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Association of Chromosome 9p21 with Subsequent Coronary Heart Disease Events: A GENIUS-CHD Study of Individual Participant Data

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Abstract

Background: Genetic variation at chromosome 9p21 is a recognized risk factor for coronary heart disease (CHD). However, its effect on disease progression and subsequent events is unclear, raising questions about its value for stratification of residual risk.

Methods: A variant at chromosome 9p21 (rs1333049) was tested for association with subsequent events during follow-up in 103,357 Europeans with established CHD at baseline from the GENIUS-CHD Consortium (73.1% male, mean age 62.9 years). The primary outcome, subsequent CHD death or myocardial infarction (CHD death/MI), occurred in 13,040 of the 93,115 participants with available outcome data. Effect estimates were compared to case/control risk obtained from CARDIoGRAMPlusC4D including 47,222 CHD cases and 122,264 controls free of CHD.

Results: Meta-analyses revealed no significant association between chromosome 9p21 and the primary outcome of CHD death/MI among those with established CHD at baseline (GENIUS-CHD OR 1.02; 95% CI 0.99–1.05). This contrasted with a strong association in CARDIoGRAMPlusC4D OR 1.20; 95% CI 1.18–1.22; p for interaction <0.001 compared to the GENIUS-CHD estimate. Similarly, no clear associations were identified for additional subsequent outcomes, including all-cause death, although we found a modest positive association between chromosome 9p21 and subsequent revascularization (OR 1.07; 95% CI 1.04–1.09).

Conclusions: In contrast to studies comparing individuals with CHD to disease free controls, we found no clear association between genetic variation at chromosome 9p21 and risk of subsequent acute CHD events when all individuals had CHD at baseline. However, the association with subsequent revascularization may support the postulated mechanism of chromosome 9p21 for promoting atheroma development.

Journal Subject Terms:

Genetic, Association Studies; Coronary Artery Disease; Secondary Prevention; Epidemiology; Risk Factors

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Keywords

chromosome 9p21; genetics, association studies; residual risk; prognosis; myocardial infarction; recurrent event; secondary prevention

Introduction

Using a case-control approach, a large number of common genetic variants have now been associated with coronary heart disease (CHD) through genome-wide association studies, in an effort largely led by the CARDIoGRAMPlusC4D consortium.¹ Among these variants, the chromosome 9p21 locus was the first to be discovered and the variant with the largest individual effect, and is the most widely replicated genetic risk factor for CHD.²⁻⁴ Multiple studies including case-control and prospective cohort studies in general populations have reliably confirmed its effect on risk of CHD among otherwise healthy individuals.⁵

However, it is uncertain whether variants at the 9p21 locus also affect risk of recurrent or subsequent events, including mortality in those with established CHD. Elucidation of this hypothesis would help to better understand its mechanism and estimate its incremental value for stratification of residual risk. Prior studies have shown conflicting results, although most have been underpowered. A literature based meta-analysis indicated a null association of chromosome 9p21 variants with subsequent CHD events but was based on summary, not individual level data, with varying outcome definitions.^{6, 7}

The new collaborative GENetIcs of sUbsequent Coronary Heart Disease (GENIUS-CHD) consortium, described in this issue of the journal was established to investigate genetic determinants of disease progression following an index CHD event.⁸

In this paper, we use the GENIUS-CHD resource to: (1) examine the association of variants at the 9p21 locus on risk of subsequent CHD events in individuals with established CHD; (2) compare these to the association between chromosome 9p21 and any CHD observed in the CARDIoGRAMPlusC4D consortium; and, (3) explore the potential impact on these estimates of biases that might affect genetic association studies of disease outcome and prognosis.

Methods

In accordance with Transparency and Openness Promotion (TOP) Guidelines, the data, analytic methods, and study materials will be made available to other researchers for purposes of reproducing the results or replicating the procedure. Participating studies received local institutional review board approval and included patients who had provided informed consent at the time of enrolment. The central analysis sites also received waivers from their local institutional review board for collating and analysing summary level data from these individual studies. Details about the GENIUS-CHD consortium and study inclusion criteria have been published separately in this issue of the journal,⁸ while for this study full details about data sources, genetic variant selection, outcomes and statistical analyses are available in the Supplementary Material.

Results

In total, 49 studies from the GENIUS-CHD consortium contributed to the federated analysis resulting in a sample size of 103,357 individuals of European descent with established CHD and available genotype data at the 9p21 locus. Of these, 93,115 individuals had available data for the primary composite outcome of subsequent CHD death/MI, of whom 13,040 experienced these events. Contributing study details are provided in Table 1. Participant characteristics are representative for populations with established CHD with a weighted mean age of 62.9 years; 73.1% male. As expected, risk factor prevalence was high in this population, including diabetes (24.4%), hypertension (59.1%) and current smoking (25.7%). Statin use at enrollment varied by study, ranging from 5.2%–97.3%, with a median of 61.5% (Table 1).

