

Lee, PLM, CDH Sherman, LA Rollins, E Wapstra, KP Phillips. Do female amphibians and reptiles have greater reproductive output if they have more mates?

Behavioral Ecology and Sociobiology

Supplementary Information – SI1

INTRODUCTION

Table S1. Selected reviews of the causes of polyandry. Abbreviations in “Review method” indicate that the data are from experimental (Exp), natural or wild populations (Nat) or not specified (NS).

Taxonomic group	Topic	Number of species	Review method	Conclusions	Reference
Insects	Relationship between multiple mating and female fitness	78	Analytical (Exp)	Females gain directly from multiple mating in terms of increased lifetime offspring production, despite a negative effect on longevity in species without nuptial feeding	Arnqvist and Nilsson (2000)
Birds	Ecological explanations for interspecific variation in the rate of extra-pair paternity and evidence for the adaptive function of extra-pair paternity	approx. 130	Descriptive (NS)	Extra-pair paternity varies with life history, pattern of paternal care and local opportunities for promiscuity: it remains to be shown whether genetic benefits are a general explanation for extra-pair paternity in birds	Griffith et al. (2002)
Birds	Genetic benefits of extra-pair paternity	55	Analytical (NS)	Genetic benefits are not strongly supported by available empirical data	Akçay and Roughgarden (2007)
Reptiles	Benefits of polyandry	40	Descriptive (Nat)	No evidence for direct benefits to females and weak evidence for indirect genetic benefits: multiple paternity represents the combined effect of mate-encounter frequency and sexual conflict, driven by large male benefits and small female costs	Uller and Olsson (2008)
Anuran amphibians	Evidence of sperm competition in cases of simultaneous polyandry	25 (only 8 based on molecular evidence)	Descriptive (Exp & Nat)	Simultaneous polyandry could be an outcome of forced matings in some species or an adaptive female strategy in others but seems to be an evolved mating strategy for anurans in general (although hard data were limited to a small number of species)	Roberts and Byrne (2011)

Viviparous vertebrates	Relationship of multiple paternity to brood size in pregnant fishes versus pregnant mammals and other viviparous vertebrates	Fishes: 18; Mammals: 49; Reptiles & amphibians: 29	Analytical (NS)	No significant correlations between brood size and multiple paternity for fishes and mammals, but herpetological species with larger broods tended to have higher incidence of multiple paternity than those with smaller broods	Awise and Liu (2011)
Not taxonomically limited, but dominated by insects	Genetic benefits of polyandry	40	Analytical (Exp)	Weak evidence for genetic benefits (marginal evidence for an increase in egg hatching success) and direct benefits (marginal evidence for greater fertility and higher clutch production)	Slatyer et al. (2012)
Lizards	The evolution of polyandry and patterns of multiple paternity in lizards	19	Descriptive (Nat)	It is premature to understand what affects the costs or benefits of multiple mating to males and females, or the sum of these which resolves sexual conflict. Broader taxonomic coverage, longer-termed field studies and links between field and experimental approaches are required	Wapstra and Olsson (2014)
All species included, except those with unusual or inflexible mating strategies	Relationship between polyandry and ecological and genetic variables	160	Analytical (Nat)	A weak positive trend with latitude, without significant differences in the frequency of polyandry between temperate and tropical regions. A small to moderate effect size of multiple paternity being associated with multilocus heterozygosity was consistent with genetic benefits having small impact	Taylor et al. (2014)
Birds	Are extra-pair males different from cuckolded males?	20-27	Analytical (NS)	No evidence that the extra-male had better quality genetic or phenotypic traits than the cuckolded male. Older males coerce females into extra-pair mating, without obvious benefit to the female. Nonadaptive models may better explain female extra-pair matings	Hsu et al. (2015)
Birds	Does genetic similarity between the social pair	33	Analytical (NS)	Positive significant relationship between the occurrence of extra-pair paternity and the	Arct et al. (2015)

	predict extra-pair paternity in birds?			relatedness of social mates, particularly for studies using microsatellite markers	
Marine turtles	Relationship between polyandry and mate-encounter rate	7	Analytical (Nat)	Incidence of multiple paternity is significantly correlated with packing density, supporting a mating system of convenience polyandry driven by mate-encounter rate	Lee et al. (2018)
Not limited	What is the relationship between multiple paternity and brood sizes?	114	Analytical (NS)	Species either have mating systems with close to random mating and high levels of multiple paternity, or have constraints that produce low levels of multiple paternity	Correia et al. (2021)
Elasmobranchs	What are the drivers of multiple paternity?	32	Analytical (NS)	Multiple mechanisms contribute to multiple paternity, particularly cryptic female choice. Drivers vary in importance and intensity across and within species	(Lyons et al. 2021)
Amphibians and reptiles	What is the pattern of polyandry across taxa, and do females have greater reproductive success if they have more mates?	116 (28 in meta-analysis)	Analytical (Nat)	Only female salamanders, which controlled sperm acquisition, had significantly more offspring with multiple sires. . For reptiles and salamanders, population-level multilocus heterozygosity co-varies with the effect size of polyandry increasing with numbers of sires, but further evidence is required to confirm the association	This study

METHODS

Assembling the global dataset and data extraction

Searching for records

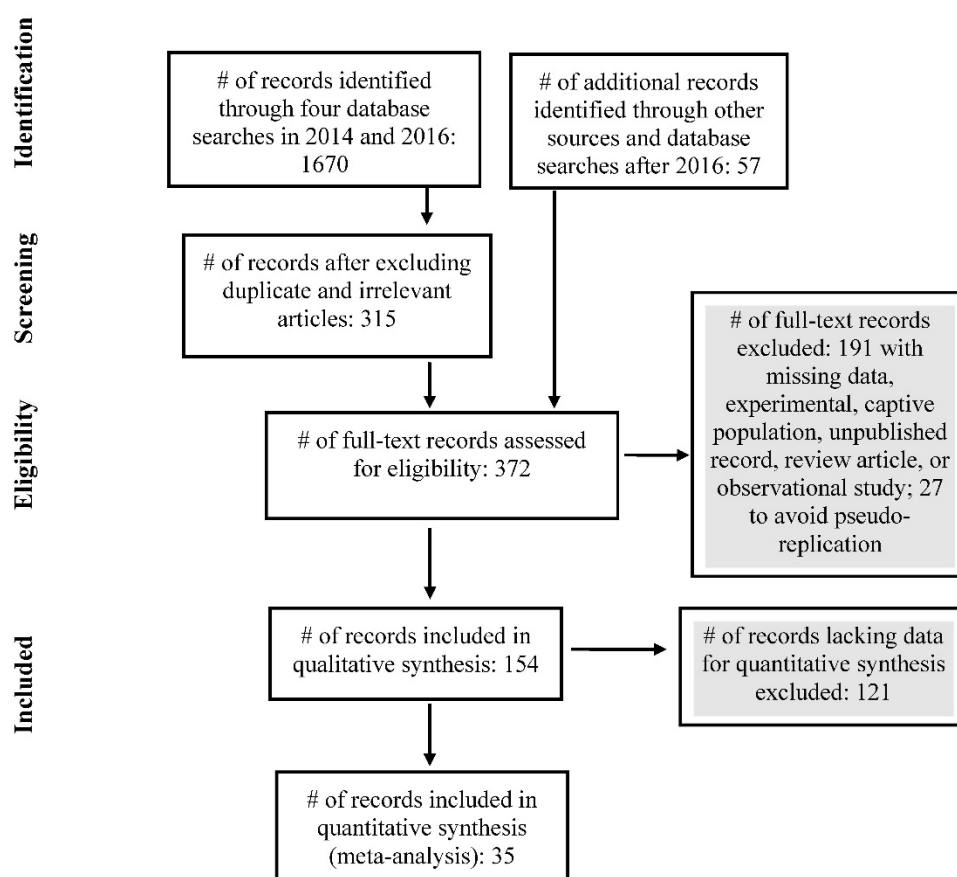


Fig. S1. PRISMA (Preferred Reporting Items for Systematic reviews and Meta-Analyses) diagram summarising the flow of information (Liberati et al. 2009). Clear boxes are items passed to the next stage, whereas darkened boxes are items removed.

We conducted four main searches of Web-Of-Knowledge and SCOPUS for records relevant to our study. In general, we searched with the following terms: “polyandry”, “multiple paternity”, “extra-pair*” or “parentage”; which were then further refined by the terms: “reptile”, “turtle”, “tortoise”, “terrapin”, “lizard”, “skink”, “gecko”, “iguana”, “dragon”, “chameleon”, “snake”, “boa”, “adder”, “viper”, “crocodile”, “alligator”, “caiman”, “gharial”, “amphibian”, “toad”, “frog”, “salamander”, “newt”, “caecilian” or “squamate”, and by: “molecular”, “DNA”, “genetic”, “microsatellite”, “loci”, “fingerprinting” or “allozyme”. The dates and the specific terms used for the four searches were as follows.

SEARCH I (9/12/2013), search terms in Web-Of-Knowledge were: “polyandry” OR “multiple paternity”, refined by “reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian” AND “molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme”. Search terms for SCOPUS were: polyandry AND “multiple paternity” in Article Title, Abstract, Keywords; and further search within results for: reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian.

SEARCH II (8/4/2014) search terms in Web-Of-Knowledge were: polyandry OR "multiple paternity", refined by: squamate AND "molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme". Search terms in SCOPUS were: polyandry OR "multiple paternity" in Article Title, Abstract, Keywords; followed by search within results for: reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian OR squamate; followed by search within results for: molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme.

