Toronto group advocates for global South–South collaborations among developing nations where feasible, and have facilitated such exchanges. They arranged for representatives of Pakistan’s Health ministry, for example, to visit an Indian-based genomics company, Shantha Biotech, to observe the latter’s vaccine research programme. Given the tensions between the nations, it was one of the first times that any cross-national collaboration had occurred in recent memory, leading the company’s founder Khalil Ahmed to comment “If biotech can help to unite people, then why not? Given the political situation, the scientific community can and should open the doors of friendship and cooperation.” This example illustrates that the strategic politicization of science and medicine is being effectively marshaled by proponents of public health genomics, as they seek to intervene in larger structures of global inequality by targeting the specific needs of poorer countries (e.g. collective not individual health interventions) and highlighting the unique contributions these countries can make to genomics more broadly (e.g. as a source of diverse genotypes). In addition to the South–South solidarity and empowerment that drives public health genomics, this is very much a market-oriented campaign in which the role of private biotech companies is central (Rajan, 2006). The Toronto group, for example, has organized international conferences and smaller meetings to facilitate collaborations between researchers and companies in order to advance this arena (Frew et al., 2006).

A fundamental critique of public health genomics, especially as it targets complex diseases, is that candidate genes are only expected to account for a small fraction in the “multifactorial web of [disease] causation” (Fujimura et al., 2008: 648). Thus, the concern goes, governments should be cautious to invest in an area that is unlikely to yield much fruit, especially while traditional public health interventions and socio-economic development strategies remain grossly under-funded (Ribeiro, 2005). A common counter-claim to this is that pharmacogenomics “can be used to increase efficiency, cut costs, reduce adverse effects and increase the efficacy of drug-development pipelines” (Daar and Singer 2005:241). An influential population geneticist, in turn, suggests that

“while [genomics] may discover risk loci that explain only a small fraction of the observed cases, the details of what loci are discovered and how they function to create the disease might give us insights into the etiology of the disease in question, and this knowledge might lead to a larger public health impact down the road. In the best cases we are learning genes we never suspected to be involved with a disease are involved, and this is revealing of novel biology and suggestive of novel interventions. Whether these ‘hints’ are worth the cost is another question!”<sup>11</sup> In sum, public health genomics is posed as an alternative to European and North American research agendas and the pursuit of ‘boutique medicine’ (Brand et al., 2007; Séguin et al., 2008a, 2008b). Paradoxically, like their counterparts in the Global North, proponents of public health genomics seek to develop the commercial platform of pharmaceutical development in their pursuit of public health advances, which may ultimately limit the affordability of future health goods.

<sup>10</sup> See “From Lab to Village: An Interview with Dr. Abdallah Daar and Dr. Peter Singer” Available at: <http://med.stanford.edu/oih/fromlabto-village.html>; Last retrieved April 1, 2009.

<sup>11</sup> Retrieved April 6, 2009 from [www.scidev.net/en/news/pakistan-seeks-to-learn-from-indian-genomics-firm.html](http://www.scidev.net/en/news/pakistan-seeks-to-learn-from-indian-genomics-firm.html).

### 2.3. Ethnic drug markets

The third strand in the genealogy of genomic sovereignty is the pharmaceutical industry's increased focus on ethnic drug markets. That is, "companies are hoping to tailor therapies ever more closely to the genetic profile of individuals or groups of consumers, [such that] identifying racial/ethnic correlations with disease is becoming big business" (Kahn, 2004). As I will explain further in the section on 'marketing' dilemmas, the link between drug response and ethnicity is not simple biological reductionism, but in some cases takes in to account the ways in which social processes (e.g. immigration) and environmental exposures (e.g. poor living conditions) may create differential health effects across ethnic groups. What is important to note at this point is that many pharmaceutical companies view increasing investment in 'niche ethnic markets' as a matter of economic survival. Companies of all sizes in both poorer and richer countries are starting to collaborate in an effort to cultivate these 'segmented' markets in which drugs can be tailored to specific genotypes. This involves not only North American drug companies working in isolation, but partnerships with non-Western researchers and governments that seek to biologically brand their own populations.<sup>12</sup> Sovereignty policies, in turn, attempt to preemptively empower non-Western scientific and political elites within such collaborations.

