Will Genomics Widen or Help Heal the Schism Between Medicine and Public Health?

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Abstract: We discuss the "schism" between medicine and public health in light of advances in genomics and the expected evolution of health care toward personalized treatment and prevention. Undoubtedly, genomics could deepen the divide between the two worlds, but it also represents an important and perhaps unique opportunity for healing the schism, given the volume of new scientific discoveries and their potential applications in all areas of health and disease. We argue that the integration of genomics into health care and disease prevention requires a strong medicine–public health partnership in the context of a population approach to a translational research agenda that includes four overlapping areas: (1) a joint focus on prevention—a traditional public health concern but now a promise of genomics in the realm of individualized primary prevention and early detection, (2) a population perspective, which requires a large amount of population-level data to validate gene discoveries for clinical applications, (3) commitment to evidence-based knowledge integration with thousands of potential genomic applications in practice, and (4) emphasis on health services research to evaluate outcomes, costs, and benefits in the real world. A strong medicine–public health partnership in the genomics era is needed for the translation of all scientific discoveries for the benefit of population health.
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> Today, the two cultures "medicine and "public health" seem to live in different, often unfriendly worlds
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> K. White[1], 1991

> The dominant issues for health and health care today can be effectively engaged only if public health and medicine work together as better partners.
>
> M. McGinnis[2], 2006

Introduction

More than 4 years after the completion of the Human Genome Project, researchers continue to express both excitement and skepticism about the near-term applications of genomics in health care and disease prevention.[3–5] Health applications of genomic research remain focused mainly on individually rare, single gene disorders,[6] which account for nearly all of the 1300 or more genetic tests currently available for practice or research use.[7] Despite impressive advances in gene discovery and characterization, researchers have voiced reservations about the potential benefits of medical applications of genomics,[8,9] pointing out the complex relationships among genetic variation, the environment, and disease, and the limited clinical validity and utility of genetic risk prediction. They also note that prematurely optimistic claims by researchers, the media, and test developers may lead to unrealistic consumer expectations and inappropriate use of genetic information. In addition, an overemphasis on the genetics of human disease may divert attention from the importance of environmental exposures, social structure, and lifestyle factors.[8]

Skepticism about genomics runs high among some public health practitioners whose traditional domains include control of infectious diseases and chronic disease prevention. Some practitioners perceive genomics research as a low-yield investment at best[9,10] and as a dangerous opportunity cost at worst, which undercuts efforts to address social and environmental causes of ill health.[11,12] In this view, genomic medicine is the enemy of public health.

Some public health scientists view genomics research on common diseases as a low priority because "the major preventable environmental causes of illness and death are tobacco use, unhealthy diet, physical inactiv-

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ity, excess alcohol use, infections, trauma and exposure to environmental toxins."[9] Some envision the only public health applications of genomics to be population screening, and argue that this approach will remain limited to newborn screening programs.[10] Others reject genomics research as an unwarranted extension of the individual risk paradigm.[11] They criticize the focus of genomics on individual characteristics on both pragmatic and philosophical grounds, citing its failure to prompt effective public health interventions while "blaming the victim."[11,13] Advocates of this viewpoint often cite the distinction between prevention in populations and in high-risk individuals, which was set out so eloquently by Geoffrey Rose[14]; however, Rose was careful to present these approaches as complementary rather than mutually exclusive.

The contribution of genomics to population health in the next 50 years remains uncertain. Some public health advocates contend that interventions based on environmental change will be more effective than those focused on individual behavior change (e.g., for obesity control[15]). The balance between population-based and individually targeted prevention strategies will become even more important in the genomic era.

The Schism Between Medicine and Public Health

The divide between medicine and public health is a longstanding problem in the United States and in many other countries. Recent comments such as, "[T]here is little need for further integration of genetic services and education into public health especially in countries in which public and private health services are dichotomized,"[10] reflect the "schism" described by Kerr White, who is a founder of the field of health services research.[1] In his 1991 book, *Healing the Schism: Epidemiology, Medicine, and the Public's Health*, White traced the historical evolution of this schism and explained how the formal separation of schools of medicine and public health in the U.S. in 1916 exacerbated the divide. He described the growing cleavage between individual- and population-based approaches to health and disease in the 20th century.[1] During this time, medicine increasingly emphasized the investigation of biological mechanisms of disease, focusing on treatment, while public health emphasized the study of environmental and social influences on health and disease, focusing on disease prevention and health promotion.[1]