SEARCH III (9/4/2014): search terms in Web-Of-Knowledge were: monogamy OR "extra-pair*" OR "parentage"; - refined by: "reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian OR squamate" followed by a search within results for: "molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme". Search terms in SCOPUS were: monogamy OR "extra-pair*" OR "parentage" in Article Title, Abstract, Keywords; followed by a search within results for: reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian OR squamate; and a search within results for: molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme.

SEARCH IV (15/09/2016): search terms (only from 2014-current) in Web-Of-Knowledge: polyandry OR "multiple paternity" OR Topic=monogamy OR Topic="extra-pair*" OR Topic="parentage"; - Refined by "reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian OR squamate" AND "molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme". Search terms for SCOPUS (21/9/2016): polyandry OR "multiple paternity" OR monogamy OR "extra-pair*" OR "parentage" in Article Title, Abstract, Keywords; followed by a search within results for: reptile OR turtle OR tortoise OR terrapin OR lizard OR skink OR gecko OR iguana OR dragon OR chameleon OR snake OR boa OR adder OR viper OR crocodile OR alligator OR caiman OR gharial OR amphibian OR toad OR frog OR salamander OR newt OR caecilian OR squamate; and a search within results for: molecular OR DNA OR genetic OR microsatellite OR loci OR fingerprinting OR allozyme.

The records found across these searches were the core of our dataset, and were supplemented by checking references in publications, setting up citation alerts (Web-Of-Knowledge and Google Scholar), and conducting repeated searches of Google Scholar and Web-Of-Knowledge (search terms as for SEARCH IV). These searches and citation alerts were particularly useful in finding records published after 2016. Our search for records terminated in August 2019.

Our process of retaining or eliminating records is summarised by a PRISMA (Preferred Reporting Items for Systematic reviews and Meta-Analyses) diagram (Fig S1). We initially screened the authors and titles of the records discovered by the searches to remove duplicates and unrelated items (e.g., studies of taxa that were not reptiles or amphibians). We then downloaded full texts of remaining records, to decide on whether the records were to be included or excluded. From the full text accounts of studies that were eligible to be included in our study, we extracted the data used in our review and meta-analysis.

Inclusion of cases

All cases that were included in the dataset were measures of naturally occurring polyandry. Six cases warrant further clarification. One population was reintroduced (Lafferriere et al. 2016), two populations included translocated individuals (Tuberville et al. 2011; Mulder et al. 2017), two studies used enclosures (Halverson et al. 2006; Gopurenko et al. 2007) and one used wild-caught individuals kept in a semi-natural enclosure (Noble et al. 2013). However, in all cases, individuals were free to mate naturally. Details of each case are below:

- (1) Mulder et al. (2017): the desert tortoises studied were a declining wild population that received a number of translocated individuals to mitigate the decline. We considered this case suitable for inclusion as individuals

lived in natural conditions. The authors waited four years to ensure that parentage analysis would adequately reflect post-translocation mating and reproduction –the authors were interested in the outcome of natural reproductive behaviour, and did not report undertaking experimental manipulation of matings or limiting access to mates.

- (2) Tuberville et al. (2011): this desert tortoise population had been introduced to an island in multiple translocations, 25-30 prior to 1994 (provenance unknown), 74 wild-captured individuals in 1994, and 13 captive/rehabilitated individuals since 1994. The tortoises were free to engage in natural behaviour on the island. Sampling for parentage analysis was conducted in 2006-07, which was over a decade after the majority of individuals had been translocated to the area. The authors did not report undertaking any experimental manipulations of matings or limiting access to mates; they were interested in the natural reproductive success of individuals from different release groups.
- (3) Lafferriere et al. (2016): the Orinoco crocodile (one of the most threatened crocodile species in the world) was reintroduced with captive-bred individuals during 1990-2006 to an area where the original population had been extirpated from in the 20th century. Post-introduction, beaches were supplemented with sand to facilitate nesting, eggs were collected to prevent predation and juveniles retained until released as one-year olds in a “head-start” program to reduce mortality in the first year of life. These interventions were to promote survival and establishment of the population, but adult individuals were free to behave naturally: for example, the formation of male hierarchies was observed during the breeding season. Sampling for paternity analysis occurred 2004-2006. The authors did not report manipulating matings or limiting access to mates.
- (4) Halverson et al. (2006): ponds were enclosed with drift fences and pit traps placed inside and outside of fences to sample wild wood frogs and their offspring. Authors checked traps and searched the ponds for adults and egg masses exhaustively over the breeding season. Adults caught outside the fence were sampled (toes clipped for DNA extraction) and then released inside the fence to continue with breeding. Egg masses were collected and hatched in the laboratory so as to sample hatchlings for genetic analysis. Although the authors called these “field experiments”, they did not report undertaking experimental manipulation of matings. Rather, they intended for the adults they released into enclosed ponds to behave and reproduce naturally.
- (5) Gopurenko et al. (2007): the authors wanted to quantify sexual selection intensity in a wild breeding aggregation of small-mouthed salamanders. Adults migrating to a wetland breeding area were captured, sampled them for DNA then released into an enclosure in the wetland. All egg masses subsequently deposited in the enclosure were collected and sampled for DNA. The enclosure was netted to contain adults and eggs, with pit traps installed inside and outside to capture adults. This was termed an “experimental enclosure”, but the authors intended for released adults to behave and reproduce naturally, and did not report experimentally manipulating matings.
- (6) Noble et al. (2013): this study on eastern water skinks tested whether females gained direct or indirect benefits from multiple mating. Sexually mature individuals of both sexes captured from the wild were maintained in large semi-natural enclosures in densities similar to those found under natural conditions. The authors termed this an “experimental setup” but explicitly stated that individuals were allowed to breed naturally and did not describe any experimental manipulation of matings. Following the breeding period, females were collected and held until parturition. This setup enabled all offspring and their parents to be sampled for DNA analysis, and for physical characteristics and offspring growth rates and physical performance (sprint speed and endurance) to be measured.

Examples of PA calculation

Data for multiple clutches or litters of the same mother sampled in the same breeding season were treated as a single sample of a female with evidence (or not) of polyandry. However, clutches or litters produced in different breeding seasons were considered independent samples. We illustrate how we dealt with such data using selected examples:

Gopurenko et al. (2007) genotyped offspring from 65 egg masses and assigned them to 14 different mothers. The offspring of 12 mothers had multiple sires, so PA was estimated as $((12/14) \times 100) = 85.7\%$.

Sari et al. (2017) collected samples from 25 clutches laid by 10 different females in the same breeding season. There was multiple paternity in the clutches of 7 females, so PA = 70%.

Lance et al. (2009) sampled 92 clutches across several breeding seasons (2000-2005). As some of these clutches were produced by the same female, but in different breeding seasons, they were considered independent samples. Multiple paternity was reported as being found in 51% of the population but the number of clutches with multiple paternity was not stated, so we inferred there had been 45 clutches with single paternity and 47 with multiple paternity among 92 clutches.

Other variables

Data on the following variables were collected (included in Supplementary Data; column labels for variables in Supplementary Data are in parentheses):

- number of loci used (*N.B.*, this was limited to studies using microsatellites as markers) (Loci)
- average number of alleles per locus (Alleles)
- average number of offspring genotyped per clutch or litter (genotypedPerClutch)
- average percentage of the clutch or litter sampled (PercentageclutchSampled)
- average clutch or litter size (ClutchSizes)
- average observed (ObHet) and expected heterozygosities (ExHet) estimated for the population
- latitude (Lat) and absolute latitude (abLat) of the sampling location

Most of the data for these variables were extracted from the same studies reporting data from paternity analyses or associated literature (e.g., “primer notes” or another study by the same authors about the same population). Cases for which data were extracted from elsewhere were:

- Missing clutch size data for the study by McVay et al. 2008 (*Crocodylus moreletii*) was replaced with clutch sizes for 73 clutches (reported not to vary between years) which had been estimated for Northern Belize populations from 1992-1995 (Platt et al. 2008).
- Missing clutch size data for the study by Lance et al. 2009 (*Alligator mississippiensis*) was replaced with mean number of eggs per clutch reported for the same population (Davis et al. 2001).

Average heterozygosity (observed or expected) data were missing for Gopurenko et al. 2006, Chapple and Keogh 2005, Madsen et al. 2005, Garner et al. 2002, Barry et al. 1992, McCracken et al. 1999, and Garner and Larsen 2005.

Preliminary analyses leading to exclusion of cases with small sample sizes

While sample sizes were not significantly correlated with PA (Kendall's rank correlation tau: $z = -1.61$, $p = 0.107$), there was a high frequency of cases reporting either 0% or 100% values (21 and 22 instances respectively), with many of these having small sample sizes (70% were cases < 5 samples) (Fig. S2).

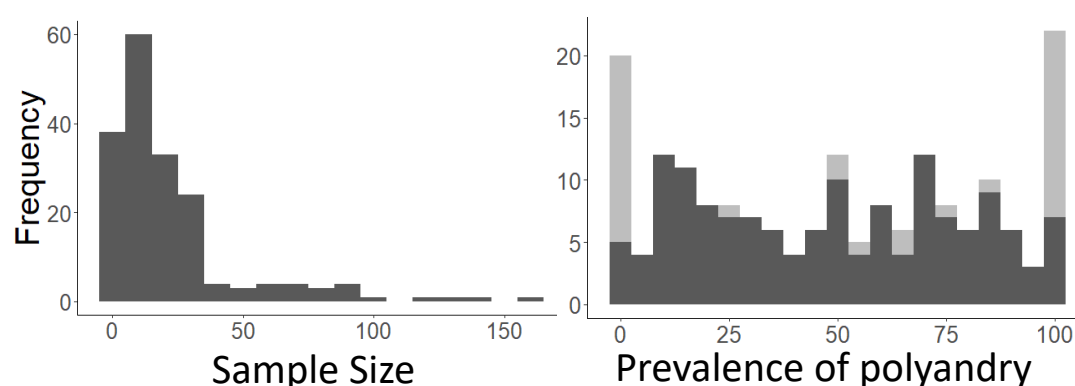


Fig. S2. The frequency (%) of sample sizes for all cases (left), and (right) the prevalence of polyandry in the population for all 184 cases (grey) and for 146 cases with sample sizes of 5 or more (black).

