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ABSTRACT

Using a genome-wide gene-by-environment (GxE) approach, we identify 37 single nucleotide polymorphisms across the genome that interact with socioeconomic position (SEP) to increase the risk of obesity. We use two-generation data from the Framingham Heart Study (FHS) in conjunction with the FBAT-I approach to examine the simultaneous influence of specific genetic polymorphisms and SEP as co-determinants of obesity risk in the 3rd generation of the FHS. Of the 37 significant SNPs, 15 are located within known genes that have been linked to body mass phenotypes, related to hypertension, and prostate and colon cancer. We also demonstrate that genetic risk for obesity may be triggered by environmental risk factors and absent these triggers, genetic factors are significantly less influential on BMI. The genome-wide GxE approach provides clues regarding the social and genetic etiology of this complex phenotype and points to physiological and behavioral mechanisms through which these associations may be operating.