ENIGMATIC VARIATIONS

Beyond Fortune-Cookie Genetics

In September 2013, an invitation to order a "your 23andMe kit today" arrived at my home in Berkeley. 23andMe is a personal genome service company that was cofounded by Anne Wojcicki (who is related to a founder of Google) in the heart of Silicon Valley. The letter claims that "the service reports on more than 240 health conditions and traits, including carrier status, disease risk and how your DNA may impact your overall health."[1] Furthermore, it added, "You can also learn about your ancestral history." This marketing gimmick underlines that "preventive health information should be accessible to everyone," thus combining a democratizing accessibility with a sunny injunction to self-management.

23andMe celebrates the dream of making DNA technology relevant to personal health, educational benefits, and cultural self-discovery. At UC Berkeley, some administrators were inspired to adopt this user-friendly approach to spark student interest in modern science. In the fall of 2010, the campus initiated a voluntary Bring Your Genes to Cal program. Incoming freshmen were invited to send in their saliva samples to be tested for different kinds of enzyme intolerance.[2] Meanwhile, 23andMe has been promoted in American popular culture for its power and potential to help individuals search for unknown ancestors. A television show on PBS hosted by the Harvard historian Henry Louis Gates Jr. used 23andMe kits to trace the genetic ancestry of famous individuals, stirring widespread

interests among African American people seeking to rediscover family lines disrupted by the kinship-shattering cataclysm of slavery. But despite concerns that exposing personal features to the public may lead to social discrimination,[3] personal genetics, packaged and exemplified by 23andMe's merging of consumer empowerment and genomic self-knowledge, is publicly touted as the intertwining of American ingenuity, democracy, and individualism, all mined through individual bloodlines and genomes.

This popular image of genomic science was dismissed as "fortune-cookie genetics" by Dr. Edison Liu, then the lead scientist at Biopolis, Singapore's ecosystem of bioscience institutions. He explained that the growth of personalized genetics companies in the United States has generated the private misuse of genetic information for clues to personal ancestry and health. While 23andMe, for Liu, a U.S. citizen, represents a typically American genomic preoccupation with individualistic conceptions of kinship and descent, he had some reservations. The fact that most people are unable to interpret the data without the intervention of physicians means that the self-knowledge acquired from a cheek swab is not useful from a medical point of view, and indeed it might even encourage individuals to make health decisions without consulting with medical specialists. Indeed, Liu's position was echoed by U.S. doctors and the American Food and Drug Administration (FDA), which disapproved of individuals learning about their own DNA for these reasons. In 2013, the FDA sought to curb the misuse of commercialized, personalized test kits that had led some individuals, on their own, to seek out serious medical procedures such as a radical mastectomy.[4] For Liu, the market packaging of user-friendly DNA is a neoliberal capitalization on individual desires for fortune-telling that only contributes to the fortune of companies and perhaps to the detriment of falsely empowered individual patients.

By invoking 23andMe, Liu seized the opportunity to differentiate an American use of genomics, which seems to project rugged individualism and valorized self-care,[5] from Biopolis, where genomics are managed by scientists for collective health needs. Although the Biopolis hub is closely informed by American scientific administration and practice, as the hub's spokesman, Liu sought to highlight a defiantly Asian difference. As a state-funded project, the Singapore genomics initiative began earlier (2003), intending not to promote personal genetics, but rather to connect genetic data and tissues already stored in hospitals and clinics in Singapore and other sites, especially in China. A community of scientists, not private companies, will supervise the work of

linking multiple existing data sources in research institutions and filling in the gaps in genomic knowledge about peoples in Asia.

The Singapore biomedical initiative also challenges the fortune-telling belief that the inheritance story is told exclusively by DNA. Liu explains: "We are in a 'new risk genomics' moment because new research shows that our inheritance is infinitely more mysterious than previously assumed in Mendelian genetics." At the turn of the century, the Human Genome Project was intended to usher in a DNA-focused approach to personalized medicine. Soon after, the focus shifted from a narrow focus on genetics to epigenetics, or the study of gene–environment effects on the performance of genes.

Scientists realize that while the genome evolves slowly through centuries, the epigenome, which turns a gene on or off, can change very quickly, within a few generations. The new science is called post-genomics. Liu prefers the term "new risk genomics," which describes a highly interdisciplinary field that includes genetics, epigenetics, biostatistics, proteomics (protein studies), and metabolomics (the study of cellular metabolites). Liu believes that, as a center for the study of new risk genomics, Biopolis has the potential to generate a tremendous amount of digital information that will revolutionize diagnostic and therapeutic methods. The high ambition of this interdisciplinary ecosystem is architecturally rendered as well in the design of Biopolis itself as a network of interconnected research towers.

Yet, despite Liu's rhetorical dismissal of recreational fortune-cookie genomics, some kind of fortune-telling is involved in genomic science, albeit in the abstract language of DNA and mathematics that still manages to work in "Asian" cultural elements. In the post-genomic landscape that Biopolis configures, and indeed mimetically hails through its architecture, it is precisely the attempt to design and then harness the "experimental future"[6] and its fortunes in Asia that is at stake. This book attempts to illuminate what is cosmopolitan science and what are the variations and differences that become coded in Asian post-genomics.

Biotechnologies today are involved in decoding the secret workings of the genome and recoding it in relation to other systems of codes and information (e.g., ethnicity, disease, nationality, geography). Genetic technologies can be likened to the Enigma machine used during World War II, a device for coding and decoding secret messages.[7] As in the mid-twentieth-century coding industry, the contemporary biomedical enterprise is resolutely multidisciplinary, driven by biological research and bioinformatics. The research milieu is a

strange place where mathematicians, biologists, engineers, and other scientists work in tension and in concert across different fields.

The work of unlocking the enigma of life—the double helix of science and passion—now includes research venues in Asia. At Biopolis, DNA databases are coded to "Asian" ethnicities and other elements, thereby redefining what "Asian" means in variations of genes, identity, disease, and space. As a supplement to the American paradigm of the new genomics, researchers in Singapore are amassing and gathering for the first time millions of data points on Asian vulnerabilities and variations, so that other scientists can develop drugs and therapies tailored to the needs of bodies within Asia. I seek to illuminate one of the latest iterations of a century-long migration of scientific and technological knowledges originating in Europe and the United States to Asia, and the situated discovery of new findings within particular biomedical assemblages that transform contemporary science.

Asia, Anthropology, and Science Studies

The path for the study of post–World War II science, technology, and medicine in East Asia was blazed by anthropologists conducting research on Japan, arguably the most scientifically advanced nation in the region. In a pathbreaking study of high-energy physicists in Japan and the United States, Sharon Traweek examined the social and discursive construction of scientific communities.[8] Margaret Lock's award-winning studies of aging and menopause, as well as of organ transplantation, also situated biomedical innovations within a Japan–North American framework.[9] Arthur Kleinman pioneered the cross-cultural study of health practices by contrasting Western and Chinese-style approaches to psychological illness in Taiwan.[10] In a similar cross-cultural vein, Lawrence Cohen explored the medical and cultural construction of senility and cultural anxieties in India and the United States.[11] By taking a comparative approach, these works highlight Asian cultural notions of community, sickness, and bodies that contrast with American scientific understanding. Collectively, such perspectives situate Asia within contrastive cultural contexts for modern sciences.

More recent studies about how scientific and medical knowledges are taken up in diverse regions tend to focus on exploitation and ensuing ethical dilemmas. Brandishing the notion of "biocapital," Kaushik Sunder Rajan framed India as a site that has been exploited by biomedical trials in search of readily available experimental subjects.[12] Other anthropologists have portrayed Asia as a region of coerced and illicit organ harvesting, supplying body

parts for transplant procedures, as well as a site of affective labors that serves a burgeoning medical tourism industry.[13] The implications are that besides the "bio-availability" of exploitable populations, cultural and social arrangements in parts of Asia abet in the biocapitalist pursuit of readily available bodies, labors, and "fresh" human organs from the developing world.

Meanwhile, the rapid deployment of specific biotechnologies in Asia requires a shift from contrastive cultural or political economic comparisons, to consider emerging competitive scientific milieus in their own right. The volume *Asian Biotech* casts light on the varied deployment of biotechnologies in Asian sites and on their enmeshment with situated forms of nationalism, biosovereignty, and ethics.[14] The newly influential journal *East Asian Science, Technology and Society* publishes articles that attempt to discover similarities and differences in the production of scientific knowledge in various historically situated but globally enmeshed contexts. Indeed, researchers in the anthropological and science and technology studies (STS) fields are studying emerging science contexts in Asia, which can generate potentially critical insights that richly expand the field beyond its originating Euro-American context.

Framed by the concept of "global assemblage,"[15] this book identifies an emerging context of what may be called Euro-American cosmopolitan science, crystallized in Singapore. First, assemblage concept departs from simplistic cross-cultural and North–South contrasts; it also challenges the STS theory of a universal science that floats beyond local mediations. The emergence of a science milieu in Asia, I argue, is the particular outcome of complex mediations between global technologies and situated forces. Second, if we understand Euro-American cosmopolitan science as regulated science, one should not assume in advance that biomedical science in other places is merely a debased form. Rather, this work will illuminate how, in order to become universal, cosmopolitan science must remediate situated elements so that it can attend to an array of "global" scientific problems. What is "global" and what is "situated" are destabilized in processes of scientific remediation across the planet. In order to be universalizable, cosmopolitan science depends on this constant effort to be particular, to remediate situated elements.

Radical uncertainties, the historian of science Steven Shapin observes, attend much of contemporary science, and "it is the quotidian management of those uncertainties"[16] that is the stuff of my investigation here. My overarching theme is productive uncertainty, in that scientific practices responding to myriad challenges are productive of new forms that in turn create uncertainty.

Different registers of uncertainty are at play in conditioning the experiment at hand: from the calculation of genetic risks for diseases, to uncertainties surrounding the science and the endeavor, to the larger "known unknowns" that science confronts in attempts to secure the immediate future.

Here I take the opportunity to state that, as an anthropologist, my task is to report and interpret scientific practices and ideas in context, without advocating on behalf of actors or experiments under investigation. My approach has consisted less in judging ethical or redemptive claims about specific research objectives than in identifying the particular biomedical assemblages within which ethical problems and conundrums crystallize, which actors seek to resolve. By offering a multifaceted ethnography of bioscience at Biopolis, I aim to illuminate how science projects are complex entanglements of reason and the passions. The branding of a new biomedical center is often surrounded by promotional publicity. As such, media stories and hype are part of the affective work of the trust-making necessary for garnering legitimacy for this kind of state-supported scientific enterprise. Discursive and nondiscursive practices surrounding Biopolis illuminate what might be called a form of scientific "exuberance"[17] as well as the affective uncertainty that perturbs the orderly landscape of science.

