Title: Developmental temperature affects phenotypic means and variability: a meta-analysis of fish data

Authors and affiliations

Rose E. O'Dea[1,2], *Malgorzata Lagisz*[1], *Andrew P. Hendry*[2] & *Shinichi Nakagawa*[1]

[1]Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia

[2]Department of Biology & Redpath Museum, McGill University, Montréal, Québec, H3A 0C4, Canada

Correspondence

Rose E. O'Dea

Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia

Tel: +61 2 9385 8865

Email: rose.eleanor.o.dea@gmail.com

Abstract

Fishes are sensitive to their thermal environment, and face an uncertain future in a warming world. Theoretically, populations in novel environments might express greater levels of phenotypic variability to increase the chance of surviving – and eventually thriving – in the new conditions. Most research on the effect of the early thermal environment in fish species focuses on average phenotypic effects rather than phenotypic variability, but to understand how fishes will respond to rising temperatures we need to consider both the average response of the population, as well as the breadth of individual responses. Here we present the first meta-analysis on the effects of developmental temperature in fishes. Using data from 43 species and over 6,000 individual fish we show that a change in developmental temperature induces a significant change in phenotypic means and variability, but differently depending on whether the temperature is increased or decreased. Decreases in temperature (cool environments) showed a significant decrease in phenotypic means and no change in phenotypic variability. Increases in temperature (warm environments) showed a non-significant increase in phenotypic means, and a significant increase in phenotypic variability. Larger increases in temperature saw grater increases in phenotypic variability, but no increase in the mean phenotypic response. Together, our results suggest that fishes exhibit both directed and stochastic developmental plasticity in response to warming temperatures, which could facilitate or accelerate adaptation to a changing environment.

Keywords

bet hedging; canalization; genetic compensation; non-adaptive plasticity; spreading reaction norms; systematic review

Introduction

Fish populations are threatened by warming temperatures due to climate change. If these threats are realised, then the economic impact will be profound; fisheries represent a multi- billion-dollar industry, and support a large fraction of the human population (Dulvy *et al*. 2003; Sumaila *et al*. 2011). Fishes, like all species, are adapted to survive within a restricted range of temperatures. When temperatures shift beyond this range then populations must either adapt or perish. How can they adapt?

When the temperatures change, a species that was formerly on an adaptive peak might become maladapted (Robertson *et al*. 2013). Plasticity – the expression of different phenotypes when the same genotype is exposed to different environments – could help a population return to an adaptive peak (Ghalambor *et al*. 2007). Temperatures changes that predictably occurred within the ancestral history of a population might induce 'adaptive developmental plasticity' (*sensu* Nettle and Bateson 2015). In this case, the developmental temperature is a cue that triggers a phenotypic change in the direction of the new optimum. But severe or unprecedented temperature changes might merely impose developmental stress. In these stressful conditions plasticity is likely to be maladaptive and push the population mean further from an adaptive peak, so selection should favour a reduction in plasticity (this phenomenon is called 'genetic compensation'; Grether 2005). But so far we have only considered the *mean* population response. If we also consider individual variation (i.e. the range of individual responses) then we envisage a more hopeful alternative, which we depict in Fig. 1.

