Supplemental Information: The heritability of behavior: a meta-analysis

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Author contribution statement: TS and NAD jointly designed the project. NAD conducted analyses. All authors collected data and contributed to the writing of the manuscript.

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Supplemental Information

Table S1. Magnitudes of variation (i.e. heterogeneity) due to article ID, phylogenetic structure, sampling error, and that unattributable to any modeled source (residual). *I*2 is the proportion of total variation not attributable to sampling error. Based on reduced sample sizes of either Nreported or 100, whichever was smaller.

|  |  |
| --- | --- |
| Source of Variation | % |
| Article | 43.68 |
| Phylogeny | 0 |
| Residual | 54.66 |
| Sampling Error | 1.68 |
| *I*2 | 98.34 |

Table S2. Magnitudes of variation (i.e. heterogeneity) due to phylogenetic structure, sampling error, and that unattributable to any modeled source (residual). *I*2 is the proportion of total variation not attributable to sampling error. Less than half of the variation attributable to article ID (Table 3) is attributable to phylogeny when article ID is excluded. While some degree of conflation between phylogeny and article ID is inevitable, that most ends up as residual variation when article ID is omitted suggests that the lack of phylogenetic signature reported in the main text is not due this conflation.

|  |  |
| --- | --- |
| Source of Variation | % |
| Phylogeny | 17.9 |
| Residual | 81.48 |
| Sampling Error | 0.60 |
| *I*2 | 99.40 |

Table S3. Significance test results for the inclusion of particular moderators when sample size is included in the fitting of the model as either Nreported or 100, whichever was smaller.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Moderator | Log-Likelihood | *χ*2 | df | test df's | p–value |
| **Endo- vs. Ectotherm** | **-256.48** | **4.16** | **17** | **1** | **0.04** |
| Invertebrate vs. Vertebrate | -255.18 | 2.76 | 17 | 1 | 0.10 |
| **Behavioral Category** | **-266.44** | **24.08** | **8** | **10** | **0.007** |
| Semi- vs. Domestic vs. Wild | -256.40 | 4.00 | 16 | 2 | 0.14 |
| Field vs. Lab | -254.75 | 0.70 | 17 | 1 | 0.40 |
| Full Model | -254.40 |  | 18 |  |  |