At Biopolis, scientific entrepreneurialism as a mode of risk-taking seeks to shape an emerging region for health markets and biosecurity. This ambitious and potentially risky project is inextricably linked to narratives that establish a spectrum of "Asian" differences—in DNA, populations, disease risks, disease forms, geography, research capacities, customized therapies, markets, and collective goals. The remarks of scientists and physicians accord value not only to themselves as experts, but also to the techniques and procedures involved in the acquisition of these truths.[18] My informants often make optimistic projections about the novel value of their discoveries and techniques for "Asian" peoples, the region, even the world. Such narratives and claims are consequential: the regime of truth accepts and makes true the critical potentials of their science.

In addition, science discourses and metrics are strategic when lab findings migrate to the public realm, and science spokesmen must perform in order to continue to draw multibillion-dollar investments from the Singaporean state and from foreign entities. Collectively, promissory claims about the science being produced animate political interest and legitimacy in what citizens may view as an uncertain economic enterprise. Such political justifications have scientists posing the need for Biopolis and the post-genomic research

that occurs there in relation to the many diseases and ailments that vex and will vex Asian bodies. To gain further traction, long-standing notions of Asia, now reworked as a genomic, epidemiological, and environmental continuity, come into play. In Singapore, discourses of cultural, ethnic, and geographic differences are less about cultural jingoism than strategic claims to leverage Singapore's potentialities in global genomic science while also making the state investment in biomedical research also a reinvestment in the well-being of a vulnerable and racialized populace.

Race and Ethnicity in Medicine

The United States is a major shaper of cosmopolitan science, but it suffers from the historical convergence between structural racism, medicine, and biology that has had a devastating impact on minority populations. The history of misuse and abuse of racial data in medicine, with actual instances of eugenic and racial violence, is well attested.[19] Owing to this history of race science—one that medical anthropologists have at times participated in—racialized medicine in America is often read as an insidious and virulent science-as-racism.

As many STS scholars of the history of American racial science have argued, race was never about nature or biology in the first place. Race itself was always "interpretive," or a cultural construction, so to speak. Critics have argued that the uses of race were and are always confused about the genetics of populations, the genetics of race, and the genetic and social causes of diseases. Therefore, the reintroduction of race as a biomarker in genomic science has stirred old fears of the biologization of race, its stigmatization, and this reinforcement of social inequalities.[20] In *Backdoor to Eugenics*, Troy Duster explores the troubling social and ethical implications of genetic technologies, including the misuse of genetic theory and information, on minority groups such as African Americans.[21] Especially among those working with populations that have and continue to be drawn into a new constellation of race and medicine in the United States, rightful skepticism continues, despite the fact that the new "ethnoracial" category incorporates the interplay of nature and nurture into medical research.

Indeed, genomic medicine has propelled the transition from race to ethnicity, thus effecting a different kind of interpretation of disease vulnerability, though the race-ethnicity divide is neither finite nor entirely clear. The employment of the ethnic heuristic should perhaps not be considered as a restoration of scientific racism in genomic science, but as a new technique that is intended to be inclusionary in the mobilization of health data. The

National Institutes of Health (NIH) Revitalization Act of 1993, Margaret Lock and Vinh-Kim Nguyen note, promotes the use of race (and gender) as a scientific category in DNA sampling. They are careful to note that "population," "race," and "ancestry" (the preferred term) that variously correspond to U.S. census categories are not considered discrete dichotomous variables but are used as heuristic devices for studying the frequency of specific genetic traits. This represents a gesture on the part of the NIH at navigating the fraught historical and political terrain in which "race" in its molecularized form has often been read as a causal explanation of historical and ongoing structural social inequalities.[22] Duana Fullwilley argues that the "molecularization of race" can be viewed as intended to rectify the systematic exclusion of gendered and raced minorities in American health research.[23] The ethnic heuristic—mobilizing ethnicity in an experiment as an interpretive tool rather than as a claim to some stable and preexisting biological reality—is one way in which researchers attempt to elaborate a bioscientific enterprise that can include questions of human difference without defaulting into the pitfalls of scientific racism and racist genetic determinism.

Ambivalence remains over the use of ethnoracial genomic data because of its unintended effects on racial politics. Even Lock and Nguyen worry that DNA fingerprinting outside the lab may give rise to biomedical practices that unintentionally promote racial stereotypes, affirm ethnoracial differences, or further commoditize racial medicine.[24] At the same time, despite risks of exacerbating racial blaming and oppression, there is a growing consensus that the use of such genetic markers should be dropped.[25] After all, besides their application as a mode of biomedical inclusion, ethnoracial categories may contribute to social healing in that minority groups, through their biomedical racialization, are finally receiving the sophisticated medical attention they have long deserved. Alondra Nelson has argued that commercialized ethnic DNA can be used as building blocks for projects of reconciliation and thus may be viewed as positive elements for the future of American racial politics.[26]

As I will argue in this book, the ethnic heuristic as an inclusionary aspect of DNA fingerprinting is more unambiguously embraced overseas as an advantageous aspect of genomic science that gives texture and robustness to the DNA maps of global populations so far excluded from genomic science.

"The Difference That Makes a Difference"

We are at a moment when there is a growing international division of knowledge and labor as well as a pluralization of the life sciences. Genomic science

is a novel experiment in the interplay of biology, race, and the environment, but each national setting uses different concepts of race (historical, cultural, political, and biomedical) in relation to genomic science for different but not mutually exclusive strategies of bolstering national identity, biocapitalism, and/or biosecurity for the future.

Scientists seeking to configure new knowledge systems outside Euro-American milieus generate what Gregory Bateson calls "the difference that makes a difference."[27] Different systems constantly experiment with form where the constant value is not a thing but a contingency. Drawing on ecology and biology, Niklas Luhmann argues that in society's self-referentiality and future elaboration action is communicated through the constant creation of otherness (contingency) in relation to things that already exist. As is often the case, the largest register of difference is the West versus Asia not as stable things but as relationships among shifting contingencies identified in systems making. Differences (race, ethnicity, geography) therefore are not stable but are rather contingent values that systems use to reduce complexity but end up creating more complexity.[28] Throughout this book, "the West" and "Asia" are invoked by researchers, informants, and sometimes by me in order to indicate the registering of such contingent attributes and relationships from vantage points within different systems of knowledge making (biomedical, political, anthropological, etc.).

Difference and differentiation mark novel aspects of any scientific experiment. When American genomic science is used for non-European populations, race, used as a code for groups with distinctive clusters of genetic, epigenetic, and molecular features, is useful for developing customized medicine. In pharmacogenomics, infinitesimal genetic differences can have significant implications for disease susceptibility and therapeutic responses; and racial/ethnic markers have become a useful technology for sampling populations, testing drugs, diagnosing, and customizing therapies. For instance, variability in DNA and in immunology is scientifically significant in reproductive technologies. Charis Thompson argues that "race" in contemporary biomedical research is a heuristic for identifying the intricate interplay of nature and nurture, of genetics and epigenetics.[29] Thus, attention to "racial" biomarkers of gene–environment interactions is very critical in the success of transplant technologies.

But because race outside the lab can refer to a variety of things, the racialization of genomics often takes on political and symbolic overtones, just as it grows out of fraught histories for creating and classifying human difference.

Different national contexts of genomic science disclose various uses and meanings of race.[30] Latin American countries tend to construct "mestizo genomics" because scientists are influenced by notions of race mixture (from social, historical, and political sources) that come to shape research questions and answers.[31] In Mexico, the digital database is racialized as mestizo or mixed race, in opposition to indigeneity and in acknowledgment of interwoven histories and populations who collectively symbolize the nation. Mestizo blood samples are critical for the Mexican biomedical enterprise because they represent a form of "genomic patrimony."[32] It is interesting that genomic science in Latin America seems to be primarily concerned about constructing unified, while mixed, national races in their databases. By contrast, in Asian biomedical sites, ethnicity as "the difference that makes a difference" is deployed as an astute strategy to enhance the scope and power of genomic knowledge thus generated.

Enduring European colonial legacies in Southeast and East Asia are constructions of plural society, of coexisting races (essentialized) closely tied to language and religion. Different authoritarian political orders are based on multinationalism (China) or on multiracialism (Singapore), and the major axis of difference is between majority and minority nations/races/populations. Although there is political emphasis on protecting the group rights of minority nations/races, the majority nation/race is variously privileged and enjoys political dominance. In Singapore, electoral democracy is tempered by a communitarian ethos that extols social obligations and the importance of the common good, thus emphasizing collective over individual autonomy and rights. An official order of so-called CIMO (Chinese, Indian, Malay-Muslim, Others) multiracialism aims to balance the claims of different races in the nation. At the same time, hate-speech statutes discourage talk about race and religion, and there is a healthy public defense against disparaging the cultural practices of any "race." In this model of administrative homogenization of identities, "ascribed" race minorities are very different from "voluntary" self-inscribed minorities in liberal multiculturalism.[33]

Nevertheless, in reaction against the state's insistence on "racializing" everyone, media, academic, and "scientific" discourses increasingly use "ethnicity." Researchers in Singapore shift from the official category of race (traced through patrilineal descent) to American uses of ethnicity (based on self-identification in medical records) in their effort to model ethnic biomedical collectivities. Fortuitously, they recognize that ethnic-differentiated

medical science makes their databases more performative and mobile across multiple sites. For instance, ethnic Chinese biomedical collectivities can come to represent huge numbers of people in the world who may self-identify as Chinese. Critically as well, English—the language of science and ethnicity as normalized by international social science—is utilized to strategic advantage by Singaporean health researchers. The ethnic heuristic helps to circulate their findings, claims, and applications to places where English denotes like-ethnicities are found.

Therefore, genomic science in Singapore does not reify colonial-era notions of biological race, nor does it uphold a single national race in the genomic lab. In addition, the assumed stigmatizing effects of ethnoracial medical data in the United States do not apply in Asia. People tend to have a robust sense of their (variously constructed) racial/ethnic identities viewed through the lens not of past victimization but of ancient roots and historic achievements. Genetic technology is new, and people welcome Asia-oriented research that targets their ethnoracial group for therapeutic research. Few express fear or ambivalence about ethnic specifications in biomedical sciences, which in any case are but tools to help clinicians develop the personalized genetic data one can get on a chip and soon on the iPhone. Ethnic-differentiated tools are part of being techno-savvy medical consumers.

