Online Supplementary Materials for:

‘Behavior Outpaces Form when Linking Traits to Ecological Responses within Populations: A Meta-Analysis’

Thibaut Rota, Allan Raffard, Iris Lang, Quentin Petitjean, Lisa Jacquin, Olivier Dézerald, Simon Blanchet, Andrew P. Hendry and Régis Céréghino

Table S1: Examples of traits-to-ecological response relationships from studies constituting our dataset. Studies include measures made on individuals (‘ind’), populations (‘pop’), and colonies of social insects (‘col’). Numbers in bold and in brackets are corresponding to mechanistic *links* shown in Figure 1a.

Level	Trait(s)	Trait type	Species	Ecological response(s)	Trait-to-function relationship (hypothesis or observation)	References
ind	Tail shape	Morphology	*Hyla chrysoscelis* (amphibian)	Survival when exposed to predators (fitness)	The induced changes in tail shape of tadpoles exposed to predators (**11**) enhanced their survival, in affecting their escaping abilities (**4**)	(McCollum & Van Buskirk, 1996)
ind	Mandible shape	Morphology	*Gammarus fossarum* (arthropod)	Litter consumption rate (foraging performance)	Mandible shape did not alter the performance of amphipods to consume leaf litter (**1**)	(Rota et al., 2018)
ind	Functional morphology	Morphology	*Micropterus salmoides* (fish)	Δ C^{12,13} and Δ N^{14,15} (trophic niche)	Beyond large effects of ontogeny, no relationship between morphological traits and trophic niches was detected (**2**)	(Zhao et al., 2014)
ind	Benthic vs. limnetic morphotypes	Morphology	*Gasterosteus aculeatus* (fish)	Invertebrate community structure (community)	Benthic and limnetic morphotypes are specialised on different prey, inducing effects on community structure (**2, 8**)	(Des Roches et al., 2013)
pop	Gill rakers morphology (anadromous vs. landlocked ecotypes)	Morphology	*Alosa pseudoharengus* (fish)	Chlorophyll a (ecosystem functioning)	Anadromous and landlocked ecotypes feed on different zooplankton species according to their gill rakers morphology, thereby altering biomass of phytoplankton (**2 ,8**)	(Post et al., 2008)
ind	Corticosterone levels	Physiology	*Thalassarche melanophrys* (bird)	Number of chicks (fitness)	Elevated corticosterone levels (stress hormone) was linked to a lower reproductive output (**5**)	(Angelier et al., 2010)
ind	Mass-specific standard metabolic rate	Physiology	*Desmognathus brimleyorum* (amphibian)	Flies feeding rates (foraging performance)	Individuals with higher mass-corrected metabolic rate consumed prey at faster rates (**1**)	(Gifford et al., 2014)
ind	Elemental stoichiometry (C, N, P)	Physiology	*Procambarus clarkii & Faxonius limosus* (arthropoda)	Δ C^{12,13} and Δ N^{14,15} (trophic niche)	Elemental imbalances (C, N, P) between consumers and resources drive the diet of consumers (**2**)	(Lang et al., 2021)
ind	Mass-specific standard metabolic rate	Physiology	*Phoxinus phoxinus* (fish)	Pelagic production (community & ecosystem functioning)	Higher energetic expenditures altered community structure (**1,2,6,7**) and the pelagic production of phytoplankton	(Raffard et al., 2021)
col	Boldness, activity	Behavior	*Apis mellifera* (arthropoda)	Colony weight, survival after winter (fitness)	Colonies expressing active and bold behaviour accumulated more reserves and grew faster, increasing winter survival (**1,3,4**)	(Wray et al., 2011)
ind	Social dominance	Behavior	*Lepidodactylus lugubris* (squamate)	Crickets feeding rates (foraging performance)	Socially-dominant geckos consumed more crickets than sub-ordinate individuals (**1**)	(Short & Petren, 2008)
ind	Activity	Behavior	*Esox lucius* (fish)	Δ N^{14,15} (trophic niche)	More active pikes had higher trophic positions (**2**)	(Nyqvist et al., 2018)
ind	Activity	Behavior	*Phoxinus phoxinus* (fish)	Algal biomass and litter decomposition rate (community & ecosystem functioning)	More active minnows consumed potentially more grazers but fewer detritivores (**1,2**), increasing algal production and decomposition rate (**6,7,8**)	(Raffard et al., 2023)

Table S2: Detailed list of the 30 search term combinations (search strings) entered in each of the three search platforms (Web of Science ‘WoS’, Scopus and Google Scholar ‘GS’). The search started during year 2019 and ended up in 2020. For GS searches, we delimited our searches within the first twenty pages (i.e., first 200 results).

Search strings	***WoS***	***Scopus***	***GS***	
phenotypic AND traits AND individual AND intraspecific AND fitness	76	53	200	
functional AND traits AND individual AND intraspecific AND fitness	38	33	200	
morphological AND traits AND individual AND intraspecific AND fitness	13	15	200	
physiological AND traits AND individual AND intraspecific AND fitness	77	29	200	
behavioral AND traits AND individual AND intraspecific AND fitness	24	36	200	
phenotypic AND traits AND individual AND intraspecific AND feeding AND consumption rate	1	2	200	
functional AND traits AND individual AND intraspecific AND feeding AND consumption rate	1	0	200	
morphological AND traits AND individual AND intraspecific AND feeding AND consumption rate	2	1	200	
physiological AND traits AND individual AND intraspecific AND feeding AND consumption rate	1	1	200	
behavioral AND traits AND individual AND intraspecific AND feeding AND consumption rate	0	2	200	
phenotypic AND traits AND individual AND intraspecific AND community structure	37	25	200	
functional AND traits AND individual AND intraspecific AND community structure	73	44	200	
morphological AND traits AND individual AND intraspecific AND community structure	11	8	200	
physiological AND traits AND individual AND intraspecific AND community structure	12	10	200	
behavioral AND traits AND individual AND intraspecific AND community structure	8	8	200	
phenotypic AND traits AND individual AND intraspecific AND ecosystem functions	26	19	200	
functional AND traits AND individual AND intraspecific AND ecosystem functions	54	46	200	
morphological AND traits AND individual AND intraspecific AND ecosystem functions	13	13	200	
physiological AND traits AND individual AND intraspecific AND ecosystem functions	6	11	200	
behavioral AND traits AND individual AND intraspecific AND ecosystem functions	6	8	200	
phenotypic AND traits AND individual AND intraspecific AND isotopic niche	1	1	200	
functional AND traits AND individual AND intraspecific AND isotopic niche	1	1	200	
morphological AND traits AND individual AND intraspecific AND isotopic niche	1	1	200	
physiological AND traits AND individual AND intraspecific AND isotopic niche	1	2	200	
behavioral AND traits AND individual AND intraspecific AND isotopic niche	0	1	200	
phenotypic AND traits AND individual AND intraspecific AND trophic niche	10	6	200	
functional AND traits AND individual AND intraspecific AND trophic niche	11	8	200	
morphological AND traits AND individual AND intraspecific AND trophic niche	4	3	200	
physiological AND traits AND individual AND intraspecific AND trophic niche	1	3	200	
behavioral AND traits AND individual AND intraspecific AND trophic niche	2	3	200	
TOTAL (with Duplicates)	**511**	**393**	**6000**	**6904**