The rs1333049 single nucleotide polymorphism (SNP) was genotyped in 42 studies, with the remaining 7 studies using highly correlated proxies (R -squared > 0.90); rs10757278 (4 studies) or rs4977574 (3 studies) when the primary SNP was unavailable. Genotyping details are provided in Supplementary Table 1. For rs1333049, the average risk allele frequency across the participating studies was 0.518 ranging from 0.453 to 0.587 (Supplementary Figure 1).

From CARDIOGRAMplusC4D, after excluding 6 cohorts which had contributed data to both consortia, data were available for association with chromosome 9p21 from 41 studies, including 47,222 cases with CHD and 122,264 controls free of any CHD. Power to detect different effect sizes, including the effect size identified in CARDIOGRAMplusC4D, using a two-sided alpha of 0.05, are provided in Supplementary Table 2

Chromosome 9p21 Association with Subsequent CHD Events

Study-specific results for the association between chromosome 9p21 and risk of the primary outcome of CHD death or myocardial infarction among individuals with established CHD at baseline, adjusted for age and sex are presented in Supplementary Figure 2.

The per-allele odds ratio for the primary outcome during follow-up was 1.02 (95% CI 0.99–1.05). The effect estimate again for the primary outcome, based on a time to event analysis and using a Cox regression model, was also similar with a HR of 1.02 (95% CI 0.99–1.04, Supplementary Figure 3).

In contrast, a meta-analysis of CARDIOGRAMplusC4D data (excluding studies also contributing data to GENIUS-CHD), revealed a per-allele odds ratio for a CHD event similar to that reported previously (OR 1.20; 95% CI 1.18–1.22). There was evidence of statistical heterogeneity between the estimates (Interaction $p < 0.001$), Figure 1.

Subgroup Analyses

We found minimal evidence for heterogeneity in effect estimates when stratifying by CHD subtype at baseline (interaction p -value 0.801), with no clear evidence for an effect of chromosome 9p21 genetic variation on subsequent CHD death or MI in individuals enrolled with ACS (OR 1.02; 95% CI 0.97–1.06), those with coronary artery disease with a prior MI

(OR 1.01; 95% CI 0.96–1.05) and those with coronary artery disease without prior MI (OR 1.01; 95% CI 0.95–1.08, Figure 1).

We further examined the effect of chromosome 9p21 on the primary outcome in prespecified subgroup analyses. We noted a borderline nominally significant interaction with sex, suggesting a greater risk among women with the chromosome 9p21 risk allele, for subsequent CHD death/MI (interaction p value = 0.04), while non-significant trends were noted for greater risk in those without hypertension (p value = 0.08) or without renal impairment (p value = 0.17). There were minimal differences in effect estimates by other patient level characteristics including age and diabetes, or according to statin or anti-platelet use or LV impairment at baseline (Supplementary Figure 4).

Similarly, when stratified by study level features, we observed minimal evidence for heterogeneity in effect estimates by study size, geographical region, study design or length of follow up (Supplementary Figure 5). However, when ordered by date of first enrollment, there was no evidence for variation in effect by time of enrollment (Supplementary Figure 2).

Secondary outcomes

We additionally examined the association between chromosome 9p21 and other subsequent events available for this analysis within the GENIUS-CHD Consortium, listed in Supplementary Table 3, with summary estimates provided in Figure 2. Of note, the per-allele effect of risk variants at chromosome 9p21 on subsequent revascularization during follow up was 1.07 (95% CI 1.04–1.09). The effect on the composite outcome of any CVD, which includes revascularization, was also significant at 1.04 (95% CI 1.02–1.07). However, there was no clear evidence of association for the remaining secondary outcomes, with only a marginal trend to protection for both subsequent heart failure (OR 0.97; 95% CI 0.93–1.01) and CVD death (OR 0.97; 95% CI 0.94–1.01), as shown in Figure 2.

Selection Bias

To explore the potential for index event bias we looked for differences in associations between chromosome 9p21 and known cardiovascular risk factors in the UKB, among the subset of participants with established CHD, compared to the full UKB cohort (Supplementary Table 4). While there were differences between the groups in the prevalence or values of the tested risk factors, we did not find clear evidence to indicate a distortion in associations between chromosome 9p21 and age, blood pressure, diabetes or smoking. There was, however, a small difference for BMI, with a greater statistical association between the chromosome 9p21 risk allele and lower BMI identified in those with established CHD than in the general population (nominal interaction p value 0.02, Supplementary Table 4).

We also observed that the chromosome 9p21 risk allele frequency in those surviving with CHD, both in UKB (0.529) and in GENIUS-CHD (0.518, Supplementary Figure 1), was higher than the general population in the UKB (0.481) and European reference populations from the 1000 Genomes (Phase 3),⁹ (0.472). This difference in frequency confirms the association of chromosome 9p21 with CHD and also indicated absence of a crude survival bias with loss of large numbers of risk allele carriers to fatal events prior to entry into CHD

cohorts. We did however observe a trend to an age association in those with established CHD as well as the general population in the UKB, with lower chromosome 9p21 risk allele frequencies with advancing age, relative to younger carriers (Supplementary Figure 6).