By adopting the ethnic heuristic, Singapore can leverage an ethnic-rich genetic database and brand itself as a biomedical center for a broader Asia. Multiethnic DNA is less about investing in national unity (as in the Mexican case) than a pragmatic strategy to produce a statistical infrastructure for demographic and geographical reach. It is this convergence of the use of ethnic heuristics in cosmopolitan science and the existence and malleability of official racial classifications in Singapore and Asia through which this infrastructure emerges. Racial categories for population administration provide a convenient and salutary statistical framework for the biomedical sciences. Biopolis's American-style biomedical research is thus resolutely global in its ambition; and the ethnic heuristic, detached from specific national moorings, facilitates a transnational inclusiveness because majority populations (Chinese, Malays, and Indians) in the region who were previously excluded from "universal" biomedical research can now be brought under the molecular gaze. In recognition of this universalizable power of the ethnic heuristic, the NIH selected Singapore's "trans-ethnic" DNA project to develop statistical research on the DNA of "non-European" populations.[34] In a sense, American scientists furnished the ancestry/ethnic heuristic, as Lock and Nguyen have

argued, and their Singaporean counterparts apply it to majority (not minority) populations in Asia.

This book is an experiment in what I call an anthropology of the future. How can anthropology—the study of the diverse ways of being human—be made relevant in the twenty-first century? Whereas anthropologists have long assumed that "culture" has always had a monopoly in defining the human, Stephen J. Collier and I maintain that science and technology actively mediate cultural notions, thereby proliferating novel ideas of the human, living, and life itself. The task of anthropology therefore is to investigate how contemporary science participates in and transforms preexisting cultural ideas about the anthropos in multiple registers today.[35] In an age of hopes for science and technology, ethnographies are critical for illuminating how cultural, philosophical and political differences translate and shape experimental systems and milieus.[36] Following a visit to China, Nikolas Rose has observed that the racializing trend of pharmaceuticals in Asia should not be dismissed as due to simply cultural differences. Instead of a reflexive critical suspicion, he cautions, we might seek answers in "new relations of genomics, identity, biosociality, and bioeconomics."[37]

In the chapters that follow, my study of Biopolis in Singapore, with a glance at BGI Genomics in China, goes beyond cross-cultural and cross-disciplinary translations to interrogate how science itself becomes transmuted in the process of designing anticipatory futures. This book is an ethnographic study of Biopolis, Singapore's City of Life, a global milieu that seeks not only to incubate a new life science in and of Asia, but also to mobilize new political and ethical horizons for managing uncertainties in a uniquely connected and vulnerable region. Even as therapies are becoming more and more individualized for the wealthy, as in the sequencing of Steve Jobs's genome in order to treat his pancreatic cancer, pharmaceutical innovations continue to demand the capture of huge swaths of new data. But whereas biomedical science is amazing in promising to unlock the codes of life, our diverse and shared fortune as anthropos is not so easily predictable or prepared for.

The new biology evolving in Singapore and elsewhere is an interdisciplinary field, bringing together the diverse expertise of biostatisticians and classically trained biologists, engineers, and doctors who often do not see eye-to-eye but do depend on the same sources of state or overseas funding. Different techniques are fashioned from dry labs and wet labs: that is, sites for the analysis of computer-generated data and classic bench-top experiments with biological materials. My investigation focuses on some research

programs integrated with clinical and academic research communities, including genetics, oncology, stem cell research, and tropical diseases. I explore the biomedical assemblage from the inside to illuminate how the work of science is infused with intensities, optimism, and anxiety.

As part of its quest to be a global biomedical hub, Singapore shifted from a British medical tradition focused on high-quality patient care to an American style of training physician-researchers engaged in innovative evidence-based practices. In 2003, Biopolis was established by the Agency for Science, Technology and Research (A*STAR). Biopolis comprises a cluster of public research institutions and corporate labs involved in many areas of biomedical science activities. Outside the Biopolis precincts, there are many international medical programs, including the Duke-NUS Graduate Medical School and the Johns Hopkins Cancer Center as well as major teaching hospitals and global drug laboratories. Biopolis is then itself less a singular site and more a network of institutions stretched across the island and beyond. With the term, "Biopolis complex or ecosystem," I refer to this extended network of universities, hospitals, clinics, research institutions, and pharmaceutical companies in Singapore and overseas.

Singapore has gathered an international community of life experts (biostatisticians, geneticists, stem cell experts, neuroscientists, bioethicists), the so-called new specialists of the soma,[38] to meet such challenges. The bioscience research community draws from the public and private sectors, composed of more than two thousand scientists. Foreign and local-born researchers have been trained at leading world institutions such as Cambridge University, University of Edinburgh, Harvard University, MIT, Johns Hopkins, and many more in Europe and Australia, as well as Singapore's own world-class universities. Science luminaries supervise labs, unfairly dubbed "research factories," where hundreds of PhDs recruited from top-ranking universities in China, India, and Singapore work in some obscurity. Despite their busy schedules of work and travel, all scientists whom I contacted were responsive to requests for interviews. Biopolis has many corporate labs, but scientists there were unavailable for interviews because of concerns about intellectual property issues.

This book draws on research conducted between 2004 and 2013 during multiple summer visits to Singapore. In all, I interviewed a few officials and scores of researchers in fields such as population genetics, medical genetics, oncology, bioethics, infectious diseases, and stem cell research in the extended Biopolis complex. My investigation focuses on research practices

rather than on therapeutic activities, and my informants tend to be scientists (principal investigators) who often are clinician-scientists. Most of my interview data were collected in the spring of 2010, when I was a research fellow at the Asia Research Institute of the National University of Singapore. Some scientists were interviewed later at UC Berkeley and the UC San Francisco Medical School in California, and BGI Genomics, China.

Besides hour-long interviews (and repeat visits in many cases) at the offices of science institutes, I attended the many international conferences and lectures at Biopolis and the Duke-NUS Graduate Medical School. I also visited major teaching hospitals and clinics throughout the island, and I generally imbibed the biomedical culture brewing in Singapore. I hung around different medical campuses and ate in cafeterias serving international cuisine. This fieldwork, driven in part by my capacity to connect with individual researchers, offers captivating ethnographic and philosophical moments that highlight the invisible work, as well as the uncertainty, going on in some of the labs.

I am grateful to all respondents, from principal investigators to lab workers, from American scientists to mainland Chinese technicians, for their desire to explain to a nonspecialist what it is they are doing. I was generally impressed by their ardent interests, strong dedication, and professed optimism for the future. The identities of informants are disguised except where otherwise indicated. Scientists with public roles and well-known reputations—such as Edison Liu, director of the Singapore Genome Institute (2003–2010), and Henry Yang Huangming, a founder of BGI Genomics, among others—retain their own names. I appreciate the time and effort they took to engage someone who is concerned about the anthropos in other guises.

Not all scientists I encountered participated in the project of ethnic-stratified medicine, and many projects at Biopolis do not mark their data or claims in ethnic terms. But as one among other Asia-born researchers, my presence may have stimulated a degree of candidness seldom encountered by other anthropologists. In Singapore, cultural discourses suggest an overlap between race and ethnicity, and that will be evident in quotes scattered through this book. At the same time, most researchers frequently invoked "Asia" and/or "Asian" to highlight some dimension or element—in genetic variants, beliefs, values, way of life, and geography—that is a necessary and significant part of their work in forming this globalized biomedical milieu.

location, the city-state's potential vulnerability to many intersecting traffics also creates its potential for controlling flows of deadly diseases. By understanding the relations and places that Singapore gathers as a hub, the airport needs to act as a political spigot controlling different flows in the event of emergencies. In Israel, the state garrisons itself against its purportedly unfriendly Muslim neighbors as well as potential pandemics. In Singapore, the state as spigot can operate most explicitly as a cordon for the world against "Asia" wrought as a disease-ridden place (but also as a source of potential terrorists). A quarantine against deadly infectious diseases interacts with military-political barriers against the body politic, writ large. While radical uncertainty remains, such preparations are among the best to prevent the leaking of tropical diseases into the rest of the world.

NINE

THE "ATHLETE GENE" IN CHINA'S FUTURE

Life is of sequence—A.G.C.T.
Life is digital
Information is the language of life
Not the analog.

In his epigrammatic style, Dr. Henry Yang Huangming, the founder and then president of BGI Genomics, China, set out his "philosophy" of "why life is life" at a 2010 Harvard-sponsored conference about Asia's vision in the twenty-first century. Yang was introducing BGI Genomics (henceforth BGI) to the rest of Asia, describing it as "the largest genome sequencing center in the world." The institution aims to sequence the genomes of any and every living thing: humans, animals, plants, fungi, and microbes. On the basis of increasing the ease in mapping the long lists of nucleotides and combinations of DNA markers for individual organisms, Yang declared, to gathering unease in the crowd, "Bioscience and bioeconomy will shake up the world in the twenty-first century."[1]

When asked whether, in his vision of life as a genome sequence, he was missing "life's complexity, the legend in the map," Yang replied, "We are far, far away from knowing life. What we are doing is very superficial and sequencing is only the beginning, comparable to the periodic table in chemistry." Here he indexed the heuristic nature of modern experimental science; historically, the rendering of chemistry in tabular form enabled the standardization of a

language between disciplines, which helped to push life science from natural history to an experimental science of life, biology, and, later, genetics.

But the audience was less concerned with a question over the heuristic nature of modern experimental science than the ethical problem of its potential applications. Yang responded to skepticism of his organization by clearly distinguishing BGI's power to rewrite the program of life from the synthetic biology unfolding in the West as exemplified by J. Craig Venter's goal to reengineer life at the cellular level. But perhaps what BGI is doing is not that different from what scientists at Harvard, MIT, and Berkeley are doing, only it is at a more stunning scale.

Yang emphasized that there is a critical East-West difference in the uses and implications of post-genomics biology. In Yang's view, in technologically advanced countries, the public worry is about the harm that science can do, whereas in developing countries such as China, science is viewed as a problem solver, and there is the need to be concerned about the ethics surrounding its uses. Yang seems to be saying that in China, and Asia more generally, the ethical justifications take a different form from "Western" scientific responsibility, which, in his estimation, hinges on the supposition that it is the way scientific applications are used and mobilized that renders whether something is good or bad, ethical or not ethical.[2] By comparison, in the developing country case, Yang suggests, these justifications take a different form. They focus less on the ethics of potential applications and so are not hung up on what appears to be time-wasting committees or scare journalism, but instead are poised toward their usefulness in informing actual and practical decisions, positions, preparations, and coordinated action. In other words, scientists from the People's Republic of China (PRC) are not claiming to reinvent the wheel like the Americans; the claims and aims of BGI, for instance, are not first to do good with science, but to do good science, with the hope of the results of that work ramifying as a collective social good down the line. It seems a more humble ethos in the application of science for the common good. But "good science" in the BGI incarnation is about many things: being a good scientific citizen, and generating good values for human welfare through an efficient system of corporate science.

