

Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden

A Collaborative Meta-Analysis

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Objectives	This study sought to ascertain the relationship of 9p21 locus with: 1) angiographic coronary artery disease (CAD) burden; and 2) myocardial infarction (MI) in individuals with underlying CAD.
Background	Chromosome 9p21 variants have been robustly associated with coronary heart disease, but questions remain on the mechanism of risk, specifically whether the locus contributes to coronary atheroma burden or plaque instability.
Methods	We established a collaboration of 21 studies consisting of 33,673 subjects with information on both CAD (clinical or angiographic) and MI status along with 9p21 genotype. Tabular data are provided for each cohort on the presence and burden of angiographic CAD, MI cases with underlying CAD, and the diabetic status of all subjects.
Results	We first confirmed an association between 9p21 and CAD with angiographically defined cases and control subjects (pooled odds ratio [OR]: 1.31, 95% confidence interval [CI]: 1.20 to 1.43). Among subjects with angiographic CAD (n = 20,987), random-effects model identified an association with multivessel CAD, compared with those with single-vessel disease (OR: 1.10, 95% CI: 1.04 to 1.17)/copy of risk allele). Genotypic models showed an OR of 1.15, 95% CI: 1.04 to 1.26 for heterozygous carrier and OR: 1.23, 95% CI: 1.08 to 1.39 for homozygous carrier. Finally, there was no significant association between 9p21 and prevalent MI when both cases (n = 17,791) and control subjects (n = 15,882) had underlying CAD (OR: 0.99, 95% CI: 0.95 to 1.03)/risk allele.
Conclusions	The 9p21 locus shows convincing association with greater burden of CAD but not with MI in the presence of underlying CAD. This adds further weight to the hypothesis that 9p21 locus primarily mediates an atherosclerotic phenotype. (J Am Coll Cardiol 2013;61:957–70) © 2013 by the American College of Cardiology Foundation

Genome-wide association studies (GWAS) first identified the 9p21 locus as associating with coronary heart disease (CHD) in 2007 (1–3). A plethora of replication studies have since confirmed and validated this association in a series of different ethnic populations, making this the most robust genetic finding for CHD to date. The need for large study samples in many of these studies has led to phenotypic heterogeneity with inclusion of cases with acute or stable clinical presentations with presumed healthy control populations and varying definitions of CHD, including clinical or noninvasive diagnosis of coronary artery disease (CAD), angiographic CAD, validated myocardial infarction (MI),

or a combination of these (4,5). This lack of phenotypic clarity has resulted in uncertainty about the primary phenotype mediated by the 9p21 locus, specifically whether it predisposes to atherosclerosis or promotes a more abrupt plaque rupture or thrombotic process leading to MI. This in turn has hampered contextualization of early functional studies attempting to resolve the underlying mechanism (6).

There have been several attempts to tease apart the closely related phenotypes of CAD and MI (7–9). In the most comprehensive analysis to date, Reilly et al. (8) demonstrated that, although 11 variants had shown robust association with MI in GWAS when compared with healthy control subjects, they did not associate with MI when both cases and control subjects had underlying CAD. It was thus proposed that the primary association for these variants was likely to be with development of CAD rather than predisposition to plaque rupture or thrombosis per se. It follows then that carriers of the risk allele at the 9p21 locus should demonstrate a greater burden of coronary atherosclerosis compared with non-risk carriers. Although studies with computerized tomography have demonstrated a correlation between 9p21 and greater coronary artery calcification, indicating a role in predisposing to atheroma formation (10,11), studies using invasive coronary angiography as a more direct and widely available means of visualizing plaque have demonstrated discrepant results, leading to ongoing uncertainty with regard to the mechanism of risk (12–15).

To address this lack of consistency we sought to establish a collaboration of genetic studies and perform a comprehensive meta-analysis of the association between 9p21 and angiographically defined CAD burden as well as to replicate the lack of association with superimposed MI in subjects with underlying CAD.

Methods

Search strategy and selection criteria. We performed a systematic published data search for studies of 9p21 variation in relation to CAD/MI, published before June 2011 on MEDLINE and EMBASE, combined with cross references and manual searches. Search terms included “coronary artery disease,” “myocardial infarction,” or “atherosclerosis,” in combination with “9p21.” No language restrictions were used. A hand-search of articles and cited reference search were also performed to identify all articles that cited the index publication. Experts contributed to identification of cohorts with published and unpublished data (M.R./N.J.S.). For each included cohort, data were tabulated for angiographic presence or absence of CAD, burden of CAD, number of MI cases in subjects with underlying CAD, and the diabetic status of all subjects. Published data search, data collection/abstraction, and entry were performed independently and reconciled by 2 trained investigators (K.C. and R.P.).

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