**Supplementary Materials**

**849 unique records on 12 June 2019**

**SEARCH 1:** *Web of Science*

TOPIC: (“female ornament\*” OR “mutual\* ornament\*”)

Timespan: All years

Databases: WOS, BIOABS, BIOSIS, CCC, DRCI, KJD, MEDLINE, RSCI, SCIELO

**SEARCH 2:** References from five highly cited articles in the topic and all publications citing those five articles

Amundsen T. 2000. *Trends Ecol. Evol.* **15**, 149–155

LeBas NR. *et al.* 2003. *Proc. R. Soc. Lond. B* **270**, 2159–2165

LeBas NR. 2006. *Trends Ecol. Evol.* **21**, 170–173

Kraaijeveld K. *et al.* 2007. *Anim. Behav*. **74**, 657–677

Tobias JA. *et al.* 2012. *Philos. Trans. R. Soc. Lond. B* **367,** 2274–2293

**EXCLUSION criteria:**

* Data files (29)
* Analysis scripts (5)
* Conference documents (9)
* Reviews (53)
* Theoretical studies (20)
* Comments and editorial articles (34)
* Book or book chapters (16)
* Comparative studies (81)
* Papers on methods (2)
* Taxonomic studies (2)
* Descriptive studies (16)
* Artificial selection (4)
* Male only studies (35)
* Genetic architecture (7)
* Genetic correlation (4)
* Mechanism (14)
* Mating system (4)
* Non-morphological traits (86)
* Non-ornamental traits (40)
* Species recognition (3)
* Fossil records (3)
* Human studies (11)
* Assortative mating (9)
* Other unrelated topics (53)

**Total exclusions = 540**

**309 records**

(Title and abstract screening)

**INCLUSION criteria:**

* Peer-reviewed articles
* Birds
* Species in which both sexes are ornamented
* Ornament ↔ fitness/condition

**25 additional peer-reviewed articles on males with extractable data**

**INCLUSION criteria:**

* Same inclusion criteria as above
* Cited in studies on female ornaments only (from the studies selected previously)
* From the same populations as those studies on females citing them

**125 records**

(Full-text screened studies with extractable data)

**META-ANALYSIS DATA:**

**150 studies** (64 species)

967 effect sizes

**Figure S1.** PRISMA flowchart of the literature search strategy and study selection process

Chart, scatter chart

Description automatically generated

**Figure S2.** Sexual dimorphism seems to affect condition-dependence of ornaments. Shown are the effect sizes of ornament elaboration and body condition per sex. However, a significant effect of sexual dimorphism was only influenced by four outliers corresponding to an extreme case of sexual dimorphism in the Willow Ptarmigan *Lagopus lagopus* (more details in *Results*). The size of the bubbles is proportional to the inverse of the standard errors (often referred to as ‘precision’), thus the larger the bubble the greater the precision of the effect size. Regression lines are plotted by sex based on the posteriori distributions of the model (details in *Methods* and Table S1.7).

Diagram, engineering drawing

Description automatically generated

**Figure S3.** Funnel plots for each model data set presented by sex (F: females, M: males). Model numeration according to Table S1. Effect sizes are plotted against the inverse of their standard errors, or precision (1/SE). Each filled dot represents actual effect sizes calculated from our literature compilation, while the empty circles are fabricated effect sizes using the trim-and-fill method to force funnel plots to be symmetric. The mean effect size is defined by the vertical line along with pseudo 95% confidence intervals defined by dotted lines (mean effect size ± 1.96x[1/SE]), which created the funnel shape. In the absence of publication bias, actual effect sizes are expected to lie within this funnel and be evenly distributed on both sides of the vertical line. Deviations from the symmetric funnel shape may indicate publication bias. Results from Egger’s tests to test for funnel asymmetry are shown in Table S5.