In this chapter, I discuss BGI in order to illuminate its differences from Biopolis, the main focus of this book. I begin by noting the rapid rise of BGI, a nonprofit institute and company in China, which is not affiliated with the Chinese state but now dominates the world in DNA-sequencing prowess. Unlike Biopolis, which is an extension of Euro-American cosmopolitan science using "Asian" materials, I suggest that BGI is a new model of Chinese global

research and business that stirs both skepticism and anxiety among Western observers, both for the sheer magnitude of its sequencing operations and for the ways in which it is taken to embody, rightly or not, a number of worries over Chinese science in its deviation from cosmopolitan scientific structures and strictures. I then shift to the dual faces of BGI, contrasting its international and domestic modalities of biodiversity for research on emerging life forms. On the national front, I argue, BGI deploys ethnic classification in a signal study of Tibetan DNA that seems to foreshadow China's biomedical preparation for global uncertainty.

Not Just a Global DNA Assembly Line

BGI Genomics is a private, nonprofit organization founded as the Beijing Genome Institute in 1999 to participate in documenting 1 percent (the "Chinese" component) of the Human Genome Project. The cofounders, Henry Yang and Wang Jian, along with two other colleagues, were members of the "lost generation" who grew up during the Cultural Revolution (1966–1976). Some of the most entrepreneurial leaders in China today are from this cohort. They went through hardships, including the closing of all schools, but later managed to go to college and even enroll in universities in the West. The future BGI leaders were trained in genomic science: Henry Yang at the University of Copenhagen, and Wang Jian at the University of Washington, Seattle. With their cosmopolitan experiences, Yang and Wang are very unlike China-trained scientists employed in state institutions. BGI started as a nonprofit research entity affiliated with the Chinese Academy of Sciences, but it split off into a private organization in 2007 when state funding dried up. BGI leaders also chafed against the bureaucracy and conservatism of the Chinese state science world that was skeptical of such an expensive science venture. In addition, national agendas did not permit freedom in biological research within the state system. BGI decided to be formally and institutionally independent of the state, I was told by a corporate representative, in order to be free to choose its own projects without risking possible abuses of science.

In 2009, the Shenzhen government offered BGI close to US$13 million to move to its Special Economic Zone, near the border of Hong Kong. Commenting on the move from the nation's capital, a BGI investor said, "Shenzhen is as far from Beijing as you can get. You can't be independent in Beijing."[3] Recast as BGI Genomics Shenzhen, the company operated out of a former shoe factory, enjoying the same cheap land rates and tax breaks as its neighbors, including the giant Foxconn factory that manufactures Apple digital products

for world markets. Shenzhen is the technological incubator of China, providing prime opportunities to combine a mass assembling infrastructure with DNA research. As BGI's international sequencing business grew, the company opened BGI Hong Kong in another former shoe factory, putting the company close to global transportation networks that allow a quick turnover in processing DNA samples and performing medical diagnoses for overseas clients. Having grown accustomed to Biopolis's high-tech and resortlike enclave, I was surprised at how basic and unglamorous BGI Hong Kong is, situated in an outdated industrial zone.

Although BGI had divorced itself from PRC political and scientific funding establishments, it has benefited from funds and tax breaks offered by the Shenzhen and Hong Kong governments. By this time, BGI had made the central government proud for putting Chinese genomic science on the world map. In 2010, the Development Bank of China offered BGI a loan of US$1.5 million to purchase sequencing machines from the United States, making it the world's largest facility. The company headquarters at BGI Shenzhen has more than 158 sequencing machines, and it claims to have sequenced some 57,000 human genomes to date.[4] The institute employs four thousand people, including two thousand PhDs. There are over a thousand young employees in bioinformatics alone, many of whom live in company dormitories. But BGI Shenzhen has grown beyond being a sequencing platform to designing new medicines and food products. Institutionally, BGI Shenzhen is a bit like the Biopolis campus in that it has different divisions, dedicated to diagnostics, animal cloning, and agricultural research.

In a bold innovative move, BGI in 2013 acquired the assaying company Complete Genomics in Mountain View, California, and now has the capacity to produce the machines that produce the data. It is estimated that BGI has at least 25 percent of the world's total gene-sequencing services, followed by Illumina of San Diego and the Broad Institute of Harvard and MIT.[5] In the world, BGI is mostly known for being the world's largest sequencer of genetic data on animals, plants, microbes, and humans, giving BGI the capacity to shape the evolving global ecosystem of genomic science.

The meteoric rise of BGI has stirred trepidation in the world of bioscience. For observers in the West, BGI has been viewed as the apparent spitting image of the PRC industrial behemoth, literally built into former factory spaces hiding in plain sight in China's industrial zones. The uncertainty for those on the outside is that BGI is a chimeric entity; this view is heightened because, with China's ascending global economic power, "security" concerns are the expression

of a suspicion over the categorical hybridity of Chinese institutions in general, and of the gigantic capacity to dominate global industries from manufacturing shoes to manipulating genomes. The narrative of Singapore's Biopolis—U.S.-influenced, cosmopolitan, capitalist—contrasts with BGI's image as one of those strange PRC hybrid entities, a chimera of socialism with Chinese characteristics: Is it or is it not a factory? Is it a private or a state entity? Is it a research or a capitalist institution? As a biomedical milieu, is it doing ethical or unethical things?

In foreign science journalism, the digital mechanization that drives Shenzhen's industrial powerhouse has been transposed to the fast informatization of living forms. In 2010, a writer for *Nature* magazine dubbed BGI "the sequence factory" and skeptically asked whether "its science will survive the industrial ramp-up."[6] After BGI's purchase of Complete Genomics, a *New Yorker* piece repeats the factory theme, branding BGI "the gene factory."[7] An image of "assembly-line" DNA is used to describe BGI's global reach.[8] From Western journalistic and science perspectives, calling BGI a genome factory implies that because of its Foxconn-like, mass-assembling approach to data, there is a skepticism as to whether the company can be an innovator in science.

Dr. Svensen, a geneticist, previously at Biopolis but now at the University of California, San Francisco, remarked to me, "Genome sequencing is just a global service, that is, stupid work that should be industrialized. Once sequenced, it is up to the scientist to analyze how genomic information is different." His comments suggest that China's science power lies in its cheap labor, not intellectual creativity; there is also the suggestion in factory imagery that workers are exploited in assembly-line data production. At the same time, Svensen seems to miss a different truth, which is that genomic sequencing is a platform for scientific experimentation. While the genomic sequencing infrastructure is not the current aim of the science, a monopoly of global data points exerts a kind of biostatistical power to monopolize markets, to write new algorithms, to plan a novel design of life.

There is trepidation about whether BGI is a state-driven institution that challenges how international science is conducted. Related to this worry is BGI's fusion of research and business in a new kind of global science facility. When I asked Dr. Chen of BGI Hong Kong to address such criticisms, he said emphatically that BGI is not a state agency but "a nonprofit and a commercial venture, a research and a marketing project." He went on to say that BGI may be "hybrid" but not in the sense of being a joint state venture; instead it is like any American private company (like Google) that vertically integrates

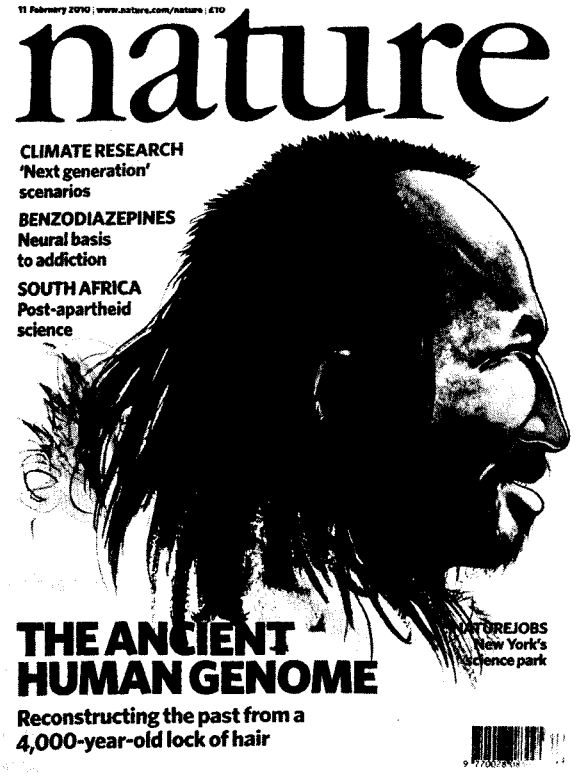

FIG. 9.1 BGI's study of the "ancient human genome" makes a splash. Courtesy of *Nature* Magazine.

multiple research and business units. As such, as the world's largest genomics center, BGI is attractive to investors worldwide, including the Silicon Valley venture capital firm Sequoia Capital. At Berkeley, Dr. Rasmus Nielsen, an evolutionary biologist who works closely with BGI (see below), noted that anxiety about BGI as a "genome factory" should not be about BGI as doing something unethical. Rather, there has been concern about the speed of BGI's rise and its ever more complex logistics and bioinformatics, all factors that decisively inform its global competitiveness. But, as we shall see, BGI is a new kind of science company that is innovative on different fronts.

The "sequence factory" label was first earned when BGI analyzed the DNA of an ancient human from a hair fragment found in Canada's ice wastelands. Featured on the cover of *Nature* magazine (February 2010), the study put Chinese life sciences for the first time on the global map (see figure 9.1). The arresting portrayal of an ancient human became a kind of ethical branding of BGI. In its

plan to digitize, eventually, the entire human pool, proceeding from Asia to Africa and South America, BGI has won another moniker: "a library of digital life."

As an ambitious science organization, BGI has been innovative in forging international collaborations with major research institutions and joint labs in the West. Projects with the University of Copenhagen, where Yang trained, include the sequencing of the Danish pig and the study obesity in Denmark. Under the umbrella of BGI Americas, in Cambridge, Massachusetts, BGI is helping to build a DNA analysis center at the Children's Hospital of Philadelphia, and it is developing programs in food security and human, animal, and environmental health at the University of California, Davis. There are new BGI branches in South America and Africa. As a global sequencing powerhouse, BGI is a critical provider of bulk services to U.S. institutions.

BGI has also deployed its sequencing capacities in its role as a global citizen of science. After the Asian tsunami in 2008, BGI experts sequenced the DNA of victims to help with the identification of their nationalities (aligned with ethnic profiles of their DNA). In 2011, after a mysterious outbreak of food-borne diseases in Germany, BGI sequenced the *E. coli* strain found in contaminated sprouts within three days and made the data freely available, which helped to put an end to the contamination. When it comes to Asia, BGI offers scientists, including those at Biopolis, reduced costs for sequencing services as a way to boost their research.

