
Re-presenting Global Genomics Through Asian Genomics: Stories from the Periphery ... or the not so Periphery¹

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Abstract

By exploring different spaces of Singapore genomics I show attempts to re-shape or 'e-race' certain meanings of race in the new genomics while simultaneously 'Asian' genomics works to redefine global genomics.² I contend that 'Asian' genomics, databases, and genomes should be seen in a relational, indeed an interactional, way to 'global' genomics and local spaces. The elaboration of this point is crucial to a better understanding of transnational flows of global genomics because it illuminates that meanings and practices in the new genomics, including race, are contested and negotiated in complex ways. Subsequently, it highlights that hegemonic narratives of global genomics focused, for example, on the Human Genome Project (HGP) are insufficient. Meanings and practices of global genomics do not simply spread out from some centre, generally regarded as Western / US genomics.

'Asian genomes, Asian genomics, Asian populations, Asian scientists'— is the descriptor about race or something else? In this short paper, I attempt to understand the workings of 'Asian' by exploring spaces of global genomics. I argue that 'race' and 'Asian' are being re-shaped in the transnational flows of information and human bodies in the new genomics and that, in the process, 'race' is implicated in contestations and negotiations over what is the new global genomics. The paper is broken down into three parts. The first briefly presents my conceptual tools. The second presents examples from Singapore genomics to implement this framework. In the third, I make concluding remarks about this web of race, nations, and global genomics.

In the conclusion, I suggest the following: (1) that we need new conceptual tools for articulating the complexities and interactions between the global and the local in new technosciences especially in regard to capturing

better transnational flows and diasporic contributions, actors, and practices to the new genomics and (trans)national efforts and (2) that national scientific efforts to remain competitive in the 21st century play significant roles in the re-shaping and possibly reifying of certain concepts of race in their local context and that these have important consequences for genomics research and the global genomics community that may be overlooked.

Spatiality, absence / presence, and the flame metaphor

'Race' is a tricky concept. By now, most are aware that it has multiple meanings based on historical context and location. Science and technology studies scholars in North America have recently and importantly retrieved the topic of race and biology, showing how debates over biological versus social construction theories of race have never really been settled, as many have supposed (Reardon, Dunklee & Wentworth 2005). My task here differs. I am less concerned with the genomics community debate over social construction versus biological theories of race. Rather, I will be more concerned with how 'race' is mobilized, put into practice, contested, (re)-shaped, or (e)-raced in the transnational flows of the new biotechnosciences of human genomics.

With this in mind, I want to hold off on any a priori definition of race (e.g., in terms of colour, as it is popularly or dominantly understood in the US). I suggest that given that there are multiple understandings of race in academic, popular, and national discourses, it stands to reason that this may also be the case in the new genomics. By looking for (re)-shapings of race I turn to race as a verb: racing. Out of the realm of the static, I move to that of process, to look at associations and relations. To talk about 'relations' requires a discussion about space or spatialities; this is what I want to talk about here. Spaces are locations in which objects lie, but spatiality, characterized by space and time, allows me to focus on processes in which objects must move, be re-presented and translated, in the sense of 'transformed'.

The new genomics—I dare say 'global genomics'—is translated (read: transformed) in multiple spaces. 'Global genomics' hides this situation. Generally regarded as taking place in genomics space (read: Western /

American), it spreads out evenly from the centre. By surveying multiple spaces, including virtual spaces (e.g. websites representing the state), spaces for new genomics to take place (e.g. science parks), media spaces (e.g. mainstream US media, technical journals), diasporic spaces ('Pan-Asian' scientists), I complicate the smooth move out of the centre. I suggest that spaces overlap creating bumps and terrains that require attention.

Bruno Latour is known more for actor-network theory (ANT). My interest here is focussed on later versions of ANT. Early ANT presented the technoscientific network, its building and sustenance, as everything—the universe. This led, correctly, to many criticisms of a functional managerialism or colonialism. Colonialism—because it left no room for the Other, that is, anything outside or non-related to the network or nodes in the network. In other words, this analytical tool may be good for describing imposing structures, but what critics, especially feminist and post-colonialist scholars, recognized with early ANT was the lack of space for alterity of Otherness. This alterity is what I am concerned with in this interrogation of the new biotechnosciences and conceptual tools of STS to study them.

