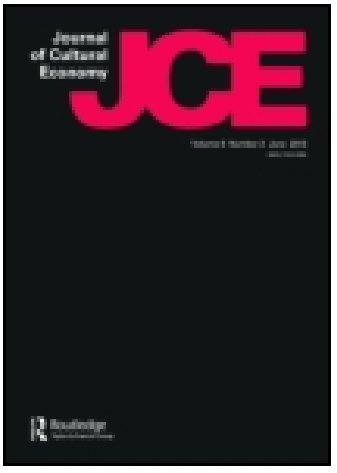

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Why Singapore Trumps Iceland

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WHY SINGAPORE TRUMPS ICELAND
Gathering genes in the wild

Aihwa Ong

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The article explores how a National Institute of Health policy of racialization-as-inclusion in research informs the building of Asian DNA databases at Biopolis, an emerging biomedical hub in Singapore. Citing variability in DNA and populations in the Asian region, Singaporean biostatisticians challenge DeCode Genetics of Iceland as an exemplary model of genomic research. They claim that genetic traits among populations in Asia that are relatively new to medical genomics – and being gathered 'in the wild' – gain value from being calculated and databased. The infrastructure deploys the ethnic heuristic in different registers. First, the network of ethnicity becomes a supple membrane coextensive with the network of genetic data points. Second, ethnicity is rendered an immutable mobile that circulates databases beyond tiny Singapore, making the infrastructure at once situated, flexible, and expansive. Third, the ethnic signifier carries affective value that enhances a sense of what is at stake in the building, mobilization and implications of such Asian databases. In short, the origami-like folding together of multiple, flowable, and perfomative data points shapes a unilateral topological space of biomedical 'Asia.'

KEYWORDS: Biopolis; Singapore; genetic variability; ethnic heuristic; performative database

Things that Hold

Over the past decade, I explored DNA research in a biomedical frontier in Singapore called Biopolis. In 2010, I met Dr Yang, a tall Singaporean whose vivacious personality belied the nerdy image of a biostatistician. He welcomed me in the manner of the bright young scientist on the cusp of something big. During his stint in the Singapore army, a requirement of all able-bodied male Singaporeans, with the unit of defense science, Dr Yang became interested in 'how genetics affect traits in Singapore.' For instance, he said, '99% of the Chinese here are myopic. Obesity (among ethnic Chinese and Malays) and diabetes (high rates among ethnic Indians) are the foci of defense science in the island-state.' The biosecurity picture he referred to conjures the island as differentiated pools of genetic material and vulnerability. After his army service, Yang returned to Oxford University to work on a doctorate in biostatistics, when he was awarded a Wellcome Trust grant. Yang described this still emerging field of biostatistics thusly: 'There has been a logical progression in biology, physics, and chemistry from observation to math science. We deal with data quantitatively rather than deterministically, that is the interaction of genes and environment. When risks are found, people will manage their health better.'[1]

Yang and his colleagues are incubating a new kind of biological science originating in the West. They use genome-wide association studies (GWAS) to scan complete sets of DNA of people in order to develop probability profiles of associations between ethnic

groups and a disease under study. Studies also link data on genes and the lifestyle of large samples of ethnic groups in order to find statistical patterns of risk for certain diseases such as type 2 diabetes. Statistical studies also try to find differences between ethnic populations in responses to medicine. Big data designed for probability studies in health risks have become a growing part of national administration in Singapore.

Statistical reasoning, it has been argued, is central to modern nation-state formation. Two mathematical techniques – the probability calculus and the 'stable' object to be measured – are involved in Singapore's genomic project of producing biomedical data for managing health risks. First, it has been argued that national governments depend on mathematical techniques as the basis of rational decisions for mastering uncertainty (Desrosieres 1998; Hacking 2006). Michel Foucault (2007) observes that the pervasive calculation of biological events – morbidity, mortality, and risk – is vital to the biopolitics of security or biosecurity. Power over life is continually reorganized, and the interplay of different statistical normalities in human society permits the evaluation of probabilities of collective risk. Genomic science is an extension of the statistics of normalities and probabilities of risk at the molecular level.

Second, Alan Desrosieres (1998) notes that mathematical reasoning depends on the measurement of 'things that have a stable meaning, allowing comparisons to be made and equivalences to be established' across the national space (pp. 6, 9). As Yang's quote above disclosed, things that hold in Singapore genomics are not only identifiable health risks, but also ethnic categories central to administrative practices in many Asian countries. As we shall see, the historical legacy of British colonial rule includes not only statistical science but also Anglophone racial and ethnic categories that have stable meanings across national borders in postcolonial Asia. Because they can escape their national contexts, Asian racial categories have become heuristic devices of comparative value in the work of universalizing situated genomic science.

Racialization of DNA in Different Sites

The Human Genome Project, completed in 2003, drew on the genes of a few individuals to map a 'universal' human genome, one that does not exist in the body of any specific person. US-based scientists were interested in representing humanity in general, albeit dominated by genes from the maverick scientist-entrepreneur J. Craig Venter, whose company Celera Genomics (now Synthetic Genomics) had launched the sequencing of the human genome in 1998, but decided to join forces with the National Institute of Health (NIH) endeavor. The joint efforts of Celera and the NIH came together in the version of the Human Genome Project that was presented to the world.

Paradoxically, this model of generalized, deracinated genomic vision of humanity seems to challenge an earlier NIH policy that promotes the racialization of human genomes.

