ATHEROSCLEROSIS

International Journal for Research and Investigation on Atherosclerosis and Related Diseases

AUTHOR INFORMATION PACK

TABLE OF CONTENTS

ISSN: 0021-9150

DESCRIPTION

Atherosclerosis brings together, from all sources, papers concerned with investigation on **atherosclerosis**, its risk factors and clinical manifestations. *Atherosclerosis* covers basic and translational, clinical and population research approaches to **arterial** and **vascular biology** and **disease**, as well as their risk factors including: **disturbances of lipid and lipoprotein metabolism, diabetes** and **hypertension, thrombosis**, and **inflammation**. The Editors are interested in original or review papers dealing with the pathogenesis, environmental, genetic and epigenetic basis, diagnosis or treatment of atherosclerosis and related diseases as well as their risk factors.

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AUDIENCE

Researchers and clinicians working on atherosclerosis and related diseases, including: lipoprotein metabolism, arterial and vascular biology and disease, thrombosis, inflammation, and cardiovascular risk factors.

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SPECIAL GUIDELINES

Clinical Trials

The International Committee of Medical Journal Editors (ICMJE) defines a clinical trial as any research project prospectively assigning human participants to intervention or comparison groups to study the cause-and-effect relationship between an intervention and a health outcome. Interventions include but are not limited to drugs, surgical procedures, devices, behavioral treatments, process-of-care changes, and the like. All manuscripts reporting clinical trials, must include a copy of the trial protocol including the complete statistical analysis plan, a flow diagram (CONSORT flow diagram), and a completed trial checklist (the CONSORT checklist and template flow diagram can be found at http://www.consort-statement.org/. The trial registration number must be included on the title page of the manuscript reporting a registered clinical trial and in the Materials and methods section. Failure to do so will prevent entry to the peer review process.

Registration of clinical trial

Registration in a public trials registry is a condition for publication of clinical trials in Atherosclerosis in accordance with International Committee of Medical Journal Editors (ICMJE) recommendations. Trials must be registered at or before the onset of patient enrolment. Purely observational studies (those in which the assignment of the medical intervention is not at the discretion of the investigator) will not require registration.

Clinical trial results

In line with the position of the ICMJE, Atherosclerosis will not consider results posted in the same clinical trials registry in which primary registration resides to be prior publication if the results posted are presented in the form of a brief structured (less than 500 words) abstract or table. However, divulging results in other circumstances (e.g., investors' meetings) is discouraged and may jeopardise consideration of the manuscript. Authors should fully disclose all posting in registries of results of the same or closely related work.

Randomized control trials

Reports of randomised trials must conform to CONSORT 2010 guidelines. All manuscripts reporting randomized clinical trials, must include a copy of the trial protocol including the complete statistical analysis plan, a flow diagram (CONSORT flow diagram), and a completed trial checklist (the CONSORT checklist and template flow diagram can be found at http://www.consort-statement.org).

Guidelines for genetic association papers

Atherosclerosis is interested in publishing genetic association papers that present data that is novel, statistically robust, clinically relevant and that add significantly to the field. Authors are advised to follow the reporting guidelines outlined in the STREGA Statement (http://www.strega-statement.org) [1], and to achieve this, the following criteria should be met.

1. All the following aspects should be addressed appropriately and Methods used should be reported:

a) Population stratification should be addressed in case of admixed populations;

b) Test on Hardy-Weinberg-Equilibrium must be carried out and the p value reported;

c) LD-structure between SNPs (if multiple SNPs are reported) must be presented;

d) Genotyping errors / call rate must be reported;

e) Appropriate correction for multiple testing (if multiple independent SNPs are reported) must be included;

f) Possible relatedness between studied subjects must be documented and addressed if present.

2. All papers must include a power calculation to estimate the effect the size the study has the power to detect, based on sample size and minor allele frequency of the included SNPs. If power calculations are not included the paper is likely to be rejected without review. It should be stated whether or not power calculations were performed before or after study completion. Comment: The study should have an adequate sample size. Ideally, power calculations should have been performed before conducting the study since post-hoc power calculations are often a self-fulfilling prophecy. It should be stated whether or not power calculations were performed before or after study completion. Several programs are available to perform power and/or sample size calculations for genetic association studies, e.g. the "Genetic Power Calculator" (http://pngu.mgh.harvard.edu/~purcell/gpc) [2], and see table 1 below. Sample size and /or Power calculations on two-stage designs can be calculated e.g. by using the program CATS (http://www.sph.umich.edu/csg/abecasis/CaTS) [3] for case-control studies and QpowR (https://www.msu.edu/~steibelj/JP_files/QpowR.html) for studies on quantitative traits. Since genetic association studies often involve more complex study designs involving meta-analysis or several replication stages, simple answers on required sample sizes cannot be given. Authors are advised, however, to keep this issue in mind and give a good rationale, if the study is clearly underpowered.