Thinking about spatiality is important to thinking about human genomics because genomics rarely, if ever, takes place in one geographic location (much of it takes place in virtual space). Network is one form of space and ANT has been important to study the new technosciences. However, here I borrow from the work of John Law and Annemarie Mol, who have extended actor-network, especially in regard to using it to think about spatiality. They include other forms of space to network theory, such as, Euclidean, fluid, and fire spaces (Law & Mol 2000). It is the latter that I think is most helpful to think about race and the new genomics in relation to mapped spaces. Primarily, I use fire as a metaphor, specifically its characteristic flicker, to represent the simultaneous absence / presence to create its shape. For me, race space / object in the new genomics often works in this way.

As the multiple mapped spaces of the new genomics interface and interfere, the shape of the race flame emerges in which some absences weigh in more heavily at times than others. Through three vignettes, I explore the spatialities of Singapore genomics in order to locate (re)shapings of race at

78 Pei Pei Koay

the crossroads of 'global genomics,' 'transnational flows,' and 'national science'. Race is re-shaped through simultaneity of certain absences in the discourses in the new genomics. This is important not only because it shows the strategies of various actors in the new genomic discourses that are working to re-shape certain notions about race in global genomic practices, but also that these re-workings are implicated primarily by economic concerns.

The new genomics: Stories from Singapore

A. Virtually 'real' space: Biopolis and Singapore / Asian genomics

Conceived in 2001 (publicly known first in cyberspace), Biopolis opened in 2003 as Singapore's multi-billion dollar flagship biomedical science park. Its current locations are dual:

- Physical: Buena Vista, Singapore
- Virtual: <http://www.one-north.com/pages/lifeXchange/index.asp>

Furthermore, more than a place to work, it is part of a broader built living space known as 'one-north'. Both locations are situated within one-north (its website and physical space), which in turn is situated in / by / through Singaporean virtual and physical locations.

One-north's website describes Biopolis as:

a thriving community for scientists, researchers and technopreneurs to work, live, play and learn, in an environment bounded only by the imagination.

JTC Corporation, which describes itself as the industrial architect of Singapore, created this new technopolis for this small city / nation-state, but in the process, the state's aim is to re-envision Singapore through Biopolis.

This is where taking space into account in its many forms is especially important. Notably missing in the descriptions of Biopolis (read: the new Singapore) is its current population and everyday living. The government has had problems in attracting foreign workers and keeping homegrown ones. Recent surveys show that one in every four Singaporeans is foreign

born. With the new biotechnology initiative, the government has aggressively sought to obtain high-tech workers from abroad. There has been an effort to draw from Asian nations—China (PRC) and India in particular—but more so from the usual pool of high-tech, highly educated, professional workers from the United States, Britain, Australia, Europe, and to some extent Japan and South Korea. A government-industry website ‘BioMed Singapore’, has been a central space to reach these workers (BioMed-Singapore.com; Wong 2002). However, this highly educated, cosmopolitan workforce is still a small percentage of its total foreign born workers. In contrast, the majority of its foreign workers are low-tech—employed in construction and as domestics. These individuals mostly hail from other Southeast Asian countries—in particular, the Philippines, Sri Lanka, Indonesia, Malaysia, and to some extent the PRC (although this may be shifting to high-tech workers), who are often neglected and discriminated against.

The main point here is that the state has used Biopolis to re-imagine Singapore as more multi-racial, multi-ethnic, multi-national and has been able to displace discussions of its own domestic racial politics and non-knowledge worker immigration issues for which it has been often criticized. The enormous amount of resources poured into Biopolis—both virtual and non-virtual—is telling of the collaborative efforts of the state, industry, and scientific community to re-make Singapore as well as global genomics at this site. This is further shown in the next section as Singapore genomics and state space overlap with database science and regional geopolitical space. I will return to Biopolis later but here I want to further interrogate this idea of ‘Asian’ genomes and genomics.

B. Regional space: Pan-Asian SNPs and Asian genomes

Elsewhere I have described the importance of large-scale human population bio/databanks to human medical genomics (Koay 2004). To summarize, genomic scientists argue that these bio/databanks are necessary for medical research in three regards:

- (1) to pinpoint genetic predisposition of complex diseases; that is, to search for susceptibility genes for common diseases

80 *Pei Pei Koay*

- (2) to pinpoint differences in pharmaceutical / treatment responses
- (3) and to pinpoint variation in disease response.