Although sample sizes ranged up to 157 (mean 23.11, SD 27.30), there were many with few samples (36 cases < 5 and 61 cases < 10 samples; *N.B.*, 2 cases did not report the sample size) and the majority were < 30 (Fig. S2, left). If cases with fewer than five samples and those with unreported sample sizes were excluded (Fig. S2, right), there was little change to the mean PA (48.67%, SD 29.91%, N = 146, compared with 49.33%, SD 33.71% for all 184 cases), but the number of 0% and 100% values was reduced to just a dozen.

Effect size data

Conversion formulae for Z_r

Calculations followed those of Borenstein et al. (2009). The bias corrected standardised mean difference, *Hedges' g* (called SMD in *metafor*) was converted to its uncorrected form, d :

$$d = \frac{\text{Hedges' } g}{J}$$

Correction factor, J was calculated:

$$1 - \frac{3}{4df - 1}$$

With df = degrees of freedom, calculated as $n_1 + n_2 - 2$ (where n_1 was the sample size of the first group, and n_2 was the sample size of the second group).

Following this, correlation r was calculated, using a correction factor, " a ":

$$r = \frac{d}{\sqrt{d^2 + a}}$$

$$a = \frac{(n_1 + n_2)^2}{n_1 n_2}$$

Conversion from correlation r to Fisher's z score, Z_r was then calculated:

$$Z_r = 0.5 \times \ln \left(\frac{1 + r}{1 - r} \right)$$

The variance of Z_r (Var_{Z_r}) was approximated with:

$$Var_{Z_r} = \frac{1}{n - 3}$$

Excluded studies

Table S2. Studies examining the relationship between the number of sires and the number of offspring, but excluded from the meta-analysis because they did not report means, variances and sample sizes of their test groups. These studies also did not report the correlation coefficient r between the number of offspring and the number of sires, and lacked the raw data with which to calculate r . “PA %” is the prevalence of polyandry and “N”, sample size, as estimated in the current study. The statistical test used, and the resulting p-value (a significant value is emphasised with an asterisk) are those reported by each study. Further clarification of some of the studies or their tests are in footnotes.

	PA %	N	Statistical test and result	P	Reference
Lacertilia					
Crotaphytidae					
<i>Crotaphytus collaris</i>	70	64	T-test: $t_{(71)} = 0.1$	0.920	York and Baird (2019)
Lacertidae					
<i>Zootoca vivipara</i> ¹	50	14	T-test: $t = 0.13$	>0.100	Laloi et al. (2004)
<i>Zootoca vivipara</i> ¹	68	44	T-test: $t = 0.39$	>0.100	Laloi et al. (2004)
Scincidae					
<i>Eulamprus quoyii</i> ²	68	60	ANCOVA ³ : $F_{(1,50)} = 10.55$	<0.010* ⁵	Noble et al. (2013)
Serpentes					
Colubridae					
<i>Elaphe obsoleta</i>	88	34	Multiple ordinal logistic regression: Wald $\chi^2 = 0.507$	0.476	Blouin-Demers et al. (2005)
Natricidae					
<i>Nerodia sipedon</i>	58	45	ANOVA ⁴ : $F_{(1,42)} = 0.60$	0.440	Prosser et al. (2002)
Testudines					
Cheloniidae					
<i>Caretta caretta</i>	93	15	Ordinal logistic regression ⁴ : $\chi^2 = 7.76$, $df = 1$	0.005* ⁶	Zbinden et al. (2007)
<i>Caretta caretta</i>	75	72	GLM: $\chi^2_{(1,71)} = 0.16$ (based on GERUD estimate); $\chi^2_{(1,71)} = 0.24$ (based on COLONY estimate)	0.690 (GERUD); 0.626 (COLONY)	Lasala et al. (2013)
Emydidae					
<i>Chrysemys picta</i>	33	12	T-test: $t = -2.40$	<0.01* ^{6, 7}	Pearse et al. (2002)
<i>Chrysemys picta</i>	14	157	GLMM ⁴ : $Z = -0.32$	0.752	McGuire et al. (2011)
<i>Emydoidea blandingii</i>	42	77	GLMM ⁴ : $Z = 1.998$	0.046* ⁸	McGuire et al. (2013)

1. Two different populations.

2. Wild-caught individuals were kept in enclosures at densities similar to those found under natural conditions.

3. Female body condition and size were controlled for.
4. Model included multiple variables.
5. Multiply mated females attained greater fertility.
6. More fecund females attracted more mates.
7. Females oviposited more eggs in response to multiple mating.
8. Larger and old females attracted more mates.

Statistical analyses

Controlling for phylogeny

We used meta-analysis models that incorporated a correlation matrix of phylogenetic relationships to account for phylogeny as a random effect. We used the *R* package *rotI* to interface with the 'Open Tree of Life' (opentreeoflife.org), to retrieve a phylogenetic tree (Fig. S7), which was then used to construct the correlation matrices.

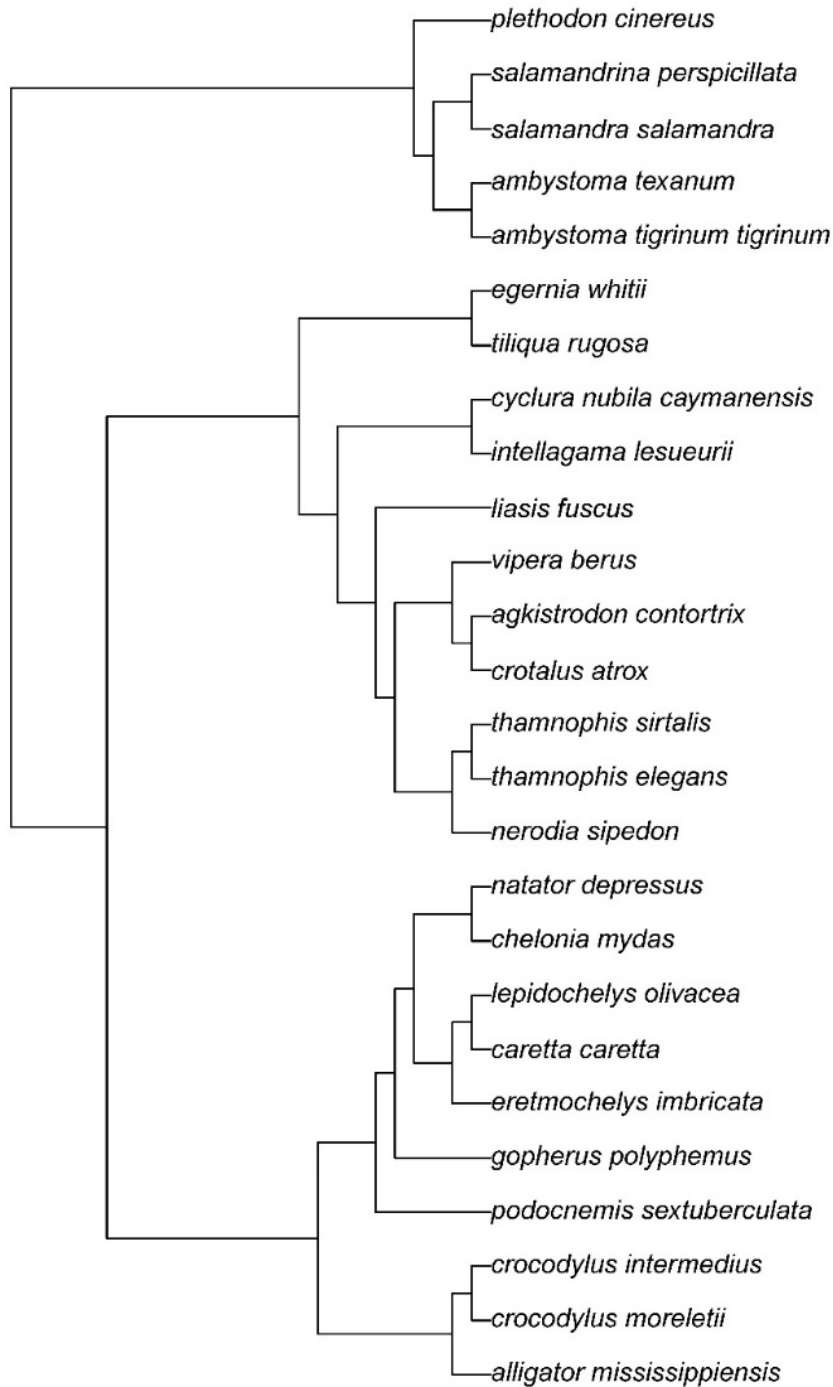


Fig. S3. Tree retrieved by the *R* package *rotI* from the 'Open Tree of Life' project (date of retrieval: 9 December 2021)