The increasing importance of ethnic drug markets for the survival of the pharmacogenomics industry, in turn, is part of a larger shift in the life sciences wherein human tissue, and specifically genetic information, is patentable and potentially profitable (Etzkowitz, 1998).<sup>13</sup> The DNA of populations is increasingly expected to be a resource (Cooper, 2008; Franklin, 2006; Rajan, 2006; Rose, 2007; Waldby, 2002; Waldby & Cooper, 2008) for preventative healthcare and targeted medicine. This increase in 'biovalue' is tied to the growing industry excitement around 'emerging economies' whose chronic disease load is rapidly multiplying. Countries such as Mexico and India among several others have been tagged by corporate insiders as "Pharma's Promised Land" because they are expected to account for one fifth of global drug sales by 2020.<sup>14</sup> Proponents of public health genomics view this industry trend as an opportunity for 'emerging economies' (Hardy, Seguin, & Darr, 2008). That is, if pharmaceutical companies fail to demonstrate safety and efficacy of a particular drug based on a clinical trial conducted in North America, they may be able to demonstrate the drug works in another population, such as India or China (Daar & Singer, 2005). They see this as serving the dual function of recouping the companies' investment in drug R&D, while also addressing the health needs of 'pharmaceutically marginal' populations (Ecks, 2005).

Producing drug treatments requires that targeted populations first supply DNA to be studied by genomic researchers and drug developers. Genomic sovereignty claims seek to regulate both ends of this process—tissue supply and drug distribution—to minimize harm and maximize benefit to the national population. Daar and Singer (2005) explain it thus: "...Developing countries are not only potentially huge markets for drug therapeutics but are also depositories of important human genetic diversity. Understanding this diversity is valuable because it better defines those population subgroups that will benefit more from a particular drug than others, and allows the detection of side-effects that might not be seen in populations that are mainly Caucasian" (Daar & Singer, 2005: 245). But some analysts warn against a 'pharmaceuticalization of philanthropy' (Biehl, 2007) and the related 'pharmaceutical citizenship' in which corporations stand to be the primary 'winners' in initiatives to redress socio-political marginality with medicine (Ecks, 2008). Montoya (2007), in turn, critically analyzes the increasing popularity of 'bioethnic conscription' in the context of Mexican Americans enrollment in diabetes research and drug marketing, explaining that "The 'emerging market' trope is a commonly accepted demographic truism. That is, to succeed, businesses must now appeal to the ethnic market..." (114). Daar and Singer's implicit contrast between Caucasians and non-Caucasians above—despite numerous and repeated attempts by analysts to debunk and substitute other modes of classification (e.g. geographic ancestry, cf. Foster & Sharpe, 2002) for this crude racial concept—is not simply a sign of carelessness but a reflection of how national genomics initiatives are being strategically crafted as niche ethnic markets.

<sup>12</sup> These include China, Cuba, Brazil, Egypt, Gambia, India, Iran, Kuwait, South Africa, South Korea, and Zimbabwe among others. See, Hardy et al. (2008). *As genomic medicine takes off, some emerging economies show leadership*. Retrieved April 6, 2009 from [http://www.mrcglobal.org/files/HGV\\_Release.pdf](http://www.mrcglobal.org/files/HGV_Release.pdf).

<sup>13</sup> See also *Global Science and National Sovereignty* (2009), explain that 'In an era when global science has become a producer of innovations and of products that are patented and appropriated according to national legal systems, the norms of universalism and communalism, which presupposed that science would create universally accessible goods, are no longer upheld' (Mallard, Paradeise, & Peerbaye: 4).

<sup>14</sup> "The Emerging Seven: Pharma's Promised Land". Retrieved April 6, 2009 from <http://www.pharmaceutical-technology.com/features/feature48666/>.

