
LINKAGE ANALYSIS OF A COMPOSITE FACTOR FOR THE MULTIPLE METABOLIC SYNDROME (MMS): THE NHLBI FAMILY HEART STUDY

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Recent studies have demonstrated significant genetic as well as phenotypic correlation underlying the clustering of traits involved in the multiple metabolic syndrome (MMS). The aim of this study was to identify chromosomal regions contributing to MMS-related traits represented by composite factors derived from factor analysis. Data from the NHLBI Family Heart Study was subjected to a maximum likelihood-based factor analysis. These analyses generated a MMS factor that was loaded by body mass index, waist-hip ratio, subscapular skinfold, triglycerides, HDL, homeostasis model assessment index, plasminogen activator inhibitor-1 antigen and serum uric acid. Genetic data were obtained for 2467 subjects from 387 three-generation families (402 markers, Marshfield sample), and 1082 subjects from 256 sibships (243 markers, Utah sample). Multipoint variance component linkage analysis (GENEHUNTER version 2.1) of the MMS factor was conducted in the Marshfield and Utah samples. The greatest evidence for linkage was found on chromosome 2 (LOD = 3.46 at 233 cM for the Marshfield sample; LOD = 2.26 at 241 cM for the Utah sample; LOD = 3.34 at 240 cM for the combined sample). The 1-LOD-unit support interval from the Marshfield and combined samples completely overlapped and included the region with the maximum LOD score from the Utah sample. Suggestive linkage (LOD > 2.5) was also observed for regions on chromosomes 7, 12, 14, and 15. In summary, a genomic region on chromosome 2 may contain a pleiotropic locus contributing to the clustering of MMS-related phenotypes.