Indeed, genome sequencing on a large scale is a relatively easy way to achieve a global presence for Chinese science. As a commercial enterprise, BGI has been an inexpensive and speedy sequencer for researchers around the world. It is a very complex, multifaceted genomic science enterprise, with different divisions focused on the technologies of sequencing, screening human DNA for medical applications, and developing plant and animal hybrids for food security. BGI promises to change the infrastructure, business, and innovations of cosmopolitan science. In an email, a BGI manager describes the following scenario: "China is rapidly positioning itself to become an important—and hugely disruptive—player in the industry's future trajectory."[9] By putting its sequencing prowess at the service of the world, BGI has already made an impact in sequencing the planet's biodiversity.

Modalities of Biodiversity

A question for an imperiled world today is whether we should value the whole of biodiversity for its own sake or for the differences composing that

diversity. DNA sequencing is therefore about mapping life on earth and, in the process, discovering findings that can sustain the health of our species and the planet. I suggest in the rest of the chapter that BGI, in building its sequencing databases, prioritizes two models of biodiversity by using different metrics of species and ecological levels. I compare BGI's modeling of the "tree of life" in two ways. The first universal tree prioritizes species that are important to economy and science (i.e., values of the ecological sustainability of our planet), while the second "Chinese" tree identifies the scientific and aesthetic values of iconic species within the cultural-ecological habitat of the national motherland.[10]

BGI's approach to the book of nature is to model DNA databases in terms of their specific scientific findings, but it makes a distinction between the general planetary biosphere and a Chinese biosphere. The classical image of the tree of life is up for revision in BGI's vision. At the conference where Yang encountered skepticism from the audience, he professed his company's goal of "flying the science and humanity banner," an intention he expressed in a flamboyant style.[11] In 2010, BGI launched the 1000 Genomes Project in order to generate reference genomes for a thousand "economically and scientifically important plant/animal species."[12] On the webpage, a tree of life (see figure 9.2) diagrams a certain logic of assemblage in that *Homo sapiens* is not at the top of the tree but ironically reoccupying a position near the center of the biospheric tree. The trunk of this global tree is a double helix, suggesting that the species leaves are related because of the various combinations of nucleotides in DNA rather than the splitting branches and bifurcations of evolution. Indeed, there are no branches at all, suggesting a biosphere or atmosphere of life rather than the arborescent tree. Also there are openings to the sphere, which suggests more worlds of life and form beyond the selected one thousand genomes of flora and fauna important to human beings. What kind of anchor is the modern human positioned therein, relative to the surrounding circles of animal and plant species spinning on the top of a blue planet Earth? As a figure of both immanence and transcendence, this tree of life is haunted by the intertwining interests of ecological sustainability and corporate branding. The diagram depicts the interrelationships among different animal and plant species, suggesting that genomic findings would yield tools for sustainability that can be economically made accessible to all of humankind.

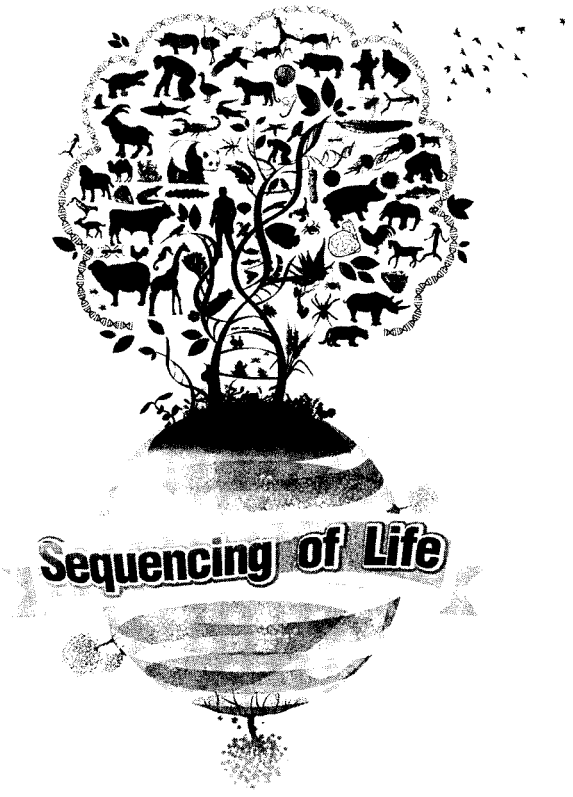

FIG. 9.2 BGI's tree of life for the 1000 Genomes Project. Courtesy of BGI Shenzhen.

Meanwhile, within the lobby of the BGI office in Hong Kong, there is another tree of life (see figure 9.3), one with the particular Chinese lens of biodiversity within China's particular ecological, cultural, and political sphere. The intrusion of a Chinese biocosmology into DNA mapping is perhaps unsurprising. BGI scientists, especially the president Wang Jian,[13] present themselves as patriotic citizens of the PRC who want to do science that contributes to China's sustainability, prestige, and national identity. There is a race to sequence the DNA of humans, animals, plants, and microbes, that is, to mobilize the knowledge of life forms considered part of the national patrimony. The project is not driven by the state, and indeed Chinese state science institutions are neither coordinated nor entrepreneurial in the way that BGI is.

But beyond its resolutely international orientation, BGI has a homegrown interest in building a Chinese genomic treasure house that can contribute to

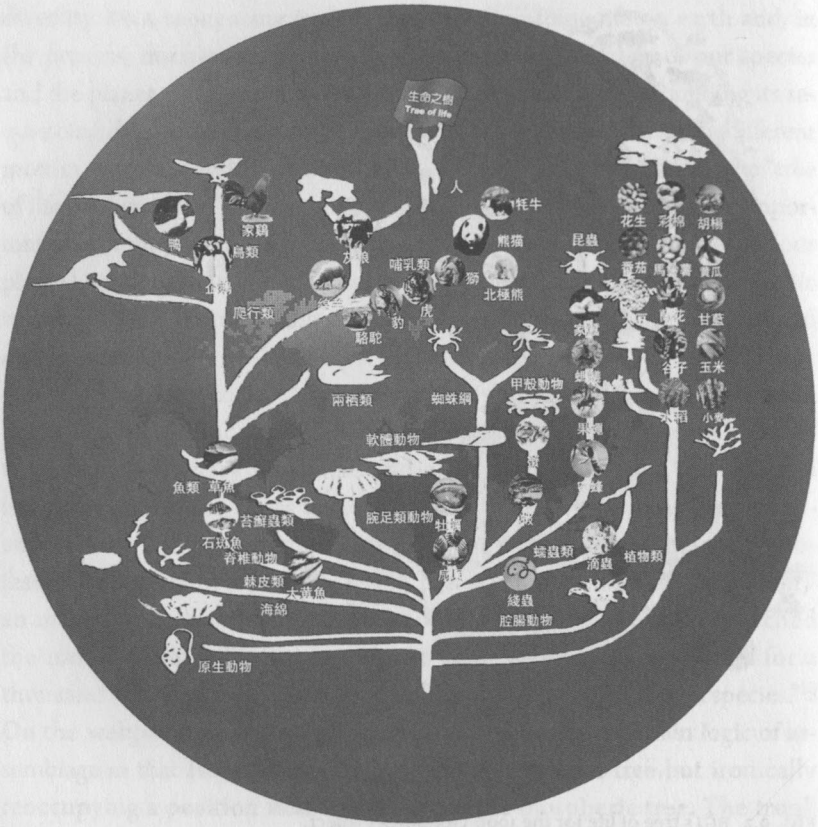

FIG. 9.3 BGI's other tree of life. Photograph by Rena Lam; courtesy of BGI Shenzhen.

the health and biosecurity of the nation. Thus, while aiming to model the entirety of life, BGI also focuses on generating genomic maps of Chinese forms of life, especially charismatic species like the giant panda, the stork, and the silkworm, as well as flora (soybeans, golden ancient poplars, mushrooms) that are specific to the Chinese ecosystem, which is coextensive with China's modern territorial boundaries. Nonnative animals and plants—chicken, rice, peanuts, tomatoes, maize—have long been Sinicized as food crops vital to the civilization.[14] The China-centered ecosystem emphasizes differences between life forms in order to generate commodifiable value for research and medicine. The increasing facility and speed of the bioinformatics software have greatly improved Chinese scientists' capacity to respond to major arenas of concern for the PRC: to develop genetically modified foods (e.g., rice and maize) and cloned livestock and to develop stem cell research to treat

human diseases. The first step in wielding this bioscience prowess is to stake scientific and symbolic claims on China's charismatic and necessary biological forms.

The BGI's Chinese tree of life, a projection of the artist's imagery, thus enacts China as a distinctive genomic branch of the tree of life. This branch image suggests a very different conception of evolution and relatedness among species than the amorphous DNA cloud depicted in the other tree model. The unified origin of Chinese species, where people (at the top) branch off from primates, first suggests a unified descent in place, which seems to suggest a deep territorial-evolutionary relationship to China as a historical-cultural complex. Besides native species, the tree incorporates nonindigenous ones that are historically part of the glorious Chinese food culture. The Chinese tree is very different as well from the more conventional Biopolis notion of populations resulting from the migration of an already-evolved human species.

This powerful representation of Chinese life forms evokes not only their innate qualities but also their cultural and even mythical roots and routes to China's present, with iconic species mapped onto the flat time of national culture heritage, ending with a Chinese-identified human figure at the top. Mimicking the aesthetics of classic porcelain design, this diagram contains and delimits Chinese forms of life as so many branches of a nationalized multispecies tree within the shape of a blue plate. As a patterning of genomic truth claims, the tree metaphor embodies the very singular *oikos* of an emergent globalizing Chinese ethnos.

Ethnic Classification and Governing through Blood

As mentioned above, BGI has bigger ambitions than PRC state-run science institutes, but BGI also has its own dream for Chinese biomedical science. It has turned its algorithmic power toward differences composing human biological diversity in China. The goal is to develop medicine that can be customized for different groups in the country.

There are, however, significant differences between BGI and Biopolis, in the deployment of the ethnic heuristic and itineraries of medical information. Elsewhere, I illuminate how researchers in insular Singapore use the ethnic heuristic for constructing DNA databases that can create broader environments for making the categories fluid and fungible. The ethnic-specified digital knowledge makes ethnicized DNA convertible and substitutable across different domains of science valuation so that these objects can represent majority "Asian" populations in the world.

