**Genetic liability to rheumatoid arthritis in relation to coronary artery disease and stroke risk**

**Running head:** Rheumatoid arthritisand cardiovascular disease

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**Abstract**

**Objectives** To assess the causality of the associations of rheumatoid arthritis **(**RA) with coronary artery disease (CAD) and stroke using Mendelian randomization approach.

**Methods** Independentsingle nucleotide polymorphisms strongly associated with RA (n=70) were selected as instrumental variables from a genome-wide association meta-analysis including 14,361 RA cases and 43,923 controls of European ancestry. Summary-level data for CAD, all stroke, any ischemic stroke and its subtypes, intracerebral hemorrhage, and subarachnoid hemorrhage were obtained from meta-analyses of genetic studies, international genetic consortia, the UK Biobank, and the FinnGen consortium. We obtained summary-level data for common cardiovascular risk factors and related inflammatory biomarkers to assess possible mechanisms.

**Results** Genetic liability to RA was associated with an increased risk of CAD and intracerebral hemorrhage. For one unit increase in log odds of RA, the combined odds ratios were 1.02 (95% confidence interval, 1.01, 1.03; *p*=0.003) for CAD and 1.05 (95% confidence interval, 1.02, 1.08; *p*=0.001) for intracerebral hemorrhage. Genetic liability to RA was associated increased levels of tumor necrosis factor and C-reactive protein (CRP). The association for CAD attenuated after adjustment for genetically predicted CRP levels. There were no associations of genetic liability to RA with the other studied outcomes.

**Conclusion** This study found that genetic liability to RA was associated with increased risk of CAD and intracerebral hemorrhage and that the association for CAD might be mediated by CRP. The heightened cardiovascular risk should be actively monitored and managed in RA patients, and this may include damping systemic inflammation.

**Keywords:** coronary artery disease; intracerebral hemorrhage; Mendelian randomization; rheumatoid arthritis; stroke

**Introduction**

Rheumatoid arthritis is the most common autoimmune arthritis with a prevalence of 1%, and cardiovascular disease (CVD) is the leading cause of mortality worldwide (1, 2). Interestingly, CVD risk is substantially increased in RA, and to a similar extent as other established risk factors such as diabetes (3). Both cardiovascular morbidity and mortality have been found in meta-analyses to be 1.5-fold elevated in RA over the general population (4, 5). The reasons for this remain poorly understood, but may relate to shared risk factors (e.g., obesity and smoking), or an influence of RA on traditional cardiovascular risk factors (e.g., side effects of anti-rheumatic therapies or reduced physical activity due to pain). Importantly though, traditional risk factors do not fully explain the augmented CVD risk in RA and observational studies suggest that RA may be a novel, and independent risk factor for coronary disease (6-9). CVD and RA have overlapping pathophysiologic mechanisms which may contribute, such as systemic inflammation, with cytokines raised in RA known to be important in driving atherosclerotic diseases (10). In line with this, systemic markers of inflammation associate with cardiovascular risk in RA (11, 12). However, previous observational studies may have been limited by residual confounding or reverse causality. As such, whether RA is an independent and causal risk factor for cardiovascular diseases and cardiometabolic risk factors remains equivocal.

Mendelian randomization (MR) analysis is an epidemiological approach that can strengthen causal inference by using genetic variants as instrumental variables for the exposure (13). The method can minimize the influence of residual confounding since genetic variants are randomly distributed at conception and therefore unrelated to self-adopted lifestyle and environmental confounders (13). In addition, the method can diminish reverse causality because the germline genotype cannot be modified by the onset and progression of the disease (13). Here, we conducted a two-sample MR study to examine the associations of genetic predisposition to RA with coronary artery disease (CAD), stroke and its subtypes and cardiometabolic risk factors. We aimed to provide important evidence regarding the causal role of RA in causing a range of CVD, and whether this could be through influencing traditional risk factors or systemic inflammation.