As I explore in greater depth elsewhere (Benjamin, 2010), the creation of segmented markets not only ‘resuscitates’ drugs that have undergone unsuccessful clinical trials in North America, as proponents of public health genomics advocate. Marketing to specific ethnic populations also resuscitates ethnoracial taxonomies that serve as proxies for biologically meaningful genetic variation. Among the many lessons from the BiDiI case involving the first “ethnic drug” marketed for African American hypertension, there is a recursive relationship between population labels at the time of sampling and research and the ways in which groups will be marketed to downstream (Kahn, 2004). In the context of postcolonial genomics, there is a commercial drive to ensure that the genetic classifications produced through national ‘diversity mapping’ can be calibrated with salient social groups to which drugs can be marketed. Advertising a diabetes drug to carriers of some particular haplotype is, arguably, much less effective than a ‘public health campaign’ directed to an ethnic subpopulation. However, as with BiDiI, the ways in which different biopolitical constituencies are affected by the strategic calibration of biological and ethnic groupings in drug marketing is highly unpredictable and often contentious.

To focus only or even mainly on the beneficent potential of this global shift to ethnic drug marketing is to close one eye to the lessons learned in the U.S. context. “Recontextualizing the race debate” by urging scholars “not [to] criticize industry on the basis of profit motive” (Séguin, 2008c: 172) disregards the continued salience of race even when members of medically-neglected populations are the ‘beneficiaries’ of pharmaceutical interventions, as in the BiDiI case and ethnic niche marketing more broadly. Racialization is not simply a short-term methodological problem to be overcome with the development of more precise bioinformatic techniques nor is it usually deployed in explicitly nefarious ways. Rather, the logic of embodied ethnoracial difference is playing a defining role in segmenting pharmaceutical markets and resuscitating an ailing industry, often with the stated aim of producing biomedical goods for ethnoracial populations that are under-served. Thus, the ‘value’ of race is central to the development of public health genomics and requires sustained analysis.

### 3. Dilemmas for genomic sovereignty

The previous sections have outlined three strands in a mixed genealogy of genomic sovereignty policies, outlining some of the concerns about how such trends take shape within existing structures of power and inequality. This section goes in greater depth in to two broad dilemmas that tie some of these issues together within specific national and institutional contexts. It draws upon case material from Mexico and to a lesser extent India, to illustrate key points.

#### 3.1. Mapping human taxonomies

The first dilemma that genomic sovereignty policies face is the way in which different methods of classifying human beings—as biological, social, or political—compete, clash, and complement one another in unpredictable ways. In the course of everyday life, individuals draw on different understandings of human difference to suit specific needs with minimal consequence if they lack coherence. However, when institutions and governments employ such classifications, their rational may come under greater scrutiny. Societies employ numerous types of classificatory schemes to sort and hierarchize populations, so that analyses about the ways in which race, nation, genomics, and identity are co-constituted in the Euro-American context (Fortun, 2008; Fullwiley, 2008; Rabinow, 1999; Reardon, 2004; Tallbear, 2005; Soo-Jin Lee et al., 2001; Montoya, 2007) are not readily transplantable to societies with very different histories of social group-making.

The two most salient categories that structure social life in Mexico, for example, are ‘mestizo’ (ethnoracially mixed citizen-subject) and ‘indigenous’ (comprised of approximately 65 ethnic groups). Within these, geography and language are strong determinants of self-identity, socio-economic status, and life chances. It is in no way surprising, then, to find that the work of the Mexican Institute for Genomic Medicine is heavily couched in the discourse of ‘mestizaje’, seeking to discern the genomic underpinnings of this unique Mexican cultural–biological hybridity. Mestizaje is an already circulating discourse which proponents of Mexican genomics have used to cultivate public support for the initiative. It serves as a biological brand for the nation-state to attract foreign financial investment and scientific interest, and to neutralize antagonism from critics from among the country’s Catholic Church, public health- and academic communities.