In human population genomics, it is not the individual who is studied, but rather the entire group to which that individual belongs. A project in human population genetics could examine the presence or absence of certain forms of genes in the population (e.g., a gene implicated in the development of X disease). Such a study could observe both the frequency of physiological characteristics (e.g. blood pressure) or of disease (e.g. cardiac illnesses) within the population. It could also examine the interactions between environmental and genetic factors.

The main idea is that this type of project involves a large number of people whose information, in aggregation, allows statistical analyses. These bio/databanks also include not only tissue samples and genome sequences of individuals, but one or more of the following: genealogical, medical, and lifestyle information about the individuals. Increasingly, then, what have arisen are local large-scale populational databases. Pharmaceutical companies have been instrumental in promoting these databases along with state officials. Singapore has its own national bio-bank, the Singapore Tissue Network (STN), announced in 2002.

What I wish to discuss here, however, is the Pan-Asian SNP initiative. Singapore is also an important player in this project. Edison Liu, the executive director of the city-nation-state's flagship biomedical initiative, Genome Institute of Singapore (GIS), is one of the leading coordinators and spokespersons for this project. Announced in 2004, this is a regional genomic database project developed by scientists from eleven 'Asian' states. These include: China, India, Indonesia, Japan, Korea, Malaysia, Singapore, Nepal, the Philippines, Thailand, and Taiwan. Its target is to unravel what members and advocates of the initiative call the 'Asian gene pool'.

Specifically, the objectives are to show the pattern of migration and settlement throughout the continent and bring scientists a step toward identifying genetic characteristics associated with certain diseases. The objectives of the project can be divided into anthropological and medical projects, but these are not exclusive. Anthropologically, the project aims to elucidate Asian genetic history, migratory patterns, and cultural

development, but medically, it is to identify genetic differences between Asian populations, especially those that affect the risk of disease. The diseases that they aim to study are those that have been especially shown to affect primarily Asian populations. However, the reasons may be either primarily genetic or environmental. This point has not been made entirely clear in media spaces.

What has been made clear is that unlike its European counterparts, the funding for these enormous tasks is low. The budget is estimated by its scientists to be only about US\$ 3 million. Scientists on this project will collect a total of 2600 human samples (20–100 coming from each ‘ethnic’ group). The collection process will take place over two years. It began in 2005 and the data collected will be put into an open database.

Unlike other regional and national genomic population databases, neither of these projects has received much coverage in popular or scientific media. While heralding the Pan-Asian initiative, its scientists are also cognizant of this and their status in the global genomic community. Liu stated, ‘We are aware, scientifically, the impact of this work may be considered by some as incremental. But we are convinced that this heralds the rise of Asian biosciences’ (Normile 2004).

When represented in international media, the Pan Asian and STN projects have been presented as Asian genomics or race-based techno-science in contrast to other genomics database projects, e.g. Iceland. However, direct links to race have been avoided by spokespersons, including Liu. Instead, they make the point that this is an opportunity to represent themselves by representing their interests in research that they deem to have been ill-represented in Western / American-European global genomics. In other words, Asian scientists have used this effort to be spokespersons or to represent ‘Asian’ genomes as diverse but similar. Liu’s position is that there are many different populational genomes among their country’s population (his examples, China and Singapore). The other leading spokesperson—from Japan—has not publicly made such a claim for Japan and ‘Japanese’ genomes. However, both point out there are similarities among ‘Asians’. Still, publicly, the overwhelming emphasis is to contrast ‘Asian’ similarities with Europeans, the Americas, and elsewhere.

While these two projects have been described by international scientific and mainstream media as race-based, race is more than rhetoric as elaborated below. When the multiple spaces of the new genomics are highlighted—Singapore state space, media space, global and regional genomic spaces—race is shown to be contested and negotiated and thus importantly implicated in these genomics endeavours.

These scientists also have used this project in efforts to re-present Asian genomics and biosciences in general. Not simply as peripheral—grassroots—genomics, small and incidental to Western / American genomics, but as something bigger—something that is constitutive of global genomics. Next, through Liu, I interrogate further transnational spaces at the intersection of Singapore, American, and genomics spaces.