Box 1. Decision path ensuring that effect sizes were not related (or the least possible), to body size

A. When no correlation between body size/mass and the trait of interest nor the ecological response were shown in primary studies, we assumed that the relationship between the trait and the response was not resulting from variation in body size, and we included the effect size, but at two conditions.

1) First, no strong relationship between body size and the response nor the trait was expected theoretically by the MTE (Brown et al., 2004).

2) Second, the analyses have been performed on a group of individuals or populations of a same size class, age or cohort.

B. For the cases where body size was theoretically expected to affect both trait and response (e.g., body size links both to metabolic and feeding rate; Brown et al., 2004), we only extracted statistics :

(i) From partial relationships (i.e., body size has been accounted for on the response and the trait)

(ii) When authors tested the relationships on mass-specific traits and mass-specific responses.

C. When the effect of body size was expected on the response, but not on the trait (e.g., body size relating to feeding rate, but not to boldness) :

(iii) We also included statistics from semi-partial relationships (i.e., accounting for the dependent effect of body size on the response, but not on the trait).

D. When trait-to-response relationships were obviously a result of variation in body size, or when we had a doubt, we did not include the effect size(s).

Table S3. Formulae used to convert statistical values found in initial publications into *r* correlation coefficient (see Koricheva *et al*., 2013; Nakagawa & Cuthill, 2007).

Statistic	Formula used to obtain *r*
t	$\sqrt{\frac{t^2}{t^2 + df}}$
F	$\sqrt{\frac{df_n F}{df_n F + df_d}}$
χ2	$\sqrt{\frac{\chi^2}{N}}$
Hedges' g	$\sqrt{\frac{g^2 n_1 n_2}{g^2 n_1 n_2 + (n_1 n_2) df}}$
R²	$\sqrt{\frac{1 - ((n-1) * (1 - R^2))}{n - k - 1}}$

