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Genomics and Public Health at CDC

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Genomics is the study of the entire genome, including all genes and their interactions with each other and with the environment (*1*). The scope of public health genomics is even broader, encompassing genetic variation in populations, both human and microbial. Molecular typing of pathogens---a mainstay of infectious disease surveillance, prevention, and control---already is used to trace epidemics (*2*), provide information for vaccine development (*3*), and monitor drug resistance (*4*). Now genomic research is producing powerful new tools for public health; for example, a newly described, microchip-based method promises to diagnose influenza infection, distinguish among viruses of human or animal origin, and detect mutations that suggest increasing virulence---all in a matter of hours (*5,6*).

Until recently, public health applications of human genetics were limited largely to state-mandated programs that screened newborn infants and ensured access to genetic services for affected children and families. Now genomic research and technology have generated new molecular targets and new tests for newborn screening, kindling renewed debate on their relative benefits, risks, and costs (*7*). Public health investigations of diseases with infectious and environmental causes also are beginning to evaluate the contribution of human genetic variation to susceptibility and natural history (*8*).

Most population-based research in genetic epidemiology has focused on common, chronic diseases, as reflected in approximately 22,000 scientific publications during the last 5 years (*9*). The results point to complex interactions among multiple genes and environmental factors, which remain poorly understood. However, small successes in translation illustrate the potential for public health genomics in three areas: stratifying risk to guide multilevel interventions, understanding environmental causes of disease, and identifying new opportunities for prevention.

Family health history, which captures information about shared inherited and environmental factors, is a simple and inexpensive genomic tool for identifying persons and families at high risk (*10*). For example, a Utah study indicated that the 14% of families with positive family histories for coronary heart disease (CHD) accounted for 48% of all persons with CHD and for 72% of CHD events occurring before age 55 years (*11*).

Population-based data and careful cost-effectiveness analysis are needed to determine whether combining traditional, population-level prevention strategies with more intensive interventions for families at increased risk will improve the return on investment in prevention (*12*).

Public health interventions are based on understanding and modifying environmental risk factors. For example, recognition of inadequate folate status as a cause of neural tube defects led to an effective public health intervention to increase folic acid intake among reproductive-aged women (*13*). A systematic review of epidemiologic data on birth defects in relation to folic acid intake and variation in the *methylenetetrahydrofolate reductase* (*MTHFR*) gene illustrates "Mendelian randomization" (*14*), in which the effects of specific environmental exposures, such as dietary elements, drugs or toxins, are either accentuated or mitigated in persons with different variants of genes involved in physiologic response. Because genotype is "randomized" at birth, biologic information thus can strengthen evidence obtained from traditional environmental risk factor studies and provide a less biased framework for interpreting data on gene-environment interactions (*15*).

Public health genomics can provide information about population-level interventions that do not depend on 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 (*16*). 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.

Just as genomics will enhance the knowledge base for public health research and practice, public health principles and methods can provide information for genomics research and translation. Rigorous application of population-based methods for collecting, evaluating, and interpreting the evidence on genetic variation in relation to health and disease will improve research quality, promote knowledge synthesis, and help identify research gaps. By keeping the focus on population-level implications, the public health perspective helps ensure the entire population benefits from public investment in genomics research.

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