C. Diasporic spaces: Asian bodies and 'glocal' genomics

In 2001, Liu, a Hong Kong born, US educated, scientist became the director of Singapore's GIS. He re-migrated halfway across the world, but his biography also traverses the WWW—from the Singapore Medical Association (SMA) to blogs of individuals identifying themselves as from Malaysia to Asian Americans. His narrative is a diasporic one. According to these stories, Liu migrated to the United States with his family as a young boy, was educated in the States, received multiple degrees from Stanford, California, and after working hard and paying his dues, became the Director of the Division of Clinical Sciences at the US National Cancer Institute in 1996. Well-accomplished in the area of molecular oncology, Liu focused on breast cancer research, which his academic publications mostly target. My representation is highly abbreviated in comparison to the lauding, lengthy biographies reproduced especially around various websites of Singaporean institutions and associations.

The narrative is not simply a biography of an individual—a member of the Chinese diaspora returning to Asia—as news stories suggested. It is much more complex. The relationship between Liu and GIS is also presented as teacher / student (the West as mentor, the East as student). Liu is described by Singaporean political and science officials as head hunted for the position: a prestigious American scholar and researcher

who could help raise not just Singapore, but Asia as a whole to the level of Western science. In 2002, Liu delivered the SMA lecture. The SMA Council presented him with a citation and in his introducing of Liu, John Wong, who helped pioneer GIS, describes how their relationship came to fruition,

we asked one of America's leading scientists to be a mentor, guru, and guide, for Singapore's Biomedical Sciences Initiative. Ed had numerous other offers, all far more prestigious than we could muster. Yet, his genuine desire to help out Asia, and bring the best of American science and medicine to this part of the world, led him to accept the position of Executive Director to, Genome Institute of Singapore (Wong 2002).

This relationship can be read more symbolically as between the central Western (American) science and a minor Eastern (Asian) science. The connotation of America's superior science is represented in the statement that prestige can only emerge there.

By 2005, Liu turned the tables on the superiority of American science and communicating to a much wider audience. Through the Singaporean state controlled newspaper, *Straits Times*, he ventured that the world would now look to Singapore as its model, mentor, guru, and guide to tomorrow's new life sciences. Here, the 'American scientist' scathingly criticizes the US for its hypocrisy in its criticism of Singapore as ruled by an authoritarian government, pointing to its own authoritarianism in its passing of the US Patriot Act after 9/11. But less openly, he also criticizes what we may gather is China's hypocrisy. Liu repositions Singapore geopolitically as well as himself and the new genomics community in this article.

He is a scientist with a faith in science and technology as the world's means for betterment, but his faith should not be equated with Enlightenment, Western capitalist and colonialists' unquestioning faith in science and technology, and with that, freedom and autonomy of science. Liu is not only a child of Western science and American capitalist society; he is also a child of colonialism and American racialization. Science and technology along with all the good they have brought have also caused enormous pain. He gives these examples: mining processes, modern warfare, deforestation, and ocean depletion. It is no coincidence that these are all

technologies practiced and supported by colonialism in Southeast Asia. With his not quite complete faith in those who *manage* science and technology, he argues that Singapore is a fine adopted home. With its history of looking towards science and technology as the roads to progress as well as strict controls and management, Singapore can guide science and technology and show the West a new way, in his words, the ‘arrogance of people from countries of plenty’ and be the model for the world.

His article is meant, at least in part, as a persuasive argument for retaining indigenous (Singaporean) talent rather than recruiting foreign educated workers. The argument has been that if Singapore wants to build up its biomedical science infrastructure quickly—which it must if it wants to compete with larger and regional countries—it must turn to foreign scientists to fill the dearth in Singapore’s workforce. The Singapore government has already relaxed immigration policy, but as Liu suggests, Singapore must learn to keep its citizen scientists at home as well. It must answer the question of how to provide an environment in which Singaporean scientists will want to stay. Singaporeans have been known to educate their children elsewhere, many of whom do not return. Liu never gives Singaporeans an answer, only the comments that it can do better and that what it has going for it is the government. In particular, he stresses the following aspects: ‘the quality of its leaders, a political culture of economic pragmatism and flexibility and the country’s ability to integrate complex systems’ (Liu 2005).