**Table S1.** Summary of meta-analysis model parameters along with 95% credible intervals. Reference level in models 2 to 7 for interactions with Sex is ‘female’, in model 2 for Fitness is ‘condition’, in model 3 for Condition parameters is ‘condition’, in model 4 for Fitness parameters is ‘timing of breeding’, and in models 5-7 the Intercept refers to ‘female’.

| **Model** | **Parameter** | **Posterior mean** | **Lower 95% CI** | **Upper 95%CI** | **Effective sample size** |
| --- | --- | --- | --- | --- | --- |
|
|  |
| **1: Sex**  (Condition & Fitness combined) | Female | 0.1885 | 0.1147 | 0.2776 | 5000 |
| Male | 0.2180 | 0.1119 | 0.3320 | 5000 |
| Publication year (centred mean) | -0.0062 | -0.0096 | -0.0028 | 4608 |
| Phylogeny variance (female) | 0.0059 | 2.45x10-10 | 0.0165 | 5000 |
| Phylogeny variance (male) | 0.0132 | 2.25x10-10 | 0.0312 | 4772 |
| Phylogeny covariance (fem/male) | 0.0040 | -0.0028 | 0.0144 | 4279 |
| Species ID variance (female) | 0.0047 | 3.30x10-8 | 0.0123 | 5000 |
| Species ID variance (male) | 0.0034 | 4.26x10-11 | 0.0120 | 4746 |
| Species ID covariance (fem/male) | 0.0011 | -0.0025 | 0.0060 | 5000 |
| Residual variance (female) | 0.0662 | 0.0551 | 0.0775 | 5000 |
| Residual variance (male) | 0.0532 | 0.0429 | 0.0647 | 5000 |
| Residual covariance (fem/male) | 0.0149 | 0.0040 | 0.0258 | 5000 |
| **2: Sex\*Condition or Fitness** | Female | 0.2232 | 0.1484 | 0.3021 | 5000 |
| Male | 0.2550 | 0.1558 | 0.3738 | 5000 |
| Fitness | -0.0864 | -0.1474 | -0.0240 | 5433 |
| Sex:Fitness | -0.0135 | -0.0972 | 0.0709 | 5000 |
| Publication year (centred mean) | -0.0072 | -0.0108 | -0.0039 | 5000 |
| Phylogeny variance (female) | 0.0042 | 4.29x10-10 | 0.0134 | 4547 |
| Phylogeny variance (male) | 0.0117 | 2.64x10-9 | 0.0290 | 4585 |
| Phylogeny covariance (fem/male) | 0.0022 | -0.0035 | 0.0106 | 4126 |
| Species ID variance (female) | 0.0051 | 1.94x10-10 | 0.0126 | 5000 |
| Species ID variance (male) | 0.0039 | 3.06x10-11 | 0.0130 | 4503 |
| Species ID covariance (fem/male) | 0.0010 | -0.0028 | 0.0060 | 4798 |
| Residual variance (female) | 0.0652 | 0.0542 | 0.0766 | 4796 |
| Residual variance (male) | 0.0522 | 0.0421 | 0.0628 | 4681 |
| Residual covariance (fem/male) | 0.0137 | 0.0033 | 0.0243 | 5000 |
| **3: Sex\*Condition parameters** | Female | 0.1804 | 0.0911 | 0.2848 | 4804 |
| Male | 0.2402 | 0.0843 | 0.4032 | 5000 |
| Body size | 0.0480 | -0.0629 | 0.1524 | 5000 |
| Immunity | 0.0064 | -0.1473 | 0.1604 | 4753 |
| Stress | -0.0226 | -0.1713 | 0.1263 | 5000 |
| Environment | 0.1233 | -0.0767 | 0.3097 | 5000 |
| Parasites | 0.0901 | -0.1388 | 0.3063 | 5000 |
| Sex:Body size | -0.0915 | -0.2580 | 0.0634 | 5000 |
| Sex:Immunity | -0.0248 | -0.2418 | 0.1836 | 4773 |
| Sex:Stress | 0.1533 | -0.0690 | 0.3766 | 5000 |
| Sex:Environment | -0.0454 | -0.2963 | 0.1988 | 5217 |
| Sex:Parasites | -0.1282 | -0.4363 | 0.1602 | 5000 |
| Publication year (centred mean) | -0.0036 | -0.0108 | 0.0035 | 5000 |
| Phylogeny variance (female) | 0.0039 | 1.01x10-10 | 0.0159 | 5000 |
| Phylogeny variance (male) | 0.0200 | 2.87x10-10 | 0.0616 | 4346 |
| Phylogeny covariance (fem/male) | 0.0023 | -0.0063 | 0.0155 | 4715 |
| Species ID variance (female) | 0.0060 | 4.37x10-9 | 0.0181 | 5000 |
| Species ID variance (male) | 0.0133 | 3.07x10-12 | 0.0362 | 4499 |
| Species ID covariance (fem/male) | 0.0033 | -0.0044 | 0.0139 | 4511 |
| Residual variance (female) | 0.0628 | 0.0460 | 0.0800 | 5000 |
| Residual variance (male) | 0.0539 | 0.0401 | 0.0693 | 5000 |
| Residual covariance (fem/male) | 0.0031 | -0.0087 | 0.0148 | 5000 |
| **4: Sex\*Fitness parameters** | Female | 0.1437 | -0.0044 | 0.2869 | 5182 |
| Male | 0.1701 | 0.0324 | 0.3169 | 5000 |
| Reproductive success | 0.0375 | -0.0768 | 0.1611 | 5315 |
| Offspring quality/condition | 0.0722 | -0.0700 | 0.2187 | 5000 |
| Parental quality | -0.0712 | -0.2279 | 0.0767 | 5000 |