Discussion

In this study, we examined the effect of genetic variation at the chromosome 9p21 locus on risk of subsequent events in 103,357 individuals with established CHD using the newly formed GENIUS-CHD consortium.⁸ We found that: (1) in contrast to the known strong association with CHD observed in CARDIoGRAMPlusC4D, there was a markedly attenuated and non-significant association with subsequent CHD events in GENIUS-CHD; (2) effect estimates in GENIUS-CHD were broadly consistent in stratified analyses based on features related to study design, patient characteristics and type of index CHD event and (3) exploratory analyses suggested that selection biases were unlikely to explain the discrepancy. However, we did find evidence of an association between these variants and a secondary outcome of future revascularization events. Our findings, taken together with those from others, support the view that chromosome 9p21 promotes CHD through progressive stable atheroma rather than through development of an unstable phenotype.

The chromosome 9p21 locus is the most widely-replicated genetic risk locus for CHD identified to date, with an estimated 15–35% increased risk in carriers of the variant allele in prospective population and case-control studies.⁵ However, studies examining the effect on subsequent CHD events in people with known CHD at baseline have reported conflicting results.^{10–14} Our group previously examined this in a literature-based meta-analysis, based on 15 studies with median sample size of 1,750 individuals, accruing 25,163 cases of established CHD, and reported no clear evidence of an effect of variants at chromosome 9p21 on the risk of subsequent events.¹⁵ An analysis by the CHARGE consortium of 2,953 MI survivors also reported no association with subsequent mortality.⁷ However, the limited size of most prior studies and the limitations of literature meta-analyses indicate that many possible explanations, including errors in risk allele coding and selection biases, could not be adequately explored, precluding meaningful interpretations for any mechanistic or clinical implications.

The emergence of the GENIUS-CHD Consortium has now permitted a robust evaluation of the role of chromosome 9p21 in subsequent CHD event risk, revealing a clear lack of association with a common composite coronary endpoint. This is in marked contrast to findings from studies comparing cases to CHD-free controls, as confirmed through meta-analysis of CARDIoGRAMPlusC4D data. Furthermore, we were able to add to previous findings by showing that the type of CHD at baseline, whether acute coronary syndrome or stable CHD with or without prior MI, does not alter this association. We also interrogated several widely-proposed explanations that could account for our findings through pre-specified subgroup analyses, and confirmed that most of these, specifically older age, medication use at baseline (statin or antiplatelet), study size or follow up duration, did not appreciably alter the association findings. Our finding of a possible interaction with sex, warrants further investigation, but should be considered hypothesis-generating given the borderline evidence of an interaction.

Selection bias (i.e., index event bias or collider-stratification bias) could potentially explain reversed or attenuated associations in disease progression studies like this, operating by inducing relationships between (otherwise independent) risk factors through the selection of individuals with disease.^{16, 17} Specifically, individuals surviving a first event consequent on exposure to a particularly strong risk factor may have lower levels of exposure to other individually weaker, independent risk factors, which can then attenuate the association of the risk factor of interest with subsequent events. However, the distribution of common risk factors by chromosome 9p21 genotype did not differ when compared between the general population and the subset with CHD in the UKB, using interaction tests. The only exception was for BMI, a potentially differential association with chromosome 9p21 in those with CHD compared to the general population was noted. However, the effect size was small in both populations and on its own is unlikely to indicate presence of substantial index event bias.

Selection bias may also theoretically occur by focussing on subjects surviving a first event, where chromosome 9p21 risk allele carriers at risk of fatal CHD events are lost prior to enrollment into CHD cohorts, thereby diluting the future impact of the variant on subsequent CHD events. In this scenario, we would expect a lower risk-allele frequency in those surviving CHD and entering CHD cohorts, but we found no evidence for this. Among those with CHD in the UKB, and among the whole UKB cohort, we did find a progressive loss of risk allele carriers with increasing age, consistent with prior findings of a greater association with CHD, among younger individuals in case-control studies.⁵ Given patients with CHD are generally older, it is possible that a subtle survival bias may still be influencing our findings, although all analyses were adjusted for age. However, based on simulation modelling, sample size and projected SNP effect size, we and others have previously estimated that selection biases are only minimally operating in this context and would be unlikely to account for our observed findings.^{18, 19} Although our findings potentially argue against important selection biases in the analysis for the primary outcome, they are relatively insensitive assessments and may not fully elucidate such biases.