Liu indicts the US in its exclusionary practices in his history of ‘Western’ science and colonialism. He is less critical and more selective of Singapore’s history. Describing the government and the legacy of its first prime minister, Lee Kuan Yew, as less than authoritarian and paternalistic, is at the least revisionist, but he also does not mention Singapore’s race relation issues, minority discrimination, and Chinese bias. According to some Singaporean ‘minority’ authors these may help explain why it is difficult to keep some of its citizens from leaving. In overlaying the multiple spaces of genomics (American space, Singapore space, Biopolis space, genomics space) the interfaces present us with race as an interference. This interference, this flame, is shaped by the absence of Singapore race relations and the presence of American and colonialist sorry history and

renewed efforts to create a multi-cultural, multi-racial high-tech city. The flicker is made essential for this new global genomics.

Of course, it is still too early to ascertain if Singapore will become the model for the new genomics. Singapore hopes to re-create itself as the bio-polis of Asia and global genomics. However, according to some Western media reports, there is still some doubt as to whether it is an environment in which Singapore citizens and foreign residents will want to stay. Furthermore, as represented by this diasporic body embodied in Liu, efforts in Singapore are underway to remake the Singapore citizen as well as to reclaim the Asian body with the help of the new global genomics.

However, in this diasporic space, I now want to examine more closely the interference and interfaces of spaces for Liu's discussions about race. In Singapore space and genomics, 'race' has largely been absent from Liu's proclamations. In hegemonic global genomics and American spaces, we can get a glimpse of Liu's views on race and genetics as discussed in a scientific community setting while working for the NCI in the US. In a conference on minorities and cancer, he presented his view of the relationship between race and genetics within the American context. In fact, he is careful to frame race through the lens of America's historical and social situation, writing,

In this country (US), the determination of race is terribly inaccurate, mainly because of the dynamic nature of the American population (Liu 1998, 1766).

This is different from saying that there can be an accurate determination of race if the population were static. However, Liu's understanding of the role of genes is complex. He follows his discussion of race, cancer, and genetics with, 'there is no single race gene' and continues,

there is no single race gene that is linked to a single cancer gene by genetic proximity. Because there is no obvious Darwinian selection for cancer in defining a race, there is no natural reason why a cancer should congregate with skin color (Liu 1998, 1766).

Specifically, he equates the idea of biological race with genes implicated with skin colour, but this understanding of race as equivalent to skin colour emerges from US history.

Having taken on the role of leader of Singapore genomics, Liu's discourse has shifted. It is true that we can view Liu's words in the above quote as merely rhetorical, but doing this would surely be a loss. Rather if we retrieve this idea of race with his attempts to explain 'Asian genomes' in more recent interviews, we find that they follow this historical thread of race (Hutchinson 2001). We, then, begin to see that he works to re-shape race in global genomics, but at the same time, his representational work displaces Singapore's domestic racial politics in the new genomics.

What I want to suggest is that diasporic / (trans)national scientists are embodiments of (e-)racing efforts. I take (e-)racing as efforts to efface discussions about race especially in / by / through informational sciences, but they can also be instances of re-shapings of race. These new high-tech transnational scientists are examples of transformations in practices of race.

Biological sciences are implicated in (e-)racing efforts, especially in the transnational flows of its workforce and information. The (e-)racing of national and regional populations is another way in which the new genomics and 'Asian' scientists like Liu are also implicated. On the one hand, Singapore's online resources promote a new harmonious, cosmopolitan, diverse, high-tech community embodied in Biopolis. On the other, research efforts are marked by genomics research itself, much of which has neglected non-European and North American populations, hence scientists, like Liu, argue the need for STN and the Pan-Asian Initiative. However, as discussed above, the exclusionary strategies of real human bodies and populations continue to persist. Race is shown not as a stable representation and / or reproduction but *still* in existence in multiple, sometimes overlapping, and at other times contradictory guises.