**Methods**

**Study design**

We first examined the genetic correlations and MR associations of genetic predisposition to RA with CAD and stroke and its subtypes. To assess potential mechanisms, we investigated the associations of genetic predisposition to RA with common cardiovascular risk factors and related inflammatory biomarkers. We then conducted multivariable MR analysis to examine the mediation effects of RA-associated factors in the associations between genetic predisposition to RA and the cardiovascular endpoints. This study was based on summary-level data from international consortia, UK Biobank, and the FinnGen consortium. All included studies had obtained ethical permits from corresponding ethics committees. The UK Biobank received ethical permits from the North West Multi-centre Research Ethics Committee, the National Information Governance Board for Health and Social Care in England and Wales, and the Community Health Index Advisory Group in Scotland. All participants provided written informed consent. The present MR analyses were approved by the Swedish Ethical Review Authority (2019‐02793). This study was conducted in accordance with the MR guideline (14).

**Instrumental variable selection**

Single nucleotide polymorphisms (SNPs) strongly associated (*p*<5×10-8) with RA were obtained from a genome-wide association meta-analysis including 14,361 RA cases and 43,923 controls of the European ancestry (15). All RA cases were defined by the 1987 criteria of the American College of Rheumatology for RA diagnosis or by a professional rheumatologist (15). Linkage disequilibrium in selected SNPs was estimated using the 1000 Genomes European reference panel. SNPs in high linkage disequilibrium (*r*2 >0.01 or clump windows <10,000 kb) were excluded and the SNP with the lowest *p* value for the genome-wide association with RA was retained. A total of 70 independent SNPs with beta and standard error coefficients scaled to log-transformed odds of RA were used as instrumental variables (**Supplementary Table 1**). To provide estimates with a more intuitive interpretation, we estimated absolute genetic associations with RA using linear regression and used these summary-level data for SNP-RA associations in a supplementary analysis (**Supplementary Table 1**). This enables the calculation of MR estimates that represent odds ratios for the studied CVDs per 1% increase in the absolute probability of RA. Genetic associations were estimated in participants of genetic European descent in UK Biobank. The outcome was defined using electronic health records (ICD-9 714.0, ICD-10: M05 or M06). Linear regression was performed with adjustment for age, sex, and 10 genomic principal components.

**Data sources for outcomes**

Summary-level data for the associations of RA-associated SNPs with CAD, all stroke, any ischemic stroke and its subtypes, intracerebral hemorrhage, and subarachnoid hemorrhage were obtained from meta-analyses of genetic studies, international genetic consortia (16-19), the UK Biobank, and the FinnGen consortium (20). There was minimal sample overlap between the exposure and outcome datasets. Detailed information, including case and control number and covariates adjusted for in the genome-wide association analysis, is shown in **Table 1**. The associations of RA-associated SNPs with above outcomes are presented in **Supplementary Table 2.**

**Data sources for cardiovascular risk factors, inflammatory biomarkers, and inflammatory bowel disease**

We obtained summary-level data for cardiovascular risk factors (including body mass index (21), blood pressure (22), fasting glucose and insulin (23), high-density and low-density lipoprotein cholesterol and triglyceride (24), smoking initiation (25), and moderate to vigorous physical activity (the Neale Lab data, http://www.nealelab.is/uk-biobank) and inflammatory biomarkers (interleukin-6 (26), tumor necrosis factor (26), and C-reactive protein (27)) from international consortia and the UK Biobank (the Neale Lab data). Summary-level data on inflammatory bowel disease were obtained from a genome-wide association meta-analysis study including 59,957 individuals of European descent (28).Detailed information on the studies used are shown in **Supplementary Table 3.**

**Genetic correlation analysis**

Genome-wide pairwise correlations between RA and studied CVD outcomes based on consortia data were estimated using linkage disequilibrium score regression (LDSC) that leverages genome-wide association analysis summary-level data and linkage disequilibrium to estimate genetic correlation (29). This method estimates universal genetic correlation by measuring correlation of effect size between SNP-exposure and SNP-outcome associations across all genetic variants in the genome. The correlation with *rg* >0.7 was deemed as a strong correlation. The correlation with the *p* value <0.006 (0.05/8 outcomes) was treated as significant in LDSC analysis.

