ATHEROSCLEROSIS

International Journal for Research and Investigation on Atherosclerosis and Related Diseases

AUTHOR INFORMATION PACK

TABLE OF CONTENTS

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DESCRIPTION

Atherosclerosis brings together from all sources papers concerned with research and investigation on **atherosclerosis**, its complications, and related diseases, including: **lipoprotein metabolism**, **arterial** and **vascular biology** and **disease**, **thrombosis**, **inflammation**, disorders of **lipid transport**, **diabetes** and **hypertension** as related to atherosclerosis, and cardiovascular risk factors. The editors are also interested in clinical papers dealing with case studies of specific or general interest, new or unusual **lipid syndromes**, and the genetic basis and familial incidence of atherosclerosis and related diseases. High quality reports of controlled clinical trials of drugs or diets will be considered provided the paper deals with the mechanism of action of the drug or diet.

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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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(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.

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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.

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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. This table can be used as a rough guidance.

1 **MAF**
GRR assumed
per Allele Cases required
in a balanced design 0.01 1.1 40000 1.3 4700 1.5 1800 0.05 1.1 8400 1.3 1000 1.5 380 0.1 1.1 4500 1.3 500 1.5 200 0.2 1.1 2500 1.3 300 1.5 125 0.3 1.1 2000 1.3 250 1.5 100 0.4 1.1 1700 1.3 230 1.5 100

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