Moving to new spaces

The issue of making spaces for the alterity of Otherness is important when exploring discourses of globalization of science if we are to be able to attend to explorations that capture relations and shaping. We need analyses that go beyond structure and hegemony, yet take them into account. To show this Otherness I borrowed from the works of some

after-ANT researchers, who have turned to theorizing / practicing spatiality. Specifically, I borrowed the idea of multiple interfacing / interfering spaces to show the (re-)shapings of global technosciences and their objects—like genomes, databases, and race travel. In this paper, I focused on race. Here, these conceptual moves, to relational approaches and to take absence, the ‘Other’, and space seriously, are important for two major reasons:

- (1) Concepts are always in-formation in so far as they are always situated in time and place. ‘Race’ is a moving, variable concept even in the form of ‘biological race’. Scientists are not in agreement as to what it means or even what to do with it, but, many are not willing to get rid of it either. Furthermore, race is made even more difficult to study because so many scientists, political leaders, and people on US streets are unwilling to speak about it. Therefore, these moves help to better locate ‘racing’ (in other words, to somehow take snapshots of it, pin it down a bit, hold it for a moment). I have argued more directly elsewhere that the narrative of the universal genome of the HGP is linked to stories about nations, race, and identity-making (Koay 2006). The supposedly stable, constant, global source of knowledge and 21st century icon of human identity—the HGP—is implicated in contested stories and shapings of regional and local human population database projects. I explored what race is *not* supposed to shape in the new genomics: the universal human genome. This is to get at race through its absence.
- (2) Related, then, these conceptual moves help to elucidate complex connections between race, genomics and what we mean by global science / globalization of science. In particular, what concerns me here is how non-Western / American science is represented or not represented in academia, in global politics, and international media. Technoscience tends to occur in the United States, Canada, the UK, Western / Northern European countries, and Japan. First, technoscience happens in other countries as well. There is genomics in Eastern Europe, in Mexico, South America, Africa, South, East, and Southeast Asia. Second, they may not be peripheral or incidental to global science. My contention is that genomics in these areas are global genomics, but perhaps *all*

88 Pei Pei Koay

are better described as 'glocal' science and, the latter, not simply cases of local genomics or striving to be modern science.

The standard representation of global science seems wrong-headed to me. Furthermore, only one re-presentation of global genomics is presented here. Representations are always only partial representations and re-presentations. However, part of my argument in examining race and genomics discourses and focusing on Singapore is not simply that Singapore makes for a good case study—although it does this as well. Rather, I suggest that in contrast to what science studies, feminist scholarship, and postcolonial research have importantly shown, that is, all global science is in fact local, we might consider the argument that all local science is in fact global. What do I mean by this?

By focusing on local science, science studies have somewhat neglected certain important aspects of global. These are attempts of other countries to globalize and modernize their technosciences. Of course, technoscience and its objects, practices, and concepts do not move en-masse from one location to another. This is represented in Latour's idea of translation and transformation in ANT. However, as I implied earlier, there is a totalizing element in network theory. However, the point I make here is that ANT is good at capturing the standardizing efforts of technoscience. I think it is important to bring the global back into STS analysis because the local is also not quite right. However, I prefer 'glocal' to describe human genomics to signify both contributions to the globalizing efforts of the new genomics, the hegemonic efforts in its narrative-making, as well as the local contestations over defining genomics, race, and futures.

In this paper, I used three interweaving narratives of subjects / objects in Singapore genomics to show interfaces and interferences of spaces to think more complexly about Singapore genomics, to show the *glocalizing* processes of the new genomics at work, and to re-think race in the new genomics at the crossroads of nation-building and globalization. These examples were used to highlight that Singapore genomics is not simply particular to Singapore—yes, it is historically, socially, and culturally situated—but it is also part of a global genomics community. At the same time, race cannot be understood only in terms of race in the US. These

narratives of which I could only give brief descriptions here, show complex re-shapings of race in diasporic bodies of scientists, genomic populations, and bio-cities. They also indicate that the genomic narratives of Singapore are not adequately explained by narratives of Western domination over the East or to a reference of supportive work to the Human Genome Narrative and the need for new conceptual tools to highlight their complexities:

- (a) Liu is a diasporic body but also a site of race making. Described as a Hong Kong 'native', but raised, educated, and worked in the US. He was a leader at the US National Cancer Institute (NCI), but then jumped the major ship for 'grassroots' genomics in Singapore. He is an Asian scientist as a representative of Asian bodies (by way of the Pan-Asian Initiative and Asian scientists) as well as a diasporic scientist re-representative of global genomics. He is an actor of an 'Other' space in which meanings and practices of race and global genomics are contested and which ANT could not capture. He is both constitutive to the making of the hegemonic global genomics network but also constitutive of what may be a new, different, and important global genomics network. He is an active participant with the Singapore government and industry in attempts to remake both the Singapore city-state and a new global genomics.
- (b) The state and Liu have been central in re-presenting Singapore, its history, its citizens, residents, and future. Liu has been instrumental in working to re-locate Singapore and Asian genomics in the new global genomics discourse linked to GIS and database research, specifically by way of STN and, especially, the regional Pan-Asian Project. Still, locally, in representations of STN there are absences of everyday Singaporean citizens. There are absences of Malaysian, Indian, Chinese bodies in the decision-making processes and their histories as well as a near absence of contesting and ambivalent voices of the supposed harmonious racial relations in Singapore media to the international audience. I suggest that this absence of human bodies and voices is needed in genomic strategies to convey the diversity of Asian bodies that are much desired by a large circle of the human genomics community as well as the state strategies to convey a Singapore that can be 'the gateway to Asia' as one of its campaigns suggest.

- (c) Biopolis is to be the new environmentally friendly, multinational, multi-cultural, technoscientific city for the new millennium. Existing now in both cyberspace and physical space—plugged into each other—this space is both re-presentative of a new Asian / global science and future society (as a harmonious, voluntarily multiracial cosmopolis).³ ‘Will it become such a place?’ is the question still waiting to be answered. Currently, the state-industry ‘Biomed Central’ website seeks foreign, high-tech recruits, providing easy access to visa forms and assurance of eased immigration procedures for that specific worker population. More important where are former Singapore populations?

These are not simple stories with simple lessons. What was at issue for me here is how to make local variation visible while at the same time not to reify the traditional dichotomies of East / West, modern / traditional, genes / environment, nature / social. If we want to understand how natural and social orders are made in our post-modern world, including those that concern race, we must be able to articulate global science beyond the local, or simply differencing, and the globalizing. Relational approaches worked for my purposes (there may be other approaches as well). Related to this is the fact that there is a critical—in the sense of productive—project here that must be taken up. It is not enough to simply make differences visible. By showing differences and localization of science, I presented the case for increased responsibility in discourses and practices of the new genomics, not somehow flattening out responsibility—that is, to re-distribute it to the extent that somehow no-one need take responsibility for the practices being engendered. The discourses on race and genomics revolve around this revived debate about ‘is race real?’ (read: biological), but, to some extent, this question is a red herring since race continues to be practiced, contested, and negotiated in the new genomics.⁴ I do not endorse the views that complexity and non-causal associations imply an inability to implicate. Attempts may be made to (e-)race but one of the hard lessons may be that actors in the new global genomics may still be reinforcing certain old notions of race (in the US or Singapore) that emphasize exclusion in the transnational flows of this new global (capitalist-driven) genomics.

While the narratives of global genomics are much more complex than the story of Western / US domination of science, it should be clear that not everything is well and good with Singapore and Asian genomics. There are issues of Singapore domestic politics that need to be addressed. In terms of representation, or the ability to re-present, more of my concern here, there are also larger constraints that these scientists and the state feel they need to respond to, namely the institutionalization of Western science (read: US hegemony of global genomics). The details are beyond the scope of this paper. However, while the capitalist drive to re-create or rather replicate populations based on race, ethnicity, and / or nations for pharmaceutical purposes is difficult to dissociate from American spaces of state, industry, and science, Singapore state and science spaces and actors are increasingly interfaced with these spaces and redescribing 'Asian' in geo-capital politics as well as 'glocal' genomics.

Notes

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- ² In other places, I argued that local genomic population databases (be they national, regional, and / or race-based) were integral technoscientific objects for what we call 'global genomics'. In other words, I argued that they were not merely supportive. If we must use the term central, then these databases were as central as the Human Genome Project (HGP) databases and HapMap. By this I mean that the importance—the centrality—of the material and symbolic practices of the Human Genome Project databases and the International HapMap Database could not be so without these other databases and projects.
- ³ Currently, the 'harmonious race relations' are enforced through government multi-racial policies, including housing policies. For an overview of such policies see Chua (1998).

92 Pei Pei Koay

⁴ For a good overview of these debates see Reardon (2004).

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Re-presenting Global Genomics Through Asian Genomics 93

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