In earlier stages of Mexican nation-building, ‘mestizaje’ was utilized by the national intelligentsia as “a potential route to national consolidation and as a positive mark of national identity” contra notions of ‘hybridity as degenerate’

(Lund, 2006: 86). The recent popularity of calculating levels of ethnoracial mixture in genomics (rather than determining pure types), gives added value to the Mexican genome brand within the global scientific community. Complicating genomic nation-building, however, is the salience of the ‘indigenous question’ for Mexico’s national identity and collective biology: In the same way that *mestizaje* serves as a resource for Mexican genomic advocates, critics of the Initiative have a ready counter-narrative in the long struggle over indigenous rights: “the Indian as necessary participant in and erasure from the national project; an included exclusion that forms the very logic of *mestizaje*. Indigeneity, then, is a feature of genomic national building whereby the dual process of inclusion and exclusion persists. The Indian participants in the building of a new race and a new spirit, yet is excluded from the modern” (Lund, 2006: 83).

Soon after its founding in June 2005, for example, the Mexican Institute initiated an ambitious programme to collect DNA samples from more than 2000 individuals, an initiative dubbed the National Crusade Genomic Map of Mexico. Representatives of the agency and a battalion of health workers visited states in which governors and local leaders had agreed, through prior consultation and negotiation, to allow the agency to recruit DNA donors. As an official Institute document reports, the Crusades were “intended primarily to collect blood samples of 100 men and 100 women originally from each of the participating states. . . They turned into academic events of three days during which were given public presentations and discussion tables in universities, high schools and public forums, both for the student community, as for the general public”.<sup>15</sup> Some agency officials and observers expressed heightened anxieties during the sampling process about, ‘human subjects protection’ for indigenous communities, such that local elders and community representatives (often anthropologists with connections to the group) were recruited as intermediaries and consent documents were translated from Spanish in to the local languages. In addition, the informed consent process placed emphasis on explaining to the communities that their donations would be used to map the genetic diversity of the country *and* for research as yet unknown, but that they should expect *no* direct medical benefit from their participation (Schwartz, 2008).

Even more fundamental than issues of consent and future access to therapies, the collection of indigenous samples also illustrates the potential for ontological conflict between what donors think their DNA represents and what their tissue is made to represent in the framework of national genomics. Over the course of the Mexican Institute’s outreach and sampling, ethnographer Ernesto Schwartz reports a situation in which a Tepehuanes (indigenous) elder who was serving as community spokesman at one of the blood sampling sites in the state of Durango asserted, “We are not Mexicans. We are Tepehuanes, and you are looking for the genome of the Tepehuanes!”<sup>16</sup> The elder’s statement contrasts that of the project director who, when asked whether indigenous research subjects require special defense against harm or discrimination, replied “the protection is the same, finally they are Mexicans, the same as us”.<sup>17</sup> This relatively benign mismatch in which a community gatekeeper and genomics director disagree over the relationship of an indigenous group to the Mexican body politic, is an instance of taxonomic mismatch. In this case, the different points of view between researchers and Tepehuanes participants, did not thwart collection of indigenous blood samples. In part, this reveals how the very elaborate community engagement and informed consent protocol of the HapMap process is not designed to identify much less address fundamental conflicts in classification.

To turn to the Indian Genome Variation Consortium, as a brief point of comparison, one of the project’s first findings suggest that two warring groups, Hindus and Muslims from the Kashmir region, share more genetic similarity with one another than with their in-group cousins in other parts of the country. One of the researchers, Partha Mazumder, admitted that “The social hierarchy of caste groups is not fully reflected in their genetic profile”.<sup>18</sup> The report further explains that scientists consider some of the findings about genetic proximity and disease risk data “so sensitive that they have decided not to make the identities of the communities public for now”. One project

<sup>15</sup> “National Crusade Genomic Map of the Mexicans”. Retrieved April 3, 2009 from <http://www.inmegen.gob.mx>.

<sup>16</sup> Ernesto Schwartz interview with Cesar Lara, Chief Bioethicist, ELSI Department of the INMEGEN. June 18, 2008. With authors permission, cited from Schwartz, E. (2008). *Genomic sovereignty and the creation of the INMEGEN: Governance, population and territoriality*. Master’s dissertation, Exeter University Genomics in Society programme.