Possible biological explanations could also exist for our findings. Pathological studies indicate differences between chronic stable atherosclerotic plaques that cause ischemia through progressive vessel occlusion and vulnerable plaques with thin caps, prone to sudden plaque rupture, unheralded MI and coronary deaths.²⁰ In a seminal study dissecting the phenotype of CHD, a lack of effect for chromosome 9p21 and MI was noted, when both cases and controls had underlying atherosclerosis.²¹ Our group and others have in parallel shown that chromosome 9p21 robustly associates with atherosclerotic phenotypes,²² while functional studies have also implicated this region with molecular activity that drives atheroma.²³ Furthermore, in this study we show that the only outcome positively associated with chromosome 9p21 is incident revascularization, perhaps reflecting more severe atherosclerosis burden. Collectively these data support the concept that chromosome 9p21 promotes progressive atheroma formation and does not confer risk via plaque rupture.

In this context, it is worth noting that chromosome 9p21 associates more robustly with CHD in case-control studies than in prospective cohort studies.⁷ The difference, as proposed by others, could hypothetically be accounted for by incidence–prevalence bias, with

chromosome 9p21 carriers more likely to *survive* a CHD event and thus be *over*represented among CHD cases (the opposite to survival bias described above).⁷ This becomes more likely as stated above if chromosome 9p21 drives a more progressive and stable atheroma phenotype. If this holds true then among survivors with established CHD, one might expect that chromosome 9p21 carriers could hold a small favourable advantage over those who experience CHD in its absence, due instead to other more dangerous or vulnerable characteristics, and despite undergoing more subsequent revascularization, these chromosome 9p21 carriers do not experience more dangerous or fatal events.

These findings have important implications. Clinically, they indicate that a degree of caution should be applied when considering or evaluating patients for chromosome 9p21 in order to predict disease progression or residual risk. They also highlight the need to appreciate important biases that may inflate or attenuate association findings in the setting of subsequent events for individuals with established disease. Mechanistically, these findings support existing and emerging efforts seeking to elucidate the mechanism of the most robust genetic discovery for CHD in recent decades.

There are important limitations to consider. First, among individuals in GENIUS with established CHD, the timing of the first CHD event or age of onset was often unknown so we could not account for this variable in our analyses. However, the lack of association in the ACS studies, which had documented timing of the first event, suggests this did not impact the findings. Second, we had limited information on whether subsequent revascularization events were late staged procedures, which would count as part of the index CHD event or unplanned and symptom driven and thereby a true subsequent event, which may have diluted the effect estimate. Third, while we did not observe a specific interaction for statin or aspirin use, we cannot rule out an effect of combined or additional medication usage attenuating the association signal, given the high prevalence of secondary prevention drug use in this setting compared to general population cohorts. Fourth, our analyses were restricted to participants of European descent as most of the included studies only recruited these individuals and so we were markedly underpowered to explore associations in other ethnic groups. Unfortunately, this remains a wider problem of genetic research and global efforts are ongoing to address this imbalance. Finally, variability of follow-up duration across studies is an analytical challenge and could have impacted our findings, through misclassification. However, a sensitivity analysis stratifying on the follow-up duration of individual studies (<5 or 5+ years) revealed minimal evidence ($P=0.62$) of heterogeneity in effect estimates (Supplemental Figure 5), suggesting that this is unlikely to have influenced our findings significantly as effect estimates were concordant across studies with different lengths of follow-up. Our major strengths however include the size of the study and the large number and types of subsequent events and an effort to examine for selection biases. We also sought to mitigate potential miscoding of the risk allele, given rs1333049 is a palindromic SNP, and also the risk allele C changes from being a minor allele in population cohorts to the major allele in CHD cohorts. Finally, this analysis benefitted from the collective expertise and input of over 170 investigators and analysts, many of whom have previously reported on chromosome 9p21.