| Survival | -0.1380 | -0.3007 | 0.0257 | 4745 |
| Sex:Reproductive success | -0.0479 | -0.2156 | 0.1122 | 5000 |
| Sex:Offspring quality/condition | -0.0912 | -0.2941 | 0.1065 | 6587 |
| Sex:Parental quality | 0.0105 | -0.1997 | 0.2031 | 5483 |
| Sex:Survival | 0.0079 | -0.2143 | 0.2457 | 4794 |
| Publication year (centred mean) | -0.0088 | -0.0126 | -0.0045 | 5000 |
| Phylogeny variance (female) | 0.0085 | 3.17 x10-9 | 0.0295 | 5000 |
| Phylogeny variance (male) | 0.0057 | 2.51x10-12 | 0.0201 | 5000 |
| Phylogeny covariance (fem/male) | 0.0009 | -0.0052 | 0.0089 | 5302 |
| Species ID variance (female) | 0.0069 | 9.26x10-9 | 0.0181 | 5000 |
| Species ID variance (male) | 0.0024 | 1.63x10-12 | 0.0095 | 5000 |
| Species ID covariance (fem/male) | 3.97x10-5 | -0.0041 | 0.0040 | 4765 |
| Residual variance (female) | 0.0761 | 0.0613 | 0.0937 | 4515 |
| Residual variance (male) | 0.0661 | 0.0499 | 0.0827 | 5000 |
| Residual covariance (fem/male) | 0.0159 | 0.0014 | 0.0336 | 5000 |
| **5: Sex\*Sexual dimorphism** (Condition data only) Removing outliers | Female | 0.2020 | 0.0928 | 0.3245 | 5000 |
| Male | 0.1478 | 0.0236 | 0.2772 | 5000 |
| Dimorphism | -0.0132 | -0.0759 | 0.0428 | 5000 |
| Sex:Dimorphism | 0.0287 | -0.0475 | 0.1072 | 5000 |
| Publication year (centred mean) | -0.0106 | -0.0219 | 0.0005 | 5000 |
| Phylogeny variance (female) | 0.0072 | 1.60x10-10 | 0.0285 | 5000 |
| Phylogeny variance (male) | 0.0107 | 2.55x10-10 | 0.0372 | 5325 |
| Phylogeny covariance (fem/male) | 0.0017 | -0.0060 | 0.0126 | 5000 |
| Species ID variance (female) | 0.0050 | 1.31x10-9 | 0.0195 | 5000 |
| Species ID variance (male) | 0.0072 | 1.23x10-9 | 0.0240 | 4549 |
| Species ID covariance (fem/male) | 0.0009 | -0.0052 | 0.0086 | 5000 |
| Residual variance (female) | 0.0853 | 0.0574 | 0.1156 | 5000 |
| Residual variance (male) | 0.0702 | 0.0470 | 0.0939 | 5662 |
| Residual covariance (fem/male) | 0.0072 | -0.0123 | 0.0274 | 5000 |
| **6: Sex\*Sexual dimorphism** (Fitness data only) | Female | 0.1269 | -0.0070 | 0.2713 | 5000 |
| Male | 0.1358 | -0.0222 | 0.2761 | 5000 |
| Dimorphism | 0.0012 | -0.0573 | 0.0596 | 5000 |
| Sex:Dimorphism | -0.0222 | -0.0944 | 0.0545 | 5000 |
| Publication year (centred mean) | -0.0074 | -0.0172 | 0.0012 | 5592 |
| Phylogeny variance (female) | 0.0095 | 2.40x10-9 | 0.0363 | 4856 |
| Phylogeny variance (male) | 0.0097 | 3.61x10-9 | 0.0355 | 5000 |
| Phylogeny covariance (fem/male) | 0.0014 | -0.0077 | 0.0130 | 4611 |
| Species ID variance (female) | 0.0039 | 1.26x10-10 | 0.0154 | 5000 |
| Species ID variance (male) | 0.0046 | 1.43x10-9 | 0.0171 | 4559 |
| Species ID covariance (fem/male) | 0.0002 | -0.0040 | 0.0048 | 5886 |
| Residual variance (female) | 0.0725 | 0.0488 | 0.0973 | 5000 |
| Residual variance (male) | 0.0737 | 0.0501 | 0.1023 | 5000 |
| Residual covariance (fem/male) | 0.0192 | 0.0013 | 0.0381 | 5000 |
| **7: Sex\*Sexual dimorphism** (Condition data only) Without removing outliers | Female | 0.1936 | 0.0858 | 0.3116 | 4793 |
| Male | 0.1344 | 0.0051 | 0.2796 | 5243 |
| Dimorphism | 0.0037 | -0.0306 | 0.0392 | 5000 |
| Sex:Dimorphism | 0.0454 | 0.0003 | 0.0912 | 5000 |
| Publication year (centred mean) | -0.0119 | -0.0225 | 0.0002 | 5000 |
| Phylogeny variance (female) | 0.0067 | 2.53x10-10 | 0.0266 | 5000 |
| Phylogeny variance (male) | 0.0118 | 5.43x10-9 | 0.0399 | 5000 |
| Phylogeny covariance (fem/male) | 0.0021 | -0.0059 | 0.0145 | 4769 |
| Species ID variance (female) | 0.0050 | 3.48x10-10 | 0.0198 | 5000 |
| Species ID variance (male) | 0.0079 | 1.45x10-9 | 0.0265 | 4960 |
| Species ID covariance (fem/male) | 0.0012 | -0.0043 | 0.0092 | 4519 |
| Residual variance (female) | 0.0873 | 0.0595 | 0.1194 | 5000 |
| Residual variance (male) | 0.0698 | 0.0480 | 0.0959 | 4676 |
| Residual covariance (fem/male) | 0.0084 | -0.0107 | 0.0280 | 5000 |

