

O'Dea, R.E., Lagisz, M., Jennions, M.D., Koricheva, J., Noble, D.W., Parker, T.H., Gurevitch, J., Page, M.J., Stewart, G., Moher, D. and Nakagawa, S. (2021), Preferred reporting items for systematic reviews and meta-analyses in ecology and evolutionary biology: a PRISMA extension. *Biol Rev.* doi:10.1111/brv.12721

Checklist item	Sub-item number	Sub-item	Reported by authors?	Notes
Title and abstract	1.1	Identify the review as a systematic review, meta-analysis, or both		
	1.2	Summarise the aims and scope of the review		
	1.3	Describe the data set		
	1.4	State the results of the primary outcome		
	1.5	State conclusions		
	1.6	State limitations		
Aims and questions	2.1	Provide a rationale for the review		
	2.2	Reference any previous reviews or meta-analyses on the topic		
	2.3	State the aims and scope of the review (including its generality)		
	2.4	State the primary questions the review addresses (e.g. which moderators were tested)		
	2.5	Describe whether effect sizes were derived from experimental and/or observational comparisons		
Review registration	3.1	Register review aims, hypotheses (if applicable), and methods in a time-stamped and publicly accessible archive and provide a link to the registration in the methods section of the manuscript. Ideally registration occurs before the search, but it can be done at any stage before data analysis.		
	3.2	Describe deviations from the registered aims and methods		
	3.3	Justify deviations from the registered aims and methods		
Eligibility criteria	4.1	Report the specific criteria used for including or excluding studies when screening titles and/or abstracts, and full texts, according to the aims of the systematic review (e.g. study design, taxa, data availability)		
	4.2	Justify criteria, if necessary (i.e. not obvious from aims and scope)		

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Finding studies	5.1	Define the type of search (e.g. comprehensive search, representative sample)		
	5.2	State what sources of information were sought (e.g. published and unpublished studies, personal communications)		
	5.3	Include, for each database searched, the exact search strings used, with keyword combinations and Boolean operators		
	5.4	Provide enough information to repeat the equivalent search (if possible), including the timespan covered (start and end dates)		
Study selection	6.1	Describe how studies were selected for inclusion at each stage of the screening process (e.g. use of decision trees, screening software)		
	6.2	Report the number of people involved and how they contributed (e.g. independent parallel screening)		
Data collection process	7.1	Describe where in the reports data were collected from (e.g. text or figures)		
	7.2	Describe how data were collected (e.g. software used to digitize figures, external data sources)		
	7.3	Describe moderator variables that were constructed from collected data (e.g. number of generations calculated from years and average generation time)		
	7.4	Report how missing or ambiguous information was dealt with during data collection (e.g. authors of original studies were contacted for missing descriptive statistics, and/or effect sizes were calculated from test statistics)		
	7.5	Report who collected data		
	7.6	State the number of extractions that were checked for accuracy by co-authors		

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Data items	8.1	Describe the key data sought from each study		
	8.2	Describe items that do not appear in the main results, or which could not be extracted due to insufficient information		
	8.3	Describe main assumptions or simplifications that were made (e.g. categorising both 'length' and 'mass' as 'morphology')		
	8.4	Describe the type of replication unit (e.g. individuals, broods, study sites)		
Assessment of individual study quality	9.1	Describe whether the quality of studies included in the systematic review or meta-analysis was assessed (e.g. blinded data collection, reporting quality, experimental <i>versus</i> observational)		
	9.2	Describe how information about study quality was incorporated into analyses (e.g. meta-regression and/or sensitivity analysis)		
Effect size measures	10.1	Describe effect size(s) used		
	10.2	Provide a reference to the equation of each calculated effect size (e.g. standardised mean difference, log response ratio) and (if applicable) its sampling variance		
	10.3	If no reference exists, derive the equations for each effect size and state the assumed sampling distribution(s)		
Missing data	11.1	Describe any steps taken to deal with missing data during analysis (e.g. imputation, complete case, subset analysis)		
	11.2	Justify the decisions made to deal with missing data		
Meta-analytic model description	12.1	Describe the models used for synthesis of effect sizes		
	12.2	The most common approach in ecology and evolution will be a random-effects model, often with a hierarchical/multilevel structure. If other types of models are chosen (e.g. common/fixed effects model, unweighted model), provide justification for this choice		