RESULTS

Global distribution of cases

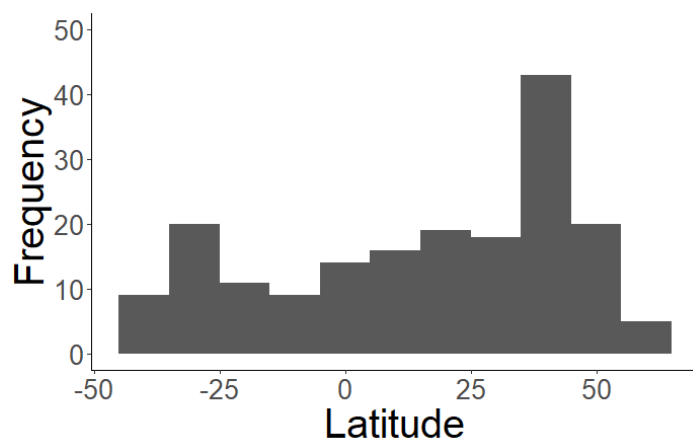


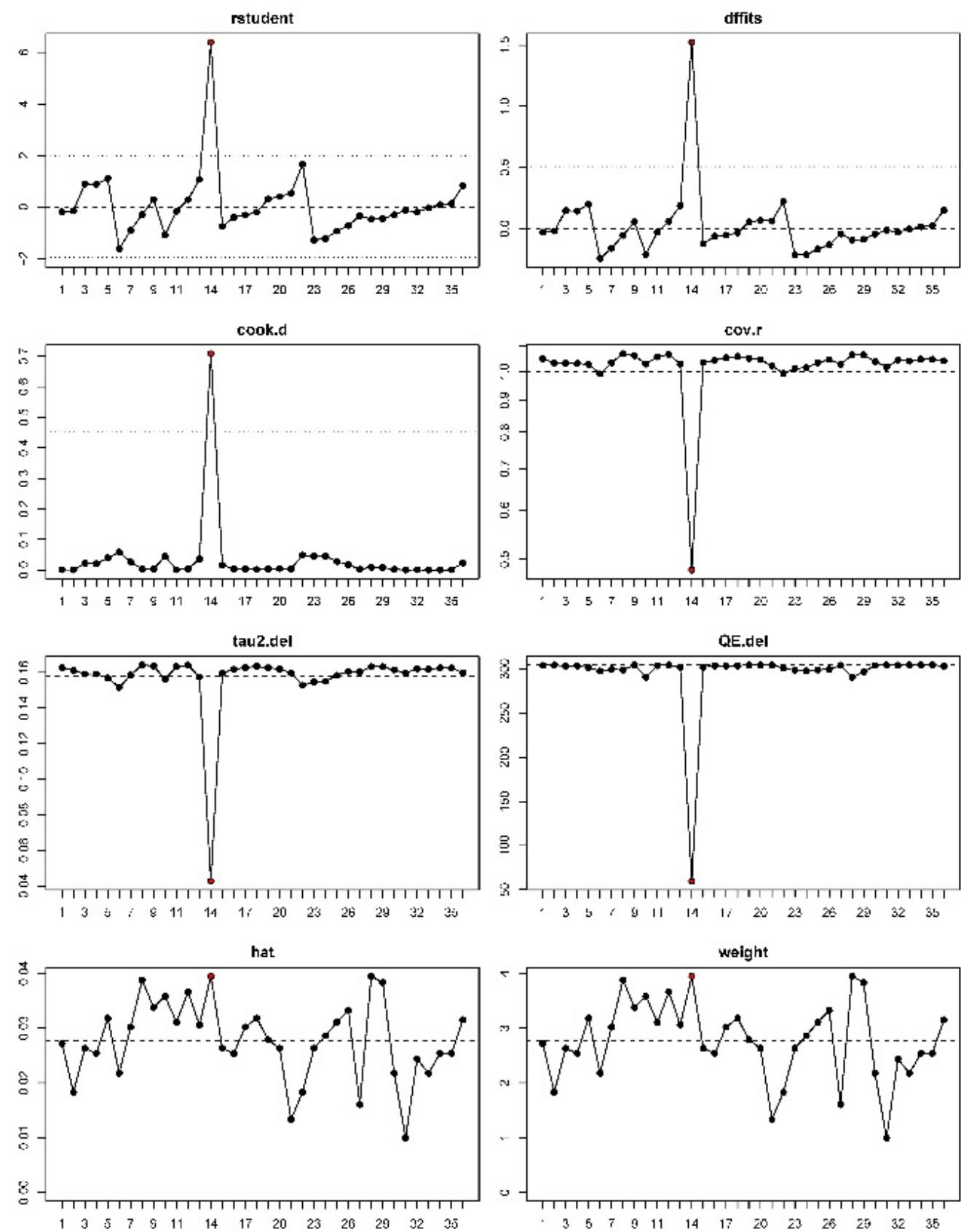
Fig. S4. Frequency graph for latitude for cases excluding those with fewer than five samples. There were more cases in the northern hemisphere (mean latitude in the northern hemisphere: 33.4° , $SD\ 14.0^\circ$), with a second smaller peak of cases in the southern hemisphere (mean latitude in the southern hemisphere: -21.0° , $SD = 14.0^\circ$).

There were more cases in the northern hemisphere and at higher latitudes than in the tropics or in the southern hemisphere. However, there was no significant correlation between PA and the absolute latitude (Kendall's rank correlation tau: $z = 0.84$, $p = 0.402$, excluding cases with fewer than five samples).

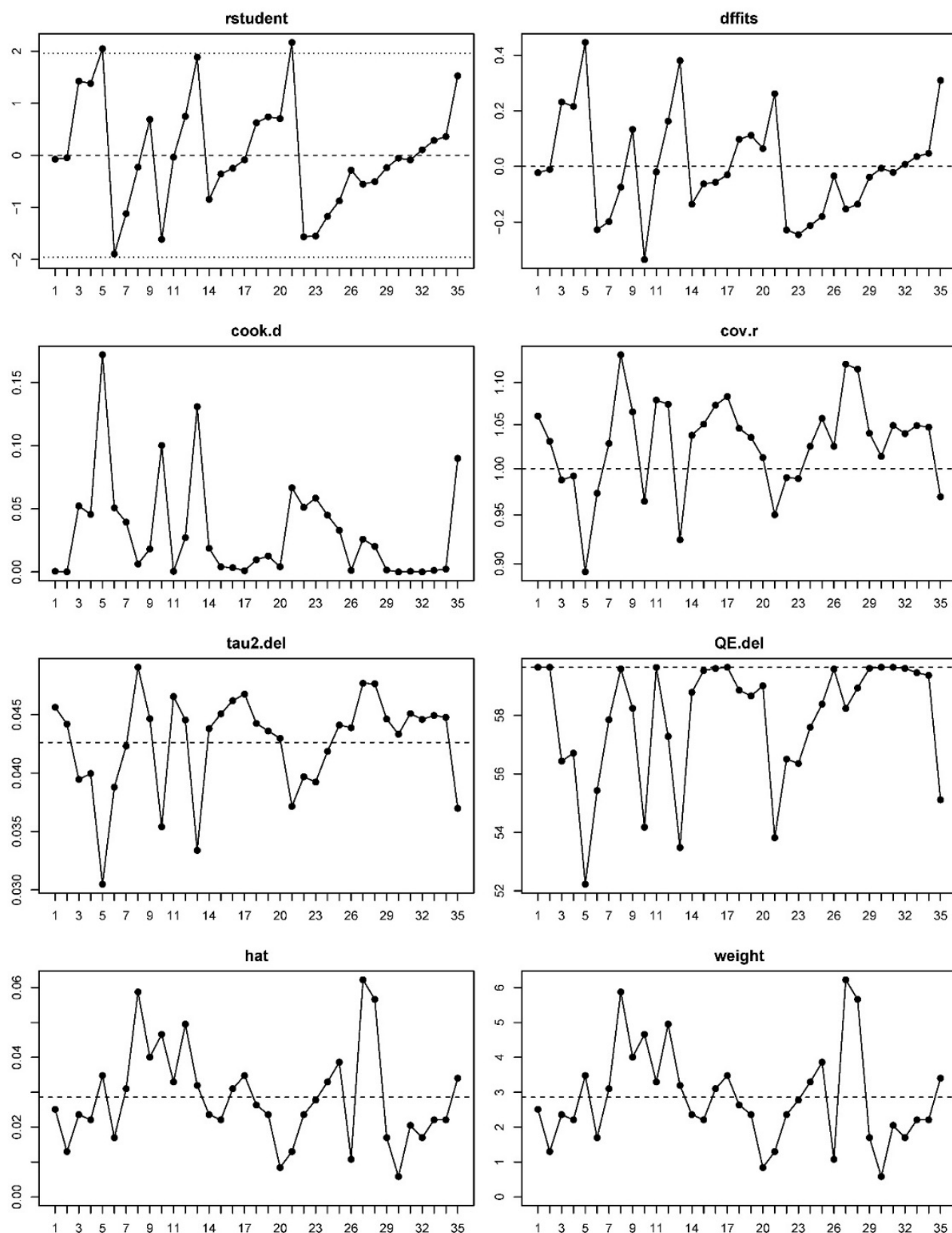
Identifying outliers and testing for publication bias

1) Influential case diagnostics

An influential case is an outlier, which if excluded from analysis, leads to substantial changes in the fitted model (Viechtbauer 2010). We examined whether there were influential cases in the model results using the *influence.rma.uni()* function in *metafor*. The test revealed one particular case, Eizaguirre et al. 2007 (Eizaguirre et al. 2007), as an influential outlier (Fig. S5, case marked with a red dot, panel A). When this case was excluded, the remaining cases did not exert any particularly strong influences on the model (Fig. S5, panel B).