**Statistical analysis**

We aligned the SNPs based on allele letter and allele frequency. SNPs that were missing in the outcome datasets were replaced by proxy SNPs, which were searched in <https://ldlink.nci.nih.gov/> by setting *r*2 >0.8 and European populations as reference groups. Missing SNPs without proxies were excluded from the analysis. We searched phenotypes associated with RA-associated SNPs at the genome-wide significance level in PhenoScanner V2, a database of human genotype-phenotype associations (30).

The inverse variance weighted method under the multiplicative random effects model was used as the main method to calculate the associations of genetic liability to RA with cardiovascular outcomes, cardiovascular risk factors and inflammatory biomarkers. The method can provide the most precise estimate; however, it is sensitive to horizontal pleiotropy and outliers. Several sensitivity analyses, including the weighted median (31), MR-Egger (32), MR-PRESSO (33), and contamination mixture (34) methods, were used to examine the consistency of results and detect and correct for horizontal pleiotropy. The weighted median analysis can provide consistent causal estimates, providing that more than half of weight derives from valid SNPs (31). The MR-Egger regression can detect the horizontal pleiotropy by its intercept test and provide estimates after correcting for pleiotropic effects; however, the analysis is less powerful for most scenarios (32). In a comparative study, power to detect causal effect is usually greater for the inverse variance weighted method compared to the MR-Egger method in scenarios of different status of pleiotropy and satisfaction of InSIDE (Instrument Strength Independent of Direct Effect) assumption (32). The MR-PRESSO method can also correct for horizontal pleiotropy by identifying and removing outlying SNPs (33). The contamination mixture method is good at analysis based on multiple genetic instruments and can generate causal estimates even when instruments contain invalid SNPs (34). In addition, we used scatter plots to visualize the heterogeneity in estimates of used SNPs and whether the association was driven by certain SNPs. Estimates from different datasets, but for the same cardiovascular disease, were combined using the fixed-effects meta-analysis method where study-specific estimates were weighted based on the amount of information captured by that study (i.e., more weight to a large study with many cases than in a small study with few cases). Given that the *HLA* gene regions are shared by RA and other autoimmune disorders (35), we performed a sensitivity analysis after removal of SNPs in these gene regions (including *HLA\_A, HLA\_B, HLA\_C, HLA\_DPA1, HLA\_DPB1, HLA\_DQA1, HLA\_DQB1, HLA\_DRA, HLA\_DRB1,* and *HLA\_DRB3*). We used the multivariable MR analysis to estimate the mediation effects of RA-associated factors in the associations between RA and cardiovascular outcomes. The multivariable MR analysis was based on the same set of genetic instruments (SNPs for RA) and the model was based on summary-level beta coefficients and the corresponding standard error for RA, the outcome, and the mediator. In addition, we conducted a multivariable MR analysis to adjust for genetic liability to inflammatory bowel disease (a common autoimmune disease) to minimize its influence. Likewise, this analysis used the same genetic variants as the main analysis and MR estimates were obtained from a multivariable inverse variance weighted analysis on the association between genetic liability to RA with a CVD outcome with adjustment for genetic liability to IBD. Cochran’s Q value and p value for MR-Egger intercept were used to assess the heterogeneity and horizontal pleiotropy, respectively. The Bonferroni correction was used to account for multiple testing in examining the association between RA and cardiovascular diseases. Associations with a *p* value <0.006 (0.05/8 outcomes) were deemed significant association in order to correct of multiple testing. All tests were two-sided and were conducted using the TwoSampleMR and MendelianRandomization package (36, 37).

**Results**

Results of the search in PhenoScanner V2 are presented in **Supplementary Table 4.** Several RA-associated SNPs were found to be associated with other autoimmune diseases, like inflammatory bowel disease, systemic lupus erythematosus, type 1 diabetes, at the genome-wide significance levels. A few other traits, like immune cells, were identified to be associated with used SNPs. There were few strong genetic correlations between RA and studied cardiovascular outcomes (**Supplementary Table 5**). RA showed a weak significant association with overall stroke (*rg,* 0.20; *p*=0.003).