In conclusion, using the newly formed GENIUS-CHD consortium, we demonstrate that variation at chromosome 9p21 shows no clear association with risk of subsequent CHD events when all individuals have established CHD at baseline. This is in marked contrast to prior case-control studies examining odds of CHD presence compared to disease-free controls. We could not account for the attenuation of effect in terms of selection biases or subgroup effects. However, we did find a greater risk for incident revascularization in those with established CHD and although residual bias may be at play, our findings collectively support the view that chromosome 9p21 promotes CHD through progressive stable atheroma rather than through development of an unstable phenotype.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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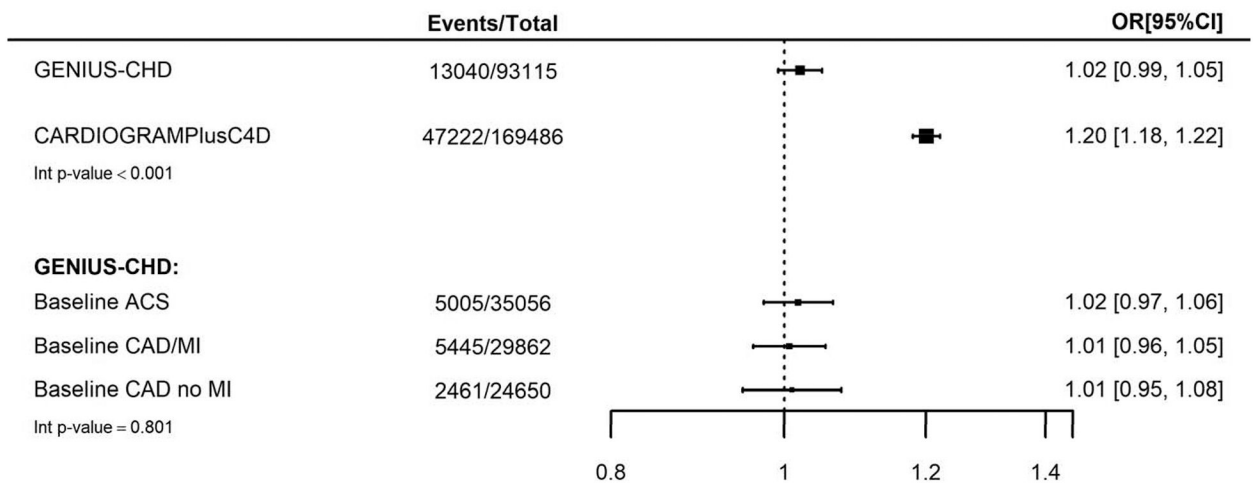


Figure 1:
 Association between chromosome 9p21 and subsequent CHD events in all participants with baseline CHD (GENIUS-CHD) compared to association in CHD cases and CHD-free controls (CARDIOGRAMPlusC4D)
 For the CARDIOGRAMPlusC4D meta-analysis estimate, 6 studies [LURIC, LIFE-Heart, GoDARTS, OHGS, PROSPER, WTCCC] were excluded as they were also included in GENIUS-CHD.
 Estimates for GENIUS-CHD are also presented by subtype of CHD at baseline including acute coronary syndrome (ACS), stable coronary artery disease without prior MI (CAD/no MI) and Stable CAD with prior MI (CAD/MI). All estimates were adjusted for age and sex.

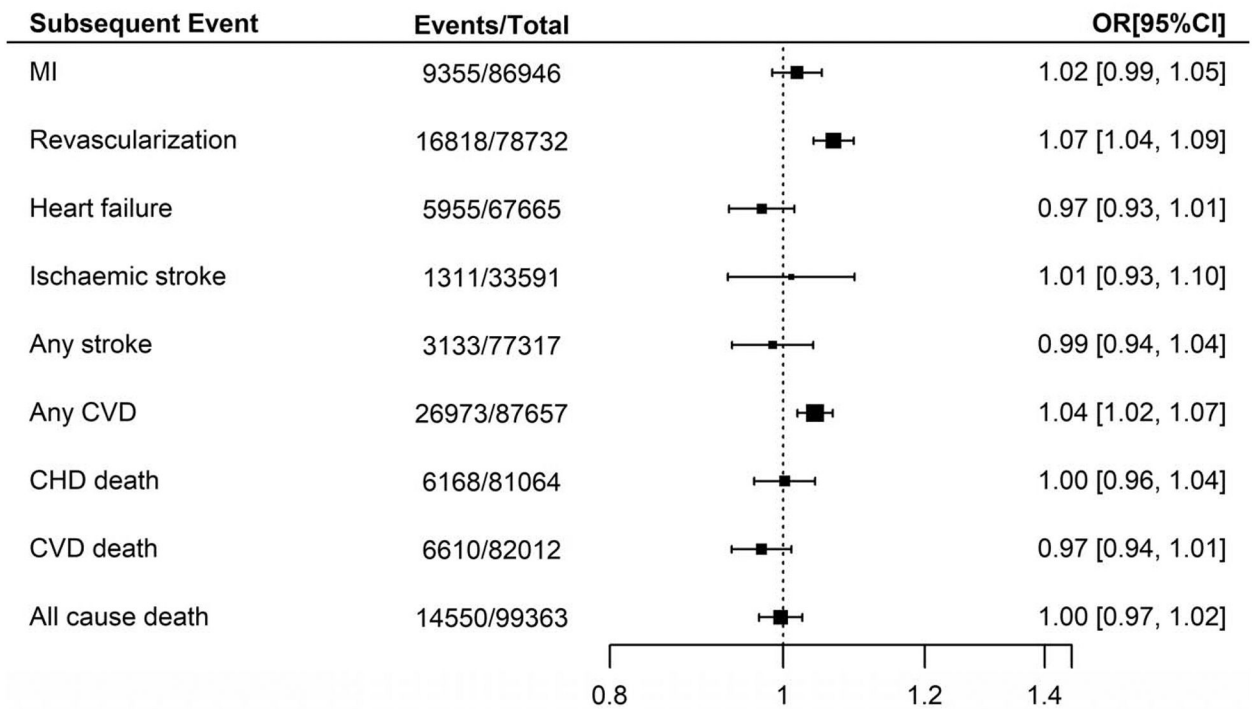


Figure 2: Association between chromosome 9p21 and secondary outcomes in participants with baseline CHD, within GENIUS-CHD. All meta-analysis estimates were adjusted for age and sex.