3. For any novel association a replication study must be included in the submitted manuscript. Any novel association not including a replication study may be rejected without review. Comment: The presentation of novel association results requires replication in most cases, if appropriate replication studies exist. However, if the first study has already an appropriate sample size (considering that very large studies with several thousands of individuals are available) and if the results show a strong association, it might not be necessary to provide a replication. Furthermore, giving additional evidence from other sources could replace replication studies, if they are convincing, e.g. results from functional experiments. Meta-analysis on the discovery stage or other outstanding studies do also not require replication in every case, but it should be clear that these are exceptional cases and have to discussed in that way to be acceptable for publication.

4. For any association study replicating a previously published finding, there should be sufficient novelty to add significantly to the literature. This could include confirming the effect size in a different ethnic group, or extending the association observations to additional intermediate traits or disease groups. Any study not having sufficient novelty is likely to be rejected without review.

5. We require all SNPs to have their designated RS number and for the numbering of base pair changes and amino acid changes and gene symbols to be using agreed nomenclature. For example see the following website: http://www.hgvs.org/mutnomen.

6. Generally, authors should present the rationale as to why gene regions and SNPs have been selected. Association studies using SNPs where previous studies have demonstrated that the base change has an effect on protein function or gene expression will be favored over those using SNPs where no functionality has been previously determined. Studies using a tagSNP approach will also be considered, where these add additional data to the already known variations, in order to further explain observed associations.

References

[1] Little J et al: Strengthening the Reporting of Genetic Association Studies (STREGA): an extension of the STROBE statement. PLoS Med. 2009 Feb 3;6(2):e22.

[2] Purcell S, et al. Genetic Power Calculator: design of linkage and association genetic mapping studies of complex traits. Bioinformatics 2003, 19(1):149-150.

[3] Skol AD et al. Joint analysis is more efficient than replication-based analysis for two-stage genome-wide association studies. Nat Genet (2006) 38:209-13.

In the following table, some sample sizes are given, calculated from the "Genetic Power Calculator", assuming an alpha-level of = 0.05, an additive inheritance model, an assumed prevalence of disease of 30% and a power of 80% for a balanced case-control study (1:1 case:control ratio) for varying minor allele frequencies (MAF) and genetic relative risks (GRR). Relative risks of between 1.1 and 1.3 are in the range that can be expected in genetic association studies on complex diseases.

ATH_GfA_example_table.jpg

Guidelines for meta-analyses

In principle, literature-based meta-analyses should be reported in that way, that any interested researcher is able to reproduce the results. To ensure this, authors are strongly advised to follow the guidelines listed below and are further encouraged to use the PRISMA (http://www.prisma-statement.org/PRISMAStatement/Default.aspx) and the MOOSE statements (http://jama.ama-assn.org/cgi/content/full/283/15/2008) as a guide. Therefore, as much information as needed should be provided. However, for the average reader only the most mandatory information should be reported in the main paper with additional information given in the Supplementary Material.

1. Specification of objective and primary study outcome. If there are previous meta-analyses on the same outcome available, the authors should specify clearly the differences and added value of their meta-analysis in a separate section ("Added value to previous meta-analysis on the same topic").

2. Detailed specification of search strategy, study selection strategy (including approaches to reach unpublished studies) and eligibility criteria for studies. It is highly recommended to use a graphical Flow Chart (templates available at http://www.prisma-statement.org/PRISMAStatement/Default.aspx).

3. Description of possible sources of bias and confounding and strategies to prevent them. This includes:Bias in individual studiesBias across studies (e.g. publication bias, selective reporting within studies)Quality and comparability of studies (study types, study outcomes, sample size)

4. Description of Statistical Methods: What is the primary summary measure (Difference in Mean, OR, etc.)? How was it extracted from the individual studies (e.g. calculated from raw numbers or tables or taken as reported)Methods to assess heterogeneity and biasMethods used for the combined analysis (fixed effects, random effects) including a rationale for using this method.

5. Reporting of results:Individual study characteristics (including sample size, study type, population/ethnicity, primary outcome, reference)Individual study results (effect estimates including confidence intervals or standard errors). Graphical presentations is preferred (Forest plots).Meta-analysis results: Combined effect estimate, confidence intervals, some measure of heterogeneity, results of bias assessment (preferably using graphical presentations, e.g. Funnel plot)

6. Additional for meta-analysis of genetic association studies: meta-analysis on a single SNP with certain selected outcomes suffer from the problem that they completely ignore the other genetic variability within a certain gene region. Many of these meta-analyses also completely ignore already available results from genome-wide association (GWA) studies on the investigated outcomes. These GWA studies might not have studied the very SNP of interest but highly correlated ones in the same genetic region which can add valuable information to the meta-analysis. The authors must either discuss the findings from these GWAS or - even much better - approach the authors from these GWAS for a lookup of the meta-analyzed SNPs. Meta analyses that do not cover these issues will be rejected without review. Furthermore, these studies have to report the following information:Specification of the genes / polymorphisms (rs numbers) and rationale for selection of the specific polymorphismsGenotyping methods in each individual studyGenotype characteristics (genotyping success rate, minor allele frequency, frequencies of genotypes, Hardy-Weinberg-equilibrium).