Study title: Effects of parental care on the magnitude of inbreeding depression: a meta-analysis in fishes

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Study summary: This study is a meta-analysis testing whether variation in the magnitude of inbreeding depression is related to among-species differences in parental care in fishes. We synthesised 536 effect sizes across 56 studies and 18 species, spanning 47 years of research.

Author contributions: CP carried out the majority of the data extraction and code writing with guidance from NP.

Versions of packages and software used:

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> sessionInfo()
R version 4.3.1 (2023-06-16 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 11 x64 (build 22621)

Matrix products: default

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] metameta_0.2       MCMCglmm_2.35      coda_0.19-4        orchaRd_2.0
 [5] emmeans_1.8.8      R.rsp_0.45.0       patchwork_1.1.3    lubridate_1.9.2
 [9] forcats_1.0.0      stringr_1.5.0      dplyr_1.1.2        purrr_1.0.2
[13] readr_2.1.4        tidyr_1.3.0        tibble_3.2.1       tidyverse_2.0.0
[17] devtools_2.4.5     usethis_2.2.2      lme4_1.1-34        ape_5.7-1
[21] rotl_3.1.0         ggplot2_3.4.3      metafor_4.2-0      numDeriv_2016.8-1.1
[25] metadat_1.2-0      Matrix_1.5-4.1

loaded via a namespace (and not attached):
 [1] remotes_2.4.2.1    rlang_1.1.1        magrittr_2.0.3     compiler_4.3.1
 [5] callr_3.7.3        vctrs_0.6.3        profvis_0.3.8      pkgconfig_2.0.3
 [9] crayon_1.5.2       fastmap_1.1.1      ellipsis_0.3.2     labeling_0.4.2
[13] utf8_1.2.3         promises_1.2.1     sessioninfo_1.2.2  tzdb_0.4.0
[17] ggbeeswarm_0.7.2   ps_1.7.5           nloptr_2.0.3       cachem_1.0.8
[21] jsonlite_1.8.7     progress_1.2.2     later_1.3.1        parallel_4.3.1
[25] prettyunits_1.1.1  R6_2.5.1           stringi_1.7.12     boot_1.3-28.1
[29] pkgload_1.3.2.1    estimability_1.4.1 Rcpp_1.0.11        pacman_0.5.1
[33] R.utils_2.12.2     httpuv_1.6.11      rentrez_1.2.3      splines_4.3.1
[37] R.cache_0.16.0     timechange_0.2.0   tidyselect_1.2.0   rstudioapi_0.15.0
[41] miniUI_0.1.1.1     curl_5.0.2         processx_3.8.2     pkgbuild_1.4.2
[45] lattice_0.21-8     shiny_1.7.5        withr_2.5.0        desc_1.4.2
[49] urlchecker_1.0.1   pillar_1.9.0       tensorA_0.36.2     generics_0.1.3
[53] rprojroot_2.0.3    mathjaxr_1.6-0     hms_1.1.3          munsell_0.5.0
[57] scales_1.2.1       minqa_1.2.5        xtable_1.8-4       rncl_0.8.7
```

[61] glue_1.6.2 cubature_2.1.0 tools_4.3.1 fs_1.6.3
[65] mvtnorm_1.2-3 XML_3.99-0.14 grid_4.3.1 colorspace_2.1-0
[69] nlme_3.1-162 beeswarm_0.4.0 vipor_0.4.5 latex2exp_0.9.6
[73] cli_3.6.1 fansi_1.0.4 corpcor_1.6.10 gtable_0.3.4
[77] R.methodsS3_1.8.2 digest_0.6.33 farver_2.1.1 htmlwidgets_1.6.2
[81] memoise_2.0.1 htmltools_0.5.6 R.oo_1.25.0 lifecycle_1.0.3
[85] httr_1.4.7 mime_0.12 MASS_7.3-60

Information about spreadsheet: Each row represents one effect size. Descriptions for each column heading are provided below.

Paper_ID = numerical ID assigned to each paper included in the dataset

Dvar_ID = unique ID for each individual effect size

First author = first author of the paper from which data were extracted

Year = paper publication year

Study = study identifier, by combining the first author and publication year columns

Genus = genus

Species = species

GENUS_SPECIES and GENUS_SPECIES_corr = combined genus and species columns

Study setting = describes whether the study was conducted in the lab, field, or under semi-natural conditions

F-value = inbreeding coefficient F

Care provided = describes whether offspring received some type of parental care in the study or not

Sex providing care = describes whether offspring received care from the male parent, female parent, or neither parent

Timing of care = describes whether there was prehatching, posthatching, or no care provided

Focal sex = sex of animals that inbreeding depression was measured for

Fitness parameter = type of fitness train that inbreeding depression was measured for

Stress = provides information on whether inbreeding depression was measured under stressful or benign conditions

Life stage = describes whether inbreeding depression was measured at an early life stage or in adulthood

Shared control = provides information on any shared control treatments across different effect sizes

Hedges g = standardised mean differences (Hedges' g effect size)

Hedges g var = variance in the Hedges' g effect size

N total = total sample size for each effect size

Data_source = source of raw data used to calculate effect sizes (e.g. Table 1, Figure 2)

N_oubred = sample size for outbred individuals

Mean_outbred = mean value of fitness trait for outbred individuals

SD_outbred = standard deviation of fitness trait for outbred individuals

N_inbred = sample size for inbred individuals

Mean_inbred = mean value of fitness for inbred individuals

SD_inbred = standard deviation of fitness trait for inbred individuals

In cases where there were no means/SD provided for a fitness trait, we extracted test statistics and then converted these to Hedges' g effect sizes using the appropriate formulas.
Test = type of test statistic (e.g. chi-square, t-test)

Statistic = value of the test statistic