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Software	13.1	Describe the statistical platform used for inference (e.g. <i>R</i>)		
	13.2	Describe the packages used to run models		
	13.3	Describe the functions used to run models		
	13.4	Describe any arguments that differed from the default settings		
	13.5	Describe the version numbers of all software used		
Non-independence	14.1	Describe the types of non-independence encountered (e.g. phylogenetic, spatial, multiple measurements over time)		
	14.2	Describe how non-independence has been handled		
	14.3	Justify decisions made		
Meta-regression and model selection	15.1	Provide a rationale for the inclusion of moderators (covariates) that were evaluated in meta-regression models		
	15.2	Justify the number of parameters estimated in models, in relation to the number of effect sizes and studies (e.g. interaction terms were not included due to insufficient sample sizes)		
	15.3	Describe any process of model selection		
Publication bias and sensitivity analyses	16.1	Describe assessments of the risk of bias due to missing results (e.g. publication, time-lag, and taxonomic biases)		
	16.2	Describe any steps taken to investigate the effects of such biases (if present)		
	16.3	Describe any other analyses of robustness of the results, e.g. due to effect size choice, weighting or analytical model assumptions, inclusion or exclusion of subsets of the data, or the inclusion of alternative moderator variables in meta-regressions		
Clarification of <i>post hoc</i> analyses	17.1	When hypotheses were formulated after data analysis, this should be acknowledged.		

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Metadata, data, and code	18.1	Share metadata (i.e. data descriptions)		
	18.2	Share data required to reproduce the results presented in the manuscript		
	18.3	Share additional data, including information that was not presented in the manuscript (e.g. raw data used to calculate effect sizes, descriptions of where data were located in papers)		
	18.4	Share analysis scripts (or, if a software package with graphical user interface (GUI) was used, then describe full model specification and fully specify choices)		
Results of study selection process	19.1	Report the number of studies screened		
	19.2	Report the number of studies excluded at each stage of screening		
	19.3	Report brief reasons for exclusion from the full text stage		
	19.4	Present a Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA)-like flowchart (www.prisma-statement.org).		
Sample sizes and study characteristics	20.1	Report the number of studies and effect sizes for data included in meta-analyses		
	20.2	Report the number of studies and effect sizes for subsets of data included in meta-regressions		
	20.3	Provide a summary of key characteristics for reported outcomes (either in text or figures; e.g. one quarter of effect sizes reported for vertebrates and the rest invertebrates)		
	20.4	Provide a summary of limitations of included moderators (e.g. collinearity and overlap between moderators)		
	20.5	Provide a summary of characteristics related to individual study quality (risk of bias)		

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Meta-analysis	21.1	Provide a quantitative synthesis of results across studies, including estimates for the mean effect size, with confidence/credible intervals		
Heterogeneity	22.1	Report indicators of heterogeneity in the estimated effect (e.g. I^2 , τ^2 and other variance components)		
Meta-regression	23.1	Provide estimates of meta-regression slopes (i.e. regression coefficients) and confidence/credible intervals		
	23.2	Include estimates and confidence/credible intervals for all moderator variables that were assessed (i.e. complete reporting)		
	23.3	Report interactions, if they were included		
	23.4	Describe outcomes from model selection, if done (e.g. R2 and AIC)		
Outcomes of publication bias and sensitivity analyses	24.1	Provide results for the assessments of the risks of bias (e.g. Egger's regression, funnel plots)		
	24.2	Provide results for the robustness of the review's results (e.g. subgroup analyses, meta-regression of study quality, results from alternative methods of analysis, and temporal trends)		
Discussion	25.1	Summarise the main findings in terms of the magnitude of effect		
	25.2	Summarise the main findings in terms of the precision of effects (e.g. size of confidence intervals, statistical significance)		
	25.3	Summarise the main findings in terms of their heterogeneity		
	25.4	Summarise the main findings in terms of their biological/practical relevance		
	25.5	Compare results with previous reviews on the topic, if available		
	25.6	Consider limitations and their influence on the generality of conclusions, such as gaps in the available evidence (e.g. taxonomic and geographical research biases)		

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Contributions and funding	26.1	Provide names, affiliations, and funding sources of all co-authors		
	26.2	List the contributions of each co-author		
	26.3	Provide contact details for the corresponding author		
	26.4	Disclose any conflicts of interest		
References	27.1	Provide a reference list of all studies included in the systematic review or meta-analysis		
	27.2	List included studies as referenced sources (e.g. rather than listing them in a table or supplement)		