At the end of the 20th century, several health policy groups attempted to address this schism, including the Institute of Medicine (IOM)[16] and the Robert Wood Johnson Foundation (RWJF),[17] the American Medical Association (AMA) and the American Public Health Association (APHA). A 1997 IOM report warned of the drawbacks of separating medicine from public health, noting that "for too long, the personal health care and public health systems have shouldered their respective roles and responsibilities for curing and preventing separately from each other, and often from the rest of the community as well. However, working alone and independently, our formal health systems cannot substantially improve population health at the level of fundamental determinants."[18]

Recognizing the potential benefits of enhanced collaboration, professional organizations in medicine and public health have launched several joint initiatives. For example, in 1994 the APHA and the AMA established the Medicine and Public Health Initiative to develop innovative solutions for meeting the health needs of the U.S. population. The initiative promoted joint strategic planning and stimulated collaborative efforts at the national, state, and local levels.[19] More than 10 years later, the 2006 AMA Health Care Advocacy Agenda chose "improving the health of the public" as one of the six most important issues facing medicine.[20] Likewise, three of five items on APHA's 2006 legislative agenda focused on improving access to health care.

Genomics and the Schism

Just how genomics will affect the schism between medicine and public health is not yet known. In an increasingly technologically driven healthcare system, genomics could easily widen the schism, as biology and technology drive one camp, and policy and behavioral and social sciences drive the other. A 2006 IOM report pointed out a critical need for transdisciplinary research that would integrate genomics and the biological sciences with the behavioral and social sciences, thus joining "nature" and "nurture."[21]

Substantial investment in genomic research has been accompanied by high expectations for translation from basic science to clinical applications. These expectations have focused the spotlight on translational research,[22,23] as reflected in the National Institutes of Health (NIH) roadmap initiative.[24,25] The translation framework is defined primarily in terms of the discovery of new drugs and their accelerated use in human clinical trials, and it places little or no emphasis on prevention. Thus, the "bench to bedside" paradigm covers only part of the distance from discovering new knowledge to delivering better health at the population level, where the benefits of prevention are most apparent.[26,27] In 2003, Claude Lenfant, the retiring director of the NIH National Heart, Lung and Blood Institute, described many discoveries of curative or preventive interventions that never reached the end of the translation highway and asked, "Let's be realistic. If we didn't do it with aspirin, how can we expect to do it with DNA?"[28]

The "lost in translation" problem, in genomics and in other areas, is complicated by the increasing costs of healthcare delivery and persistent inequities in access

to health care. In a 2004 IOM meeting on the implications of genomics for public health, William Foege, a prominent public health leader, expressed concern that genetics may widen the health disparities gap: "The challenge to public health genomics is to overcome inequitable allocation of benefits, the tragedy that would befall us if we made the promise of genetics only for those who could afford it and not for all society."[29] The potential inequitable distribution of new health technologies to widen health disparities is not unique to genomics. However, as discussed by Sankar et al.,[30] we need to be particularly careful not to oversell the suggestion that genomic research will solve the health disparities problem in the U.S.: "Over-emphasis on genetics as a major explanatory factor in health disparities could lead researchers to miss factors that contribute to disparities more substantially and may also reinforce racial stereotyping, which may contribute to disparities in the first place."

Attempts to extend the translation research agenda beyond the "bench to bedside" paradigm have called for type II and type III translation research,[31,32] including both applied research on the best ways to deliver or disseminate interventions that work in real-life settings (delivery research) and to evaluate health outcomes and population impact (outcomes research). A comprehensive approach to translating gene discovery into health applications could help foster a true partnership between medicine and public health.

Genomics, Public Health, and Population Health

Public health has traditionally been identified with state, federal and local public health agencies; however, a recent, more inclusive view defines public health professionals as all those who work on improving health from a population perspective.[33] According to this definition, "public health professionals" include not only those employed in government but also those employed in healthcare delivery, academia, community organizations, and the private sector; together, they are actors in the "public health system,"[34] which works to ensure conditions under which a population can be healthy. This expanded view of public health as population health allows genomics to be placed more easily at the interface of between medicine and public health.

Can Genomics Contribute to a Joint Vision of Medicine and Public Health?

