Obesity and Ischemic Heart Disease
Defining the Link

Ruth McPherson

Obesity is a complex metabolic disorder that afflicts 35% of the adult population in the United States. As an important risk factor for ischemic heart disease (IHD) and its metabolic precursors, it has become one of the most serious health problems in many parts of the world. Nordestgaard et al have previously reported that an allelic score for obesity based on 3 single nucleotide polymorphisms (SNPs) associates with IHD and in accord with other findings supports a causal relationship. As reported in this issue, they have sought to define the intermediates underlying the increased risk.

The major finding is that common genetic variants for intermediary variables explain a significant but small proportion of excess IHD risk from genetically determined obesity, these being LDL-C (8%), systolic BP (7%), remnant cholesterol (7%), diastolic BP (5%), and glucose (4%) with no contribution from either HDL-C or CRP. The latter finding is in accord with other findings supports a causal relation.

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Here, it should be noted (their Figure 2) that the observational association of measured BMI with LDL-C and remnant cholesterol flattens or even reverses for individuals with a BMI >30 kg/m². Indeed, mean LDL-C levels in obese individuals are generally close to the population average. Thus, the findings need to be interpreted accordingly and apply most importantly to the effect of variation in BMI across the normal (<25 kg/m²) and overweight (25–30 kg/m²) rather than obese range.

Given that one of the most important obesity-associated IHD risk factors is diabetes mellitus, it seems surprising that glycemia-associated SNPs were not strongly associated with excess coronary artery disease risk. Here, it could have been useful to include a diagnosis of diabetes mellitus or A1c levels in lieu of a single glucose measurement. Other measures of adiposity more directly related to metabolic traits, such as abdominal girth, might also have strengthened this finding.

There are other limitations inherent in this analysis. The SNPs included predict a small portion of each intermediary variable and in many cases are limited to few genes (LDLR, APOB, PCSK9 for LDL-C; ATP2B1, CYP17A1 for BP; LIPC, ABCA1 for HDL-C). Because different biological pathways lead to variability in these traits, the interpretation of the results should be limited to the processes regulated by the genes included in the analysis. If data are available, it would be preferable to construct a genetic risk score based on a larger number of risk SNPs for each phenotype. For example, recent genome-wide association studies have identified 157 significant loci for plasma lipid traits and 98 loci for variation in BMI. A requirement for Mendelian randomization is lack of pleiotropy. However, pleiotropic effects are evident for all 3 genes showing associations with remnant cholesterol. TRIB1 also associates with LDL-C and HDL-C and APOA5 with HDL-C and LDL-C. Genetic variants near GCKR (encoding the glucokinase receptor) are associated with increased fasting glucose and CRP but reduced triglycerides (and hence remnant cholesterol).

Overall, the findings are of interest and extend previous reports from this group linking a genetic risk score for BMI to IHD, to metabolic risk factors for IHD including remnant cholesterol and to BP and CRP. The extent to which IHD risk was found to be mediated by BMI-associated risk factors may seem small, given the general belief that obesity increases cardiovascular risk only to the extent that metabolic abnormalities arise. However, the concept of metabolically healthy obese has recently been questioned and an increased incidence of cardiovascular disease is also evident in obese subjects without overt metabolic dysfunction. In the absence of data indicating that hypertension or dyslipidemia confer greater IHD risk in obese versus normal weight individuals, a main conclusion of the study, that lipoprotein-associated risk factors should be treated in obese individuals who are unable...
to achieve and sustain weight loss, is merely consistent with present guidelines for the general population.

On this basis and other recent studies, the authors stress the need for large clinical intervention trials examining whether a lowering of remnant cholesterol in individuals with elevated levels will reduce IHD risk. Here, it is important to remind ourselves that remnant cholesterol and triglycerides are closely correlated. In this study, except for subjects with severe hypertriglyceridemia, remnant cholesterol was not measured directly but derived from a formula based on the estimated cholesterol content of triglyceride-rich lipoproteins. Despite the findings reported here and several genetic and Mendelian randomization studies17–19 supporting a causal link between triglycerides and cardiovascular risk, recent large randomized controlled trials testing pharmacological agents that lower triglycerides and remnant cholesterol most effectively, namely nicozin20 and fibrates,21,22 have been profoundly disappointing.

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None.

References

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Figure. On the basis of the tenets of Mendelian randomization, provided all covariates are met, if genetic variants associated with a given trait associate with a disease phenotype, the trait and phenotype are presumed to be causally related. Varbo et al20 demonstrate the significant associations of measured body mass index (BMI) with ischemic heart disease (IHD) and each of the above intermediary traits. An allelic risk score based on a limited number of single nucleotide polymorphisms (SNPs), for each of the remnant cholesterol, low-density lipoprotein cholesterol (LDL-C), and blood pressure (BP) also associates with IHD and explains a significant but small proportion of excess risk from genetically determined adiposity, supporting a causal relationship. In contrast, although measured BMI correlates well with each of high-density lipoprotein cholesterol (HDL-C) and C-reactive protein (CRP), the genetic variants associated with the latter traits do not alter IHD risk, indicating a noncausal relationship.
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