BGI's participation in racialized medicine has different international and domestic aspects. Internationally, it provides information for the Asian Cancer Research Group, a nonprofit company that investigates cancers that are prevalent in Asia, primarily focusing on liver, gastric, and lung diseases. Eli Lilly in Singapore, with Merck and Pfizer, takes the lead in organizing the collection of profiled tumor samples and data throughout Asia. Big pharma is clearly aligned with racialized medicine. A Pfizer scientific officer explains that "environmental and genetic factors are believed to underlie the dramatic differences in the molecular subtypes and incidence of cancers in Asia and other parts of the world. Although some progress has been achieved in the last few years in understanding and treating these cancers, they remain a huge unmet need and a disproportionate health burden to Asian patients."[15] BGI's is the first-of-its-kind genomewide study of recurrent hepatitis B virus that causes the most common form of liver cancer in China, with the highest rates in the world. The Asian cancer group is a new trend in which big drug companies engage in a precompetitive collaboration, combining their resources and expertise to accelerate research of disease and disease processes.

While the Asian Cancer Research Group uses the "Asia" marker as an immutable mobile in a Biopolis-like manner, BGI's own projects on genetic diversity and ethnic differences are about identity in and of place, as classified within the territory of China. Whereas Biopolis projects deploy ethnic-differentiated DNA in an expansive, origami-like digital configuration of "Asia," BGI's projects identify ethnic DNA differences as points of encounter in the stream of flows all firmly bounded by China's official history and borders. The comparative ethnic DNA mapping in China is about the social ordering of ethnic differences and associations that are not substitutable outside the Chinese world. Below, I will discuss this China-centric orientation in the Yanhuang and Tibetan projects. But, first, a brief account of China's pervasive ethnic classificatory scheme is necessary.

Human sciences in the PRC are institutionally obliged to follow the system of official nationalities. Since the sequencing of the human genome occurred, PRC-born researchers, following the official ethnic classification of the Chinese nation, have used Han Chinese as the master ethnicity. The Ethnic Classification Project (*minzu shibie*) of 1954 determined the fifty-six ethnic nationalities (*minzu*) entitled to political representation within the territorial expanse of the PRC. These fifty-six *minzu* compose a single master nationality, "Chinese" (*zhonghua minzu*), making China a multinational nation, of which people identified as Han make up the vast demographic majority. Thomas

Mullaney argues that a pre-1947 British imperial sociolinguistic taxonomy for classifying groups in Yunnan, and Stalinist criteria for the categorization of "plausible communities" becoming nationalities influenced the PRC classification of *minzu*. By 1984, a definitive and nonmodifiable fifty-six *minzu* classification was completed, thus establishing a primordial model. Official discourses entrenched this *minzu* scheme as central in the maintenance of the territorial, political, and economic integrity of the country.[16] This scheme highlights two important details: the differences between majority Han (*hanzu*) versus non-Han populations, and the "official-national identity" (*zhonghua minzu*) that is the umbrella of the multinational state. Not surprisingly, scientists are institutionally bounded to work within this official fifty-six *minzu* framework in order to sample and conduct DNA research.

The conflation of the official *minzu* classification and microevolutionary theory seems officially fortuitous in China. Human evolutionists identify an epigenetic rule of gene–culture coevolution that correlates groups evolving in relative isolation with a susceptibility for genes for certain diseases. One may perhaps trace the birth of Chinese genomics to a 1994 project initiated by the Chinese Academy of Medical Sciences to assemble the "immortalized cell lines" of different Chinese populations. A group of geneticists and ethnologists from leading universities (at Beijing, Harbin, Kunming, etc.) set out to collect "relatively pure genes" of "isolated" minority groups on the continent. The Chinese scientists feared that such gene pools were increasingly diluted through exposure to other populations. Dubbed "the world's largest ethnic DNA bank," this state project provides a kind of baseline for subsequent ethnic-associated genome studies in the country.[17] While state institutions individually pursue such DNA research trends, there appears to be no unified state coordination simply because the China science milieu is profoundly underregulated. Rather, researchers have been impelled by sociopolitical beliefs in ethnic differences and patriotic zeal to pursue convergent projects that give shape to an emerging racial biomedical science.

BGI dipped its toes into ethnic-specified medicine when it joined an international effort to establish the most detailed catalog of human genetic variation ever assembled. The international 1000 Genomes Project, launched in 2008, includes BGI Shenzhen, the Wellcome Trust Sanger Institute, Cambridge University, and the National Institutes of Health in Bethesda, Maryland. The consortium aims to sequence the genomes of at least one thousand anonymous participants from different ethnic groups. In the process of making a detailed map of human genetic variation, the goal is to find rare genetic

variants related to diseases. With BGI taking the lead, China became the first country to begin to sequence the whole genomes of larger numbers of individuals. At that time, worldwide, only two individuals had had their genomes sequenced: James Watson and J. Craig Venter. BGI has since sequenced the genomes of two Chinese individuals, one of whom paid about US$1.4 million for the analysis. By 2014 BGI, with its accelerating sequencing powers, had exceeded the one thousand genomes limit and hoped to expand to a one million genomes project for human beings, as well as for animals and plants.

For the past decade, (non-BGI) Chinese geneticists in Chinese universities have been busy analyzing the DNA of the Han nationality, which is genomically distinct from related ethnic minorities in Southern China. A study by PRC scientists calls the Han Chinese "the largest single ethnic group in the world, consisting of ten branches." One study of the Y chromosome and mitochondrial DNA demonstrated, the researchers claim, "a coherent genetic structure of all Han Chinese." Researchers identify an "older branch of the Han Chinese" in the Pinghua group that is represented by ethnic minorities (*shaoshu minzu*) in Guangxi Province (the Dai, Hmong-Mien, Zhuang, Kam, Mulam, Laka).[18] The majority of these scientists are not linked to BGI, but the research institute has begun in a more targeted way to map the genomes of Han and non-Han populations. For instance, BGI has sequenced the genome of a Mongolian subject, said to be a thirty-fourth-generation descendant of Genghis Khan (Mongolian is one of China's official nationalities).

In the international one thousand genomes effort, BGI's contribution is called the Yanhuang Project, which has sequenced the entire genomes of one hundred Han Chinese individuals. The Yanhuang (YH) genome map shows the relationship between YH genotypes and phenotypes and their associations with fatal diseases that threaten ethnic Chinese populations. By making genetic maps of populations in China, BGI provides an unprecedented biomedical resource for developing personal medicine that promises to benefit ethnic Han Chinese. The BGI Shenzhen website posted the following claim: "We Chinese people have our own genetic background, disease susceptibilities and drug response, which differ dramatically with other populations. For instance, Caucasians are reported to suffer more from skin cancer while Chinese suffer more from liver cancer."[19]

The mapping of DNA along the *minzu* axis cannot help but more firmly intertwine the search for ethnic-specified health vulnerabilities with the politics of Han-majority rule. Leading China anthropologists have argued that the post-1949 invention of ethnic minorities not only distorted the past but also involved

Han civilizational attempts to impose dominant values while heightening the sense of ethnic differences.[20] Louisa Schein has explored the postmarket reform's "minority rules"—expressed in media, identity performances, and tourism—as an ongoing cultural production of "internal orientalism," especially with regards to the Miao as a "feminine other."[21] Nevertheless, cultural and linguistic differences between Han and minority groups, especially the Tibetans, may be more blurred than official representations would have us believe.[22] Besides Tibetans, powerful disenfranchised minorities such as Muslim Chinese are constructing their own "ethnic nationalism," in a protracted politics of center-periphery struggles through which the Han majority come to define themselves.[23]

Not surprisingly, an interethnic genomic database of China is both contextual and performative, in that it remediates *minzu* as a biological form and interrelationship, even as "race" was only one of several criteria in the original official classification of groups, tied as it was to conceptions of ethnicity adapted from Stalinism and its conceptions of social-political evolution rather than biological unity. Ethnic-differentiated genetic data perform knowledge affects, drawing on the authority and social order within which they are produced. After all, the Yanhuang name is historically and culturally extremely significant, for it is the conjoined names of mythic ancestors of the northern (Huang) and southern (Yan) branches of an ancient group, the Huaxia, who are believed to be ancestors for the Han peoples. In this chauvinist move, substantive genetic unity is created out of the national origins story that traces Han roots in historical groups from the northern and southern halves of this vast continent. Thus, BGI's one hundred genomes project for Han Chinese and other studies genetically establish the Han Chinese as the original national population in a genomic majority-minority scheme of ethnic groups.

When I discussed the Yanhuang name, the historian Wang Gungwu said that trouble begins when geneticists use historical names out of the fog of history to designate the historical and genetic originary compositions for contemporary groups in China. This sort of biologization of a deep cultural-historical memory is a technological aspect of what Benedict Anderson calls "imagined communities," a prerequisite and ongoing process in the creation of nationalisms.[24] Wen-ching Sung has argued that the "imagined national-ethnical identities turn genomic research into vehicles for recapitulating and substantiating the notion of Chinese ethnicity."[25] Han ethnicity (and the broader ethnic scheme of the PRC) gains substantiation through bioinformatics, and this not only shores up hegemonic racial formations but also aims

to establish the long historical-national claim to an antique Han domination and racial unity. The YH project propagates a genetic consciousness that reinforces beliefs in the biological "sameness" of diverse ethnic communities gathered as "Han" in China. The YH project, Dr. Chen of BGI claimed, is only a "primary model" in building "the China Genome data bank as a national bank." The main concern is to find disease susceptibility genes and learn more about hereditary diseases as a way to maintain the health standards of Chinese people. It seemed reasonable to focus first on the Han as the largest ethnic political entity, Chen continued, but other groups will be included in future DNA studies. Ethnic-differentiated genetics is not merely ideological but constitutive of a new way for managing the biological health of the nation.

Besides the multi-*minzu* political order, the rise of genomic science in China also requires a new mode for accessing human samples. After generations of blood-donation public health campaigns, Vincanne Adams, Kathleen Erwin, and Phuoc V. Le have argued, contemporary China has increased its supply of safe, transfusable blood. By compensating blood donation that is not commercialized, "reciprocal obligations between citizens and the state are managed in and through blood." A systematic program of "governing through blood" ruptured traditional notions of blood as a precious family essence or *qi* (spirit or energy), and it infused a popular embrace of blood donation as "an act of altruistic patriotism."[26] Organized by workplace units (*danwei*), obligatory compensated blood donations (starkly contrasted to "blood selling") have become a normalized way to participate in socialist welfarism. With biology politically actualized by this mode of blood governance, work-unit quotas for patriotic blood donations would elicit samples from *minzu* groups across the nation.

This mode of Chinese biopolitical governance thus opens channels to blood samples, allowing genomic scientists, including those in BGI, to create ethnic-specific genetic mappings through which people can be analyzed and thus administered for the well-being of people in China. By banking Chinese genomes, Chen explained, BGI is building the foundation of "a prevention model versus a disease model." The reasoning seems to express a kind of preemptive social eugenics propelled and necessitated by China's demographic heft and anticipated health, social, and political problems in the near future. Chen indicated that this preventive approach was especially urgent because China's one-child policy has greatly increased the burden—the psychological, social, and individual costs—that the younger generation bears in caring for their aging parents. Large-scale genetic studies of China's populations, he rea-

soned, would yield potential DNA information that can inform medical solutions to anticipated genetic health problems and thus ameliorate associated social effects among second and future generations.