In 2005, participants at an international workshop sponsored by the Rockefeller Foundation on public health and genomics, arrived at a consensus[8] about how to develop genomics optimally for the benefit of population health. They determined that accomplishing this goal will require systematic knowledge integration and transdisciplinary collaboration. Critical efforts in reaching the goal include applied research, evidence-based knowledge integration, efforts in policy development, critical evaluation and development of health services, stakeholder engagement, and provider and public education to ensure that genomic information is used for the health benefit of all segments of the population.

Although genomic applications in practice are far from mature, the increasing recognition of genomics as an important driver of public health and health care in the 21st century[2] has stimulated development of the field of public health genomics. This is "a multidisciplinary field concerned with the effective and responsible translation of genome-based knowledge and technologies to improve population health."[8] As discussed by Burke et al.,[8] public health genomics specifically addresses the differing perceptions of the medical and public health worlds and aims to bring them together. One of the challenges in the evaluation of genomic applications to healthcare is the integration of studies of the ethical, legal, and social implications (ELSI) with those of health outcomes. In fact, ELSI questions are inherent in the research needed to address healthcare delivery and outcomes. In addition to disease biology and the efficacy of interventions under research conditions, translational research must develop knowledge about the challenges and constraints involved in delivery of genomic services, including preferences of health care providers and patients, resource constraints, appropriate informed consent procedures, strategies for professional and public education, and deliberative processes to develop policies guideline development and equitable delivery of services. A report from the Canadian Health Services Research Foundation[35] noted the need for diverse sources of evidence in developing healthcare guidance. In addition to evidence concerning the outcome of medical interventions, appropriate evaluation of emerging healthcare services requires evidence on the system in which health care will be delivered, the needs and interests of various stakeholders, and legal and social context. Appropriate procedures for deliberation and decision making are also important. Development of transdisciplinary teams that include social scientists, bioethicists, policy analysts, and other ELSI researchers will help to ensure the appropriate scope of evaluation.

A Framework for a Medicine–Public Health Partnership in the Genomic Era

In this section, we discuss a framework for an enhanced partnership between medicine and public health that can guide translation from research to practice in the genomics era. This framework consists of four principal, overlapping areas that contribute to the discovery and application of genomics-based knowledge: a focus

on prevention, a population perspective, a commitment to evidence-based knowledge integration, and an emphasis on health services research. We also suggest that this partnership can be extended from translation of genomics research to translation of other scientific discoveries for the benefit of population health.

Focus on Prevention

Advances in genomics could provide new opportunities for prevention—the main focus of public health—at the individual level or through population-wide interventions. Understanding genetic effects and gene–environment interactions in disease processes could produce recommendations that certain subgroups avoid defined exposures or receive targeted interventions. Stratification by genotype or family history already provides a means for tailoring screening tests for early disease detection (e.g., colorectal cancer screening in genetically susceptible persons),[36] and this paradigm is likely to be extended to early detection of other conditions.

A review of the public health implications of genomic research related to asthma illustrates the potential opportunities and challenges for translating new knowledge into improved prevention and treatment of a common disease.[37] Asthma is a chronic lung condition characterized by inflammation, hyper-reactivity, and reversible obstruction of the airways. Strong evidence supports a causal role for both genetic and environmental factors. Genomics research has identified numerous gene loci associated with asthma, and further studies of biological pathways associated with asthma are likely to yield new approaches to prevention and therapy. The earliest clinical applications will be in pharmacogenomics, using genetic information to optimize therapy and to prevent adverse events.[38]

Translating results of genomic research to population-level interventions will not always require genetic testing and knowledge of individual genotypes. For example, a study in Mexico of children with asthma found that supplementation with the antioxidant vitamins C and E improved lung function in children with a common polymorphism of *glutathione S-transferase M1* (*GSTM1*) who are exposed to ozone.[39] If confirmed by other studies, this finding might suggest a simple intervention—antioxidant vitamin supplementation—for children with asthma who are exposed to ozone. Without genotype-specific analysis, a potentially important population-level intervention could have been overlooked.