In 1993, the NIH Revitalization Act established guidelines for 'the inclusion of women and minorities as subjects in clinical research.'[2] In contrast to the Human Genome Project, the NIH's earlier racialization-as-inclusion is part of some attempt at social justice or more representative data. In the USA, progressive scholars did not seem to have any issue with the universalized model of the human genome, but they did with the policy racializing human genomes. Social scientists have railed against the racial marking of genetic risks or biomarkers because of possible stigmatizing effects on minority subjects. However,

medical anthropologists Margaret Lock and Vinh-Kim Nguyen cautioned that the NIH used self-identifications of gender, race, ethnicity, or the preferred term 'ancestry,' not as discrete categories but 'as heuristic devices for studying the frequency of specific genetic traits' in at risk groups (2010, p. 353). The quest to racialize human genetic fingerprints is the latest instance of how the biological sciences are increasingly engaged in the digital project of 'making up people' (Hacking 2006).

Human genomics is thus simultaneously a universalizing and a particularizing technology, conjuring differences against the backdrop of a shared 'human' genome.[3]

Across human individuals and groups, our DNA is 99.9% the same, and only 0.1% of the human genome accounts for tiny differences. In the course of human adaptation to the environment, gene–culture interactions engender microevolution at the cellular level.

Fluctuations in gene frequency and genetic drift stimulated genetic variation in anatomy and physiology, including differences in hair, skin, and eye color, as well as variable susceptibility to disease. In modern times, such genetic variants have frequently been culturally identified as 'racial' differences. In order to find such genetic variants or mutations, researchers often identify racial or ethnic communities as differentiated groups to be scanned.

Because the human genome project was initially limited to sequencing DNA from four regional groups, it set off a race to study human genetic variations across the world.

Pharmacogenomics quickly became a global growth industry and created huge demands for high volumes of data on genetic defects associated with deadly diseases for which drug companies seek to develop new therapies. For the Biopolis complex, the generation of new DNA data aggregated by Asian races/ethnicities was a strategic response to carve out a global niche for pharmaceutical research. Thus, the NIH research practice of racialization-as-inclusion migrated to Singapore, but here the races/ethnicities included are not minorities but majorities in an emerging global region.

An American scientist working at Biopolis noted, 'Most genomics research has been done on Caucasians based in Europe or the US and we are only just starting to understand about how applicable these findings are to worldwide or Asian populations.'[4] Capitalizing on raced genomics shaped by US law, geneticists in Singapore are studying genetic diversity among minority and majority populations in Asia, in a different project of racial inclusion and social justice, as well as a different relationship between the state and its citizenry. From the vantage point of the island, there is a range of potential values that can be generated from integrating race/ethnicity as codes in the DNA software. In the process of mapping DNA-Asian ethnicities, 'Asia' as a category has mutated into a series of genetic codes as well as a mutating territory of biomedical governance. Science practices in Singapore, I argue, exploit and reveal the comparative advantages between different kinds of DNA variants, between different kinds of ethnic-correlated database, and between DNA from different geographies.

Today, racialized genomes or 'the molecularization of race' is at the cutting edge of personalized medicine, where race or ethnicity becomes a 'barcode' for gauging genetic susceptibilities. Because the sequencing of human genomes has barely begun in Asia, the hunt is on in Singapore to map human genes as they occur 'in nature.'[5] From the vantage point of the island, there is a range of potential values that can be generated from combining genetic and racial variables. The state is not only the venture capitalist of biomedical science, but a biopolitical guarantor of medical services and an organizer of samples that correspond to the multiethnic citizenry. Dr Yang, our enthusiastic biostatistician, is a leader of the Singapore Genome Variation Project, one of the many multiracial databases assembled in the island-nation.

The anthropology scholarship on race and genomic science has made powerful arguments that situated national histories and politics have given particular cultural and institutional forms to Euro-American DNA projects (e.g. Kay 1993; Rabinow 2002; Jasanoff 2007; Rheinberger 2010). In particular, Iceland and deCode Genetics, the company with exclusive rights to develop a comprehensive database on Icelanders, were hailed for the quality of medical records and the sense of civic virtue that informed collaborations among the state and the academy. In their study, Gisli Palsson and Paul Rabinow (2005) suggest that 'Just as India is the official site for caste, Iceland is emerging as *the* site of biotech and bioethics' (italics in the original, p. 92). But in the decade since, as genomic science spreads unevenly across the postcolonial world, triumphant European models of genomics are less likely than once thought. As assemblage concept has indicated, historical conjunctures and global flows crystallize diverse contexts of scientific experimentation that fold universalizing science into situated systems of meanings and practices (Collier & Ong 2005; Rheinberger 2010, p. 10).

Given its situated conditions of emergence, genomic science, I maintain, exploits and reveals the comparative advantages between different kinds of DNA variants, between different racial objects, and between DNA from different geographies. In postcolonial configurations, race carries different meanings depending on history, politics, and national identity. For instance, the building of a digital genomic database in Mexico emphasizes mestizo or mixed race, in acknowledgment of interwoven histories of different populations, as a symbol of nationalist identity (Wade, Beltran, Restrepo, and Santos, 2014). By contrast, British colonial legacy in Singapore produced a model of multiracialism with essentialist notions of native (Malay-Muslim) and immigrant communities (Chinese, Indians, and others). With the advent of genomic science in Singapore, different racial categories that can also indicate majority races in Asia are wielded as a device to brand Asian genomic science.