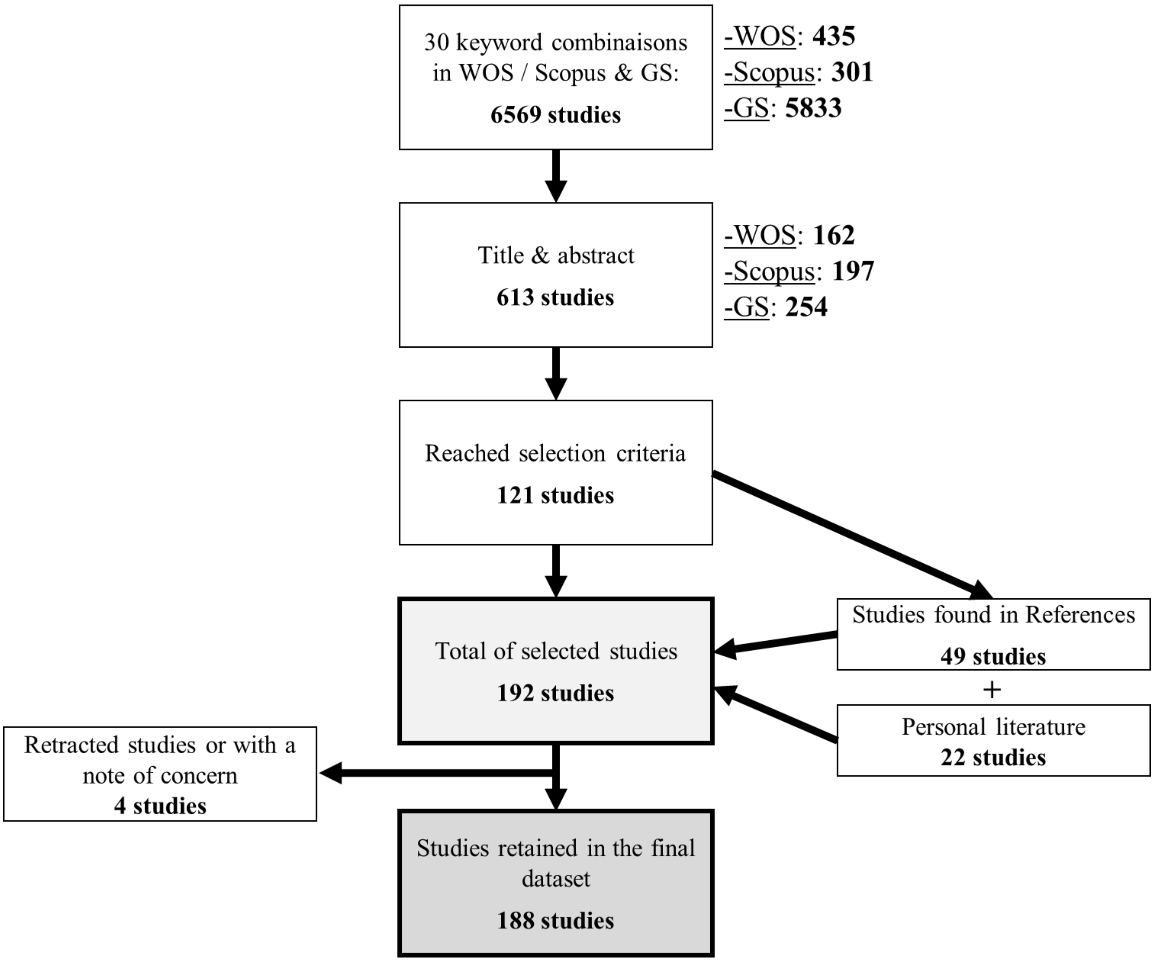

Figure S1: Path of the workflow of the systematic review. We used three search engines (WOS: Web Of Science; Scopus; GS: Google Scholar) for each of 30 combinations of keywords (Table S1). We considered the first 200 results from GS for each search term combination. We stopped the systematic review on 29th May 2020. Results at the two first stage of the literature search are results without the duplicates.

Results associated with the analysis of the whole dataset

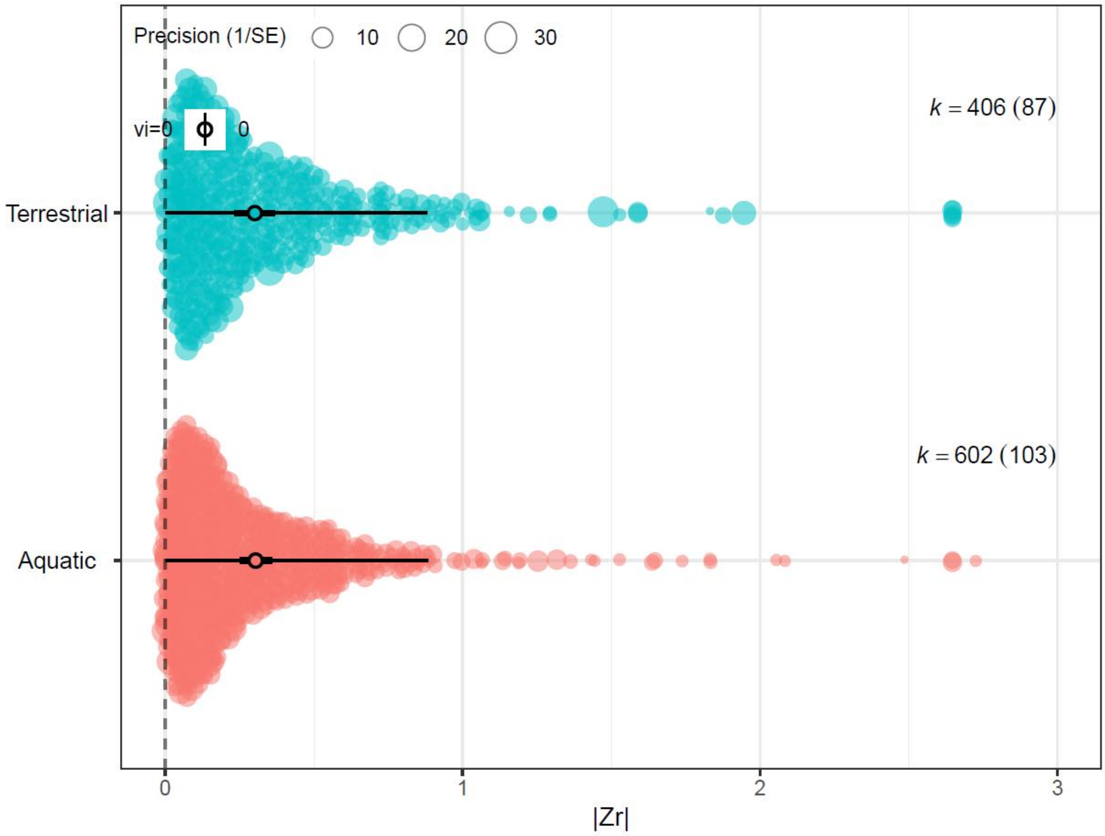

Figure S2: Orchard plot of raw effect sizes and mean estimates, 95% confidence intervals (bold error bars), and 95% prediction intervals (error bars) for aquatic and terrestrial realms. The size of bubbles is proportional to their precision (1/SE).