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Table 1:

Overview of studies contributing to chromosome 9p21 analysis and participant characteristics

Alias	Cohort	Total N genotyped	Study Design	CHD Type	Male (%)	Age (SD)	BMI (SD)	Diabetes (%)	Smoking (%)	Systolic BP (SD)	Total Cholesterol (SD)	Startin use (%)	Creatinine (SD)	Prior Revasc (%)	Prior MI (%)	PubMed ID
4C	Clinical Cohorts in Coronary disease Collaboration (4C)	1538	Cohort	CAD	62.1	62.2 (11.95)	30.2 (5.67)	23.4	-	133.9 (23.7)	4.69 (1.10)	26.4	99.3 (83.2)	22.6	15.5	-
AGNES	Arrhythmia Genetics in The Netherlands	1316	Cohort	ACS	79.3	57.7 (10.81)	26.5 (3.87)	7.6	59.3	-	5.28 (1.04)	9.8	-	-	-	20622880
ANGES	Angiography and Genes Study	588	Cohort	Mixed	65.5	64.1 (9.55)	28.1 (4.36)	30.8	14.7	-	4.84 (0.84)	69.4	83.0 (32.0)	42.4	24.7	21640993
ATVB	Italian Atherosclerosis, Thrombosis and Vascular Biology Group	1465	Cohort	ACS	90.4	40.0 (4.40)	26.8 (4.07)	8.4	78.7	132.3 (20.6)	5.76 (1.39)	56.2	-	-	-	21757122
CAB Genomics	Coronary Artery Bypass Genomics	1542	Cohort	Mixed	80.1	64.7 (10.08)	29.7 (5.71)	10.1	11.2	-	4.21 (0.95)	75.2	-	-	42.8	25649697
CDCS	Coronary Disease Cohort Study	1800	Cohort	ACS	71.5	67.5 (11.96)	27.3 (4.66)	15.4	5.8	129.2(21.6)	5.00(1.09)	46.5	100.5 (40.0)	26.9	30.3	20400779
COROGENE	CoroGene Study	1489	Cohort	ACS	70.9	64.7 (11.87)	27.6 (4.84)	18.2	34.4	-	4.63 (0.99)	5.2	84.0 (44.3)	-	-	21642350
CTMM	Circulating Cells	605	Cohort	Mixed	68.9	63.0 (9.83)	27.6 (4.45)	20.7	20.7	135.4 (19.1)	4.43(1.05)	-	86.4 (34.9)	-	30.1	23975238
CURE	Cure-Genetics Study	4242	RCT	ACS	59.3	64.7 (10.99)	27.9 (4.44)	19.9	22.6	135.7(21.9)	-	-	93.0 (33.9)	13.9	31.8	11102254
EGCUT	Estonian Biobank	2408	Cohort	CAD	51.0	67.1 (10.88)	28.9(5.16)	18.7	19.2	135.6 (18.0)	5.64(1.17)	27.3	-	15.7	36.0	24518929
EMORY	Emory Cardiovascular Biobank	2411	Cohort	Mixed	70.1	64.5 (11.06)	-	30.7	9.8	-	4.49(1.02)	76.0	99.0 (45.1)	61.7	27.9	20729229
ERICO	Estrategia de Registro de Insuficiencia Coronaria	438	Cohort	ACS	55.5	63.8 (13.36)	27.0 (5.06)	39.1	31.0	99.2 (38.4)	-	23.8	-	11.3	25.9	23644870
FINCAVAS	Finnish Cardiovascular Study	1671	Cohort	Mixed	69.4	60.9 (11.03)	27.8 (4.35)	18.4	24.3	140.2 (22.1)	4.74 (0.90)	57.3	90.8 (66.8)	32.6	39.0	16515696
FRISCH	FRISCH Study	3106	RCT	ACS	69.4	66.2 (9.80)	26.8 (3.87)	12.7	27.1	143.3(22.4)	5.80(1.12)	12.3	90.6 (18.8)	12.1	27.2	10475181
GENDEMP	GENEtic Determination of Myocardial Infarction in Prague	1267	Cohort	ACS	75.8	56.4 (8.63)	28.6 (4.68)	18.8	60.8	137.0 (20.8)	5.51 (1.17)	16.6	-	29.7	41.6	23249639
