

# The Power of Genome-Wide Haplotype Analyses for Complex Traits

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## Abstract:

The “haplotype map” effort initiated by the U.S. National Institutes of Health, Private Industry, and many European organizations was motivated by a two-fold desire to understand the genetic structure of human populations and to facilitate the discovery of disease-predisposing genes via association mapping. Association mapping, however, is complicated by a number of factors, not the least of which is the fact that, in the absence of a prior knowledge about the location of a disease gene, one may have to test literally tens of thousands of possible genomic sites for association with the disease. Multiple testing of this sort can potentially lead to many false positive results. Although the haplotype map project will yield information that can easily reduce the potential for false positive results by allowing one to focus on larger and therefore fewer total genomic regions, the power of this approach has not been adequately addressed. Here we use the analytic strategy recently outlined by Schork (*American Journal of Human Genetics* (2002) 70:1480-1489) and the haplotype block data recently described by Gabriel et al. (*Science* (2002) May 23) to assess the power of genome-wide association studies that make use of haplotype information. Our results provide very realistic answers to questions regarding the utility of genome-wide mapping efforts for complex disease and the haplotype map initiative.