New gene discoveries are reported daily and have produced divergent views on the value of genetic information for prevention. For example, the discovery in 2006 that a variant of the *TCFT7L2* gene is associated with increased risk of type 2 diabetes[40] was noteworthy for several reasons. First, type 2 diabetes is a serious disease and a major public health problem. Family history is an important risk factor but, until now, few genetic associations have been identified. The investigators replicated the association with *TCF7L2* in three independent populations and presented molecular evidence that the gene product is a high-mobility group box–containing transcription factor related to blood glucose homeostasis. The gene product may act through regulation of proglucagon gene expression via the Wnt signaling pathway.[40]

The senior investigator commented to the *New York Times* that a practical consequence of the discovery could be a diagnostic test to identify people who are at increased risk of type 2 diabetes. He speculated that "these people, knowing their risk, would be motivated to exercise more and adopt a healthier diet."[41] However, a relatively simple analysis is sufficient to show that a test for *TCF7L2* variants by itself would have very poor predictive value, adding little to the risk information already provided by family history, and would have limited utility for prevention.[41] In particular, the hypothesis that genetic risk information of this kind will motivate behavioral change remains to be tested. Further, we have little information at present to evaluate the psychological effects of widespread use of tests to identify genetic risks for common disease, or the communication strategies that might minimize risks of stigma or fatalism.

Once a genetic variant is discovered, producing a molecular test to detect it is theoretically straightforward. However, the clinical validity of such a test is highly dependent on population characteristics; these include not only prevalence of the genetic variant and the strength of its association with disease, but prevalence of the disease and interactions between this genetic variant and many other risk factors. Clinical utility is even more difficult to establish because it depends on the availability of a specific, effective intervention that adds value to existing practice. Although most gene discoveries for common diseases are not ready for prevention applications, they have, nevertheless, initiated a common interest in medical and public health to develop a common framework for how such discoveries can be evaluated for their potential applications for disease prevention.

Population Perspective: The Crucial Role of Public Health Sciences

The process of gene discovery and characterization is a basic science enterprise. Until recently, the search for gene–disease relationships was mainly conducted in highly selected patient groups. The population perspective is crucial for validating these associations and estimating their contribution to disease occurrence in other groups and the population as a whole. Indeed, Omenn[42] describes the post-genomic era as a "golden age" for the public health sciences, which include

epidemiology, biostatistics, environmental health, health education, behavioral and social sciences, and many other fields. As Kerr White predicted at the start of the Human Genome Project, "molecular biology, especially once the human genome is mapped must surely turn increasingly to the study of populations."[1] In fact, genetic and epidemiologic methods are converging and beginning to move the field of genetic epidemiology beyond gene discovery.[43,44]

The term "human genome epidemiology" was coined to denote the systematic application of epidemiologic methods in studies of human genetic variation in association with health and disease in populations.[43] The topics addressed in human genome epidemiology range from basic to applied population-based research on discovered human genes. Human genome epidemiology can be used to assess: (1) the prevalence of gene variants in different populations, (2) the magnitude of disease risk associated with gene variants, (3) the magnitude of disease risk associated with gene–gene and gene–environment interactions, and (4) the validity and effectiveness of genetic tests for screening and prevention.[43]

Epidemiologic approaches are fundamental to the population-based biobanks being proposed for gene discoveries and characterization,[45] as well as to large case–control studies of common diseases using whole genome association analysis.[46,47] Nevertheless, a schism continues to divide the ways that biomedical and clinical researchers assess the prevention value of such information and how public health practitioners assess the value of genetic information from the population perspective. A population perspective makes it possible to evaluate whether an intervention based on genotype adds value to existing recommendations for disease prevention. Answering this question requires additional information on (1) the prevalence of high-risk variants in the populations where testing is considered, (2) a population-based estimate of risk, (3) information about modification of risk by other genetic and environmental factors, and (4) behavioral and social science research to determine whether and how genetic information can be used to promote behavior change.[48] Because of the well-known difficulties of implementing behavior change for the prevention of common diseases, it is not clear whether information on genotype adds anything to available information on behavioral risk factors.