<sup>17</sup> Ernesto Schwartz interview with Gerardo Jimenez-Sanchez, Director General and co-founder of the INMEGEN. August 21, 2008. With author’s permission, cited from Schwartz, E. (2008). *Genomic sovereignty and the creation of the INMEGEN: Governance, population and territoriality*. Master’s dissertation, Exeter University Genomics in Society programme.

<sup>18</sup> See Mudur (2008). Retrieved April 3, 2009 from [http://www.telegraphindia.com/1080425/jsp/frontpage/story\\_9186161.jsp](http://www.telegraphindia.com/1080425/jsp/frontpage/story_9186161.jsp).

coordinator, Mitali Mukerjee, explains that researchers “had intense debates on whether to reveal the names of communities. . . I don’t think scientists are prepared yet to understand the full social ramifications if such information is made public.”<sup>19</sup>

Despite the ambivalence expressed about the findings, and as evidence of a particular history of nationalist rhetoric in India that champions internal diversity, the genome project director Samir Brahmachari commented that, “In fact the term ‘Indian’ is a misnomer in population genetic studies, as it indicates the population to be homogenous. This is evidently now untrue.”<sup>20</sup> Unlike the insistence by the head of the Mexico’s Institute that the country’s indigenous populations are “Mexican”, Brahmachari is eager to *denaturalize* the nation-state and admit the ways in which social groupings do not calibrate with scientifically-produced groupings.

Even so, the Indian Genome director’s rhetoric should not be viewed as a straightforward exercise in denaturalizing national identity with genomics. Rather, it draws upon and strategically deploys historical tensions implicit to Indian nationalism. This is a nationalism that one prominent commentator refers to as a “rare animal. . . the nationalism of an idea—rooted in the spirit of diversity.”<sup>21</sup> This contrasts Mexican nationalism which is rooted in hybridity (not diversity) and celebrates the *merging together* of European, Amerindian, and African lineages, embodied in the ‘Mestizo’. But as Mexican scholars and activists critical of the genome project assert, “A project attempting to prove that there is a ‘mestizo genome’ will fail if it pretends to correlate race and disease. Mestizo is a label, not a race.”<sup>22</sup> Albeit through different conceptions of heterogeneity, both national genomic initiatives marshal already existing national discourses about biological and cultural affinity in their quest to genetically map variation and link these differences to disease risk. In so doing, they must contend with the ways in which linking genetic and social groupings become politically controversial.

### 3.2. Drug marketing and genetic proxies

The second dilemma that genomic sovereignty policies face is the way in which ethnic diasporas and indigenous nationals potentially undercut the biological brand of national HapMaps, with both economic and political ramifications. As mentioned previously, during the second phase (2005–2007) of the U.S. led International HapMap project, samples were collected from seven populations, among which were several diasporic populations including “Mexican Americans in Los Angeles” and “Guajarati Indians in Houston.” As anthropologists working with the Guajarati population in Houston explain, part of the appeal in targeting them was their relative compliance to the sampling protocol (Reddy, 2007). They and other diasporic populations serve as a convenient way to sidestep national sovereignty restrictions at both sampling and drug testing stages of genomic research. Ignoring or downplaying the existence of the International HapMap database, both Indian and Mexican genome institute spokesmen frame their own initiatives as providing a unique genomic map of its national population.

Genomic sovereignty policies are intended to protect against foreign companies producing therapeutics targeting their population without their involvement. To the extent that such policies only have national reach, however, they are unable to assert sovereignty claims over the millions of Indians and Mexicans who were either born or live outside of their ancestral country and are free to donate their DNA to foreign researchers or, in the future, participate in genome-based clinical trials. To begin to understand the economic implications, consider that PricewaterhouseCoopers (PwC) estimates that “the number of diabetes sufferers in India is projected to reach 73.5 million in 2025, with the direct cost of treating each individual at about \$420 per person per year.” PwC predicts that “if these costs remain the same, India’s total bill for diabetes alone

<sup>19</sup> Mudur, G. S. (2008, April 24). Stamp on Tagore’s India Genetic map blurs lines. *The Telegraph*. Retrieved April 3, 2009 from [http://www.telegraphindia.com/1080425/jsp/frontpage/story\\_9186161.jsp](http://www.telegraphindia.com/1080425/jsp/frontpage/story_9186161.jsp). Note: In the end, researchers did make the discord between genetic and socio-political classifications public; the effects of this on long-term identity politics, however, are unclear, and are the focus of the author’s long-term project.