A



B

Fig. S5. Plots of diagnostic measures for the meta-analysis model with: (*panel A*) all cases included (the case identified as an outlier with substantial influence on the model is case 14 in red); (*panel B*) plots with the outlier excluded. Diagnostic measures were: externally standardised residuals, DFFITS values, Cook's distances, covariance ratios, estimates of τ^2 and test statistics for residual heterogeneity when each study is removed in turn, hat values, and weights. See Viechtbauer (2010) for explanations of diagnostic measures.

2) Funnel plots, Egger's tests, fail safe numbers and cumulative plots

Funnel plots, Egger's tests and estimation of fail-safe numbers were undertaken using functions provided in *metafor* for the full dataset, the dataset excluding the influential case identified with influential case diagnostics (Eizaguirre et al. 2007), and for taxonomic subsets of the data (Fig. S6). Funnel plots generated by *metafor* show the observed outcomes (Zr) on the horizontal axis against their corresponding standard errors (the square root of the sampling variances) on the vertical axis; the vertical line is the summary effect size estimated by the model for the group of cases, with a pseudo confidence interval region around this line to show $\pm 1.96 \cdot SE$ (SE being the standard error value of the vertical line) (Viechtbauer 2010). The fail-safe number is the number of missing studies required before the cumulative effect becomes statistically insignificant (Rosenthal 1979), while Egger's test detects significant asymmetry in the funnel plot (Egger et al. 1997). According to Egger's test, none of the datasets were significantly asymmetrical, and fail-safe numbers were zero for all except Caudata, Lacertilia and the full dataset. However, once the influential case identified with influential case diagnostics (Eizaguirre et al. 2007) was removed from the latter two datasets, the cumulative effect sizes were no longer significantly different from zero (thus, fail-safe numbers were zero). The funnel plot for Lacertilia further revealed two cases as outliers, which likely contributed to the heterogeneity of this taxonomic subgroup.

A forest plot of cumulative meta-analysis was conducted according to year of publication. This plot (Fig. S7) show how the initial cumulative effect sizes had high values influenced by a few early cases, but as time goes on and more cases were added, the cumulative effect sizes settled close to zero.

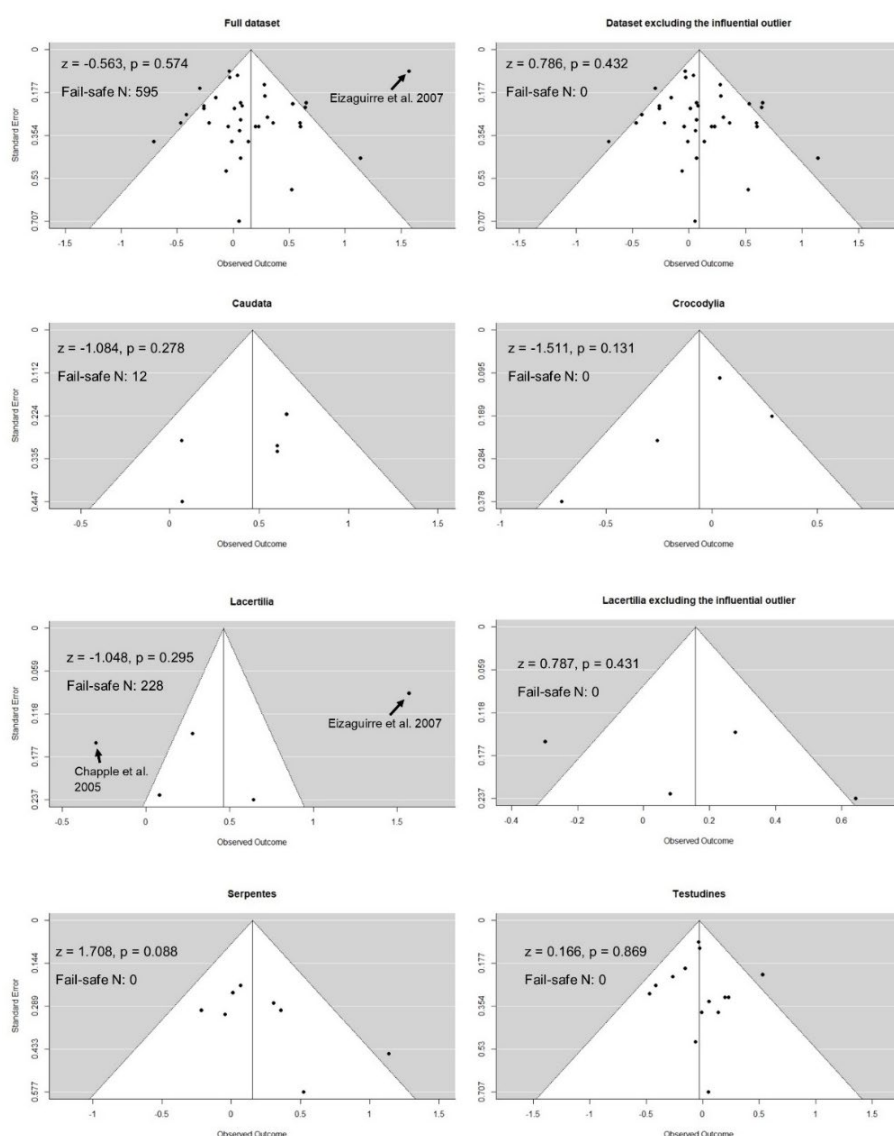


Fig. S6. Funnel plots for the full dataset, the data excluding the influential outlier Eizaguirre et al. 2007, and the various taxonomic subgroups. Test results for Egger's test and fail-safe numbers are shown for each dataset. Two outliers in Lacertilia are labelled.

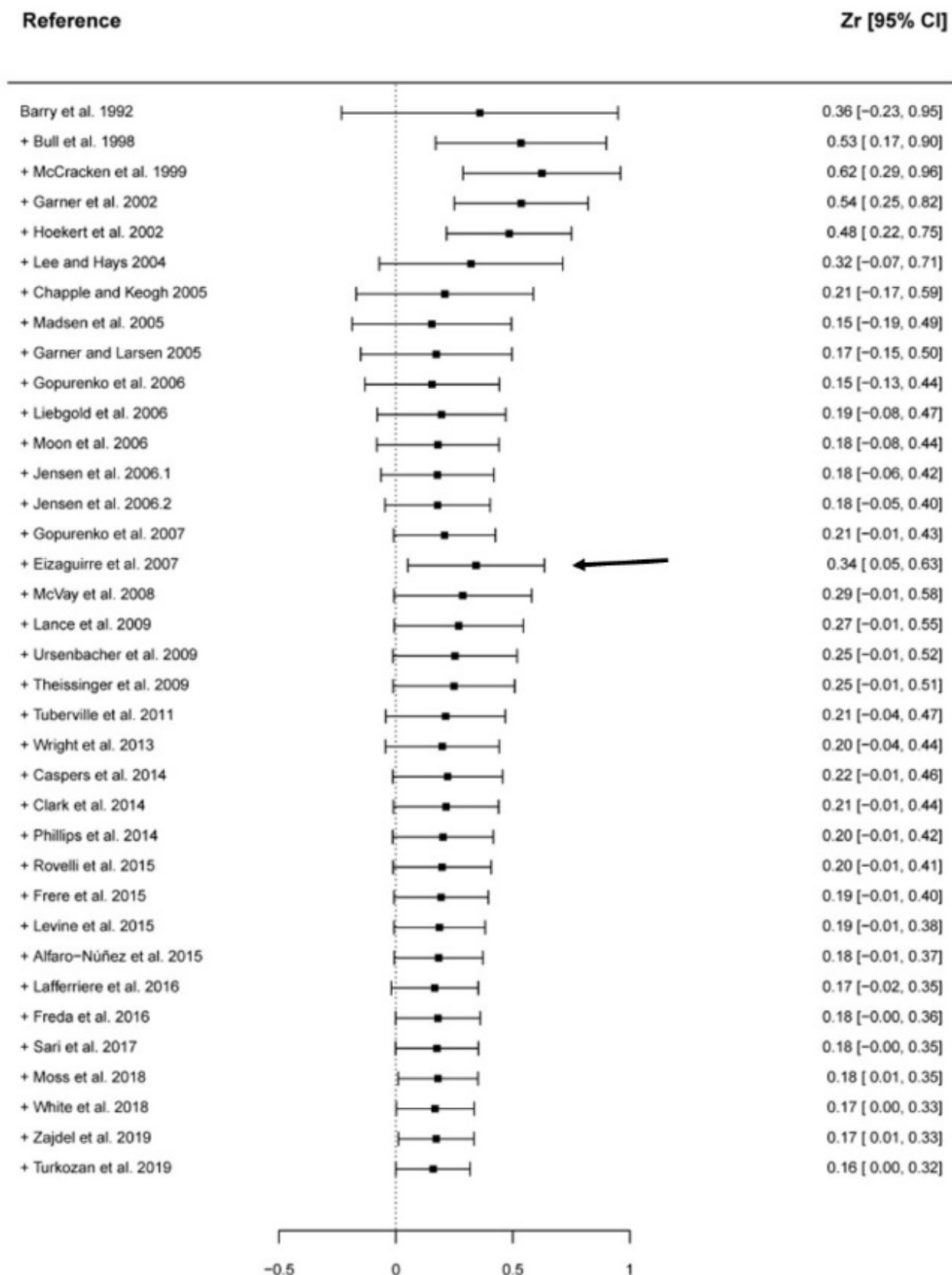


Fig. S7. Cumulative meta-analysis by year of publication. The impact of the influential case on the cumulative effect size of the full dataset at the time of its publication is marked with an arrow.