At the same time, this preemptive strategy makes use of a cross-ethnic DNA comparison to track the differential distribution of biological weaknesses and capacities across ethnic groups scattered across the vast continent. The operating logic is ethically problematic, rooted in the supremacist pragmatism that any genetic weaknesses identified in the Han majority can be potentially rectified by analyzing genetically beneficial traits found in ethnic minorities. To this end, BGI has multiple branches throughout China, an institutional distribution that mirrors the territorial location of significant minority groups and research topics: Hangzhou (livestock, plant, and health genetics), Xishuangbanna (Dai and other minorities, tropical biodiversity), and Lhasa (Tibetan). At the broadest level, BGI is combining research on biodiversity in plants, in animals, and of human beings almost as iconic species of a singularly China-specific biosphere.

Tibetans and Peak Performance

In the BGI contribution to the one thousand genomes project, the institute first did the Yanhuang study of Han DNA and then moved on to the sampling of Tibetan DNA. The decades-long history of Tibetans' struggle for autonomous rule from the PRC has made them a politically potent people at home and abroad. But BGI's framing of the comparative genetic study seems almost whimsical, not political. Jian Wang, the charismatic president of the institute, had picked up mountaineering while he was a research fellow at Seattle University in Washington (he did postdoctoral work at the University of Texas and the University of Iowa). Returning to China, he became a serious mountain climber and has successfully scaled Mt. Everest. On his climbs, he developed a personal and professional interest in the different capabilities of Han and Tibetan hikers. He was reported as confessing, "I have found that Tibetans are much better than all of us [Han Chinese] on the high mountain, and I wanted to know why."[27]

This desire materialized in a BGI Tibet-Han project—comparing allele frequencies correlated with adaptations to high altitudes—that was published in 2010. BGI researchers identified fifty Tibetan villagers living above an elevation of 14,000 feet (where there is 40 percent less oxygen than at sea level) and gathered blood samples in order to analyze oxygen saturation, red blood concentration, and hemoglobin levels (see figure 9.4). The peak performance

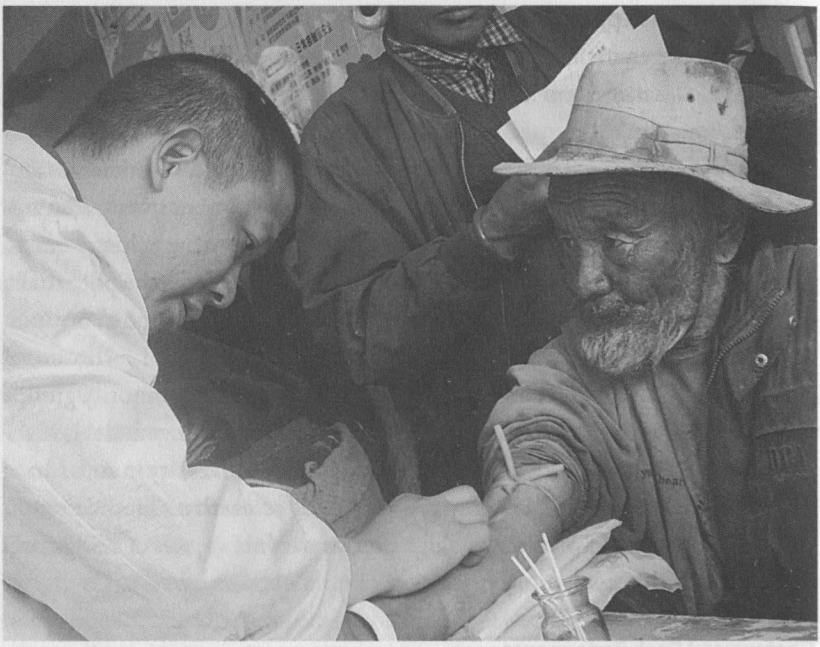

FIG. 9.4 Collecting a blood sample from a Tibetan subject. Courtesy of BGI Shenzhen.

of Tibetans in the Himalayas then was compared with the lung capacities of forty lowland Han Chinese subjects from Beijing.

The Tibetan-Han data then shifted to Rasmus Nielsen, a professor at my home campus in Berkeley and a collaborator on the project.[28] His subsequent computational findings using BGI data received a lot of media attention for their evidence on human evolution. Nielsen and his team analyzed the genes of fifty Tibetan individuals and identified thirty genes with DNA mutations, including a mutation for the EPAS1 gene, which is linked to lower levels of hemoglobin. The EPAS1 gene seems to restrain the overproduction of red blood cells at extreme altitudes, endowing Tibetans with greater resistance to altitude sickness than other groups. The EPAS1 mutation and physiological mechanisms for high-altitude hypoxic adaptation were much less prevalent in the DNA data derived from the Beijing Han sample.

Nielsen shared his view that most geographic variants in anatomy and physiology (often culturally identified as "racial") are due to "genetic drift" or random fluctuations in gene frequency, or the migration of mutation-bearing individuals to other sites. Populations in highlands are good gene pools due to their geographic isolation, but they do share genes back and forth with other

groups. By comparing the SNP (single nucleotide polymorphism) analyses of the Tibetan and Han samples, he determined that the two groups, which share many genetic traits, diverged nearly three thousand years ago. For Nielsen and his team, as well as BGI, the Tibetan study is a coup, and it established their findings as indicating the fastest case of environmentally driven genetic micro-evolution in a human population. In a 2014 report, Nielsen and colleagues traced the ancestry of the EPAS1 variant to relatives of early humans, the Denisovans (contemporaries of the Neanderthals) in Siberia.[29] The Tibetan DNA study is a triumph for the population geneticists, and it was well featured in the American media as a stunning case of natural selection and human evolutionary adaptation.

But given the politically charged nature of Tibetan-Han relationships, and the political implications of genetic Han-Tibetan comparisons, this study is not permitted to be solely about phenotypic plasticity. Therefore, despite the scientific celebration of their evolutionary prowess, Tibet scholars and leaders have rejected the genetic findings, especially any claim of Tibetans' descent from Han Chinese. Critics pointed to evidence that the culturally identified Tibetans have lived on the Tibetan plateau for more than ten thousand years, far exceeding the timeline of divergent population evolution offered by genomic researchers. Robert Barnett, a scholar of Tibet at Columbia University, was quoted as saying that Tibetans viewed the findings as a strategy to provide scientific evidence that Tibet and Tibetans were integral parts of Han China as a race, a people, and a nation. Seeking to diffuse such fears, Professor Nielsen defended himself in the press: "What identifies a people isn't genetics, it's cultural heritage. I don't think this study has any implications for the debate about Tibetan independence and their right to self-determination."[30] From the perspective of BGI scientists, the significance of the findings was not sociopolitical but pharmaceutical, which, of course, has its biopolitical weight as well.

In his campus office, Nielsen remarked that, as an evolutionary biologist, his main interest lies in figuring out genetic exchanges between continents by tracking the DNA of early human migrations to China. Therefore, to him, "the Tibetan case regarding adaptation is great. . . . Not all have direct applications for evolutionary biology. It's a bit like studying different kinds of birds in migration." That sounded like a faux pas, comparing Tibetans to birds, but Nielsen was well aware of anthropological unease over the conflation of cultural and genetic collectivities, and of political charges of potentiality of eugenics. He expressed frustrations at damage done by American media that

sometimes misrepresent bioscientists as thinking that "race is real," as a *New York Times* journalist had said. This suggestion that scientists traffic in biological essentialism and are unaware of potentialities of eugenics research is "nonsense," at least for Euro-American experts. After all, Nielsen pointed out, Euro-American science culture is permeated by an anti-eugenics ethos, "but debate has not yet begun in BGI."

The EPAS1 gene is an evolutionary adaptation to compensate for decreased oxygen level, or an example of phenotypic plasticity, not genetic change. In this study of evolutionary adaptation, Nielsen remarked, the critical difference lies in geography, as in his analysis where Tibetan genetic adaptation to high altitudes was measurable in different hemoglobin responses to thin air. Instead of using ethnic categories, he could have as easily substituted "highland group" for Tibetans and "lowland group" for Han Chinese in the two data sets, replacing a state ethnic heuristic with an ecosystem one. But BGI researchers had already conducted their sampling by using self-identified ethnic groups. For now, ethnic designations are a convenient gloss for population differences, one with implicit state endorsement and through which BGI can explicitly align its research with the well-being of extant groups in the tapestry of Chinese ethnicities.

Nielsen suggested that in the future geneticists will move beyond using ethnic collectivities because within each group "the genetics may not be the same." When I asked him whether ethnicity has been deployed in genomic research as a shortcut to DNA variation, he demurred. Now that large-scale genomic data have been compiled, he added, "We can throw away the ethnic association and go directly to the genetic variant, the high rate of frequency associated with it." He stated, with some heat, that an "ethnic differentiated database is *not* that useful . . . it is a choice." The statement is sufficiently ambiguous so that one may surmise that BGI ethnic-specified DNA information is still somewhat useful because, after all, he went along with the project, even though only at the point of computational analysis and design. Is this an American way of demurral, a vulgarization of science to the public?

Perhaps Nielsen is being disingenuous here, refusing to associate with the ethicized mode of sampling while enjoying the prestige and other benefits that came with working on such a trailblazing project. After all, the pathbreaking nature of the Tibetan project depends precisely on the determination, genomically, of the moment of ethnogenesis, so that it would need ethnic groups (Tibetan, Han) to make comparative sense. When ethnicities are determined by specific gene variations, can one continue to speak in terms of "populations"

in disassociation from the official ethnic labels? As a BGI collaborator, Nielsen seemed to participate in the use of ethnic identifiers as a way of complying with Chinese political necessities in order to gain access to the samples. It would be challenging indeed to disentangle himself from the official Chinese ethnic matrix that provides the conditions of possibility for this experiment.

Air Hunger

Outside the lab, the EPAS1 variant is called the "athlete gene" for its link to a physiological trait—the increased production of hemoglobin—that is key to physical performance in high altitudes. Therefore, the Tibetan DNA project may be considered a strategy of the BGI ambitions for pharmacogenomics of practicality and efficiency, values one associates with an earlier era of confident, high modern Western science. But back at BGI, Chen framed the comparative ethnic DNA study in terms of the science governance of the nation's peoples. Unlike his colleagues educated at leading Western universities, Chen received his medical degree from a university in Hong Kong. He worked as a businessman selling British and U.S. biomedical equipment in China before joining BGI to develop the Hong Kong site as its international business hub. Chen may be more prone to blunt statements, speaking without the nuances that one finds in the remarks of Wang Jian and Henry Yang, the more cosmopolitan and culturally adroit leaders of BGI.