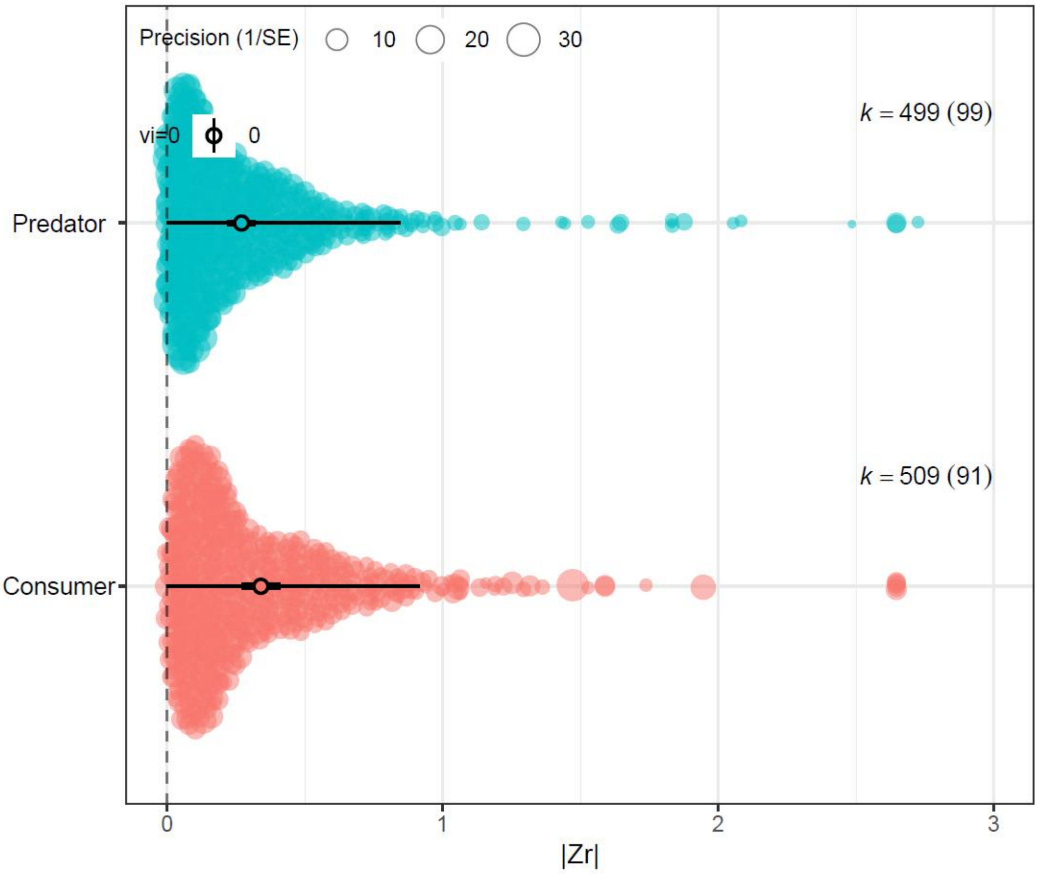

Figure S3: Orchard plot of raw effect sizes and mean estimates, 95% confidence intervals (bold error bars), and 95% prediction intervals (error bars) for predators and consumers. The size of bubbles is proportional to their precision (1/SE).

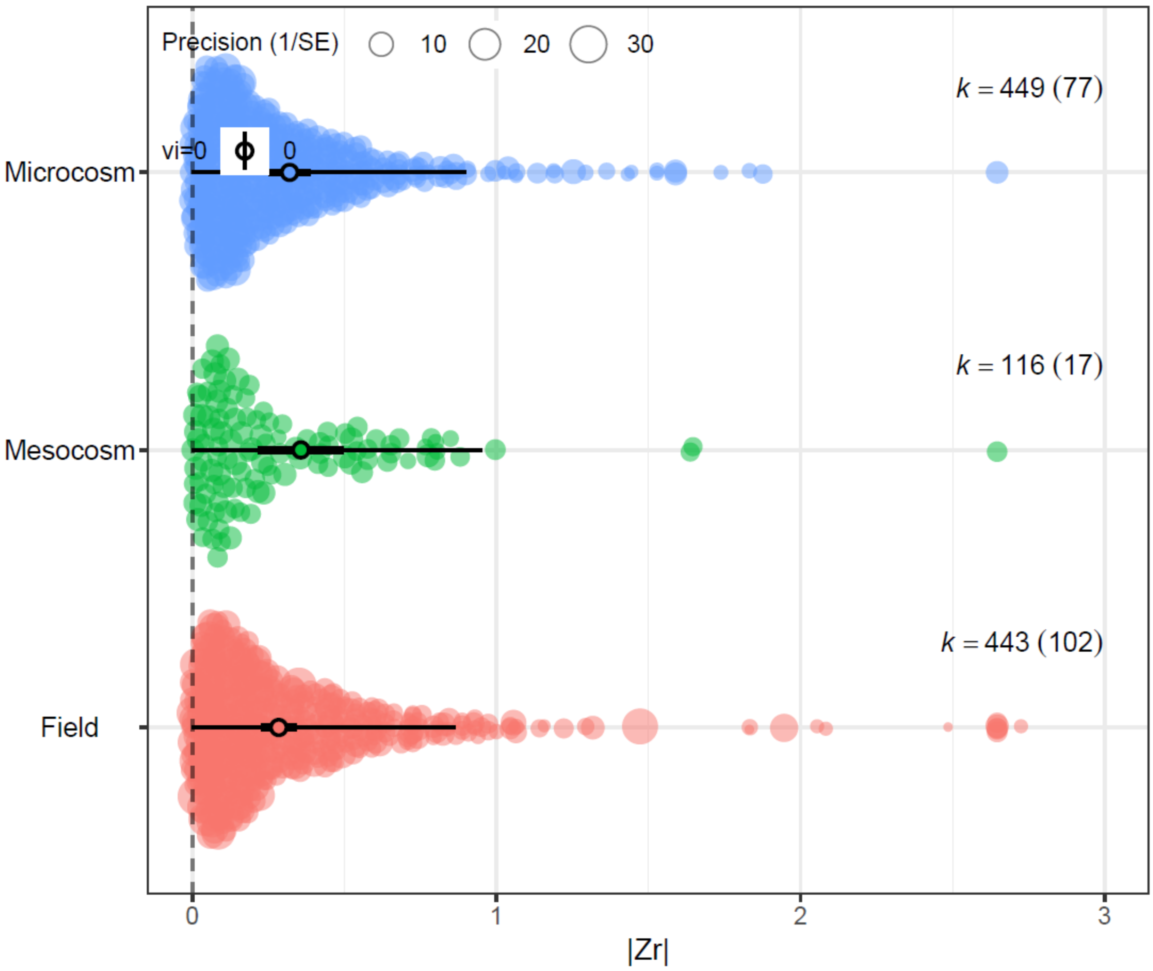

Figure S4: Orchard plot of raw effect sizes and mean estimates, 95% confidence intervals (bold error bars), and 95% prediction intervals (error bars) for microcosm, mesocosm, and field settings. The size of bubbles is proportional to their precision (1/SE).