**Table S2.** Summary of parameters along with 95% credible intervals used to construct Figure 2.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Model** | **Parameter** | **Sex (*n*)** | **Estimate** | **Lower 95% CI** | **Upper 95%CI** |  |
| 1: Sex  (Condition & Fitness combined) | Sex only | F (505) | 0.188 | 0.115 | 0.278 |  |
| M (462) | 0.218 | 0.112 | 0.332 |  |
| 2: Sex\*Condition or Fitness (Condition & Fitness separated) | Condition | F (220) | 0.223 | 0.148 | 0.302 |  |
| M (200) | 0.255 | 0.156 | 0.374 |  |
| Fitness | F (285) | 0.137 | 0.061 | 0.217 |  |
| M (262) | 0.155 | 0.045 | 0.273 |  |
| 3: Sex\*Condition parameters | Body condition | F (74) | 0.180 | 0.091 | 0.285 |  |
| M (72) | 0.240 | 0.084 | 0.403 |  |
| Body size | F (63) | 0.228 | 0.130 | 0.339 |  |
| M (51) | 0.199 | 0.036 | 0.375 |  |
| Immunity | F (30) | 0.187 | 0.042 | 0.351 |  |
| M (28) | 0.224 | 0.040 | 0.432 |  |
| Stress | F (33) | 0.158 | 0.018 | 0.304 |  |
| M (19) | 0.374 | 0.159 | 0.583 |  |
| Environment | F (11) | 0.303 | 0.109 | 0.487 |  |
| M (21) | 0.318 | 0.120 | 0.525 |  |
| Parasites | F (9) | 0.271 | 0.057 | 0.484 |  |
| M (9) | 0.202 | -0.038 | 0.436 |  |
| 4: Sex\*Fitness parameters | Reproductive success | F (123) | 0.181 | 0.076 | 0.315 |  |
| M (121) | 0.160 | 0.057 | 0.285 |  |
| Offspring quality/condition | F (55) | 0.217 | 0.079 | 0.360 |  |
| M (49) | 0.152 | 0.008 | 0.291 |  |
| Parental quality | F (44) | 0.072 | -0.075 | 0.228 |  |
| M (41) | 0.112 | -0.031 | 0.275 |  |
| Timing of breeding | F (39) | 0.144 | -0.004 | 0.287 |  |
| M (33) | 0.170 | 0.032 | 0.317 |  |
| Survival | F (24) | 0.008 | -0.151 | 0.180 |  |
| M (18) | 0.042 | -0.112 | 0.220 |  |

