

## **Explore the Emerging Role of Public Health in Integrating Genomics in Surveillance, Outbreak Investigations, and Control and Prevention of Infectious Diseases**

### **WORKING GROUP DESCRIPTION**

#### **Background**

According to the 2005 Institute of Medicine workshop report on the implications of genomics for public health, “public health genomics” can be defined as “an emerging field that assesses the impact of genes and their interaction with behavior, diet and the environment on the population’s health.” The priorities for this field are to:

1. Accumulate data on the relationships between genetic traits and diseases across populations
2. Use this information to develop strategies to promote health and prevent disease in populations
3. Target and evaluate population-based interventions

The “public health system”, which includes federal agencies such as the Centers for Disease Control and Prevention, state health departments, and academic public health institutions, is beginning to work closely with basic scientists, professional organizations, consumer groups, and the private sector to “translate” advances in genomics into actions to prevent and control infectious diseases at the population level (Centers for Disease Control and Prevention, n.d.). Increasingly, genetic information from pathogens, the human hosts, as well as vectors will be used to understand the pathogenicity, natural history, and genetic susceptibility to infectious agents. These new types of data could have profound influences on how the public health system conducts its surveillance functions, acute outbreak investigations (Lingappa and Lindegren, 2003), and community-level programs for targeting interventions, such as vaccines and medications. A major challenge is how to apply this information on the population level to

affect reduction of the burden of infectious diseases in communities. Current public health education has not fully integrated genomics into its basic competences and core curricula. The practicing public health workforce is not adequately prepared to meet the genomics challenge (Institute of Medicine, 2003; Shortell et al., 2004).

### **The Problem**

What should public health systems do to prepare and respond to the emergence of genomic tools in infectious diseases, in terms of surveillance, outbreak investigations, developing and deploying new interventions (e.g., vaccines), and in its efforts to control of infectious diseases, including bioterrorism events, at the population level?

1. Consider how public health systems should incorporate genomics into acute public health investigations such as outbreak response? What should be the current priorities? Because host genomic factors are involved in determining who will be sick from infectious agents, should public health systems routinely collect such information in their investigations? Should they develop biologic specimen repositories involving pathology tissues, human DNA, etc., to explore the host response to infectious agents and gene and protein expression profiles?

2. Consider how public health systems should integrate genomics into surveillance functions for infectious disease occurrence and tracking in the population. While it may be easier to consider pathogen genomics in surveillance, is there a role for routine collection of human genetic information in such data collection? What tools are needed to make epidemiologic surveillance efforts more in real time?

3. Consider the ethical, legal, and social implications of integrating genomics into public health surveillance and response (e.g., privacy and confidentiality, informed consent) and provide recommendations for action and policy change.

4. Consider the role of genomics in developing and evaluating community interventions for the control of infectious diseases. Such programs include administration of vaccines and working with communities and providers to implement control and prevention measures. Consider the social factors that also play a role in who gets sick from infectious agents (e.g., poor nutrition because of low socioeconomic status could influence one's immunity). What

should public health systems do to interact with and educate the public and the provider communities in genomics?

5. Consider the traditional public health data collection categories (e.g., race and ethnicity). Recent articles have underscored one of the consequences of the mapping of the human genome by calling into question our traditional notions of race. Consider how we should categorize individuals given that traditional notions of race and ethnicity are being challenged.

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## WORKING GROUP SUMMARY

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## Summary

This multidisciplinary group was given the task of exploring the interplay between public health and genomics. Recognizing the wealth of information and opportunities that genomics offers public health, the group discussed ways of bridging the gap between gene discovery and the application of genomic tools to surveillance, outbreak investigation, and prevention and control of infectious diseases. These issues were considered broadly, in the context of politics, economics, ethics, race, culture, religion, and the practical limitations of technology and cost.

The first of four working group sessions opened with a discussion about whether recommendations should emphasize tools to detect pathogens or technologies for studying the response of hosts, namely, human beings at risk of catching a disease. Pathogen-centered genomic tools could aid development of rapid diagnostic tests to identify where a pathogen or outbreak originated and whether organisms are drug resistant. Host-oriented genomic tools could be used to assess individual susceptibility to infection and predict response to immunization or specific treatment regimes. Members concurred that genomic tools could broaden scientific understanding of both elements in the host-pathogen equation; they also agreed that neither approach is free of complications.