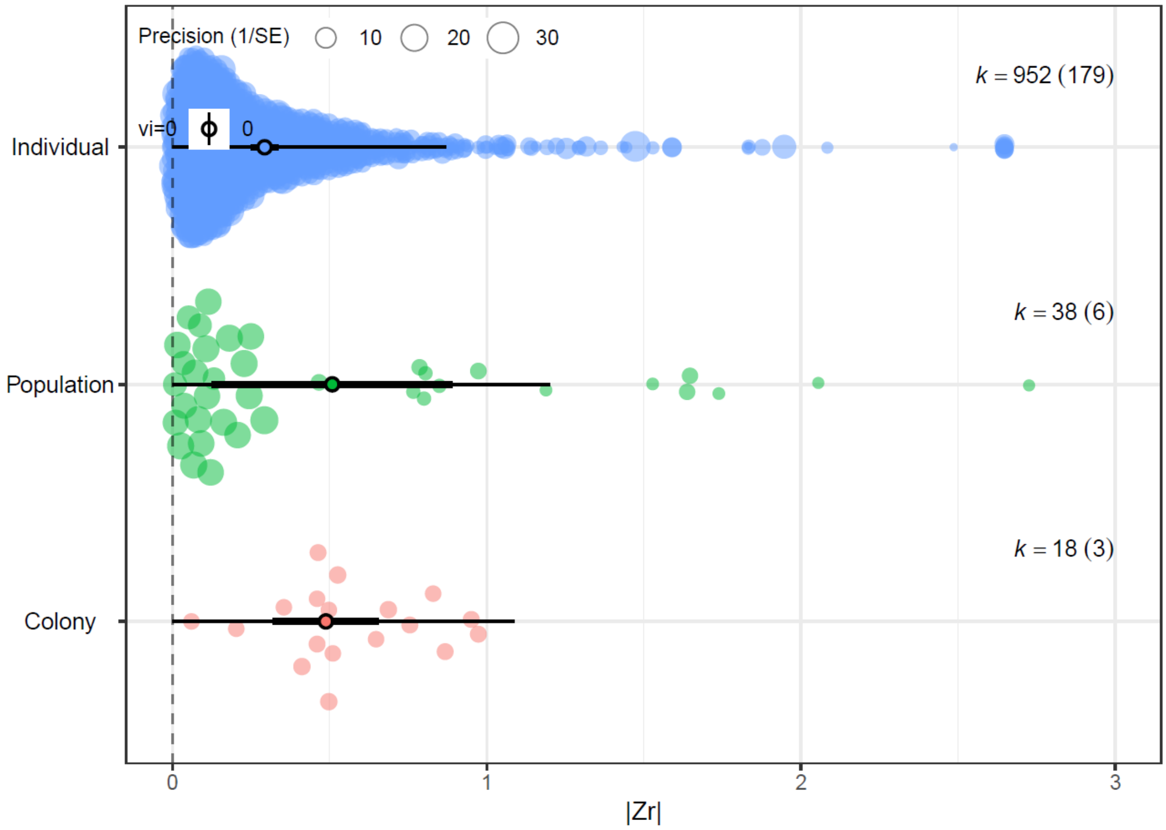

Figure S5: Orchard plot of raw effect sizes and mean estimates, 95% confidence intervals (bold error bars), and 95% prediction intervals (error bars) for colonies of eusocial insects, populations, and individuals within populations. The size of bubbles is proportional to their precision (1/SE).

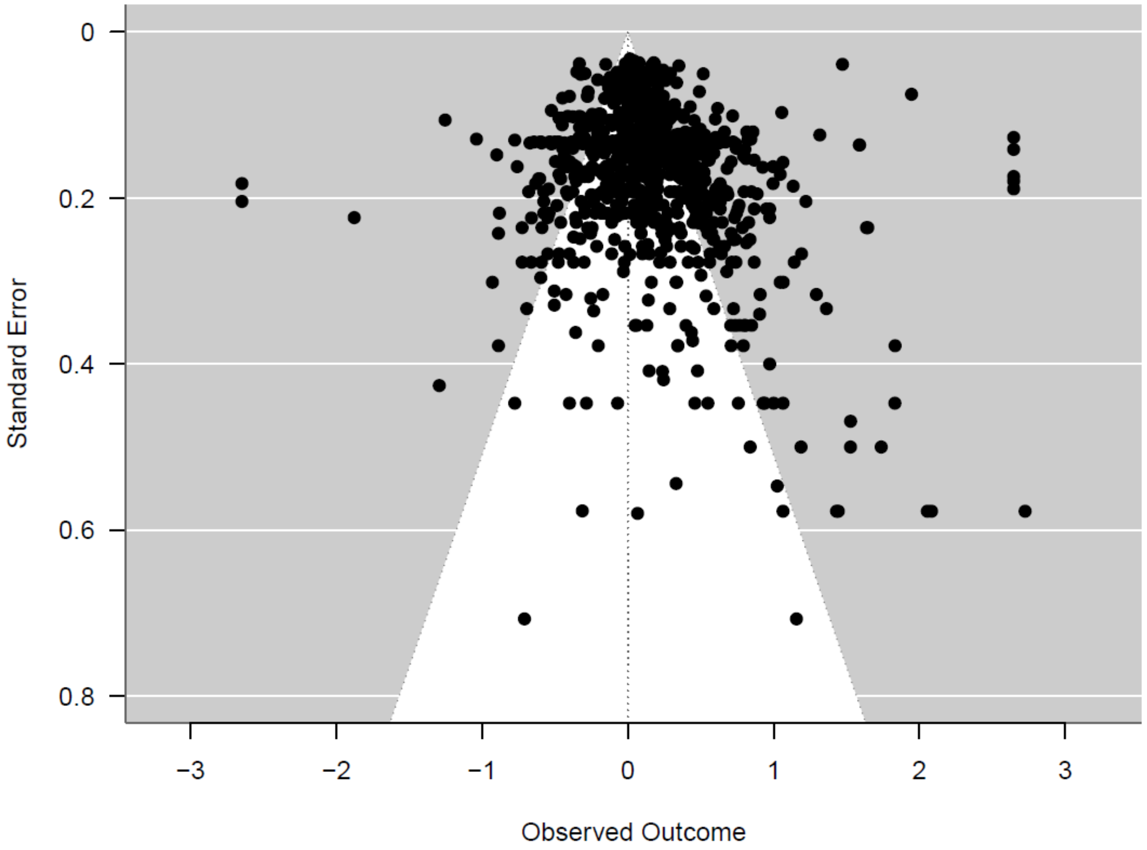

Figure S6: Funnel plot of the precision (1/SE) and effect sizes |Z*r*|.