This article argues that genetic traits among populations in Asia that were, up until recently, relatively new to medical genomics – and thus 'in the wild' – gain value from being calculated and databased. First, the Singapore case is interesting for making clear the comparative advantage of geopolitical location in a multiracial region where genomic science is relatively novel. I will discuss why Singapore's scientists claim that the heterogeneity of their DNA database has more marketable value than homogeneous ones in Europe. While the ethnic heuristic in the Icelandic database promotes DNA homogeneity, the Singaporean database celebrates Asia-wide DNA diversity. Second, beyond its competitive purposes, DNA-ethnic information helps Asian countries to corral their biological resources and shape a field in the genetics of 'Asian diseases.' Third, the ethnic accrual of data value is further realized through the deployment of ethnicity as an immutable mobile (Latour 1985) that is accumulative of diverse peoples and places. A range of techniques that generate distinctiveness in Asian genetics can respond to the question, 'How can the mapping of DNA variants in an island gather up, as it were, an entire continent'?

Genes in the Wild

Gilles Deleuze maintains that the dice throw of modern knowledge seeks to clarify the chaos of nature by discovering originary difference and repetition (Deleuze [1994] 1969, pp. 199–200).

In building a database, a Deleuzian movement of difference and repetition seems to animate the bipolar rationality of value creation that sustains the relationship between

risk-probability and risk-potentiality. Thus, difference in risk/DNA/ethnicity played on multiple levels of repetition engenders productivity via flexibility in the representative powers of Asian databases. The neoliberal hunt for DNA in Singapore intervenes into the relatively unmapped human biological resources in Asia, and in the process, designs a flexible, performative knowledge system in which the signifier risk/ethnicity is folded into the mapping of the signified DNA/mutation.

Modern knowledge captures, calculates, and invests in the multiple, variable, and unpredictable flows of things in the world. Thus, to discover unknown DNA variants, scientists need to look at genes 'in nature', or 'in the wild,' or in places still outside the realm of calculations. In biostatistical research, the axis of comparison is between the normal and the wild. This 'wildness' is less a place than a condition of the genomes of populations that is nonstandard for being outside normative databases. Because databases are by definition comparative, the uncatalogued genomic diversity of populations in Asia can be made to yield new information that challenges the normativity of existing databases elsewhere.

By databasing DNA in a scientific frontier, scientists in Singapore hope to achieve a comparative advantage over already existing Euro-American genetic databases that have been dominant in the worlds of science and pharmaceutical research and development. Thus, 'in the wild' does not only mean outside the lab, or not databased, in general, it also means outside Western databases, even if the genes from Asian peoples are also increasingly databased. By finding genes 'in the wild,' scientists map into existence a new biomedical resource with its own genetic databases, probability measures, and market potentials. Researchers building a new DNA database capitalize on potentially productive correlations of genetic and social variables.

A novel DNA database is thus a technology of potentiality, one capable not only of producing novel research values for drug discovery, but also of absorbing affective values surrounding 'our bodies, ourselves' in racial, ethnic, geographic, or disease terms. By choosing to correlate 'ethnicity' or 'race' with genetic variation, researchers in Singapore unleash the productive potential of a distinctive ethnic-diversified database that through the use of flexible scales can represent various groups across a vast terrain. Here is a design platform for 'genome geography' (Fujimura & Rajagopalan 2011) that deploys elastic notions of ethnicity and scale.

Anthropologist Christopher Kelty observes that information technologies do not merely connect existing groups; 'they generate the conditions of possibility for new collectivities – maybe even new kinds of collectivity' (2012, p. 2). Similarly, I maintain that Singapore's ethnic-DNA aggregation produces novel biomedical collectivities that are ethnic-associated, such as 'Malay' or 'Indian' or 'Chinese.' In addition, the ethnic variable DNA data generates new forms of difference within and between biomedical collectivities that are defined, sampled, and analyzed. In turn, the designation of ethnic-correlated biomedical collectivities also engenders novel notions of ethnicity, linking, for instance, 'Indians' in Singapore with 'Indians' elsewhere. Such ethnic variable DNA objects have, in the words of sociologist Bruno Latour, 'the properties of being mobile but also immutable, presentable, readable and combinable with one another' (1985, p. 6).

An ethnic-DNA correlated database is coded to and implicitly indexical of broad racial-national categories that stretch over a broad and dispersed swath of 'Asia.'

The accumulative repetitions of the ethnic categories in medical records and databases make them both immutable and mobile. Through reference to shared co-

ethnicity that stretches across merely political borders, an ethnic-specified DNA database can bring dispersed populations together. Such a biostatistical model is offered as a concentration and condensation of populations that comprise a wide swath of 'Asian' genomes, thus providing a new biomedical resource with regional reach. By thus correlating scientific and social variables and deploying their numbers, figures, and scales, Singapore scientists have designed a DNA matrix that gathers up a heterogeneous continent in this tiny island. Let us see how it happens.

'Gather Up as Much information as You Can'

Dr Williams, a scientist who grew up in the New York metropolitan area, still seemed slightly displaced in tropical Singapore. In April, 2010, Williams talked excitedly about Singapore's 'electronic research habitat.'[6] Invoking Venter, Dr Williams remarked, that the new method in biology is to 'gather up as much information as you can; there are no a-priori right and wrong answers.' Computational technology is producing a new way of seeing more and differently that does not rely on a moral axis of 'normal' or 'abnormal' (Canguilhem 1989). Rather, the significant principle is between what is already known and what is still unknown. The goal of genomic sequencing is to unravel such information so that 'we can come up with better interventions to sustain life.'

