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Sex differences in disease risk from reported genome-wide association study findings.

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Source

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Abstract

Men and women differ in susceptibility to many diseases and in responses to treatment. Recent advances in genome-wide association studies (GWAS) provide a wealth of data for associating genetic profiles with disease risk; however, in general, these data have not been systematically probed for sex differences in gene-disease associations. Incorporating sex into the analysis of GWAS results can elucidate new relationships between single nucleotide polymorphisms (SNPs) and human disease. In this study, we performed a sex-differentiated analysis on significant SNPs from GWAS data of the seven common diseases studied by the Wellcome Trust Case Control Consortium. We employed and compared three methods: logistic regression, Woolf's test of heterogeneity, and a novel statistical metric that we developed called permutation method to assess sex effects (PMASE). After correction for false discovery, PMASE finds SNPs that are significantly associated with disease in only one sex. These sexually dimorphic SNP-disease associations occur in Coronary Artery Disease and Crohn's Disease. GWAS analyses that fail to consider sex-specific effects may miss discovering sexual dimorphism in SNP-disease associations that give new insights into differences in disease mechanism between men and women.

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