<sup>20</sup> Cited from Koshy, Jacob P. Indian gene map links ethnic groups, diseases. Retrieved March 27, 2009 from <http://www.livemint.com/2008/04/26000244/Indian-gene-map-links-ethnic-g.html>.

<sup>21</sup> Tharoor, S. (2007, May 5). Mapping a nation: Pluralism at 60. *Outlook India*. Retrieved April 3, 2009 from <http://business.outlookindia.com/inner.aspx?articleid=332&subcatid=175&editionid=9&catid=1>.

<sup>22</sup> Interview with Leon Olive, bioethicist at Mexico’s National Autonomous University, cited from Mothelet (2008).

would be about \$30 billion by 2025.”<sup>23</sup> In this context, diasporic populations provide genome researchers and drug developers in the U.S. a way around difficult regulatory conditions by serving as genetic proxies for ‘emerging markets’.

Given what is a potential challenge to the authority and self-determination of postcolonial genomics, proponents of the latter have directly and indirectly attempted to address this dilemma posed by diasporic populations: Some suggest that studying ethnic groups living in the United States may contain some valuable information in terms of genetic susceptibilities and drug responses needed for the development of targeting medicine in other countries, but that they are not “adequate to satisfy the needs for harnessing global genetic diversity” (Daar & Singer, 2005: 243). More specifically, Mexican officials describe their work as “the first genome-wide genotyping effort of a recently admixed Latin American population in the public domain” (Jimenez-Sanchez et al., 2008: 1195). The implication is that there is a genetically meaningful distinction between Mexicans and Mexican Americans, such that the International HapMap sample collected in Los Angeles cannot stand in for the Mexican database.

At the same time that it naturalizes the nation-state, the Mexican Institute routinely reminds the public that their work has important implications beyond Mexico, serving as a portal to mestizo populations throughout Latin America. In terms of market share, this is a tremendously powerful position, one worth defending against diasporic proxies that are more accessible to genomic researchers in North America.

A second, related way in which genomic sovereignty proponents challenge the use of diasporic proxies is by claiming that samples obtained in their national initiatives are unique and more representative. But not simply because they happen to be taken from the right side of the border, but because of substantial differences in the *environments* experienced by diasporic (Montoya, 2007) versus national populations. These environmental exposures are thought to impact gene expression leading to different disease susceptibilities and drug responses, so that a database created using Mexican American and Indian American samples cannot be used to develop pharmacogenomic therapies for Mexicans or Indians in the home country.

It is important to note that in these responses to the dilemma posed by ethnic diasporas, genomic sovereignty proponents engage in what sociologist Charis Thompson refers to as ‘strategic naturalization’ (2001). This explains how people up- or downplay biological explanations when it suits them. In the context of genomic sovereignty claims, Mexican genome spokesmen make an implicit distinction between ‘national’ versus ‘diasporic’ samples and at the same time claim to be a portal to Latin America’s entire mestizo population, first naturalizing and then denaturalizing the nation-state border. Similarly in the second response, the diasporic population is not considered unrepresentative of the nation because of the different environments and their possible effects on gene expression. This suggests that Mexicans north and south of the U.S.-Mexico border may not be genetically commensurable, but that their biological distinction is in response to different environmental exposures, and is thus mutable. This line of argument is neither genetic- nor environmental-determinism, but a strategic deployment of both biological and social idioms to maximize Mexico’s gatekeeping authority over a potentially valuable ‘mestizo genome’.