**Table S3.** Summary of an additional general model testing the effect of ‘study type’ (correlational or experimental). Reference level for ‘study type’ is ‘correlational’.

| **Model** | **Parameter** | **Posterior mean** | **Lower 95% CI** | **Upper 95%CI** | **Effective sample size** |
| --- | --- | --- | --- | --- | --- |
|
|  |
| **Sex + Study type**  (Condition & Fitness combined) | Female | 0.1878 | 0.1047 | 0.2719 | 5000 |
| Male | 0.2178 | 0.1097 | 0.3273 | 5000 |
| Study type (experimental) | 0.0226 | -0.0695 | 0.1260 | 5000 |
| Publication year (centred mean) | -0.0062 | -0.0093 | -0.0029 | 5000 |
| Phylogeny variance (female) | 0.0061 | 4.68x10-9 | 0.0167 | 5213 |
| Phylogeny variance (male) | 0.0132 | 4.87x10-8 | 0.0301 | 4347 |
| Phylogeny covariance (fem/male) | 0.0041 | -0.0024 | 0.0141 | 4652 |
| Species ID variance (female) | 0.0047 | 1.14x10-9 | 0.0122 | 4523 |
| Species ID variance (male) | 0.0033 | 1.74x10-10 | 0.0118 | 5000 |
| Species ID covariance (fem/male) | 0.0010 | -0.0026 | 0.0059 | 4510 |
| Residual variance (female) | 0.0662 | 0.0548 | 0.0771 | 5000 |
| Residual variance (male) | 0.0534 | 0.0433 | 0.0645 | 5000 |
| Residual covariance (fem/male) | 0.0150 | 0.0041 | 0.0256 | 5000 |