Correlations between variables

Variables tested were: PA, latitude and absolute latitude, average number of alleles observed per locus, average genetic heterozygosity estimated for the population (observed and expected), average clutch or litter sizes in the population and measures indicating the sampling effort of the study (number of microsatellite loci sampled, average number of alleles per locus, average number of offspring genotyped and average percentage of offspring genotyped). We checked for correlations between these variables and effect sizes Z_r , and pairwise relations among variables. There were no significant relationships with Z_r , but a number of variables were significantly correlated with each other (Fig. S8).

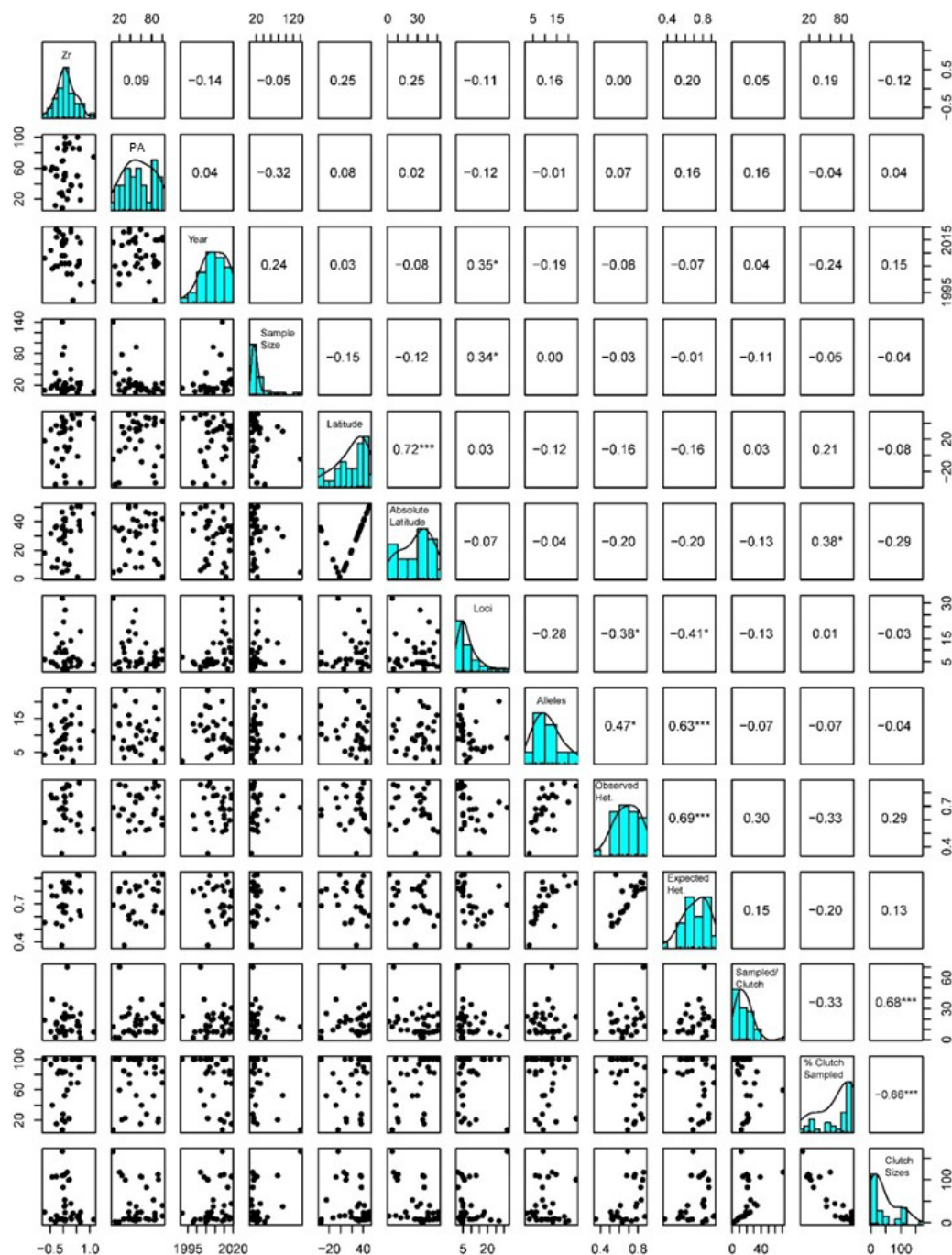


Fig. S8. Relationships among variables in the dataset used for meta-analyses, excluding the influential outlying case ($N = 35$) (test for correlation = Kendall's tau). The graphs in the lower left of the diagonal are scatter plots. The diagonal graphs are histograms, and the upper off-diagonal reports the Kendall's tau correlation, with significant p indicated in asterisks (*, **, *** = $p < 0.05$, < 0.01 , < 0.001 respectively)

There are some clearly correlated groups among the variables. As would be expected, latitude and absolute latitude were significantly correlated (the latter was derived from the former). Also as would be expected, observed and expected heterozygosities were significantly correlated, and they were also correlated with the number of loci sampled, and the average number of alleles per locus. Finally, the average number sampled per clutch and the average percentage genotyped per clutch were both significantly correlated with clutch sizes, both in different directions (positive for the former, negative for the latter).

Comparing models fitted with different numbers of moderators

We tested whether candidate variables were significant moderators and whether there were any significant remaining residual heterogeneity. We fitted a model including all candidate variables as moderators and models with single candidates. We also used corrected Akaike's information criterion values (AIC_c) to confirm the model best fitting the data. We also tested combinations of two candidates. For further details of tests and methods – see the main text.

Table S3. Results of fitting mixed-effects models that included moderators either individually or in combination, showing t or F values for tests on individual or multiple variables (omnibus), respectively. Results of tests of residual heterogeneity (QE) are also shown. Models were fitted to the dataset excluding a significantly influential case ($K = 35$ cases). Datasets for some models had fewer cases due to missing values. Model fit to the data is indicated by corrected Akaike's information criterion values (AIC_c). Boxes show AIC_c values that can be compared (i.e., models using the same dataset and having the same number of parameters): white box = single moderator and a dataset of 35 cases; light grey box = single moderator and a dataset of 26 cases; dark grey box = two moderators and a dataset of 27 cases. ΔAIC_c is the difference of the AIC_c from the lowest AIC_c value in the box; an asterisk highlights the best fitting model among the models in the box. All models controlled for time-lag bias and small study effect, and included random factors (see main text). Text in parentheses in part B in the column describing models are abbreviated text used in part C. A: result of including all moderators together in a model; B: results of models fitted with one moderator; C: results of models fitted with two moderators. To choose among models, we looked for a significant test result (individual or omnibus) with low or non-significant residual heterogeneity and relatively low AIC_c values. NS are p values > 0.05 .

Model	Cases K	Individual test		Omnibus test		Test for Residual Heterogeneity		Relative model fit	
		t	P	F	P	QE	P	AIC_c	ΔAIC_c
A: All moderators	26	-	-	0.790	NS	25.731	0.028	-	-
B: Individual moderators									
Prevalence of polyandry (PA)	35	0.570	NS	-	-	55.201	0.007	41.0	1.5
Latitude of sampled location (Latitude)	35	1.393	NS	-	-	53.850	0.009	39.5*	0
Absolute latitude of sampled location (abLat)	35	1.261	NS	-	-	56.160	0.005	39.9	0.4
Number of microsatellite loci sampled	35	0.428	NS	-	-	57.046	0.004	41.5	2.0
Average number of offspring genotyped	35	0.307	NS	-	-	57.110	0.004	40.9	1.4

per clutch or litter (Genotyped/Clutch)									
Average percentage of the clutch sampled (%Sampled)	35	0.517	NS	-	-	55.815	0.006	40.8	1.3
Average size of clutches or litters (ClutchN)	35	- 0.054	NS	-	-	55.594	0.006	41.2	1.7
Average observed heterozygosity over all loci (ObHet)	28	1.136	NS	-	-	48.590	0.003	-	-
Average expected heterozygosity over all loci (ExHet)	27	2.213	0.037	-	-	44.011	0.008	-	-
Average number of alleles per locus	26	1.694	NS	-	-	38.690	0.022	29.1	0.8
Average observed heterozygosity over all loci	26 ¹	1.706	NS	-	-	39.764	0.016	28.9	0.6
Average expected heterozygosity over all loci (ExHet)	26 ¹	1.908	NS	-	-	39.496	0.018	28.3*	0
Latitude of sampled location (Latitude)	26 ^{1,2}	0.605	NS	-	-	39.268	0.019	31.9	3.6

C: ExHet³ + other

ExHet+		2.232	0.036						
PA ³	27	- 0.779	NS	2.513	NS	42.874	0.007	35.3	0.3
ExHet+		2.201	0.038						
Latitude ³	27	- 0.278	NS	2.437	NS	43.994	0.005	35.8	0.8
ExHet+ abLat ³	27	1.952 0.007	NS NS	2.375	NS	42.312	0.008	35.8	0.8
ExHet+ Genotyped/Clutch ³	27	2.019 0.441	NS NS	2.480	NS	43.439	0.006	35.3	0.3
ExHet+ %Sampled ³	27	1.873 0.270	NS NS	2.427	NS	37.753	0.027	35.0*	0
ExHet+		2.375	0.026						
ClutchN ³	27	- 0.861	NS	2.821	NS	37.730	0.027	35.0*	0

1. To enable comparing AIC_c values with the model having only 26 cases, this model was fitted using the same dataset of 26 cases
2. Since the model with latitude specified as the moderator had the best fit amongst models fitted using the dataset of 35 cases, we also fitted the model for 26 cases to enable comparison with other models that had to be fitted with fewer cases due to missing data on the variable of interest.