'Modern biology,' Williams explained, 'is all about automated machines churning out huge amounts of data, which then have to be stored, analyzed, and visualized. … Digital computing is the servant of non-digital, brain-based computing.' In other words, genomic research seeks to bring order to huge amounts of informaticized DNA, establishing ethnic-risk–disease associations as a predictive tool or diagnostic screen that help researchers to study cellular processes like gene function and metabolism. The quest is to find predictive 'biomarkers' that links genetic defects to ethnic differences, disease susceptibilities, and prognosis. Computer readouts of genetic variants flag genetic susceptibility and ethnic association with a specific disease, helping clinicians decide on a potentially effective match of a patient with a particular drug. Genetic data are not a cure, but a strategy of disease diagnostics that works closely with molecular research. Big genomic data are foundational to experiments that put into play a synergy between DNA defects and disease pathways, computer labs and wet labs, and biostatisticians and biologists, i.e. an integrative science that is under way in Singapore's modeling of a genomic 'paradigm shift.'

The novel racial genomics practiced in Asia are the sinews of the biomedical war globally, Williams remarked. However, Singapore's model of President Nixon's 'war on cancer'[7] is differently fought through the risk-potentiality and ethical value of Asian bodies. Williams's role was to set up a computational grid for comparative genomics that draws on the DNA diversity of samples in and through Singapore. This is done by mobilizing and combining data on population genomics and medical genomics, all organized along ethnic lines. In the next decade, electronic medical records in the island's public hospitals will be made available for data mining to foster medical research. This integration of a hardware and software infrastructure is to manage digital storage and flows between the islands and other places in Asia. In authoritarian Singapore, this hybrid computational architecture enhances conditions for work experience as well as satisfies regulatory and legal requirements. In a report, Williams predicts that this 'secure, scalable

and robust' genomics enterprise is part of the strategic building of Singapore's knowledge economy (Mitchell et al., 2008).

The nature of Singapore's data, which is to say the nature of its population and the cataloging of its alluringly scalable genome, is thus central in elaborating the comparative advantage of Singaporean science. As a center of reputable science, the strategic mix of DNA heterogeneity and authoritarian politics gives Singapore leverage as a potential biobank for much of Asia. I next examine these claims in greater detail, shifting from a focus on the assembling of digital DNA data, to an investigation of why researchers think their genomic enterprise has more value than those in Europe.

Why Singapore Trumps Iceland

At the turn of the century, there were a few genomic institutions or companies, and they represented only a small range of human genetic differences in the world. The Hapmap is a haplotype catalog of variant genes that provides a shortcut to the inheritance patterns of DNA mutations. In a follow-up to the human genome project, the Hapmap has expanded its analysis of the genomes of people from 4 to 11 groups,[8] but, as Singaporean researchers noted, it covers only 5% of the world's population. They also pointed out that Iceland's deCODE Genetics is a company focused on disease gene mapping of only Caucasian populations. By contrast, in 2009, Biopolis led a 14 country-initiative to collect genetic variants (single nucleotide polymorphisms) under the umbrella of the Pan-Asian SNPS consortium. This Asia-wide database, Dr Yang remarked, 'is a great improvement' over the Hapmap and deCODE, because Asia [*and* Africa] are 'where the rare variants are.' As the development of pharmaceuticals shifts beyond the North Atlantic world, human DNA diversity data are a crucial resource. Scientists at Biopolis positioned themselves in the lead because Asian genetic variants are more valuable to Asian scientists creating a new frontier in the new genomics and to drug companies developing new drugs and new markets in the populous region.

Singapore scientists therefore found it ironic that when deCODE Genetics made its initial public offering on NASDAQ, it sold itself on the genetic homogeneity of its database. Anthropologist Michael Fortun (2008) reports that to set deCODE apart from the rest of the genomic companies, the company had to convince American investors that 'there's money to be made from Iceland's genetic purity.' But SmartMoney.com, raised objections, in an inimitable New Yorker lingo, 'OK, it may be true that Icelanders don't all look alike. But that doesn't mean you'd pick Reykjavik as the setting for a documentary called 'People of Color,' either' (232). American investors were already apprised of the need to have genetic variability in databases. In the brutal pharma markets, what were formerly selling points for deCODE's scientific acumen and justificatory appeals to its ethicality were now mere problems for business modeling.

In that global race, the richness of the data, the ethics of its management, and global marketability are all in play. While deCODE Genetics is narrowly focused on a few Caucasian groups, the Singapore database boasts representation of the three major Asian races. Besides, the Singaporean assertion would be that not only do they have a more variable and therefore marketable ethno-genomic research science, they also have their own version of genomic ethics conditioned by concerns of collective rather than individual proprietary interests.

Besides its overly homogenous data, Yang observed, deCODE is 'too upstream' in its data formation to be competitive for biotech investors. Another limitation was the propriety controls Icelandic citizens retain over their records, which limit diverse uses of medical data. In sum, where the homogeneity of Iceland's population's value depended on the creation of a data-set defined by its internal consistency, Singaporean and Asian scientists argue precisely the opposite: that homogeneity is not an asset but an impediment to robust data, and that the heterogeneous composition of Singapore's multiple ethnic-genetic pools is generative of its values, present and future.

But the Singapore–Iceland competition also reveals the volatility of 'value' in genomic business and how ethical, business, and promissory health values can converge and diverge in a fluid biomedical world. Despite its emphasis on ethical standards reflecting European value of freedom and privacy, deCODE Iceland floundered in the unruly markets for drug development. Meanwhile the kind of triumph of 'value' in diversity that Singaporean scientists extol also points to the elusiveness of the anticipated creation of conjoined health, pharmaceutical, capitalist, and social values that promise to manage uncertainties in capitalist, health, and political futures. But Singaporean scientists like to think that they are thinking ahead by designing technologies that transform the promissory quality of genomic research and the market that sustains it into shared interests and fate for a region. This would require the genomic production of values that speak to the identity and imagination of being 'Asian.'