**Table S4.** Summary of variances per sex transformed into proportions and covariances transformed into correlation coefficients, along with 95% credible intervals.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Model** | **Parameter** | **Variance** | **Lower 95% CI** | **Upper 95%CI** | **Posterior mean (*r*)** | **Lower 95% CI** | **Upper 95%CI** |
| 1: Sex | Phylogeny | F:0.07 M:0.18 | 2.6x10-9 4.5x10-9 | 0.19 0.37 | 0.4527 | -0.3351 | 0.9885 |
| Species ID | F:0.06 M:0.05 | 3.8x10-7 6.2x10-10 | 0.15 0.17 | 0.2143 | -0.6908 | 0.9767 |
| Residual | F:0.86 M:0.77 | 0.73  0.58 | 0.98 0.94 | 0.2502 | 0.0804 | 0.4228 |
| 2: Sex\*Condition or Fitness | Phylogeny | F:0.05 M:0.16 | 6.2x10-9 4.6x10-8 | 0.16 0.36 | 0.3071 | -0.5460 | 0.9941 |
| Species ID | F:0.07 M:0.06 | 2.1x10-9 5.2x10-10 | 0.16 0.19 | 0.1850 | -0.6730 | 0.9670 |
| Residual | F:0.88 M:0.78 | 0.75  0.59 | 0.98 0.94 | 0.2346 | 0.0593 | 0.4026 |
| 3: Sex\*Condition parameters | Phylogeny | F:0.05 M:0.20 | 1.4x10-9 4.1x10-9 | 0.19 0.53 | 0.1882 | -0.7108 | 0.9751 |
| Species ID | F:0.08 M:0.16 | 6.1x10-8 5.6x10-11 | 0.23 0.38 | 0.3246 | -0.5853 | 0.9970 |
| Residual | F:0.87 M:0.64 | 0.69  0.39 | 0.99 0.87 | 0.0528 | -0.1454 | 0.2516 |
| 4: Sex\*Fitness parameters | Phylogeny | F:0.09 M:0.07 | 3.1x10-8 3.1x10-11 | 0.27 0.23 | 0.1467 | -0.7364 | 0.9507 |
| Species ID | F:0.07 M:0.03 | 1.0x10-7 2.4x10-11 | 0.19 0.12 | 0.0338 | -0.7919 | 0.9225 |
| Residual | F:0.84 M:0.90 | 0.66  0.72 | 0.98  0.99 | 0.2228 | -0.0081 | 0.4533 |
| 5: Sex\*Sexual dimorphism (Condition data only)  Removing outliers | Phylogeny | F:0.07 M:0.11 | 1.6x10-9 3.5x10-9 | 0.25 0.34 | 0.1633 | -0.7646 | 0.9597 |
| Species ID | F:0.05 M:0.08 | 1.8x10-8 1.5x10-8 | 0.18 0.25 | 0.1109 | -0.7611 | 0.9658 |
| Residual | F:0.89 M:0.81 | 0.67  0.58 | 0.99  0.99 | 0.0924 | -0.1407 | 0.3443 |
| 6: Sex\*Sexual dimorphism (Fitness data only) | Phylogeny | F:0.10 M:0.10 | 2.3x10-8 2.7x10-8 | 0.34 0.32 | 0.1099 | -0.7714 | 0.9609 |
| Species ID | F:0.04 M:0.05 | 1.4x10-9 1.5x10-8 | 0.16 0.18 | 0.0300 | -0.8585 | 0.8801 |
| Residual | F:0.86 M:0.85 | 0.62  0.62 | 0.99  0.99 | 0.2616 | 0.0358 | 0.4752 |
| 7: Sex\*Sexual dimorphism (Condition data only)  Without removing outliers | Phylogeny | F:0.06 M:0.12 | 2.5x10-9 9.1x10-8 | 0.23 0.36 | 0.1867 | -0.7065 | 0.9933 |
| Species ID | F:0.05 M:0.08 | 3.1x10-9 1.8x10-8 | 0.18 0.26 | 0.1512 | -0.7237 | 0.9859 |
| Residual | F:0.89 M:0.80 | 0.69  0.56 | 0.99  0.99 | 0.1068 | -0.1301 | 0.3446 |