- See full description of the abbreviated name of the moderator in part B of the table (abbreviation is in the parentheses)

Results of moderator tests are reported in Table S3 above, but we also compared models specified with different numbers of moderators using the *anova.rma()* function in *metafor*. The comparisons of interest were among models that included average expected heterozygosity (ExHet), average clutch/litter sizes (ClutchN) and average percentage of the clutch/litter sampled (%Sampled) (see main text and Table S3). However, we found no significant differences between models (Table S4). There were also no significant differences between models with moderators and the model without any moderators.

Table S4. Results of comparing models specified with different numbers of moderators

Model with ExHet + ClutchN versus model with ExHet only

	df	AIC	BIC	AICc	logLik	LRT	pval	QE
Full	8	24.0308	34.3975	32.0308	-4.0154			37.7299
Reduced	7	22.9578	32.0287	28.8526	-4.4789	0.9271	0.3356	44.0109

Model with ExHet + %Sampled versus Model with ExHet only

Full	8	24.7762	35.1429	32.7762	-4.3881			37.7532
Reduced	7	22.9578	32.0287	28.8526	-4.4789	0.1816	0.6700	44.0109

Model with ExHet versus model with no moderators

Full	7	22.9578	32.0287	28.8526	-4.4789			44.0109
Reduced	5	21.8601	28.3393	24.7173	-5.9301	2.9023	0.2343	45.1586

Model with ExHet + ClutchN versus model with no moderators

Full	8	24.0308	34.3975	32.0308	-4.0154			37.7299
Reduced	5	21.8601	28.3393	24.7173	-5.9301	3.8294	0.2805	45.1586

Model with ExHet + %Sampled versus model with no moderators

Full	8	24.7762	35.1429	32.7762	-4.3881			37.7532
Reduced	5	21.8601	28.3393	24.7173	-5.9301	3.0839	0.3789	45.1586

Sensitivity test of expected heterozygosity as a moderator

A sensitivity test was conducted with models fitted with expected heterozygosity, which was the only variable that had resulted in a significant test as a moderator (see Table 5 in main text). This procedure tested whether leaving out just one case in the dataset could lead to a non-significant result. For the sensitivity test, we excluded one case and obtained a result for the test for moderator; we then repeated this for another case, and so forth (*N.B.*, each model was fitted with only one case excluded). The sensitivity test showed that excluding any of three particular cases did indeed result in a non-significant *p* value for the test of average heterozygosity as a moderator. These cases were Freda et al 2016, McVay et al. 2008 and Bull et al. 1998 ($t = 1.908$, $p = 0.069$, $t = 1.861$, and $p = 0.076$, $t = 1.8684$, $p = 0.075$, respectively), and are indicated in Fig. 3 of the main text.

For R scripts of these and other calculations, see below.

R SCRIPTS FOR META-ANALYSES

#Dataset preparation

#Explanations of datasets:

#data = full dataset (N = 36)

#data2 = excludes influential case Eizaguirre et al. 2007 (N = 35)

#data2b = data2 and excludes one of two populations (the 'arribada' population) from the Jensen et al. 2006 study (variables Alleles, ObHet, ExHet are the same data for the two populations) (N = 34)

#data3b = data2b and excludes cases with missing data for ExHet variable (N = 27)

#data4 = data3b and exclude cases with any other missing data (N = 26)

Sdata10 = for sensitivity test of ExHet as a moderator, this is data3b excluding the study by McVay et al. 2008 (N = 26)

#Sdata2 = for sensitivity test of ExHet as a moderator, this is data3b excluding the study by Bull et al. 1998 (N = 26)

#Create subsets of data to analyse among families

Caudata <- subset(data, Clade == "Caudata")

Crocodylia <- subset(data, Clade == "Crocodylia")

Lacertilia <- subset(data, Clade == "Lacertilia")

Serpentes <- subset(data, Clade == "Serpentes")

Testudines <- subset(data, Clade == "Testudines")

#leave out outlier from Lacertilia

Lacertilia2 <- subset(data2, Clade == "Lacertilia")

Phylogenetic matrix preparation for meta-analysis

#convert taxon names (column labelled "Animal" in this dataset) to lower cases

data\$Taxa <- tolower(data\$Animal)

#find the animals in OTT (Open Tree of Life)

library(rotl)

taxanames <- tnrs_match_names(unique(data\$Taxa), context = "Animals")

#map names in OTT to names in dataset

taxon_map <- structure(taxanames\$search_string, names = taxanames\$unique_name)

```
#get a tree
```

```
tr <- tol_induced_subtree(ott_id(taxanames)[is_in_tree((ott_id(taxanames)))))
```

```
plot(tr, show.tip.label = FALSE, main = "data")
```

```
#replace tip names with taxa names in dataset
```

```
otl_tips<- strip_ott_ids(tr$tip.label, remove_underscores = TRUE)
```

```
tr$tip.label <- taxon_map[otl_tips]
```

```
plot(tr, main = "data")
```

```
# compute BRANCH LENGTH
```

```
library("ape")
```

```
tr<-compute.brlen(tr, method = "Grafen", power = 1)
```

```
# create correlation matrix (function in ape)
```

```
matrix1<-vcv(tr, corr=TRUE)
```

```
#Repeat matrix preparation for other datasets as required, replacing "data" with dataset of interest
```

#Examining variables

```
#Obtain basic stats for multiple variables (NB: conducted for datasets of interest, replace "data" with dataset of interest)
```

```
library(pastecs)
```

```
round(stat.desc(data[, c("Zr", "PA", "Latitude", "abLat", "Loci", "Alleles", "ObHet", "ExHet", "genotypedPerClutch",  
"PercentageclutchSampled", "ClutchSizes", "Zr_sei", "year_c")]), digits = 3)
```

```
#Pairwise correlation graphs of variables (NB: replace "data" with the dataset of interest; method can be changed –  
e.g. method="pearson" is the default for the test, "spearman" can also be used.)
```

```
library(psych)
```

```
pairs.panels(data2[, c("Zr", "PA", "PubYear", "SampleSizeN", "Latitude", "abLat", "Loci", "Alleles", "ObHet", "ExHet",  
"genotypedPerClutch", "PercentageclutchSampled", "ClutchSizes")], method = "kendall", stars = TRUE, ellipses =  
FALSE, smooth = FALSE)
```

#Meta-analysis models fitted using metafor

```
library(metafor)
```

#Random-effects rma.uni model to test for influential outliers (repeat this test for other datasets as required) (N.B., this model also required for cumulative meta-analysis below)

```
rma.uni.Full1 <- rma(yi= Zr, vi=VarZr, data=data, slab = paste(data$REF))
```

```
inf1 <- influence(rma.uni.Full1)
```

```
plot(inf1)
```

#Random-effects rma.uni model of group without outlier and cases with missing expected heterozygosity removed (N.B., model required for cumulative meta-analysis below)

```
rma.uni.ExHet3b <- rma(yi= Zr, vi=VarZr, data=data3b, slab = paste(data3b$REF))
```

```
rma.uni.ExHet3b
```

#Tests for publication bias and visual detection of outliers: funnel plots, Egger's tests and fail safe numbers (repeat tests for other datasets)

```
funnel(rma.uni.Full1, main = "Full dataset")
```

```
regtest(rma.uni.Full1)
```

```
fsn(yi = data$Zr, vi = data$VarZr, type="Rosenberg")
```

#Cumulative meta-analysis by year of publication (NB: this uses a random-effects rma.uni model)

```
data.CUM <- cumul(rma.uni.Full1, order = order(data$PubYear))
```

#Cumulative meta-analysis by expected heterozygosity (NB: this uses a random-effects rma.uni model, see above)

```
data.ExHetCUM3b <- cumul(rma.uni.ExHet3b, order = order(data3b$ExHet))
```

#rma.mv model with random factors. This random-effects model accounts for phylogeny and other random factors. REF =accounting for multiple cases from the same study; Source = accounting for different sources of effect size data (Hedges' g or correlation r); Animal = accounting for multiple cases within species; Taxa = accounting for phylogeny; matrix1 = rot1 phylogeny correlation matrix. (N.B., use similar script for fitting models for other datasets such as for subgroups)

```
modelFull1 <-rma.mv (yi= Zr,
```

```
    V= VarZr,
```

```
    random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
```

```
    R = list(Taxa = matrix1),
```

```
    method = "REML", test = "t", data = data, slab = paste(data$REF))
```

```
modelFull1
```

#rma.mv model with random factors of dataset without the outlier

```
modelNoOutlier1 <- rma.mv (yi= Zr,
  V= VarZr,
  random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
  R = list(Taxa = matrix2),
  method = "REML", test = "t", data = data2, slab = paste(data2$REF))
modelNoOutlier1
```