The Right to Know 'Asian Diseases'

Besides correlating ethnic-genetic variability, scientists in Singapore also correlate ethnic-risk profiles for major diseases. Biostatisticians produce 'GWAS' that link ethnic/racial differences to disease susceptibility, thus anticipating a value-magnifying effect from using the ethnic heuristic. This is yet another way medical databases make Asian DNA 'more valuable,' not just by correlating Asian ethnicities to genetic variants and disease development, but also in giving scientists in Asia knowledge of serious illnesses that menace populations in their midst.

Dr Lee, a population geneticist trained in the USA, noted that Human Genome Organization was tracking human DNA resources worldwide, but Asian scientists should control genetic knowledge in and of Asia. In her view, we were in a 'new era now as social and economic aspects previously ignored have come into play. There were also legal implications of our capacity to predict illnesses that may not yet be visible.'[9] She thus posed political questions about who should or would own genetic knowledge of Asian peoples and thus come to control the customized medicine that develops from it. The main issue for her was the Western capture and design of biomedical knowledge, and how it serves to potentially exacerbate existing geopolitical differences in a situation where 'ethnic' differences are bandaged over deep political wounds.

She mentioned a controversy surrounding international collaborations on genetic research in China in the late 1990s. The Chinese media mentioned 'gene war,' and some Chinese scientists expressed concern that foreign involvement could lead to 'misuse' of Chinese DNA and called for a ban on exporting samples (Guo sun-wei 1997). Dr Lee noted that some Chinese thought that foreign access to 'indigenous samples engendered fears that the groups may be portrayed as genetically weak.' Such concerns about 'external' exploitation of Asian DNA underscored her insistence that scientists in Asia should control

the ethnic categories (denoting broad geographic ancestry and sociocultural features) that track the contribution of genetic factors to phenotypic variations.[10] Dr Lee phrased it this way: 'Who has the right to know? The Asian context is different from the West: we do consultations about such issues.' Authorized experts have to oversee the governance of such potentially explosive information about 'groups' (self-identified race or continental ancestry) and their gene identification that is the driving force in drug discovery. The National University of Singapore, where she was employed, was committed to developing biomedical knowledge that responds directly to diseases that affect populations of Asian ancestries.

Indeed, the emphasis on continental ancestry and biogeography in genetic research also contributes to a discourse of 'Asian diseases' in Singapore medical circles. Doctors point to for instance the prevalence of fibrosis and meningitis among whites and their absence in Singapore. Western patterns of cancer (e.g. prostate cancer), heart disease, and other common diseases have different profiles than in Asia. Furthermore, Asian populations display markedly different reactions to drugs than Western ones. Scientists in Singapore often reel off frightening figures of major diseases that disproportionately affect people in Asia. The continent, they pointed out, has the world's highest incidence of stomach cancer, lung cancer, hepatitis B, and infectious diseases. China alone has the highest rates of fatality from gastric, liver, and esophageal cancers, and over 70% of people under 40 years of age are infected by hepatitis B (Wang & Rockoff 2010). Nasal and throat cancer is prevalent among Southern Chinese. Because 60% of the causes can be traced to genetic factors, the disease is dubbed Canto(nese) cancer.[11] The focus is on the gene–environment interactions that cause high rates of prevalence, with doctors differing on which element is playing a bigger role. The general goal in labs is to pinpoint 'unique ethnic genotypes' in order to strengthen defenses against 'Asian diseases.'

Clearly, as cells derived from different ethnic groups are brought under the microscope, the term 'Asian' itself is becoming very elastic, referring, depending on context, to the genetic heterogeneity of the three major ethnicities, as a proxy for the most frequently selected group, 'Southern Chinese,' or the ecosystem that breeds conditions of possibility for a cluster of targeted diseases. While there is wide recognition that ethnicity has to do with self-identification and cultural practice, there is also a working assumption that genetic and environmental factors are firmly linked, such as ethnic Chinese with zoonotic zones in South China. The convergence of codes for DNA, ethnicity, and ancestral environments produces a mobile set of connections of scientific signification.

This mobilization around Asian diseases and genotypes is catalyzed as well by the changing global drug market, and the strategic positioning of multiracial Singapore as a research platform for all of Asia, both as a hub of biomedical expertise and data, and as a scalable genetic microcosm of the vast continent's populations. Because of aging populations, aging drugs, and rising costs of drug development in the West, the moment is ripe for growth of health markets in Asia.[12] Even though new drugs for diseases prevalent in the region are still many years away, I was told, Singapore is making a head start by assembling DNA information that create potential values beyond the island. Singapore's demographic diversity is thus offered as a pool of genetic assets in an experimental infrastructure concerned with variation over homogeneity.

As Yang noted, 'Our leverage is the multiethnic demography and the way we combine genetics sciences and traditional epidemiology.' His genome variation project is

based on assays of two million genomes in three Asian ethnic groups. DNA research benefits from Singapore's detailed medical records for at least three major ethnic groups that have long been used for teaching and research purposes on different conditions affecting each population. Doctors I spoke to regularly point out disease profiles according to ethnic breakdowns in Singapore. The high incidence of nasal cancer among ethnic Chinese has been linked to their greater susceptibility to severe acute respiratory syndrome (SARS). Ethnic Indians (mainly Tamils and Sikhs) are considered especially vulnerable to heart diseases and Muslims to obesity and diabetes. And, at a collective level, a doctor claimed, 'Hepatitis B is an Asian disease.'[13] Chinese, Indian, and Malays are considered genetically susceptible to Hepatitis B and hepatitis-linked cancer. These are all diseases and viruses that are potentially lucrative areas of research by scientists based in Singapore and likely to attract investments from drug companies. Such genome-wide scans of comparative ethnic groups are thus configuring tropical Asia as a distinct zone of bioinformatics and biostatistics, pharmaco-genomics, regenerative medicine, and newly infectious diseases, and thus as a global region of biomedical innovation.

