Informing public health approaches to obesity and smoking using genome-wide association studies: Genetic epidemiology affirms the importance of early prevention

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Abstract: Rapid advances in technology and scientific methods stimulated by the sequencing of the human genome have yielded discoveries that begin to uncover the genetic roots of common chronic health conditions. However, the implications of these discoveries for public health research and practice remain unclear. Three questions are central to building a translational pipeline that links genetic discovery research with interventions to improve health: First, when in the life course do genetic risks become manifest? Second, what are the magnitudes of risks that can be predicted using genetic information? And third, do genetic markers provide new information about risk over and above the existing technology of family health history assessment? This dissertation research seeks to address these questions for two prevalent and costly sources of morbidity and early mortality, obesity and smoking. Results reveal that (1) genetic risks manifest early in the development of obesity and smoking through processes that may be amenable to public health intervention; (2) the magnitudes of risk that can be predicted using genetic information are small; but (3) the risk information provided by genetic markers is independent of information available in a family history. These findings affirm recommendations of caution in the application of genetic information to predict health risks in individuals, but suggest promise as more powerful but less common genetic risks are discovered in the continuing evolution of genomic research. Further, these findings recommend an increased focus on childhood and adolescence in genetic discovery research and add a genetic rationale to arguments for early intervention to prevent obesity and smoking.

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