GENEBANK	Cleveland Clinic Genebank Study	2345	Cohort	Mixed	74.3	61.5 (11.06)	29.4 (5.44)	11.8	16.8	132.7(21.1)	4.46 (0.93)	71.8	-	65.3	56.1	21475195
GENES IS-PRAXY	GENEtic and Sex determinants of cardiovascular disease: From bench to beyond-Premature Acute Coronary Syndrome (GENE SIS-PRAXY)	784	Cohort	ACS	69.2	48.3 (5.62)	-	13.8	44.2	139.5 (26.5)	4.85(1.18)	93.1	75.9 (19.7)	11.3	11.4	22607849
GENOCOR	Genetic Mapping for Assessment of Cardiovascular Risk	497	Cohort	Mixed	86.7	65.2 (8.45)	-	13.3	64.4	129.5 (20.3)	4.70 (0.92)	72.1	94.8 (27.2)	13.7	63.2	22717531
GodARTS incident	Genetics of Diabetes Audit and Research in Tayside Scotland (I)	1003	Cohort	CAD	62.0	71.1 (10.62)	29.7 (5.64)	77.9	-	126.7 (NA)	4.62 (1.02)	50.8	108.0 (64.6)	0.2	1.3	-
GodARTS prevalent	Genetics of Diabetes Audit and Research in Tayside Scotland (P)	2000	Cohort	CAD	66.5	69.1 (9.20)	30.3 (5.43)	77.8	14.9	136.2 (19.7)	4.37 (0.83)	66.8	101.6(34.5)	31.4	48.9	-
GRACE_B	Global Registry of Acute Coronary Events - Belgium	699	Cohort	ACS	75.4	65.7 (12.01)	27.0 (4.35)	81.3	49.9	138.8 (25.3)	5.33 (1.19)	79.3	102.8(61.9)	-	80.1	20231156
GRACE_UK	Global Registry of Acute Coronary Events - UK	1086	Cohort	ACS	69.1	64.4 (12.04)	28.0 (5.15)	15.0	69.5	137.8 (27.1)	5.19 (1.29)	16.8	105.0 (40.0)	20.4	32.0	20231156
IDEAL	Incremental Decrease in End Points Through Aggressive Lipid Lowering (IDEAL)	6223	RCT	ACS	81.8	61.2 (9.32)	27.4 (3.80)	11.4	20.3	136.8 (19.8)	5.03 (0.98)	76.9	100.1 (16.7)	41.3	-	16287954
INTERMOUNTAIN	Intermountain Heart Collaborative Study	6763	Cohort	Mixed	66.7	61.2 (11.05)	29.5 (6.08)	20.3	10.2	141.8 (24.4)	4.96 (1.12)	38.7	99.6 (66.6)	-	6.6	20691829
INVEST	International Verapamil SR Trandolapril Study Genetic Substudy/INVEST-GENES	2145	RCT	CAD	56.6	68.7 (9.38)	-	23.9	12.8	148.6 (18.1)	-	52.8	-	47.6	-	21372283
JUMC	Krakow-GENIUS-CHD	704	Cohort	Mixed	71.6	68.3 (10.25)	26.3 (4.46)	36.9	27.5	148.1 (23.8)	5.02 (1.06)	88.3	89.9 (37.5)	50.1	39.7	28444280
KAROLA	Karola Study	1147	Cohort	Mixed	84.6	58.6 (8.13)	27.0 (3.26)	18.5	32.4	119.9 (15.5)	4.46 (0.84)	77.4	82.4 (26.5)	42.8	21.6	24829374
LIFE-Heart	Leipzig (LIFE) Heart Study	4330	Cohort	Mixed	75.5	64.0 (11.15)	29.0 (4.68)	34.4	29.0	138.3 (21.8)	5.24 (1.18)	38.9	87.3 (34.6)	-	0.1	22216169
LURIC	The Ludwigshafen Risk and Cardiovascular Health Study	2175	Cohort	Mixed	76.5	63.8 (9.85)	27.5 (3.89)	44.3	23.9	142.3 (24.1)	4.94 (0.99)	58.9	88.7 (38.5)	48.7	57.4	11258203