Role of Knowledge Integration Across Disciplines

The translation of genomic discoveries from the bench to the bedside is a long and arduous process that requires accumulation and synthesis of knowledge in many fields, including observational epidemiologic studies on gene–disease associations, gene–environment interactions, and clinical trials of efficacy of general and genotype-specific interventions. Because of the proliferation of information on genomics and health (e.g., more than 25,000 articles on gene–disease associations have been published in the past 6 years),[49] evidence must be integrated systematically before "discovery" can lead to "delivery." False leads and blind alleys have to be eliminated through an iterative process of evidence-based information synthesis, such as the efforts of the Human Genome Epidemiology Network, which promotes systematic reviews of gene–disease associations.[50]

An enhanced partnership between medicine and public health will be essential in the knowledge integration process because research that leads to genetic discoveries and their potential applications is by nature transdisciplinary.[8] Transdisciplinary partnership will require a close collaboration of professionals in basic sciences, clinical sciences, public health, social sciences, bioethics, and policy analysis. This collaboration will lead to evidence-based guidelines on the appropriate use of genetic information in healthcare practice, such as those provided by the Cochrane Collaboration,[51] the U.S. Preventive Services Task Force (USPSTF),[52] and the Guide to Community Preventive Services.[53] These efforts examine what works and what does not work to achieve a positive effect on the health of individuals, families, and populations. An extension to these efforts in the United States is the Evaluation of Genomic Applications in Practice and Prevention (EGAPP) initiative, led by the Centers for Disease Control and Prevention, which focuses exclusively on the utility of genomic applications and family history in clinical practice and disease prevention.[54]

Role of Health Services Research and Population Health Monitoring

Genomics research will hit a translation roadblock if no investments are made in evaluating the best methods for assuring delivery and monitoring safety and effectiveness of gene-based interventions, whether they are population screening programs, such as newborn screening, or early case detection and interventions delivered by clinicians. This evaluation requires a strong partnership between medicine and public health. Beyond basic research, efficacy research, and development of practice guidelines is the challenge of ensuring access to health care, which depends on adoption by healthcare providers of practice guidelines and acceptance by consumers. These factors in turn depend on public participation, workforce training, information systems, and funding.[55]

For example, the lack of training and preparation of healthcare providers has been recognized as a key barrier to the appropriate application of genetic information in health care. A collaborative effort led by

government and professional organizations created the National Coalition of Professional Health education in Genetics (NCHPEG) to enhance the competency of medical, public health, and allied health professionals applying genomic knowledge to practice.[56]

New partnership models have also been proposed, such as the national public-private partnership research enterprise, which aims to transform "clinical research . . . from its current state as a cottage industry to an enterprise-wide health care pipeline" for research translation.[55] As Zerhouni[3] and others have predicted, the advent of genomics-based healthcare delivery will require research on the best ways to integrate new knowledge into practice in ways that achieve population-level benefits.[26]

This research approach should also examine and document the impact of genomics-based health care on health disparities, stigmatization, and discrimination, thus providing important information for evidence-based policy development to address these problems. Moreover, because of the need for individualized applications of genetic information that may be in collision course with issues that relate to privacy and confidentiality, we need to develop research methods to resolve this potential conflict.

As a major new research area with real promise (as well as commercial potential), genomic medicine may offer a new opportunity to shine the spotlight on translation. For example, HMO-based research[57] and general provider surveys[58] were conducted collaboratively to assess the effect of a direct-to-consumer campaign for *BRCA1* testing on providers' attitudes, knowledge, behaviors, and practices. In another example, providers, consumers, professional organizations, and various government agencies collaborated to assess and increase the public's awareness and use of family history as an additional tool for disease prevention and public health.[59,60] Clearly, such efforts need to be sustained and extended into emerging areas such as pharmacogenomics and genetic tests in general.[61] In particular, economic evaluations of gene-based tests and interventions[62] are becoming increasingly important in the face of ever-escalating healthcare expenditures.

Invariably, translation efforts will uncover gaps in our knowledge of genetic influences on health, as well as gaps in healthcare delivery and monitoring of population health outcomes. As the use of genetic information in practice continues to expand with no systematic oversight, a medicine–public health partnership will be needed to identify these gaps, to further shape the research agenda, and to keep practitioners, consumers, and policymakers abreast of the applications of scientific discoveries that have the best potential to improve population health.

Table 1. Hereditary hemochromatosis: example of medicine–public health partnership in translation of gene discovery into health practice

Area of collaboration	Description[a]
Prevention	A joint Centers for Disease Control and Prevention–National Institutes of Health workshop was held shortly after the *HFE* gene was discovered to discuss prevention benefits of screening for *HFE* mutations in preventing complications of iron overload from hereditary hemochromatosis. This led to research and practice agendas.
Public health sciences	Mutation prevalence study in U.S. population; studies of burden of hospitalization and deaths; large cohort study to assess penetrance, natural history.
Knowledge integration	As of 2006, evidence-based knowledge synthesis and recommendations against population testing by the U.S. Preventive Services Task Force, based on best available data.
Health services research	Active, ongoing Centers for Disease Control and Prevention provider education campaign to encourage early detection and case finding. Evaluation is in progress.

