Effect-size distributions of human complex traits and diseases from genome-wide association studies

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Abstract

Although recent genome-wide association studies have led to the discoveries of many susceptibility loci, much of the heritability of the individual traits and diseases remain unexplained. Many different approaches to explaining 'missing heritability' have been proposed with different types of variants. As a recent tool for genome-wide complex trait analysis showed that a moderate amount of the heritability could be explained by common variants, we assess the effect-size distribution of common susceptibility loci by accounting for power for detecting known loci from their original genome-wide studies. With the estimated effect-size distributions for various traits and diseases such as adult height, high-density lipoprotein(HDL), Type 2 diabetes, and Crohn's diseases, we will illustrate how useful and important it is to know the effect-size distribution for various human complex traits and diseases for planning future genome-wide association studies and for projecting risk prediction.