Alias	Cohort	Study Design	CHD Type	Male (%)	Age (SD)	BMI (SD)	Diabetes (%)	Smoking (%)	Systolic BP (SD)	Total Cholesterol (SD)	Statin use (%)	Creatinine (SD)	Prior Revas (%)	Prior MI (%)	PubMed ID
NE_POLAND	North East Poland Myocardial Infarction Study	Cohort	ACS	75.0	62.4 (11.86)	24.8 (3.79)	22.2	48.1	138.9 (27.4)	5.04 (1.05)	80.7	91.6 (36.3)	1.3	10.6	26086777
NEAPOLIS	Neapolis Campania Italia	Cohort	Mixed	74.4	67.6 (10.49)	28.0 (4.18)	43.0	26.8	129.4 (14.2)	4.57 (1.02)	82.5	101.0 (68.1)	41.5	40.8	24262617
OHGS	Ottawa Heart Genomics Study	Cohort	Mixed	73.0	65.3 (11.07)	28.6 (5.00)	6.9	19.5	131.9 (19.0)	5.53 (1.03)	92.4	89.8 (21.1)	28.2	21.9	-
PLATO	The Study of Platelet Inhibition and Patient Outcomes	RCT	ACS	69.5	62.6 (10.95)	28.2 (4.51)	22.8	35.2	135.6 (21.8)	5.42 (1.23)	79.7	85.6 (26.3)	15.1	20.6	19332184
PMI	Post Myocardial Infarction Study	Cohort	ACS	78.3	62.7 (10.29)	26.5 (3.82)	12.0	28.2	117.0 (15.6)	5.98 (1.19)	46.0	87.8 (27.8)	-	17.2	12771003
POPular	The POPular study	RCT	ACS	74.3	63.8 (10.40)	-	18.9	27.5	145.0 (22.1)	4.25 (0.64)	80.7	92.7 (26.8)	33.1	43.7	26542508
PROSPER	Prospective Study of Prasastatin in the Elderly at Risk	RCT	CAD	69.9	75.4 (3.31)	26.4 (3.87)	10.3	16.2	150.0 (21.6)	5.55 (0.83)	-	109.4 (23.2)	26.0	85.9	10569329
RISCA	Recurrence and Inflammation in the Acute Coronary Syndromes Study	Cohort	ACS	75.9	61.9 (11.40)	27.2 (4.43)	19.8	30.4	-	-	46.6	100.6 (28.6)	28.2	27.9	18549920
SHEEP	Stockholm Heart Epidemiology Program (SHEEP)	Cohort	ACS	70.7	59.3 (7.21)	26.8 (4.02)	18.2	50.0	131.8 (20.6)	6.28 (1.16)	-	-	-	-	17667644
SMART	Second Manifestations of Arterial Disease	Cohort	Mixed	82.2	60.2 (9.26)	27.3 (3.63)	16.6	24.4	137.4 (19.8)	4.73 (0.96)	75.7	92.3 (22.7)	-	43.6	10468526
STABILITY	Stabilization of Atherosclerotic Plaque by Initiation of Dose-escalating Therapy trial	RCT	Mixed	82.0	64.7 (9.10)	29.9 (4.97)	38.4	21.4	131.7 (16.1)	-	97.3	-	74.6	58.6	24678955
THI	Texgen	Cohort	ACS	75.3	63.6 (10.62)	29.6 (5.59)	30.5	21.3	-	-	57.1	-	21.5	16.7	21414601
TNT	Treating to New Targets	RCT	CAD	81.3	61.3 (8.73)	28.6 (4.59)	14.8	13.4	130.9 (16.8)	4.51 (0.61)	70.3	104.8 (17.3)	-	57.3	15755765
TRIUMPH	Translational Research Investigating Underlying Disparities in Acute Myocardial Infarction Patient's Health Status	Cohort	ACS	72.4	59.8 (12.04)	29.5 (5.96)	28.6	37.4	117.8 (18.3)	-	89.0	112.5 (76.7)	27.0	18.3	21772003
UCORBIO	Utrecht Coronary Biobank	Cohort	Mixed	75.6	65.4 (10.26)	27.2 (4.34)	21.5	23.1	-	4.76 (1.18)	64.0	91.9 (42.9)	-	28.9	-
UCP	Utrecht Cardiovascular Pharmacogenetics Study	Cohort	Mixed	75.4	64.1 (9.96)	-	-	-	153.4 (21.4)	5.50 (1.10)	27.1	94.7 (24.8)	-	-	25652526
VHS	Verona Heart Study	Cohort	CAD	80.9	61.3 (9.78)	26.9 (3.57)	18.5	69.2	-	5.37 (1.10)	47.1	96.7 (32.2)	17.4	59.6	10984565
VIVIT	Vonberg Institute for Vascular Investigation and Treatment Study	Cohort	CAD	73.1	64.5 (10.44)	27.4 (4.14)	30.6	18.9	137.2 (19.2)	5.45 (1.14)	49.7	88.4 (32.7)	21.1	31.0	24265174
WARSAW ACS	Warsaw ACS Genetic Registry	Cohort	ACS	74.5	63.6 (11.72)	28.1 (4.72)	21.9	42.0	127.8 (22.6)	4.99 (1.07)	-	93.5 (41.4)	-	18.6	-
WTCCC	WTCCC CAD Study	Cohort	Mixed	79.3	60.0 (8.13)	27.6 (4.20)	11.7	12.8	143.6 (22.0)	5.28 (0.98)	71.6	-	67.1	72.0	17634449

Overview of studies contributing to chromosome 9p21 analysis and participant characteristics; alias denotes the abbreviated name of each study used in figures and tables; ACS = acute coronary syndrome, CAD = coronary artery disease; PubMed IDs are provided for individual study descriptions; mean (standard deviation) with proportions (%) are provided unless otherwise stated.