[a]For details and references, see text.

Example: Population Screening for Hereditary Hemochromatosis

We use the example of hereditary hemochromatosis to illustrate how medicine–public health collaboration in four overlapping areas has helped guide the translation of a gene discovery into health practice. A summary of the highlights is provided in Table 1.

Hereditary hemochromatosis is the most common form of hereditary iron overload disease in the U.S.[63,64] The *HFE* gene and two common point mutations associated with hereditary hemochromatosis were discovered in 1996, initiating a debate on the value of population genetic screening for this recessive disorder.[65] Developing a genetic test for these mutations (*C282Y* and *H63D*) was straightforward, and a simple intervention (regular phlebotomy) is known to be effective in reducing the risk of adverse health outcomes. However, gaps in our knowledge persist and have thus far precluded a recommendation for population screening.

In 1997, the Centers for Disease Control and Prevention (CDC) and the National Human Genome Research Institute jointly sponsored an expert panel workshop[66] to consider a medicine–public health partnership in the prevention and early detection of hereditary hemochromatosis. The panel concluded that population screening for mutations in *HFE* could not be

recommended because of uncertainty about the natural history of the disease (especially age-related penetrance), optimal care for asymptomatic persons who are found to carry mutations, and the psychosocial and societal impact of genetic testing.[66]

After the workshop report in 1998, samples from a population-based, nationwide survey were analyzed to establish the prevalence of *HFE C282Y* and *H63D* mutations in the U.S. population.[67] This study found that almost 5% of the non-Hispanic, white population of the U.S. was homozygous or compound heterozygous for these mutations. However, further epidemiologic analysis of the burden of disease using hospital records[68] and death certificates[69] found that the prevalence of diagnosed disease is much lower than the prevalence of mutations, suggesting that penetrance is low. An epidemiologic meta-analysis of the association of *HFE* mutations with the risk of clinical disease from iron overload studies showed that homozygosity for the *C282Y* mutation was associated with the highest risk of hereditary hemochromatosis; risks associated with other genotypes, including *C282Y/H63D* and *H63D/H63D*, were much lower.[70]

A large NIH-funded cohort study in the Kaiser Permanente Southern California HMO suggested that the disease penetrance for *HFE* mutations may be quite low.[71] Only 1 of the 152 subjects who were homozygous for *HFE C282Y* had symptoms of hereditary hemochromatosis. This finding, along with other data, led the USPSTF in 2006 to recommend against routine population genetic screening for hemochromatosis.[72]

Finally, to increase awareness of this common condition, the CDC has developed a campaign to educate healthcare providers and the public.[73] This campaign explains the condition and its early warning signs so that complications can be avoided by early detection and intervention in affected persons and their families. An evaluation of the provider education campaign is currently underway.

The example of hereditary hemochromatosis illustrates several ways that medicine and public health can work together to translate gene discovery for application at the individual and population levels. Government agencies whose interests span the spectrum from basic research to clinical medicine and public health can support these efforts through better collaboration and cooperation.

Conclusion

Advances in genomics—especially in relation to common diseases—are increasing the interaction and the interdependence between the traditional healthcare delivery system, which focuses on treatment of individuals, and the public health system, which focuses on prevention and control in populations. This enhanced interaction is creating a shared "population health" focus on using genomic advances appropriately and effectively to promote health and to prevent disease.

Because the field of genomics is still in its infancy, this is a crucial time for professionals in medicine and public health to work together to develop the partnership model presented here. This model—focused on prevention, population sciences, knowledge translation, and health services research and outcome monitoring—is eminently generalizable to all other areas of health.

The AMA and APHA have already taken some steps (unrelated to genomics) to heal the schism between medicine and public health. Now emerging genomic information is presenting policymakers, practitioners, and researchers with a new opportunity and new urgency to bridge the divide for the benefit of population health. James Marks from the RWJF recently observed that "no important health problem will be solved by clinical care alone, or research alone, or by public health alone—but rather by all public and private sectors working together."[74] This paradigm will certainly apply to almost all health problems in the genomics era.

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