Groups that lay claim to an *indigenous* status within a territory are another set of biopolitically rogue populations that challenge the legitimacy of genomic sovereignty claims. They do so, not by opposing scientific research as a whole, but by asserting that the fruits of genomics will not be distributed evenly or in accordance with the levels of investment that indigenous communities are being asked to participate. The dominant framing of ‘indigenous interests’ vis-à-vis genomics has typically opposes Western science as a whole, and is exemplified by the Indigenous People’s Council on Biocolonialism.<sup>24</sup> Unlike the sovereignty claims of the Council that seek to protect *against* sampling indigenous blood, the genomic sovereignty initiatives implemented by postcolonial governments, utilize indigenous populations *for* the development of national health and economic development. But, in part, because of the widespread circulation of the ‘biocolonial’ framing of genomics, genomic sovereignty advocates must often make a great effort to recruit antagonistic or indifferent indigenous communities.

In Mexico, for example, town hall-style meetings were held throughout the country several weeks prior to any blood collections, during which researchers from the Genome Institute made presentations and engaged in Q&A with

<sup>23</sup> “The Emerging Seven: Pharma’s Promised Land”. Retrieved April 6, 2009 from <http://www.pharmaceutical-technology.com/features/feature48666/>.

<sup>24</sup> This is a pan-indigenous organization that “is organized to assist indigenous peoples in the protection of their genetic resources, indigenous knowledge, cultural and human rights from the negative effects of biotechnology”. Indigenous Peoples Council on Biocolonialism. Retrieved April 6, 2009 from <http://www.ipcb.org>.

those gathered. This model of ‘community engagement’ is a source of pride on the part of the Institute, but was not allowed it to fully avoid critique by advocates of indigenous groups. For example, spokesperson for the Mexican chapter of the NGO Erosion, Technology and Concentration, Silvia Ribeiro, expresses the following suspicion:

I do not know what they mean with genomic sovereignty, but evidently what there is, is an interest by great corporations that have made consortiums with public research institutes around the world. But the results are privatized. . . My argument is for them to demonstrate that this has a public benefit. If what they call public benefit is for people to go and pay for a new medication that is not democratic [ . . . ] The genes are indigenous and the results are all transnational! (Schwartz, 2008)

So paradoxically, while the Western/non-Western dichotomy cannot be easily marshaled to criticize postcolonial genomics, proponents of the latter are still faced with the issue of ongoing national stratification in which indigenous populations and other ethnic minorities are asked to enroll as DNA donors but have limited access to biomedical interventions due to socio-economic barriers. Thus, critics of national genomic projects may utilize the everyday subordination of indigenous groups to voice suspicion towards the goals and implications of these initiatives. In Mexico, for example, the contradiction between the nation’s sacralization of its indigenous roots and everyday denigration of indigenous communities (Lund, 2006: 67)—is reinforced and complicated through the biopolitics of national genomics. More broadly, neocolonial relations of domination within countries undercut the rhetoric of national scientific empowerment that will uplift the *entire* population.

#### 4. Conclusion

In closing, the dilemmas of mapping and marketing national diversity reveal the difficulties in trying to calibrate different modes of human classification within a single biopolitical project. I demonstrate that an assertion, not defiance, of nation-state borders is the scaffold upon which knowledge and wealth is being pursued in the arena of postcolonial genomics. Furthermore, national diversity is not simply mapped by genomics, but recalibrated vis-à-vis genomic findings in attempts to genetically brand the nation as a niche ethnic market with minimal political fallout. What may, on the surface, appear to be a (re)biologization of the nation-state in the branding of “Mexican DNA” and “Indian DNA” among others, is better understood as a *strategic calibration* of different modes of classifying populations—as socio-political or biological entities—whose value is constantly mediated in the context of specific scientific, political, and economic institutions.

#### Acknowledgements

This research was supported by grant number 1R56AI072549 from the National Institutes of Health. I am grateful to UCLA’s Center for Society & Genetics for supporting this work, and to the comments of two anonymous reviewers, Catherine Bliss, Soraya de Chaderevian, Troy Duster, Amy Hinterberger, Michael Mintrom, Aaron Panofsky, Tom Pessah, Anne Pollock, Charles Taylor, Stefan Timmermans, and *Universidad Nacional Autonoma de Mexico* colleagues Carlos Lopez-Beltran, Edna Suarez-Diaz, Francisco Vergara-Silva, and Ernesto Schwartz.

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