### *Lessons from the SARS epidemic*

In 2002 an outbreak of a new disease, now called SARS (severe acute respiratory syndrome), began in Hong Kong and was quickly and inadvertently spread by infected people traveling by air. SARS had killed more than 700 people by July 2003. The World Health Organization (WHO) swiftly launched a counterattack against this novel, highly lethal disease. In just seven weeks researchers identified the pathogen and traced it back to its source. In an article that appeared in *Reason*, a nonpartisan political magazine, in April 2003, *Reason's* science correspondent Ronald Bailey wrote, "Thank goodness that SARS broke out in the Genomics Age." Perhaps if the SARS epidemic had occurred in 1992 instead of 2002, many more would have perished.

The group discussed the SARS epidemic in detail, because it illustrates classic public health issues, such as the fact that prompt identification and containment of any pathogen requires collaboration among government agencies and institutions and cooperation from the general public. In addition, the SARS experience reveals the value of such analytical tools as microarrays and computational genetics. The first step in battling any infectious disease outbreak is identifying the pathogen and its mode of transmission. In the case of SARS, new genomic knowledge enabled scientists to identify the viral culprit with stunning speed. This would not have occurred without WHO's excellent coordination efforts and collaboration among the key players in many countries. Driving this effort was public perception—shaped by massive, worldwide media coverage—that SARS was a terrible, lethal, and highly contagious airborne disease that needed to be stopped quickly.

This does not mean that the global public health response to SARS was perfect. A regrettable oversight, according to members of the working group, was the failure to gather information about host genomic factors and susceptibility to SARS from the start of the epidemic. Nonetheless, the group felt that the SARS epidemic of 2002-2003 increased awareness about the importance of good communication, coordination, infrastructure, and surveillance in running effective public health interventions.

#### *Universal issues in the use of genomic technologies: Strategies and solutions*

Whether the issue is an infectious disease outbreak or predictive testing for a heritable disease, the group identified five issues that genomic researchers and the public health community must face if genomic tools are to be used effectively. These are:

1. Educating the public
2. Identifying racial and ethnic issues in research
3. Building research capacity
4. Resolving legal and ethical issues around research
5. Targeting research to resource-poor versus resource-rich areas

After much discussion, the group decided to concentrate on two of these: public education and coming to terms with racial and ethnic issues in research.

*Educating the public: What is the best way to explain the benefits of genomic research to society?*

Scientific advances in the laboratory mean little if powerful officials, or a significant percentage of the public, oppose their use; consider how stem cell research has been slowed by public debate and opposition. Although development and use of genomic tools has not dominated the front pages like stem cell research, there is no doubt that some people mistrust biomedical research in general and are especially nervous that information about their own genetic makeup might be misused in various ways, including denial of health insurance or employment if it were found out that they had “bad” genes. These attitudes and concerns must be addressed, group members said, for genomics to be used effectively against global infectious disease. Moreover, the group felt that the public needs to be educated as to what a genome actually is.

Public campaigns aimed at building acceptance for genomic analysis of individual DNA samples should promote the social benefits of such research. Most people understand that donating blood in times of crisis is an altruistic gesture of real value to others. The group proposed that genomic research programs—where the results could speed drug or vaccine development, for example—could be marketed as an individual’s opportunity to do something good for society. It is just as important to communicate the social context of such efforts as it is to explain the facts about what genomic tests do and how new genomic tools work.

The media and entertainment industry could play a huge role in supporting, or hindering, genomics. Entertainment education is a strategy that public health systems have used for years. It consists of intentionally placing educational content in entertainment media. Often the media and entertainment industry can be persuasive in terms of behavior in ways that other advocacy methods cannot. The entertainment education strategy has been utilized successfully for numerous public health campaigns, such as HIV/AIDS prevention and for the promotion of national immunization days.

Incorporation of genomics modules into K-12 education, according to state and national science standards, will also be key to instilling long-term awareness and understanding of the relevant issues and developing a knowledgeable public. A campaign to promote acceptance of genomic testing will need to be ongoing as the field grows and advances are made. To be the most effective, genomic campaigns will need to address regional concerns, local health issues, and language differences; in fact, the individuals directing the campaign will first need to be educated about the campaign target regions in order to best serve the local public. “Buy in” from community leaders will be essential.