Genetic liability to RA was associated with an increased risk of CAD and intracerebral hemorrhage (**Figure 1**) consistently across sources. For one unit increase in log odds of RA, the combined odds ratios were 1.02 (95% confidence interval [CI], 1.01, 1.03; *p*=0.003) for CAD and 1.05 (95% CI, 1.02, 1.08; *p*=0.001) for intracerebral hemorrhage. The results were stable in all sensitivity analyses (**Supplementary Table 6**). The results were stable in all sensitivity analyses (Supplementary Table 6). In a supplementary analysis where estimates for the CVD outcomes were scaled per 1% increase in genetic liability to RA on the risk difference scale, the OR was 1.03 (95% CI, 1.01, 1,05) for CAD and 1.06 (95% CI, 1.01, 1,11) for intracerebral hemorrhage (Supplementary Table 7). We detected moderate heterogeneity in the analyses for coronary artery disease and no horizontal pleiotropy (*p* for MR-Egger intercept test >0.4) (**Supplementary Table 6**). Even though a few outliers were detected in the MR-PRESSO analyses for coronary artery disease, the associations remained consistent after removal of these outliers (**Supplementary Table 6**). As for associations for intracerebral hemorrhage in the three datasets, we observed no or modest heterogeneity, no indication of horizontal pleiotropy in MR-Egger intercept tests, and no outliers were detected by the MR-PRESSO analyses (**Supplementary Table 6**). In scatter plots of associations for CAD and intracerebral hemorrhage, we did not observe any SNPs that drove the overall positive associations (**Figure 2**). Otherwise, there were no associations of genetic liability to RA with all stroke, any ischemic stroke and its subtypes, or subarachnoid hemorrhage (**Figure 1 and Supplementary Table 6**).

The observed associations for CAD and intracerebral hemorrhage remained stable in the sensitivity analysis after removal of SNPs in *HLA* gene regions (**Supplementary Table 8**). The associations were also stable in the multivariable MR analysis with adjustment for genetic liability to inflammatory bowel disease (**Supplementary Table 9**).

With respect to cardiometabolic risk factors, genetic liability to RA was associated with reduced log odds ratio of smoking initiation, and increased levels of high-density lipoprotein cholesterol, tumor necrosis factor, and C-reactive protein (**Figure 3**). The associations remained directionally consistent in sensitivity analyses (**Supplementary Table 10**). There were no associations of genetic liability to RA with the other cardiovascular risk factors and inflammatory biomarkers studied (**Figure 3**).

Multivariate MR analyses were conducted to adjust for genetically predicted levels of tumor necrosis factor and C-reactive protein levels. The association between RA and CAD attenuated in the analysis with adjustment for genetically predicted C-reactive protein levels, but not in the analysis with adjustment for genetically predicted tumor necrosis factor. The association between RA and intracerebral hemorrhage changed only slightly in the multivariable MR analyses (**Figure 4**).

**Discussion**

We conducted a two-sample MR study to investigate the causal associations of RA with CAD and stroke using data from the large consortia and genetic studies. Few strong genetic correlations were observed between RA and studied cardiovascular outcomes. We found that genetic liability to RA was associated with elevated risk of CAD and intracerebral hemorrhage, but not ischemic stroke or subarachnoid hemorrhage. These associations were consistent across different data sources, after removal of SNPs in *HLA* gene regions, and in the multivariable MR analysis with adjustment for genetic liability to inflammatory bowel disease. Genetic liability to RA was associated with elevated levels of tumor necrosis factor and C-reactive protein. The increased levels of C-reactive protein appeared to mediate the association for CAD. We thus provide important genetic evidence supporting the link between RA and some CVDs and underscore the role of inflammation in driving CAD specifically.