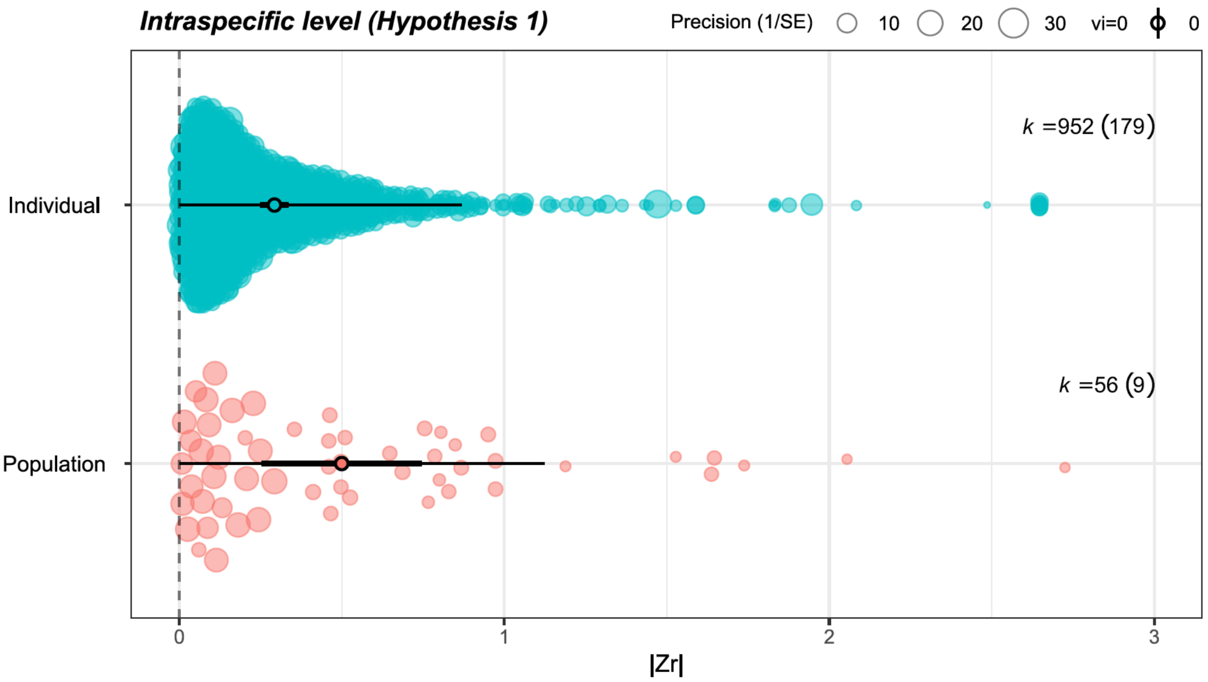

Figure S7: Orchard plot of model estimates of |*Zr*| effects sizes estimated for each intraspecific level (individual vs. population). The size of each point is proportional to the precision of the effect size (1/SE). Thick and thin error bars give 95% confidence and prediction intervals, respectively. Sample sizes (k) and number of studies (in brackets) are given for each category of ecological responses. Model estimates are reported in table 1, in the main text.

Table S4: Table of main results for the whole dataset (including effect sizes at the individual and at the population level). Mean effect sizes and 95% confidence intervals are given for response type and trait type models. Raw estimated effect sizes are given as |*Zr*| and |*r*|, as well as with their unbiased estimates (|*Zr*| – |*Zr*| null). Confidence intervals at 95% are given in brackets. For each model, (†) indicates the category with the lowest estimated effect size, and the categories shown in bold (*****) are those with significantly higher estimates compared to (†). Pairwise comparison statistics (*z*- and *P*- values) are given accordingly, in comparison to the category with the lowest estimated effect size (†). Cells remaining empty (–) are equivalent as in table 1, main text.

Parameter *(/model)*	$|Zr|$	$|r|$	$|Zr|_{null}$	$|Zr|_{unbiased}$	$|r|_{unbiased}$	**z**	***P***
(/Intercept-only)							
Global estimate	(–)	(–)	(–)	(–)	(–)	(–)	(–)
(/Intraspecific levels)							
Within-populations (individuals)	(–)	(–)	(–)	(–)	(–)	(–)	(–)
Among-populations	(–)	(–)	(–)	(–)	(–)	(–)	(–)
(/Trait types)							
Morphology **(†)** 351(69)	0.26 (0.21 – 0.31)	0.26 (0.21 – 0.30)	0.05 (0.04 – 0.06)	0.21 (0.17 – 0.25)	0.20 (0.17 – 0.24)	–	–
Physiology 204(33)	0.31 (0.25 – 0.37)	0.30 (0.25 – 0.36)	0.06 (0.04 – 0.07)	0.25 (0.21 – 0.30)	0.25 (0.21 – 0.29)	1.76	.07815
Behavior (*) 453(117)	**0.33 (0.28 – 0.39)**	**0.32 (0.27 – 0.37)**	**0.06 (0.05 – 0.07)**	**0.27 (0.23 – 0.32)**	**0.26 (0.22 – 0.30)**	**2.78**	**.00546**
(/Response types)							
Foraging (*) 186(48)	**0.32 (0.23 – 0.41)**	**0.31 (0.23 – 0.39)**	**0.06 (0.04 – 0.07)**	**0.26 (0.19 – 0.34)**	**0.25 (0.19 – 0.31)**	**2.04**	**.04130**
Trophic niche (*) 182(25)	**0.34 (0.24 – 0.43)**	**0.33 (0.24 – 0.41)**	**0.06 (0.04 – 0.07)**	**0.28 (0.19 – 0.36)**	**0.27 (0.19 – 0.34)**	**2.20**	**.02774**
Growth 130(34)	0.32 (0.23 – 0.41)	0.31 (0.22 – 0.38)	0.06 (0.05 – 0.07)	0.26 (0.18 – 0.34)	0.25 (0.18 – 0.31)	1.95	.05087
Survival 184(54)	0.27 (0.20 – 0.35)	0.27 (0.20 – 0.33)	0.05 (0.04 – 0.06)	0.22 (0.16 – 0.29)	0.22 (0.16 – 0.28)	1.55	.12176
Reproduction **(†)** 210(48)	0.21 (0.14 – 0.28)	0.21 (0.14 – 0.27)	0.05 (0.04 – 0.06)	0.16 (0.10 – 0.22)	0.16 (0.10 – 0.21)	–	–
Community (*) 56(12)	**0.41 (0.27 – 0.56)**	**0.39 (0.26 – 0.51)**	**0.08 (0.07 – 0.09)**	**0.33 (0.20 – 0.47)**	**0.31 (0.20 – 0.41)**	**2.64**	**.00822**
Ecosystem (*) 60(13)	**0.39 (0.23 – 0.56)**	**0.37 (0.22 – 0.51)**	**0.08 (0.07 – 0.09)**	**0.31 (0.16 – 0.47)**	**0.29 (0.16 – 0.41)**	**2.11**	**.03461**

Table S5: Checklist of preferred reported items for systematic reviews and meta-analysis in ecology and evolution (PRISMA Eco-evo).