Barcoding Ethnicity

As an anthropologist, I wondered whether in the attempt to come up with a general ethnic profile of risks, individual racial differences are washed over? I was therefore disconcerted when Dr Wu, a bespectacled, gray-haired, but youthful-looking geneticist, argued for a 'barcode' vision of ethnicity. He brushed aside my worries about the mapping of cultural and social categories onto cellular material as irrational and obstructionist in the urgent task of pursuing cures for Asians. It was routine, he said, for donors and patients to self-identify their ethnicity. Given the well-documented lives of Singaporeans, I suspected that researchers often used a mix of personal identity (ID) card information and medical records to construct the ethnic profile. But what about persons of mixed parentage, I asked. Dr Wu impatiently noted that in such cases, as a matter of 'practicality' or 'convenience,' as well as patrilineal bias, I may add, they used the father's self-identified ethnicity. Their aim was for the general ethnic profile and not be distracted by specific individual differences. Here, Wu was conforming to the so-called 'CIMO multiracialism' (the acronym combines the initials of the racial groups) that identifies each race/ethnic category on the basis of patrilineal descent. He continued, 'It is a matter of what resolution you want, or what scale in your sample to produce a reference database that can be used by researchers to trace disease prevalence.' He continued earnestly, 'The point is to develop a barcode that defines your ethnicity. Our final goal is to arrive at a gene that causes disease susceptibility, to finger that gene and pinpoint it.' Thus, the barcode reconfigures ethnicity in a set of statistically determined vulnerabilities that are linked to ethnic data populations.

Health Administration

This ethnic-differentiated DNA configuration is governed by rationalities of Singapore being a formally constituted multiethnic society subject to authoritarian rule. The ethnic-differentiated rationality governs different aspects of life, including health. The public is already primed to accept the notion of genetic research and the political value of developing customized medicine. Anyone in the street can tell you that Chinese are prone

to certain cancers, Indians to heart diseases, and Malays to diabetes, and the government is figuring out ways to treat them properly. For instance, the public blood bank is presented as a 'national life resource,' and parents to be are urged to donate their newborn's cord blood in order to ensure that leukemia patients in Asia will have access to 'life-saving' stem cell match.[14] This recoding of pre-existing ethnic and racial heterogeneity sustains a new regime of ethical care that is inseparable from the obligation of citizens to participate in biomedical sciences, whether as consumer, student, doctor, patient, or research subjects.

There is thus an implicit social contract with the state given in terms of the government's funding of biomedical research and the social obligation to provide one's anonymized tissue. On the one hand, the electronic infrastructure gathers up all patients and makes them participate in a vast ongoing clinical trial of potential health problems. That is, public healthcare has as its condition the use of patients' data which are 'owned' by public heath institutions. 'Best practices' govern the gathering of new samples; patients sign consent forms and in this public, there is widespread support for state-authorized biomedical research. An infrastructure for collecting and processing anonymized genetic information also sees the conversion of patient records into data points in the sample. In other words, the ethnic accrual of DNA variability is not merely economic, but it is also productive of collective legitimacy. Indeed, the researchers consider themselves to be engaged in a form of civic virtue by designing ethnic-DNA databases that are culturally identified with their 'own' communities. This robust infrastructure of health governance promotes ethnic-diversified configurations of DNA data and samples, with the goal of building 'a valuable Asian DNA biobank in Singapore.'

An Elastic Sense of Scale

The Singapore genome variant project is a technology that creates potentiality because it is the accumulative use and deployment of the three ethnic figures – Chinese, Indian, Malay – in decades-long medical records, and in the new DNA study, produces a DNA database design that that is at once contextual and performative leveraging the island's data bank to represent larger collectivities in Asia.

Dr Wu explained that variable DNA profiles exist in different geographical areas. An epigenetic rule of gene–culture interaction correlates groups evolving in relative isolation with different kinds of susceptibility genes for certain diseases. Wu gave the example of malaria tolerance in some African groups, a microevolutionary outcome of what he called '*in situ* adaptation' that is associated with one or two characteristic genes. He went on, 'Genetic pools vary in different places because they become molded by diseases prevalent there. Genetic features may account for resistance; so we are interested in finding that gene to develop a cure. Sometimes the [epigenetic] conditions that affect the vulnerable group are also taken into account.'[15]

In a post-Human Genome Project world, Dr Wu emphasized, there was potential value in using the ethnic heuristic and 'Asian' angle. He had been trained in Europe and been a visiting scientist in the USA and Japan. In the USA, he said, 'They classified all Orientals[16] together.' His point was that in Singapore and Asia, where larger scale samples were more easily available, scientists could statistically stabilize the population samples to show 'dramatic differences' among Asian races. These were categories with serious statistical amplitude. 'There are huge numbers involved in our three representative

populations: 1.2 billion Chinese (mixture of South and North Chinese); 1 billion Indians; 3/4 billion Indo-Malays, i.e. almost half the world! These are considered distinct genetic pools.' Through the use of ethnic-differentiated data, he seemed to suggest, a geometrical dynamic could be unleashed that expands the value of the data to staggering dimensions.

Yang told me boldly that the Singapore genomic data 'traces differences and similarities among Malays, Chinese and Indians, i.e. races that represent one third of the world's population.' Recently, leading hospitals, clinics, and labs on the island came together for a cohort study of gene–environment interactions in disease development among the three ethnic groups. The authors predict that 'Information obtained from the study could be applicable to India, China, and much of South East Asia' (Chew & Tai 2007, p. 1). The slippage from ethno-genome identity to ethno-nations is very telling, for suddenly genomic and disease information assembled in Singapore has the potential to be bio-medically relevant to populations in big Asian countries. How is that scientifically feasible?