RA has widely been reported as an important risk factor for CAD and impaired vascular function (32). A higher prevalence, extent, and severity of coronary plaque measured by coronary calcification (6) is found in RA patients, and this is related to disease duration, being increased in established compared to early RA (31). Similarly, invasive angiographic studies have also demonstrated RA to be associated with an increased extent of coronary atherosclerosis, with a higher prevalence of multivessel CAD, even after adjustment for some traditional risk factors(9). Importantly, this accelerated coronary atherosclerosis also appears to confer a substantially elevated risk of cardiovascular events; with incident myocardial infarction and CAD-related mortality increased by 68% and 59% in RA, according to large meta-analyses (3,4). We support a causal role for RA in driving coronary artery disease, although we report a more modest effect size of 2% in the main analysis. This likely relates to differences in outcome definition (myocardial infarction vs the softer endpoint of coronary artery disease), more healthy populations included, and the calculation of risk according to log odds of rheumatoid arthritis. Overall, though, the totality of evidence suggests coronary artery disease to be increased in RA, and our study strongly suggests a causal role in this. There are approximately 14 million people with RA globally (38). As lifetime risk of CAD for people in general is already high (39), even a small increase in odds of cardiovascular disease raises the expected number of CAD events in this population by tens of thousands compared to that expected for a similar sized group without rheumatoid arthritis. This potentially impacts public health policy around targeting of education, screening, and treatment at RA patients. Secondly, it gives insight into potential mechanisms of CAD. Even though we identified that chronic inflammation might mediate the association between RA and CAD, future research may be able to unpick exactly what more metabolic or inflammatory changes are occurring in people with RA leading to this increase in CAD, potentially identifying treatment or screening options for the whole population.

Stroke risk, of both ischemic and hemorrhagic types, has also widely been reported in observational studies to be increased in RA patients (40). Our study did not detect an association between genetic liability to RA and risk of stroke overall or ischemic stroke. This discrepancy may be related to confounding in observational studies, or increased stroke risk may not be caused by RA *per se* but certain features of RA patients. In line with this, incident adverse events, including serious infections and insufficient treatment of cardiovascular diseases have been found to be drivers of the increased risk of stroke in RA patients (41). These null MR findings might be caused by inadequate power. Our study did, however, suggest a causal role for RA in causing intracerebral hemorrhage, and supports the 68% increased risk reported in meta-analysis of observational studies (40). Our consistent findings across three datasets highly suggests the validity of this association and the underlying mechanisms warrant further investigation.

Several mechanisms have been proposed to explain the increased risk of cardiovascular disease in RA patients. Firstly, it has been suggested that RA may influence the development of traditional cardiovascular risk factors. We did not find genetic liability to RA to be associated with the majority of cardiometabolic risk factors, and only high-density lipoprotein cholesterol, a protective factor, was significantly increased. We therefore provide some mechanistic evidence against the role of traditional risk factors, although it is possible that RA may indirectly influence traditional risk factors, such as due to side effects of anti-rheumatic or anti-inflammatory medications. In addition, our null MR findings for the associations of genetic liability to RA with cardiometabolic risk factors could not completely rule out the effects of shared non-genetic factors on these associations. Furthermore, although far from significance, relatively large effect sizes were found for blood pressure in our study. In a recent published MR analysis including 461,880 hypertension cases and 337,653 controls, RA has been associated with a high risk of hypertension (42), which is an important risk factor for CAD and the main cause of hemorrhagic stroke. However, a key hypothesis is that elevated systemic inflammation and remarkably overlapping inflammatory processes between the two conditions leads to progression of cardiovascular disease (11, 43). In line with this, circulating levels of inflammatory markers such as C-reactive protein, erythrocyte sedimentation rate, and IL-6 in RA patients are associated with the risk of cardiovascular events (11, 44), and, with radiologic measures of coronary atherosclerosis (45). Our study supports that chronic inflammation drives CAD risk in RA, as C-reactive protein mediated the association between RA and CAD risk. However, our multivariable MR analysis did not suggest an important role of tumor necrosis factor for CAD or for RA-associated inflammation on intracerebral hemorrhage. Other RA-related abnormalities which may predispose to CAD or intracerebral hemorrhage may include endothelial dysfunction, oxidative stress, lipid alterations, and post-translational modifications of peptides (44). Further investigation is required into the mechanisms underlying the association between RA and intracerebral hemorrhage.