Checklist item	Sub-item number	Description	Reported	Comment	Section
Title and abstract	1.1	Identify the review as a systematic review, meta-analysis, or both	Yes	(…) A meta-analysis	Title Front page
	1.2	Summarise the aims and scope of the review	Yes		Abstract
	1.3	Describe the data set	Yes		Abstract, Introduction, Results
	1.4	State the results of the primary outcome	Yes		Abstract
	1.5	State conclusions	Yes		Conclusion
	1.6	State limitations	Yes		Discussion
Aims and questions	2.1	Provide a rationale for the review	Yes		Introduction
	2.2	Reference any previous reviews or meta-analyses on the topic	Yes	We referenced to previous syntheses on the topic aiming at describing the magnitude of ITV in plants and animals	Introduction
	2.3	State the aims and scope of the review (including its generality)	Yes		Introduction
	2.4	State the primary questions the review addresses (e.g. which moderators were tested)	Yes		Introduction
	2.5	Describe whether effect sizes were derived from experimental and/or observational comparisons	Yes	We tested three categories (observational, mesocosm and microcosm)	Methods
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.	No	We did not registered our hypotheses before the analysis.	Introduction and methods
	3.2	Describe deviations from the registered aims and methods	–		
	3.3	Justify deviations from the registered aims and methods	–		

Checklist item	Sub-item number	Description	Reported	Comment	Section
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)	Yes	PRISMA diagram included as Appendix Figure S1 and selection criteria in Methods	Methods
	4.2	Justify criteria, if necessary (i.e. not obvious from aims and scope)	Yes		Methods
Finding studies	5.1	Define the type of search (e.g. comprehensive search, representative sample)	Yes	Representative sample, with 3 different search engines	Methods
	5.2	State what sources of information were sought (e.g. published and unpublished studies, personal communications)	Yes	Data came from studies published in ecology and evolution journals	Methods, References
	5.3	Include, for each database searched, the exact search strings used, with keyword combinations and Boolean operators	Yes	See Appendix Table S2 and main text	Methods & Appendix
	5.4	Provide enough information to repeat the equivalent search (if possible), including the timespan covered (start and end dates)	Yes	We provide information on the search engines and keyword settings	Methods & Appendix
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)	Yes	See the Figure S1	Appendix
	6.2	Report the number of people involved and how they contributed (e.g. independent parallel screening)	Yes	See Autorship	Autorship
Data collection process	7.1	Describe where in the reports data were collected from (e.g. text or figures)	Yes	Text	Methods
	7.2	Describe how data were collected (e.g. software used to digitize figures, external data sources)	Yes	From the text	Methods
	7.3	Describe moderator variables that were constructed from collected data (e.g. number of generations calculated from years and average generation time)	Not applicable		
	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)	Not applicable	We did not included studies for which data were incomplete.	
	7.5	Report who collected data	Yes		Authorship

Checklist item	Sub-item number	Description	Reported	Comment	Section
	7.6	State the number of extractions that were checked for accuracy by co-authors	No		
Data items	8.1	Describe the key data sought from each study	No	We described only a few studies (see Table S1).	
	8.2	Describe items that do not appear in the main results, or which could not be extracted due to insufficient information	Not applicable		
	8.3	Describe main assumptions or simplifications that were made (e.g. categorising both 'length' and 'mass' as 'morphology')	Yes		Methods
	8.4	Describe the type of replication unit (e.g. individuals, broods, study sites)	Yes		Methods
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 versus observational)	Yes	We included a covariate for the study design (observational, mesocosm, microcosm)	Methods
	9.2	Describe how information about study quality was incorporated into analyses (e.g. meta-regression and/or sensitivity analysis)	Yes	We acknowledged and controlled for point estimates bias in adding sampling variances (*vi*) as covariates.	Methods, Statistical analysis section
Effect size measures	10.1	Describe effect size(s) used	Yes		Methods
	10.2	Provide a reference to the equation of each calculated effect size (e.g. standardized mean difference, log response ratio) and (if applicable) its sampling variance	Yes	We referred to Nagakawa et al. (2007), that we followed to calculate Z*r* values from different statistics. Sampling variances (*vi*) were calculated with the R package '*metafor*'.	Methods
	10.3	If no reference exists, derive the equations for each effect size and state the assumed sampling distribution(s)	Not applicable		
Missing data	11.1	Describe any steps taken to deal with missing data during analysis (e.g. imputation, complete case, subset analysis)	Not applicable		

Checklist item	Sub-item number	Description	Reported	Comment	Section
	11.2	Justify the decisions made to deal with missing data	Not applicable		
Meta-analytic model description	12.1	Describe the models used for synthesis of effect sizes	Yes	Hierarchical multi-level phylogenetic meta-analytic models (function '*rma.mv*' in '*metafor*' package in R)	Methods
	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	Not applicable	We used a hierarchical multi-level model (see above)	
Software	13.1	Describe the statistical platform used for inference (e.g. R)	Yes	R	Methods
	13.2	Describe the packages used to run models	Yes	('metafor' in R)	Methods
	13.3	Describe the functions used to run models	Yes	We used '*rma.mv'*	
	13.4	Describe any arguments that differed from the default settings	Yes	Codes and data are available	Methods Appendix
	13.5	Describe the version numbers of all software used	Yes		Methods
Non-independence	14.1	Describe the types of non-independence encountered (e.g. phylogenetic, spatial, multiple measurements over time)	Yes		Methods
	14.2	Describe how non-independence has been handled	Yes		Methods
	14.3	Justify decisions made	Yes		Methods
Meta-regression and model selection	15.1	Provide a rationale for the inclusion of moderators (covariates) that were evaluated in meta-regression models	Yes		Methods
	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)	Yes		Methods
	15.3	Describe any process of model selection	Not applicable	We only ran models that were of interest for our hypotheses. So we did not perform model selection	Methods