#Testing for moderators

```
library(metafor)
```

#Multilevel meta-analysis model controlling for time-lag bias (year_c) and small study effect (Zr_sei), with ExHet specified as the moderator. Mod = ~-1 removes the intercept from the model. ExHet = expected heterozygosity; Zr_sei = inverse of Zr standard error ($1/\sqrt{n-3}$), n = sample size; year_c = mean-centering of publication year (year – mean of years). Random factors: REF = accounting for multiple cases from the same study; Source = accounting for different sources of effect size data (Hedges' g or correlation r); Animal = accounting for multiple cases within species; Taxa = accounting for phylogeny; matrix3b = rotl phylogeny correlation matrix appropriate for data3b. The dataset data3b excludes the influential outlying case, and cases missing data for expected heterozygosity (K = 27). Other models fitted to test one moderator used the same script below, with ExHet replaced by the variable of interest (i.e., PA, Latitude, abLat, Loci, Alleles, ObHet, genotypedPerClutch, PercentageclutchSampled or ClutchSizes). *N.B.*, For these tests of single moderators, the result reported for the omnibus test for moderators is ignored.

```
ExHetMod3b <- rma.mv (yi= Zr,
  V= VarZr,
  mod = ~ -1 + ExHet + Zr_sei + year_c,
  random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
  R = list(Taxa = matrix3b),
  method = "REML", test = "t", data = data3b, slab = paste(data3b$REF))
ExHetMod3b
fitstats(ExHetMod3b)
```

#Multilevel meta-analysis model controlling for time-lag bias (year_c) and small study effect (Zr_sei), with all variables specified as moderators. The dataset data4 excludes the influential outlying case, and cases missing data for any of the variables (K = 26). The omnibus test for moderators excludes time lag bias and small study effect by specifying the moderators to include in the test with the btt = () instruction. For models fitted to test combinations

of two or more moderators, the same script below was used, replacing dataset data4 with the appropriate dataset for the variables of interest, and specifying btt = (1:2) for two moderators or btt = (1:3) for three moderators, etc..

```
allMods <- rma.mv      (yi= Zr,
                      V= VarZr,
                      mod = ~ -1 + PA + Latitude + abLat + Loci + Alleles + ObHet + ExHet +
                        genotypedPerClutch + PercentageclutchSampled + ClutchSizes +
                        Zr_sei + year_c,
                      random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
                      R = list(Taxa = matrix4),
                      method = "REML", test = "t", btt = (1:10),
                      data = data4, slab = paste(data4$REF))

allMods

fitstats(allMods)
```

#Create cumulative meta-analysis plot according to expected heterozygosity, and add predicted effect sizes for min, mean and max expected heterozygosity values

```
library(metafor)
```

#Predict effect sizes for min, median and max expected heterozygosity values, while holding Z_sei and year_c constant at their respective mean values, using the model fitted with expected heterozygosity as a moderator (see above for script for the model)

```
ExHetPred3b <- predict.rma(ExHetMod3b, newmods = cbind(c(0.4,0.7,0.9), 0.3, 0), addx = TRUE)
```

#Construct forest plot with predicted effect sizes based on expected heterozygosity. This uses a cumulative meta-analysis model (see above for script for the model). *N.B.*, Stars to highlight cases are manually added after the JPEG figure was generated by *metafor*, using Microsoft Publisher

```
library(metafor)
```

```
par(mar=c(5,6,4,4))
```

```
cumplotExHet <- forest(data.ExHetCUM3b,
                      ylim = c(-3, 30.5), xlim = c(-2,1.8), alim = c(-1.5, 1.5),
                      at = c(-1, -0.5, 0, 0.5, 1),
                      refline= c(-1, -0.5, 0, 0.5, 1),
                      cex=0.8, xlab = "Zr", cex.lab = 1)
```

```
text(-2, 30, "Reference", pos = 4, font = 2)
```

```
text(1.2, 30, "Zr [95% CI]", pos = 4, font = 2)
text(-1.75, 0, "Predicted", pos = 4, font = 2)
addpoly(ExHetPred3b$pred, sei = ExHetPred3b$se, cex = 0.8, mlab = c("    Heterozygosity = 0.4", "
Heterozygosity = 0.7", "    Heterozygosity = 0.9"))
```

#Sensitivity test for ExHet

```
library(metafor)
```

For dataset "data3b", repeat the meta-analysis excluding cases one by one: first, create subsets of data for each case excluded, then run the meta-analysis (i.e. to test the next case, replace Order == "1" with Order == "2", and so on, until all cases have been tested)

```
Sdata <- subset(data3b, !(Order == "1"))
SExHetMod <- rma.mv (yi= Zr,
                    V= VarZr,
                    mod = ~ -1 + ExHet + Zr_sei + year_c,
                    random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
                    R = list(Taxa = matrix3b),
                    method = "REML", test = "t", data = Sdata, slab = paste(data$REF))
SExHetMod
```

#Testing among models with different numbers of moderators

```
library(metafor)
```

#N.B., this requires "ML" set as method for the amova.rma() function to work

```
mdata <- data3b
NoMOD <- rma.mv (yi= Zr,
                V= VarZr,
                random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
                R = list(Taxa = matrix3b),
                method = "ML", test = "t",
                data = mdata)
MOD2 <- rma.mv (yi= Zr,
```

```
V= VarZr,
mod = ~ -1 + ExHet + PercentageclutchSampled +
  Zr_sei + year_c,
random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
R = list(Taxa = matrix3b),
method = "ML", test = "t",
data = mdata)
```

```
MOD2b <-rma.mv      (yi= Zr,
  V= VarZr,
  mod = ~ -1 + ExHet + ClutchSizes +
    Zr_sei + year_c,
  random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
  R = list(Taxa = matrix3b),
  method = "ML", test = "t",
  data = mdata)
```

```
MOD1 <-rma.mv      (yi= Zr,
  V= VarZr,
  mod = ~ -1 + ExHet +
    Zr_sei + year_c,
  random = list(~1 | REF, ~1 | Source, ~1 | Animal, ~1 | Taxa),
  R = list(Taxa = matrix3b),
  method = "ML", test = "t",
  data = mdata)
```

```
anova.rma(MOD2b, MOD1)
```

```
anova.rma(MOD2, MOD1)
```

```
anova.rma(MOD1, NoMOD)
```

```
anova.rma(MOD2b, NoMOD)
```

```
anova.rma(MOD2, NoMOD)
```

```
library(metafor)
```

```
#Predict the summary effect size using the model fitted with ExHet as the moderator (see above), and using mean values of expected heterozygosity, Z_sei and year_c
```

```
ExHetPred3a <- predict.rma(ExHetMod3b, newmods = cbind(0.7, 0.3, 0), addx = TRUE)
```

```
#Build labelled forest plot for the model fitted with the full dataset (see above for script for rma.mv models). N.B., the star highlighting one case was manually added with Microsoft Publisher after the JPEG figure was generated by metafor
```

```
#change margins
```

```
par(mar=c(5,6,4,4))
```

```
OffspringPlot <- forest(modelFull1, ylim = c(-3, 51), xlim = c(-6.5,5), alim = c(-2.5, 2.5), at = c(-2.5, -2, -1.5, -1, -0.5, 0, 0.5, 1, 1.5, 2, 2.5),
```

```
refline= c(-2, -1, 0, 1, 2), order=order(data$Clade1), rows = c(47:43, 40:37, 34:30, 26:19, 16:3), cex=0.8, xlab = "Zr", mlab="", cex.lab = 1)
```

```
#add text for species
```

```
text(-4.4, c(47:43, 40:37, 34:30, 26:19, 16:3), pos=4, paste(data$Animal), cex = 0.8, font = 3)
```

```
#add PA values
```

```
text(2.9, c(47:43, 40:37, 34:30, 26:19, 16:3), paste(data$ PA), cex = 0.8)
```

```
#add sample sizes
```

```
text(3.3, c(47:43, 40:37, 34:30, 26:19, 16:3), paste(data$SampleSizeN), cex = 0.8)
```

```
#Text for Jensen et al
```

```
text(-2.9, 4, pos=4, "(arribada)", cex = 0.8)
```

```
### add further summary polygons and associated text
```

```
addpoly(modelCaudata, row=42, cex=0.8, mlab="")
```

```
addpoly(modelCrocodylia, row=36, cex=0.8, mlab="")
```

```
addpoly(modelLacertilia, row=29, cex=0.8, mlab="")
```

```
addpoly(modelLacertilia2, row=28, cex=0.8, mlab="", col="grey")
```

```
addpoly(modelSerpentes, row=18, cex=0.8, mlab="")
```

```
addpoly(modelTestudines, row=2, cex=0.8, mlab="")
```

```
addpoly(modelNoOutlier1, row=-2, cex=0.8, mlab="", col="grey")
```

```
addpoly(ExHetPred3a$pred, sei = ExHetPred3a$se, row=-3, cex = 0.8, mlab = "", col="white")
```

```
text(-3.5, -1, "Full dataset", cex = 0.8, pos=4 )
```

```
text(-3.5, -2, "Without outlier", cex = 0.8, pos=4 )
```

```
text(-3.5, -3, "With moderator", cex = 0.8, pos=4 )
```

```
### add column headings to the plot
```

```
text(-6.5, 50, "Reference", cex = 0.9, pos=4, font = 2)
```

```
text(-4.4, 50, "Species", cex = 0.9, pos=4, font = 2)
```

```
text(2.6, 50, " PA%", cex = 0.9, pos = 4, font = 2)
```

```
text(3.1, 50, "N", cex = 0.9, pos = 4, font = 2)
```

```
text(5, 50, "Zr [95% CI]", cex = 0.9, pos=2, font = 2)
```

```
### add Taxon group headings
```

```
text(-3.5, 41.8, "CAUDATA", cex = 0.8, pos=4)
```

```
text(-3.5, 35.8, "CROCODYLIA", cex = 0.8, pos=4)
```

```
text(-3.5, 28.8, "LACERTILIA", cex = 0.8, pos=4)
```

```
text(-3.5, 17.8, "SERPENTES", cex = 0.8, pos=4)
```

```
text(-3.5, 1.8, "TESTUDINES", cex = 0.8, pos=4)
```

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