**Meta-analysis on Genetic Association Studies Checklist | PLOS ONE**

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|  | Item | Section name and paragraph number within manuscript |
|  | **Introduction** |  |
| 1 | Provide a detailed justification for the polymorphism studied; if a single polymorphism was analyzed, give details as to why others were not included in the meta-analysis. | Introduction: paragraph 1-4 |
| 2 | Provide a detailed justification for the population(s) and clinical condition studied. | Introduction: paragraph 1-4 |
|  | **Methods** |  |
| 3 | Provide full details of the search strategy employed; outline the full electronic search strategy –specific combination of keywords and any limits applied- for at least one database. Specify whether synonyms of polymorphisms/genes (e.g. SNP number) were searched. | Materials and methods: Publication search: paragraph 1 |
| 4 | Report full details on the inclusion and exclusion criteria applied for selecting studies.  *Please list the excluded articles and the reasons for exclusion of each article in a supplementary file.* | Materials and methods: Inclusion/exclusion criteria: paragraph 1.  Supplimentary table 2 |
| 5 | Provide details on how the quality of the studies included in the analyses was assessed. | Materials and methods: Inclusion/exclusion criteria: paragraph 1. |
| 6 | Describe steps taken to contact study authors to identify additional studies and to request missing data. | Materials and methods: Publication search: paragraph 1 |
| 7 | Describe how environmental effects were adjusted for, if this adjustment was not conducted, outline the reasons for this. | Materials and methods: Statistical analysis: paragraph 1 |
| 8 | Describe the methods of handling heterogeneity/between-study variance. | Materials and methods: Statistical analysis: paragraph 1 |
| 9 | Describe how the Hardy-Weinberg equilibrium and linkage disequilibrium were assessed. | Materials and methods: Statistical analysis: paragraph 1 |
| 10 | Describe and justify the choice of model for the analyses (per-allele vs per-genotype vs genetic model-free, random effects vs fixed effects). | Materials and methods: Statistical analysis: paragraph 1 |
| 11 | Describe whether a sensitivity analysis has been completed. | Materials and methods: Statistical analysis: paragraph 1 |
| 12 | Describe whether an assessment of the effects of population stratification has been conducted. | Materials and methods: Statistical analysis: paragraph 1 |
| 13 | Describe whether study-specific results have been assessed and if so the reasons for this (e.g. forest plot). | Materials and methods: Statistical analysis: paragraph 1 |
|  | **Results** |  |
| 14 | Include flow diagram for the studies included in the meta-analysis as the first figure for the manuscript | Results: Study Charactersitics: paragraph 1 Figure 1 |
| 15 | Report details on allele/genotype prevalence. | Results: Meta-analysis results: paragraph 1-7 |
| 16 | Report the effect size estimates and p values for each analysis. | Results: Meta-analysis results: paragraph 1-7. Supplimentary table 3 and supplimentary figure 1 |
|  | **Discussion** |  |
| 17 | Discuss the limitations of the meta-analysis, including genotyping errors/bias and publication bias. | Discussion: paragraph 11-15 |
| 18 | If the meta-analysis identifies an association within a subgroup of the population studied but not another, discuss the implications of these results, and if applicable the possibility of subgroup-specific publication bias. | Discussion: paragraph 5, 7 and 11-15 |
| 19 | Discuss the suitability of the sample size employed to the research question and the power of the study. | Discussion: paragraph 3, 6 and 14-15 |