The ethnography of scientific practices, Latour (1985) argues, reveals the transformation of lab findings into inscriptions: cascades of columns, diagrams, drawings, formulae, maps, and digital images that are combinational and mobile while remaining consistent as an optical power (1985, pp. 13–14). A useful analog is money which circulates yet remains calculable and combinational. Ethnic barcoding of DNA develops elastic properties of the ethnic figure, to condense or stretch across sites, or to move without distortion (i.e. an immutable mobile). The repetition and displacement of the ethnic figures – Chinese, Indian, Malay – flatten their differences and permit the domination of the scientific diagram to do their work, at different scales.

How is this zooming in and zooming out of data, DNA data, enabled by the use of ethnic heuristics? Ethnicity not only becomes a marker of genetic difference, it also functions as a biomedical category that can be flexibly applied to different groups in transnational space. Race or ethnicity attached to a DNA database is a mobile artifact that migrates across the landscape to represent similarly named ethnic populations in scattered places. [Scientists in Asia and the West alike deploy ethnic terms with the same aplomb that never fails to amaze anthropologists.]

For instance, the leveraging heft of the 'Chinese' figure can code for DNA variation in many sites. Dr Lin, a PRC-born oncologist at the Genome Institute, searched for genetic risks that affect the incidence of cancers in Asian populations, specifically by finding 'how genetic variation is distributed in Chinese population.' 'Why focus on Chinese groups?' I asked. Lin said, 'I have very practical reasons for having an interest in China. The population is there. We need a lot of patients, i.e. thousands of disease phenotypes. China is a major source of biomedical data [for our research here in Singapore]. We combine local and Chinese [PRC] samples.' Expressing an elastic sense of scale afforded by computational biology, he noted, 'They are all Chinese in a sense.'[17]

Using the Chinese barcode, he was able to accumulate far-flung allies and resources in one place, i.e. Biopolis. Being China-born, Lin easily forged links with many clinics and hospitals in China that supply him with the germ-line cells for different cancers. By integrating data and samples from China and overseas sites, he built a huge ethnic-correlated database that transcended borders. Furthermore, the Chinese labeled data can jump scales, by becoming a paradigmatic form for 'Asian-types of cancer.'

This projection and prognosis have to do with the frequency of cancers among 'Chinese' populations, the accessibility and scale of DNA samples, and multiplicity of

environments in which 'Chinese' peoples are distributed. The pragmatics of scientific research and design thus display how ethnic categories can slip, expand, and contract, and in this case, the relative nondetermination of 'Chinese' can be wrought into a proxy for 'Chinese' everywhere, and at times, even for 'Asia.'

The use of Anglophone ethnic names enhances the geometric power of DNA databases. English terms for different Asian ethnicities in Singapore (a legacy of colonial times) become indicators of DNA differences, so that particular ethnicities designated by the English language become aligned with differences in DNA, mutations, and disease expressions. Asian countries to which Anglophone terms refer are not only multiracial but have subethnicities, which become relevant or not depending on the way the data are cut – north and south Chinese, Sikh, and Tamil, and so on. Thus, the mix of scientific artifacts and English terms engenders a series of cascading data that can transport and transfer the implications of DNA knowledge. By thus accumulating scales and flattening diverse populations across Asia, Singapore genomics demonstrates that unlike Iceland, no island is an island.

A Center of Prognosis

The island has become a center of prognosis when it comes to ethno-genomic identities in the region. Dr Tai spells out the implications within the context of the Biopolis hub. 'Our data bank represents a much more diverse population that is reflective of what will happen in much of Asia … There are few places in the world where you can look at the effects of rapid socio-economic development on three different ethnic groups that seem to respond somewhat differently to the environment. In addition, the rather good infrastructure and communications will give us advantages over other biobanks.'[18]

By mobilizing many resources – Asian genetic diversity, global expertise and regulatory governance – Singapore projects itself as a prime center that links major ethnic collectivities to risk diagnosis, prognosis, and drug discovery. Dr Williams predicted that 'authoritarian state power and socialized medicine will ensure that rapid and systematic elements are in place for the coming together of a biobank that combines genetic and clinical data and tissues from Malay, Indian, and Chinese patients by a target date of 2020.' The collating of multiethnic databases and tissue samples, Yang claimed, 'will help make Singapore a platform from which to introduce drugs into Southeast Asian markets.' Instead of a stand-alone biobank (gesturing at deCODE), Singapore is building an integrated biomedical ecosystem mediating experiments that are proliferating in China and India (more than in SE Asia).

As noted above, China is very protective of its biological resources and does not permit the export of human samples, especially to the West. Here Singapore steps in as a research middleman who gains access to Chinese health data and is able to culturally manage PRC sensitivity that the use of its health records should be of benefit to China and Chinese people. As mentioned earlier, PRC-born Singapore-based scientists have easier access than most to Chinese health records, thus enriching Singapore's DNA and cancer databases. The information on genetic variants allows researchers to find biomarkers that they claim will ensure at least a 60% success rate for earlier phases of tests on novel customized drugs.

The island's strategic advantage, as a center for research on 'Asian cancers,' has drawn Contract Research Organizations (CROs) that handle the outsourcing for clinical

trials for drug corporations. Many trials run in Hong Kong and Taiwan focus on nose and throat cancers that disproportionately afflict Chinese populations. Given unreliable quality controls in PRC laboratories, over a hundred Chinese CROs have turned to Singapore to run experiments on new cancer drugs. Access to mainland Chinese DNA is central to the growth of clinical trials in Singapore. Scientists from Singapore help oversee ethical regulations of clinical trials in India. The intertwined scientific and economic strategies position the island as both nexus and conduit for spreading best practices in clinical experiments in the region.