**Table S5.** Publication bias does occur in data for both sexes, however results for Egger’s tests and trim-and-fill analysis suggest that publication bias is relatively small across models, with very few missing samples (*k*) identified and negligible changes in effect size after correction.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Egger's test | | |  | Trim-and-fill method | | | |
| Model | Sex | *t* | *df* | *P* |  | *k* | *Zr* | 95% CI |
| 1: Sex  (Condition & Fitness combined) | F | 0.194 | 503 | 0.846 |  | -2 | -0.012 | -0.036 ‒ 0.011 |
| M | -2.969 | 460 | 0.003 |  | 0 | -0.013 | -0.031 ‒ 0.005 |
| 2: Sex\*Condition or Fitness | F | -0.300 | 503 | 0.764 |  | -2 | -0.011 | -0.035 ‒ 0.012 |
| M | -3.383 | 460 | 0.001 |  | 0 | -0.011 | -0.029 ‒ 0.007 |
| 3: Sex\*Condition parameters | F | 1.996 | 218 | 0.047 |  | -1 | -0.016 | -0.041 ‒ 0.010 |
| M | -5.310 | 198 | <0.0001 |  | 0 | -0.0001 | -0.027 ‒ 0.027 |
| 4: Sex\*Fitness parameters | F | -0.268 | 283 | 0.789 |  | 0 | 0.002 | -0.028 ‒ 0.032 |
| M | 0.119 | 260 | 0.905 |  | 0 | -0.016 | -0.038 ‒ 0.006 |
| 5: Sex\*Sexual Dimorphism (Condition data only) | F | 0.752 | 103 | 0.454 |  | -2 | -0.020 | -0.062 ‒ 0.022 |
| M | -0.143 | 103 | 0.886 |  | 0 | 0.002 | -0.036 ‒ 0.039 |
| 6: Sex\*Sexual Dimorphism (Fitness data only) | F | 0.997 | 107 | 0.321 |  | 0 | -0.010 | -0.048 ‒ 0.027 |
| M | 1.735 | 107 | 0.086 |  | 0 | -0.015 | -0.048 ‒ 0.019 |

Egger’s test results are shown for sex-specific data sets per model (*t* values, degrees of freedom and *P* values), estimated number of missing samples with the sign indicating the direction of bias correction (*k*), mean effect size estimate after correction (*Zr*) together with its 95% credible interval.

**List of full references (Figure 1)**

[1] Quinard, A., Cézilly, F., Motreuil, S., Rossi, J-M. & Biard, C. Reduced sexual dichromatism, mutual ornamentation, and individual quality in the monogamous zenaida dove, *Zenaida aurita*. *J. Avian Biol.* **48**, 489–501 (2017).

[2] Martínez, J. E., Calvo, J. F., Jiménez-Franco, M. V., Zuberogoitia, I. & López-López, P. Colour morph does not predict brood size in the booted eagle. *Ornis Fenn.* **93**, 130–136 (2016).

[3] Penteriani, V., Alonso-Alvarez, C., del Mar Delgado, M., Sergio, F. & Ferrer M. Brightness variability in the white badge of the eagle owl *Bubo bubo*. *J. Avian Biol.* **37**, 110–116 (2006).

[4] Avilés, J. M. & Parejo, D. Covariation between bill colouration and fitness components in a nocturnal bird. *J. Avian Biol.* **43**, 565–570 (2012).

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