Elevated cardiovascular disease in RA has long been recognized, and in recent years this has been incorporated into European clinical guidelines written for use by both rheumatology (EULAR) (46) and cardiology (ESC) (47) clinicians. In particular, the importance of regular cardiovascular risk assessment every 5 years is emphasized, as is the use of a 1.5-fold multiplication factor to account for RA in risk scores based solely on traditional risk factors. However, evidence exists that cardiovascular risk factors remain undiagnosed in RA patients and, even when detected they may be undermanaged compared to in patients with other risk factors like diabetes (48). Our study provides the first MR evidence supporting the causal role of RA in driving heightened cardiovascular risk. This not only emphasizes the importance of monitoring this high-risk population, but also supports the notion in clinical guidelines that combating rheumatic disease activity is also integral to reducing cardiovascular risk. Current strategies to do this remain controversial, as some therapies have been associated with adverse cardiovascular effects (46, 49). We provide the causal genetic evidence that inflammation drives CAD risk in RA and implicate this as an effective therapeutic target. Inhibitors of tumor necrosis factor are commonly used in clinical practice and although some evidence exists for reduced cardiovascular risk in patients on such treatments (50) our results do not support this. C-reactive protein is a broad inflammatory marker raised by many pathways, including the interleukin-1/ interleukin-6 axis. Interleukin-1 inhibition reduced cardiovascular events in the CANTOS trial, and IL-6 inhibition has been found to have beneficial effects on markers of atherosclerosis such as carotid intima-media thickness (46) and to reduce cardiovascular events in RA (51). Although anti-inflammatory treatments may prove useful in cardiovascular prevention in RA, studies to date have had inadequate follow-up times and have been confounded by therapies being allocated to those with the most severe disease. Well-designed clinical trials studying the impact of anti-inflammatory therapies on cardiovascular risk in RA are required.

Given that autoimmune diseases have some overlapping genetic architecture, whether the observed RA-CAD and RA-intracerebral hemorrhage associations in our MR analysis were exclusive for RA remained undetermined even though we employed several approaches to examine this. First, the results from the search of phenotypes associated with RA-associated SNPs in PhenoScanner V2 showed no clear pattern that these used RA-SNPs could systematically mimic the effects of other immune-mediated disorders although several RA-associated SNPs were associated with several other immune-mediated diseases at the genome-wide significance level. Second, the observed associations for CAD and intracerebral hemorrhage remained stable in the sensitivity analysis after removal of SNPs in the *HLA* gene regions shared by autoimmune disorders (35), which indicated that the effects of most shared genes among autoimmune diseases did not drive the associations. Third, the associations remained in the multivariable MR analysis with adjustment for inflammatory bowel disease. However, we could not perform this analysis to adjust for genetic liability to other common autoimmune diseases due to lack of data or too many missing SNPs in corresponding analysis. Even though our exploration implies the observed associations for CAD and intracerebral hemorrhage are likely to be specific to RA, more study is needed to confirm our hypothesis.

The present study has several strengths, including MR design, the use of multiple genetic instruments, the use of different outcome data sources, the use of the multivariable MR analysis to explore possible mechanisms, and the population confinement to individuals of European descent (reducing population structure bias). In addition, lack of strong genetic correlations between RA and studied outcomes suggested that the observed associations for CAD and ICH should not be driven by shared genetic risk.

Several limitations should be considered when interpreting our findings. We observed moderate heterogeneity in the analyses for coronary artery disease in CARDIoGRAMplusC4D+UKBB and FinnGen datasets. However, the corresponding MR-Egger regression analysis did not detect any indication of horizontal pleiotropy, which suggests possible balanced horizontal pleiotropy that is unlikely to bias the MR estimate (52). In addition, the associations for coronary artery disease in two datasets were consistent across different sensitivity analyses with different assumptions. Even though there were a few outliers detected by MR-PRESSO analyses, the associations remained after removal of these outliers. We did not take anti-RA treatments into consideration in the current analysis. Nonetheless, whether corresponding treatments, such as anti-tumor necrosis factor drugs and nonsteroidal anti-inflammatory drugs, are associated with cardiovascular risk is unclear (44, 53). In addition, these treatments should not bias our causal estimation as their use follow the diagnosis of RA and would therefore be classified as vertical pleiotropy (52). The population confinement to European populations might limit the generalizability of our findings to other populations. In addition, whether the null findings for stroke and its subtypes except for intracerebral hemorrhage could be robustly holden are uncertain as the lack of significant associations might be caused by inadequate power despite the large sample size, at least for ischemic stroke. A power calculation for the current analysis was not possible due to the lack of information on phenotypic variance in RA explained by the SNPs used in the analysis as this information cannot be calculated for a binary phenotype. Thus, future studies are needed to confirm these null findings. Whether the observed associations could be applied to subgroups defined by sex and status of anti-citrullinated protein autoantibodies could not be assessed due to lack of data.