Checklist item	Sub-item number	Description	Reported	Comment	Section
Publication bias and sensitivity analysis	16.1	Describe assessments of the risk of bias due to missing results (e.g. publication, time-lag, and taxonomic biases)	Yes	See according paragraphs regarding the statistical methods and the report of the results (publication bias assessment)	Methods, Results
	16.2	Describe any steps taken to investigate the effects of such biases (if present)	Yes	We implemented several steps to investigate the effects of bias. These were random effects accounting for the multi-level non-independence of effect sizes (within and among studyID), a robust estimation of effect sizes with a variance-covariance matrix acknowledging for sources of non-independences in the dataset, acknowledging for effect size precision (sampling variance as a fixed effect), species phylogeny, a null model, time-lag with year of publication as a fixed effect (please see the statistical analysis sub-section in the Methods section)	Methods and Results

Checklist item	Sub-item number	Description	Reported	Comment	Section
	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	Yes	We unbiased effect sizes in computing null effect sizes (effect sizes expected under the null hypothesis of no effect) We fit the results on two datasets. One including the full dataset (H1), and one including only observations among individuals (H2 and H3). Results for H2 and H3 on the full dataset are given in Appendix, which led to qualitatively similar conclusions	Methods, Results, and Discussion
Clarification of post hoc analyses	17.1	When hypotheses were formulated after data analysis, this should be acknowledged.	Yes	We designed hypotheses before the data analyses. Additional analyses that were designed a posteriori are labelled as post hoc analyses (i.e., Figure 5).	Methods, statistical analysis section and results
Metadata, data, and code	18.1	Share metadata (i.e. data descriptions)	Yes	See link to data	Data accessibility
	18.2	Share data required to reproduce the results presented in the manuscript	Yes	We share the data used to perform the statistics reported in the paper	See link to data
	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)	Yes		See link to data

Checklist item	Sub-item number	Description	Reported	Comment	Section
	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)	Yes	We share the R code used to perform the statistics reported in the paper	See link to data
Results of study selection process	19.1	Report the number of studies screened	Yes	see Figure S1	Appendix
	19.2	Report the number of studies excluded at each stage of screening	Yes	see Figure S1	Appendix
	19.3	Report brief reasons for exclusion from the full text stage	Yes	The study does not fill our selection criteria	Methods
	19.4	Present a Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA)-like flowchart (www.prisma-statement.org).	Yes	see Figure S1	Appendix
Sample sizes and study characteristics	20.1	Report the number of studies and effect sizes for data included in meta-analyses	Yes		Results
	20.2	Report the number of studies and effect sizes for subsets of data included in meta-regressions	Yes	see Orchard plot figures and Tables in main text	Results
	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)	Yes	see Orchard plot figures and Tables in main text	Results
	20.4	Provide a summary of limitations of included moderators (e.g. collinearity and overlap between moderators)	Yes		Discussion
	20.5	Provide a summary of characteristics related to individual study quality (risk of bias)	No		
Meta-analysis	21.1	Provide a quantitative synthesis of results across studies, including estimates for the mean effect size, with confidence/credible intervals	Yes	Main text	Results
Heterogeneity	22.1	Report indicators of heterogeneity in the estimated effect (e.g. I2, tau2 and other variance components)	Yes	I^2 at all hierarchical levels, Q-statistic on total heterogeneity, see methods on statistics and results in main text regarding heterogeneity assessment	Results

Checklist item	Sub-item number	Description	Reported	Comment	Section
Meta-regression	23.1	Provide estimates of meta-regression slopes (i.e. regression coefficients) and confidence/credible intervals	Yes	Table 1, Figure 3–5, Main text	Results
	23.2	Include estimates and confidence/credible intervals for all moderator variables that were assessed (i.e. complete reporting)	Yes	Table 1, Figure 3–5, Main text	Results, Appendix
	23.3	Report interactions, if they were included	Not applicable	No interactions were evaluated	
	23.4	Describe outcomes from model selection, if done (e.g. R2 and AIC)	Not applicable	We did not performed model selection	
Outcomes of publication bias and sensitivity analysis	24.1	Provide results for the assessments of the risks of bias (e.g. Egger's regression, funnel plots)	Yes	Main text and figures in Appendix	Methods, Results and Appendix
	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)	Yes	We analysed main hypotheses on different subsets of data, with very little variation overall, indicating robust results	see Methods, Results, Appendix
Discussion	25.1	Summarise the main findings in terms of the magnitude of effect	Yes	Table 1, Figure 3–5, Main text	Results, Discussion
	25.2	Summarise the main findings in terms of the precision of effects (e.g. size of confidence intervals, statistical significance)	Yes	Table 1, Figure 3–5, Main text	Results, Discussion
	25.3	Summarise the main findings in terms of their heterogeneity	Yes	I^2, main text	Results
	25.4	Summarise the main findings in terms of their biological/practical relevance	Yes		Results, Discussion and Conclusion
	25.5	Compare results with previous reviews on the topic, if available	Yes		Discussion
	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)	Yes		Discussion
Contributions	26.1	Provide names, affiliations, and funding sources of all co-authors	Yes		Front page
	26.2	List the contributions of each co-author	Yes		Autorship

Checklist item	Sub-item number	Description	Reported	Comment	Section
	26.3	Provide contact details for the corresponding author	Yes		Front page
	26.4	Disclose any conflicts of interest	Yes	We have no conflict of interest to declare	Conflict of interest statement
References	27.1	Provide a reference list of all studies included in the systematic review or meta-analysis	Yes	They are marked with an asterisk (*)	Data sources
	27.2	List included studies as referenced sources (e.g. rather than listing them in a table or supplement)	Yes	They are marked with an asterisk (*)	Data sources