Introduction

There has been an explosion of genetic association studies in recent years. There has also been growing concern about the quality of association studies and the reproducibility of results. There seem to be few standards for study design, data collection, or analysis. This problem inspired an invited session at the 2003 American Society of Human Genetics (ASHG) meeting in Los Angeles, California, entitled 'Quality Standards for Genetic Association Studies in Complex Disorders'.

This special issue of Human Heredity is based on that session. We will not attempt to establish standards, but will try to sketch some norms to which genetic association studies may aspire in the future. The papers cover topics such as phenotype definition and genotype-phenotype correlation, strategies for managing phenotypic data, multipoint methods for genotype error detection, robustness of genomic control methods for case/control association in admixed populations, the relative costs (in terms of sample size increase) for different types of genotype errors in genetic model-based association, a comprehensive review of optimal SNP marker selection in disease association (e.g., determination of tagging SNPs), and the comparative information of multiple SNPs and single microsatellites. In total, there are nine papers covering a wide range of current topics related to disease association analysis.

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