In conclusion, this MR study found positive associations of genetic liability to RA with CAD and intracerebral hemorrhage and the association for CAD appeared to be mediated by high levels of C-reactive protein. These findings highlight the importance of active monitoring and prevention of cardiovascular risk to combat CAD and intracerebral hemorrhage in RA patients. We further suggest that dampening inflammation might be a preventive strategy for CAD in RA patients and well-designed clinical trials are required to assess this.

**Additional information**

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**Ethics approval and consent to participate:** All studies included in cited genome‐wide association studies had been approved by a relevant review board. The present MR analyses were approved by the Swedish Ethical Review Authority (2019‐02793).

**Availability of data and materials:** Data used can be obtained from a reasonable request to the corresponding author.

**Competing interests:** All authors declare no competing interests.

**Authorship Criteria**: SY, PC, and SCL contributed to the study conception and design. SY and PC drafted the manuscript. All authors analyzed and interpreted the data, revised the manuscript critically for important intellectual content, and approved the version of the article to be published.

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**Table 1.** Included studies and consortia

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| --- | --- | --- | --- | --- | --- |
| **Data source** | **Outcome** | **Ancestry** | **Cases** | **Controls** | **Adjustments in the GWAS** |
| CARDIoGRAMplusC4D plus UKBB | Coronary artery disease | Mixed | 122 733 | 424 528 | Not reported |
| MEGASTROKE consortium | All stroke  Any ischemic stroke  Large artery stroke  Small vessel stroke  Cardioembolic stroke | European | 40 585  34 217  3 373  5 386  7 193 | 406 111  406 111  406 111  406 111  406 111 | Age and sex |
| ISGC | Intracerebral hemorrhage | European | 3 223 | 3 725 | Age, sex, and principal components |
| Bakker et al GWAS | Subarachnoid hemorrhage | European | 5 140 | 71 952 | Not reported |
| UK Biobank (UKBB) | All stroke  Any ischemic stroke  Intracerebral hemorrhage  Subarachnoid hemorrhage | European | 12 036  6 566  1 504  1 292 | 355 525  360 995  366 057  366 269 | Age, sex and ten genetic principal components |
| FinnGen consortium | Coronary artery disease  All stroke  Any ischemic stroke  Intracerebral hemorrhage  Subarachnoid hemorrhage | European | 30 952  18 661  10 551  1687  1338 | 187 840  166 201  202 223  201 146  201 230 | Age, sex, the first ten genetic principal components, and genotyping batch |

CARDIoGRAMplusC4D, Coronary ARtery DIsease Genome wide Replication and Meta-analysis plus The Coronary Artery Disease Genetics; GWAS, genome-wide association study; ISGC, International Stroke Genetic Consortium.

**Figure legends**

**Figure 1**. Associations of genetic liability to rheumatoid arthritis with coronary artery disease and stroke. CARDIoGRAMplusC4D, Coronary ARtery DIsease Genome wide Replication and Meta-analysis plus The Coronary Artery Disease Genetics; CI, confidence interval; GWAS, genome-wide association study; ISGC, International Stroke Genetic Consortium; OR, odds ratio; UKBB, UK Biobank.

**Figure 2.** Scatter plots of associations for coronary artery disease and intracerebral hemorrhage. MR, Mendelian randomization; SNP, single nucleotide polymorphism.

**Figure 3**. Associations of genetic liability to rheumatoid arthritis with cardiometabolic risk factors and inflammatory cytokines. CI, confidence interval.

**Figure 4**. Associations of genetic liability to rheumatoid arthritis with coronary artery disease and intracerebral hemorrhage after adjustment for tumor necrosis factor (TNF) and c-reactive protein (CRP). CARDIoGRAMplusC4D, Coronary ARtery DIsease Genome wide Replication and Meta-analysis plus The Coronary Artery Disease Genetics; CI, confidence interval; ISGC, International Stroke Genetic Consortium; OR, odds ratio; UKBB, UK Biobank.