STROPS guideline

Category	#	Criteria	Page no.	Relevant text from the manuscript
Abstract				
Abstract	1	Provide in the abstract an informative and balanced summary of what was done and what was found.		
Introduction				
Background/ rationale	2	Explain the scientific background and rationale for the investigation being reported.		
	3	Provide reasons for choosing the genes and SNPs genotyped.		
Objectives	4	State specific objectives, including any pre-specified hypotheses.		
	5	State if the study is the first report of a pharmacogenetic association, a replication effort, or both.		
Methods				
Study design	6	Present key elements of study design early in the paper.		
Setting	7	Describe the setting, locations and relevant dates, including periods of recruitment, follow-up, and data collection.		
Participants	8	Give the eligibility criteria, and the sources and methods of selection of participants. For a cohort study, describe methods of follow-up. For a case-control study, state whether true controls or population controls were used. Give the rationale for the choice of cases and controls.		
	9	Report the drug and regime participants were exposed to, and the length of exposure.		
	10	For a matched case-control study, give matching criteria and the number of controls per case.		
	11	Give information on the criteria and methods for selection of subsets of participants from a larger study, when relevant.		
	12	If other publications report results for the same patient cohort, or a subset of the patient cohort, provide information on this patient cohort overlap and references to the relevant publications.		
	13	Report disease/clinical indication of patients using a standardised ontology when possible.		
Variables	14	Clearly define all outcomes, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable.		
	15	Provide justification for choice of outcomes.		
	16	Clearly define genetic exposures (genetic variants) using a widely-used nomenclature system.		

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	17	Report the rs number of each genotyped SNP.		
	18	Clearly state how haplotypes or star alleles were defined.		
	19	If referring to the minor, major, wild-type, mutant, reference, risk or effect allele of a variant, state which allele this is and for which given population/cohort.		
Data sources/ measurement	20	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group.		
	21	Describe laboratory methods, including source and storage of DNA, genotyping methods and platforms (including the allele calling algorithm used, and its version), error rates and call rates. State the laboratory/centre where genotyping was done. Describe comparability of laboratory methods if there is more than one group. Specify whether genotypes were assigned using all of the data from the study simultaneously or in smaller batches.		
	22	Describe genotype quality control methods and findings.		
	23	For quantitative outcome variables, specify if any investigation of potential bias resulting from pharmacotherapy was undertaken. If relevant, describe the nature and magnitude of the potential bias, and explain what approach was used to deal with this.		
	24	Report how adherence to treatment was assessed, and report the results of the assessment.		
Study size	25	Explain how the study size was arrived at, or provide details of the a priori power to detect effect sizes of varying degrees.		
Quantitative variables	26	Explain how quantitative variables (confounders and effect modifiers) were handled in the analyses. If applicable, describe which groupings were chosen, and why.		
Statistical methods	27	Address the following:		
	a)	Describe methods used to control for confounding		
	b)	Describe any methods used to examine subgroups and interactions.		
	c)	Explain how missing data were addressed.		
	d)	Cohort study – If applicable, explain how loss to follow-up was addressed.		

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	e)	Case-control study – If applicable, explain how matching of cases and controls was addressed.		
	f)	Describe any sensitivity analyses.		
	28	State whether Hardy-Weinberg equilibrium was considered and, if so, how.		
	29	Describe any methods used for inferring genotypes or haplotypes.		
	30	Describe any methods used to assess or address population stratification.		
	31	Describe any methods used to assess and correct for relatedness among subjects. Report results of assessments for relatedness.		
	32	Describe any methods used to address multiple comparisons or to control risk of false positive results due to a) multiple genetic variants b) multiple outcomes c) multiple assumptions regarding mode of inheritance		
	33	Describe any methods used to adjust for extent of adherence in the analyses.		
Results				
Participants	34	Report the numbers of individuals at each stage of the study – e.g., numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed.		
SNPs	35	Report any SNPs that were excluded from analysis, and provide reasons for these exclusions.		
Descriptive data	36	Give characteristics of study participants (e.g., demographic, clinical, social, ethnicity) and information on potential confounders.		
	37	Cohort study – Summarize follow-up time, e.g. average and/or total amount.		
	38	Where HWE tests have been undertaken, highlight SNPs that deviate from HWE.		
	39	Where population stratification is assessed, report the results.		
Outcome data	40a)	For a cohort study, report all outcomes (phenotypes) investigated for each genotype category over time.		
	40b)	For a case-control study, report numbers in each genotype category for all outcomes investigated.		
	40c)	For a cross sectional study, report all outcomes (phenotypes) investigated for each genotype category.		

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	41	If a study includes more than one ethnic group, provide the summary data specified in (40) per ethnic group.		
Main results	42	Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (e.g., 95% confidence intervals). Make clear which confounders were adjusted for and why they were included.		
	43	Report category boundaries when continuous variables were categorised.		
Other analyses	44	Report other analyses done – e.g., analyses of subgroups and interactions, and sensitivity analyses.		
	45	If numerous genetic exposures (genetic variants) were examined, summarize results from all analyses undertaken.		
	46	If detailed results are available elsewhere, i.e. in supplementary materials, state how they can be accessed.		
Discussion				
Key results	47	Summarize key results with reference to study objectives.		
Limitations	48	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias.		
Interpretation	49	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence.		
Generalisability	50	Discuss the generalisability (external validity) of the study results.		
Other information				
Study registration	51	State whether the study has been registered. If the study has been registered, provide details of the registry.		
Ethical approval	52	Report whether ethical approval was obtained for the collection of genetic data.		
Funding	53	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based.		
Databases	54	State whether databases for the analysed data are or will become publicly available and if so, how they can be accessed.		