Invoking natural selection and genetic adaptation, Chen said that "populations in highlands have good Asian gene pools due to their geographical isolation. In isolated territory, we can consider the gene pool [to be] more conservative than other Asian genes; the idea is that isolated populations hold onto their genes better than us" (i.e., the Han Chinese). Because isolated populations yield genetic diversity, BGI conducts DNA analysis among them to "prove that the environment will create survival benefits . . . to have stronger confidence to say that in that environment, genes rise to the challenge, or select for it." He pointed to the finding that Tibetan genetic evolution has tended toward the release of more oxygen in their oxygen-scarce, high-altitude environment. BGI researchers hope to mimic the hemoglobin-bonding oxygen molecule discovered in Tibetans so that they can develop therapies for people without the genetic and physiological adaptations for living in high altitudes.

I expected to hear about the anticipation of profits stemming from the discovery of the athlete gene. So Chen's response caught me by surprise, for its metric shifting from mere biological enhancement to capacitation of populations. Because of "climate change," Chen explained, "there will be depleted

oxygen in the future, a hundred years from now." There is a need to develop this novel medicine based on Tibetan DNA mechanisms "so that other people without this mutation will not suffer from pneumonia, headaches, and so on," if they should be forced to move to high altitudes or when the air around them thins. Suddenly a whole new vista comes into view: the need of biosciences to address China's looming uncertainties.

Here was a vision of genomic science as oriented toward anticipated ecological catastrophe. The focus is on non-Tibetans, who may need to move to the Himalayas or cope with living in climate change–induced, Himalaya-like air conditions. The projection is that biomedicine will help the Han Chinese majority, who may migrate to the highlands of their country in greater numbers, as many are already doing, with more physiological capacities than they have in their lungs to cope with poor oxygen. In this framing, the Tibetan study is a simulation of a climate-driven future in which the anticipated biothreat is not infectious diseases but uninhabitable lowlands.

In this scenario, BGI's comparative ethnic DNA approach suggests that different groups hold onto and conserve different kinds of genetic benefits for coping with a precarious future. The reasoning is that ecological isolation of the Tibetans has kept hypoxia adaptation from undergoing genomic dilution, optimizing them for their current mountainous zone. This biological advantage can provide clues to medically help other groups who are not so endowed. The casting of Tibetan's hypoxia as a kind of optimized extant, where Tibetans represent a better-prepared genetic-physiological "type" of Han, a Han future-body, has profound biopolitical implications. Han peoples come to depend on Tibetan genomes—not as distant ancestors yoked by genetics to a primordial nation that has been Chinese all along—but as a genomic resource for a coming environment. That the athlete gene has an extraordinarily specified potentiality in solving China's demographic and health problems in a climate-transformed future is itself rather breathtaking.

The PRC Genomic Analog

The sheer sample size of the genomics data that BGI is able to collect (with potential collaboration with hospitals throughout China) is the foundation to the company's global power as a research engine. BGI core researchers control and own the patents to their findings, but they also work collaboratively as a way to obtain intelligence, while still maintaining controls over the science data. In sum, the massive sequencing power of BGI, as well as its growing monopoly of DNA data on plant, animal, and human populations worldwide makes it hard to

ignore as a global scientific presence. With high-throughput sequencing technologies, BGI has laid an ambitious bioinformatics infrastructure that changes medicine from hypothesis-driven to data-driven. Such large-scale mathematical modeling is considered a necessary advance for multilevel research at the genomic, the epigenomic, and the molecular scales. These are steps toward the development of customized, cell-based medicine, pursued through international partnerships to study autism, obesity, cancers, infectious diseases, and also brain disorders. In other words, the mathematical model for analyzing gene behavior has become strategic for developing molecular interventions for treating hereditary diseases and shortcomings. Perhaps not surprisingly, the corporation faces ongoing skepticism as to its quasi-industrial approach to bioscience, the quality of its science, the role of the state, and its politico-ethical goals.

First, BGI leaders such as Henry Yang are well aware that the corporation operates under a cloud of international fear of China as a rising science power. When I interviewed him, Chen candidly admitted, "As it is, the Chineseness of BGI already raises suspicions; sometimes people think that we are a PRC state agency. There is also skepticism that maybe we are not so smart or good at our work." Therefore, BGI scientists insist that BGI is more than a factory, an assertion that perhaps echoes a growing dissatisfaction in China's current development model with being the world's workshop (home to outsourced, labor-intensive, grunt work) rather than being a bona fide center of innovation, scientific or otherwise. Western perceptions of BGI's "factory"-ness, and its associated image of being entirely profit-driven, are a mode of anxious dismissal of China's increasing scientific capacity and place in the global landscape of biological research. There is also Western anxiety over "science" coming out of China as being allied, always potentially, with the state and thus always potentially tainted. Statements of concern about BGI seem to be about fitting China into a suspicious slot, where the work is suspect, despite the company's demonstrated competences in corralling data on multiple life forms.

Second, there are misgivings that such a huge Chinese biotech corporation may be engaged in redesigning life itself, fueled perhaps by Hollywood scenes of fiendish Chinese scientists (e.g., Hollywood's depiction of *Dr. No*) taking over the world. I therefore asked Chen to compare BGI to the J. Craig Venter Institute, another major private bioscience company based in California. Chen said that BGI projects are "more natural, that is, focused on practical things. We want to avoid projects with uncertain outcomes and that will raise global controversies." By "natural," the focus is on what makes political and scientific sense to improve life and living. There is also a vision of the future

and of life and (natural) sciences in accord in China. The overriding ambition of BGI, he stressed, is to put all life on earth on the digital map (it currently produces a quarter of all genomic data), which BGI promises will be made freely available worldwide. Chen reiterated the "humanitarian" goal: "We are interested in things that can bring direct benefits to mankind: issues of illness, health, preventive medicine, even helping victims of natural disasters." I left BGI with the sense that, despite their good intentions, scientists there have not considered the question of whether bioinformatics is, at its core, an emerging enactment of life rather than merely a reduction of life to information.

Third, Chen said, "Bioinformatics assemble the unknown," compared to a "known." I was reminded of Slavoj Žižek's warning about "unknown knowns," or things we do not know that we know.[31] I therefore asked Chen how researchers at BGI decide to accumulate the unknowns, which they already seem to know in advance. "Sometimes," he responded, "disease is the prompt, its spread among different ethnicities that then get drawn into the study. We ask 'why do Koreans have a higher degree of stomach cancer?' and then compare across ethnicities. Our baseline is genetic differences." He argues that researchers must be attentive to the "economics of sample size and uniformity of data to give more cohesion," and in that sense they should already "know" or make which unknowns to be assembled. The official ethnic framing of racial medicine leads to research strategies that reproduce established ethnic hierarchies through data accumulation.

There are deep-seated beliefs in "relatively pure" genetic pools in "isolated" populations, wherein minority nationalities become potential stores of genomic resources for embattled Han bodies. There may well be political paranoia about what genetic benefits China's hardy, isolated minority nationalities harbor within them, to be mobilized to benefit a genetically deficient Han majority. Thus, the Tibetan DNA study mentioned above reveals how racial biomedicine is becoming a way of governing the near future, that is, within the realm of calculating cross-ethnic genetic benefits and weaknesses, set off against the backdrop of not only a complicated ethnic politics in China, but also the assumption of rapid environmental change at the planetary scale, with its concomitant effects on patterns of human living.

Adaptation to different ecological niches has caused "isolated" minority groups to develop adaptive genes in mountainous places while Han Chinese in other kinds of environments did not have to "hold on" to certain genes. Within this discourse of ethnic variability in acclimatization, comparative minority difference becomes a "recovery" of diluted genetic potentials. In addition, cli-

FIG. 9.5 BGI's Chinese name: "Greater China Genomics." Courtesy of Rena Lam.

mate change, which is also understood by researchers as "a near future," if not already being here, is inducing scenarios of understanding not only genetic relation but also genetic futurity, in the language of a physiological-genetic adaptation to globalized uncertainty.

Whereas, internationally, BGI promotes the sequencing of all life forms as a universal knowledge that it makes available to the world, the China-centered approach places value on genetic differences *between* human populations, especially those gathered by state nationalities' policy into the Chinese nationality (*zhonghua minzu*). Above, I discussed two BGI projects to capitalize on the value of genetic variation between ethnic groups: one to establish historical precedence of the Han, and the second to discover beneficial mutations that are unevenly distributed in order to develop new therapies for groups lacking the genetically beneficial traits. Genetic databases that seek to even out the uneven distribution of genetic adaptation between minority and majority groups express a biomedical topology of power. Here you have the emerging space spelled out in the Chinese name of BGI Genomics: "Greater China Genomics" (*Hua Da Jiyin*; see figure 9.5).

Shifting finally to a broader overview, my analysis has demonstrated contrastive Asian trends in the uses of ethnicity in biomedical sciences. BGI's approach in racial medicine may be called an "arboreal" or vertical modality, in contrast to Biopolis's rather more "rhizomatic" or lateral one.[32] Where insular Singapore's Asia is cosmopolitan and hemispheric in focus, continental China's scope is insular, in that it focuses on China's territory and the official diversity of its people as its site of investment. Han ethnicity is substantiated through projects like Yanhuang, which seems straightforward and expected. The bigger goal to build a national ethnic DNA cell bank appears to link human genetic diversity as moments in an evolutionary snapshot of iconic "immortalized cells." The genetic mapping of charismatic ethnic minorities and iconic "Chinese" species seems to reflect a way of scientifically establishing the broader genomic-national project, to think about the nation in terms of evolutionary divergences and continuities that bind the national unit *not* to a demographic latitudinal distribution across international space (as in Singapore) but, rather, to a kind of political longitudinal integration with other "Chinese" life forms within national space.

While BGI is an autonomous research institute, there are possible accommodations with officials, a shared sense of patriotism, and a sense that, outside the state system, BGI scientists can make better preparations for the nation's health uncertainties than the state sector itself. A BGI manager emailed me this from Shenzhen: "By 2020, we believe, [BGI] will be a critical player in life sciences development and pharmaceutical discovery." He projected the rise of a "distinctive model" of pragmatic collaboration among government research labs, top university researchers, and private firms that is expected to have more potential in pharmacogenomics than the 'Western' model where competing actors often work at cross purposes."[33] As a China-based and internationally oriented research institute, BGI contributes to the promises and uncertainties of genomic medicine. In Yang's words, it will "shake up" the world of cosmopolitan science.