### *Racial and ethnic issues in genomic research*

Every individual human genome is a history book. If each were read from cover to cover we would discover we are all from the same place; we would discover that we are all Africans beneath our skin. This is true whether our ancestors later went to Northern Europe and where genes for digesting lactose were selected for, or remained in Africa and developed resistance to malaria parasites. One group member pointed out that group identity is often confused with group ancestry. Instead of being obsessed with relatively minor differences that set apart ethnic groups, the group felt that spreading the message of common origin would help the public understand the importance of global solidarity in the war against disease. But this is a tricky message to convey, because social definitions of race and ethnicity are often confused with genetic origin.

In reality, human genetic makeup is a mosaic, and no gene is unique to one population. Most genetic variation is found in all populations, and occurs among individuals with only a small percentage of variation occurring at the population level. Social and ethnic conceptions of “race” are commonly understood only at the population level. This is why the notion of race is often not necessarily helpful in understanding disease. Some genes that have health effects do, however, occur more commonly in some populations, and correlate roughly with ancestry where such ancestry maps to genetically distinguishable populations. Some health-related factors may, therefore, correlate with “race” or “ethnicity,” although we should understand that the categories are only rough proxies for underlying biological differences. Most “racial” differences are likely

to be affected by social, economic, or environmental factors at least as much as genetic differences, but some differences will correlate with genetic differences, and the tools for finding those genetic differences have advanced considerably in the past decade. The important issue here is not race itself but the genes that predispose a person to disease.

The group reflected on BiDil, an antihypertensive drug to treat congestive heart failure that the Food and Drug Administration (FDA) recently approved specifically for use in self-identified African American patients. This is the first drug approved for use on a racial basis, and the FDA took this step after this medication failed to show efficacy in a large, mixed-race sample but performed significantly better in a smaller follow-up trial restricted to self-identified group of African-Americans. No genomic data were collected in the trials; instead, race—a much cruder and self-selected “identifier”—was used as the inclusion criterion for the follow-up trials.

As a consequence, the group agreed that it is impossible to determine whether race, ethnicity, or environmental factors explain why BiDil appears to work better in some people than others. More to the point, if the underlying differences are biological, attributable to gene frequency differences, then only some African populations (and hence African Americans) would have the high-frequency alleles and others would not. It is extremely unlikely, for example, that those from sub-Saharan Africa and those from northwestern Africa and those from northeastern Africa would all have the same allele frequencies, given the high level of diversity within Africa. It is also highly likely that some non-African populations also have varying allele frequencies, and so some individuals within those populations could benefit. By using a social measure, such as self-identified race, without the underlying data about genetic variations, the story cannot be understood, and clinical decisions are based on a rough heuristic. This is unfortunate when we have in hand the technologies to do the genomic analysis that could sort out the causal pathway. Overall, the group felt the BiDil study represented a missed opportunity to correlate genomic information with drug efficacy

The story of race and BiDil is a cautionary tale for host differences in response to pathogens. There are apt to be population differences, particularly for pathogens that have co-adapted in particular regions over long periods of time, so there has been selection pressure on both pathogens and human hosts that may well map to geographic areas and environmental factors that influence the prevalence of specific infectious diseases. It would be sad, indeed, if

the story stopped at “race” when in fact, the underlying story is specific environmental factors, host factors, or pathogen differences that could be illuminated by genomic tools.

### *Benefits to society*

The group felt strongly that if the wealth of information stored in human genomes is going to be harvested for the good of humankind, then social, political, and economic barriers and global collaborations must be addressed. The intersection of patients, government, politics, and genomics is often a cacophonous and confusing place. The full potential of the genomic revolution will not be easily realized. The exchange of genomic information across international borders involves delicate political negotiations as well as vast expenditures of capital, while guaranteeing individual rights and ensuring that data will be used for good, not evil, purposes. The exchange of genomic information will require leadership and will mandate education of the leadership such that local traditions and customs are respected and local “buy in” is ensured. These challenges are well worth tackling, however. Stepping back to look at the big picture, the group emphasized that the true promise of genomic technology is saving lives and preventing human misery in all the nations of the world.