

Bivariate Linkage Analysis of Obesity and Diabetes in the HERITAGE Family Study

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Abstract

Obesity is increasing world-wide and is set to become the world's biggest health problem. It is also found that obesity is sometimes accompanied by some other disorders like hypertension and diabetes. The primary aim of this study was to investigate if there are any common genes underlying the correlation of obesity and diabetes. In the present study several alternative measures of obesity and diabetes were available. However, only pairs of traits that satisfied the criteria of significant phenotypic and genetic correlation, significant heritability, and the linkage evidence at same genomic region were chosen for bivariate linkage analysis. The present study analyzed 534 subjects from 101 white families with 419 sib pairs from the HERITAGE Family Study. Variance component method was used for testing linkage. Multipoint bivariate linkage analysis was performed on Acute Insulin Response-Fat Mass and Acute Insulin Response-% Fat pairs using SOLAR software package. The maximum bivariate LOD scores for each pair of traits were localized to chromosome 1 at 179 cM (1.75 for AIRG – FM, and 2.13 for AIRG - % Fat) and to chromosome 10 at 9 cM (2.53 and 2.49, respectively). Apolipoprotein-A2 (Apo-A2) can be a possible pleiotropic candidate gene for Acute Insulin Response, Fat Mass, and % Fat in the above region on chromosome 1. Mutation in this gene can possibly affect diabetes and obesity. No such obvious pleiotropic candidate gene was found on chromosome 10 at QTL.