Dr Williams flatly noted, 'An Asian genetic architecture is much more valuable than biobanks in Euro-America because they do not carry Asian genetics.' But as I have argued above, there is more to it than the furnishing of variegated DNA of the Asian dragon. Ethnic genetic collectivities are immutable scientific artifacts as well as bio-investments, while the ethnic design of the database builds domination through the ability to capture, produce, sum up, and prognosticate on DNA for a big swath of Asia. In short, the spread of computational biology, the competition of biobanks, and the demands of big pharma are all coproducers of this 'plug and play' platform that furnishes ethnic-associated databases for speeding translational research from 'bench to bedside,' and generally 'making *more* of life' in Asia (Ong 2013)

To the researchers cited above, the 'true value' of an Asian DNA infrastructure lies in its recognition of Asian peoples as worthy subjects of cutting-edge medicine. They were inspired in part by J. Craig Venter, who in his guise as 'the god of small things' (Hylton 2012) called for 'gathering up as much information as you can.' He has been trawling the Pacific for microbes to re-engineer into pharmaceutical products. Scientists in Asia want to beat him to the chase when it comes to producing data on Asian life forms that, having been gathered and calculated, are generative of diverse values beyond that of treating disease.

Conclusion

The Singapore and PRC scientists mentioned above deploy sequencing techniques to fold the reservoir of biological potentialities in Asia into an emergent, recombinatory, and mobile DNA database. The infrastructure deploys the ethnic heuristic in different registers. First, the network of ethnicity becomes a supple membrane coextensive with the network of genetic data points. Second, ethnicity is rendered an immutable mobile that circulates databases beyond tiny Singapore, making the infrastructure at once situated, flexible, and expansive. Third, the ethnic signifier carries affective value that enhances a sense of what is at stake in the building, mobilization, and implications of such Asian databases. In short, the origami-like folding together of multiple, flowable, and perfomative data points shapes a unilateral topological space of biomedical 'Asia.'

Meanwhile, American genomic science is not adverse to the cataloging of DNA variability. Indeed, Yang's population genetics lab is one of four selected by the NIH to develop statistical research on DNA (the other participating centers are Cambridge University, Oxford University, and the University of Michigan).

Compared to Eurocentric studies, Yang noted, the key contribution of his lab is the data on multiethnic associations for disease studies and drug reactions. Questioning the applicability of the DNA discovered for European populations for non-European populations, Yang claimed 'We are leaders in the game of trans-ethnic studies' (Yang 2012).

Indeed, in positioning itself as an Asian biomedical hub, the Biopolis complex invests in the affects of biological difference and ethnic belonging. Not surprisingly, the world of digitalized science rekindles abstract feelings about genetic exceptionalism. The spirit of the experiment also seems very old, relying on discourses that project an Asian genomic history of the body–genome–environment complex back in time amongst primordial 'races' that were always in a state of flux.

This making and circulation of ethno-genomic identities raise anew the question, 'What is Asia?' By tracking the ways in which collectivities are defined, and relations are conjured, revealed, re-formed, modeled, and predicted, Asian geneticists are shaping a novel concept of Asianness that is driven by scientific optimism. For Dr Yang and his colleagues, terror incited by wild things lurking in the 0.1 sliver of the human genome can be managed by catching them in a novel web of corporeal and algorithmic self-knowledge.

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DISCLOSURE STATEMENT

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NOTES

1. Interview, Dr Yang, 10 May 2010. For reasons of confidentiality, I use pseudonyms to identify the interviewees.
2. Website of the National Institute of Health, USA. http://grants.nih.gov/grants/funding/women_min/guidelines_amended_10_2001.htm (accessed 11 September 2013).
3. The basic code of life is made up of four nucleotides: A, T, C, and G (adenine, thymine, cytosine, and guanine). In humans, the genome has over three billion of these molecules arranged together in the double helical structure of DNA.
4. IHTribune, Business Asia, 'Waiting for the Big payoff from Genomics,' 31 March 2010, 19, 21.
5. Wikipedia entry: 'Wild type (or wildtype abbreviated wt) refers to the phenotype of the typical form of a species as it occurs in nature. Originally, the wild type was conceptualized as a product of the standard, "normal" allele at a locus, in contrast to that produced by a nonstandard, "mutant" allele' (accessed 9 January 2013).
6. Interview, Dr Williams, April 2010.
7. The National Cancer Act in 1971 intended to eradicate cancer as a major cause of death.
8. International Hapmap Project (Hapmap homepage). http://hapmap.ncbi.nlm.nih.gov/ (accessed 22 March 2014).
9. Interview, Dr Lee, 14 April 2010.
10. For discussion of the usefulness of ethnic categories in assessing genetic contributions, see Mountain and Risch (2004).

11. Interview, NUS administrator, 5 June 2006.
12. China's drug markets, growing at 25% per year compared to 2–5% in the West, are the new focus of big drug makers (Wang & Rockoff 2010).
13. Doctor and researcher, National University Hospital, interviewed 1 June 1 2006.
14. Cord Blood Bank of Singapore. http://www.scbb.com.sg
15. Interview, Dr Wu, 17 June 2004. The rest of the discussion concerning Dr Wu is drawn from this interview.
16. By 'Orientals,' Dr Wu used the old-fashioned Western term for 'Asians,' with no explicit derogatory connotations.
17. Interview, Dr Lin, 14 April 2010.
18. Interview, Dr Tai, 22 April 2010.

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