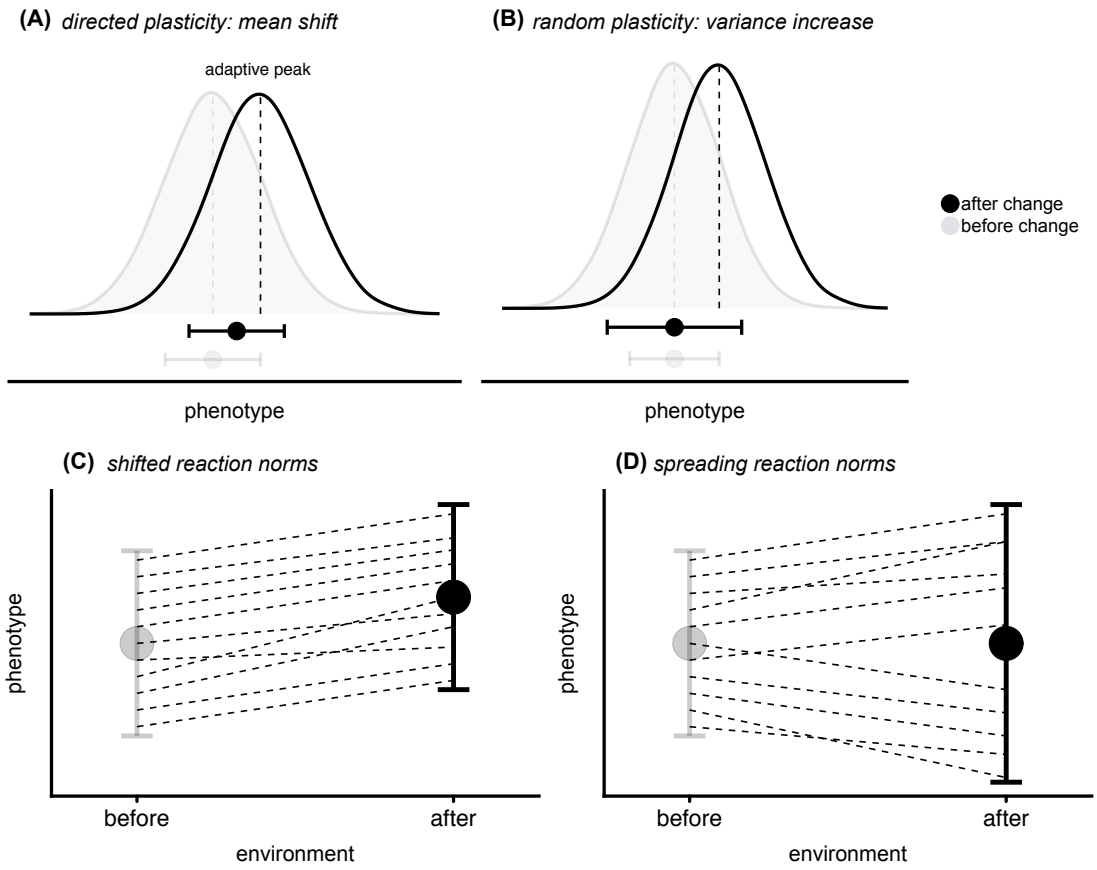

Figure 1

A change in the environment causes a shift in the adaptive landscape, which might prompt a change in the phenotypic mean and/or phenotypic variance. In **A-B**, population phenotypes (points and error bars represent mean ± SD) are shown underneath adaptive landscapes (fitness density curves). The dashed vertical lines represent the optimal phenotypes in each environment. Transparent points and curves represent the ancestral population and adaptive landscape. In **C-D**, the changes in phenotypes shown in **A-B** are depicted as reaction norms. **(A)** Under normal conditions (before the change) the phenotype of a hypothetical population is centred on the adaptive peak. After an environmental change the adaptive landscape shifts, which causes directed plasticity to shift the population mean. In this case the mean has shifted towards the new optimum, i.e. adaptive plasticity. **(B)** An increase in phenotypic variance in response to environmental change produces more individuals who are closer to the new phenotypic optimum despite no shift in the mean trait value. (**C**) The average phenotype of the population is changed due to a directional shift in the intercept of reaction norms. (**D**) Phenotypic variability is increased in the new environment due to stochastic changes in the intercept and slope of reaction norms, which cause spreading (or fanning) of the reaction norms.

A rapid change in temperature could induce greater levels of phenotypic variation within a population, which could facilitate or accelerate adaptation to a new environment (O'Dea *et al*. 2016). Ordinarily, when a population is well-adapted to its environment, we expect high 'adaptive precision' (*sensu* Hansen *et al*. 2006) so that the genotype reliably produces a particular phenotype (reducing variance around an adaptive peak). But imprecision could be a good strategy in a changing environment, to increase the chance of stumbling upon an adaptive phenotype (Hansen *et al*. 2006). Populations with greater phenotypic variance might return to an adaptive peak more quickly after an environmental perturbation, as they are more likely to contain individuals who move closer to a new phenotypic optimum. These lucky individuals could allow the population to persist in a novel environment, and provide the material for selection to act upon (Ghalambor *et al*. 2007). This scenario is reminiscent of 'bet-hedging' – if it is unclear which single phenotype will maximise fitness in the next generation, betting on a wide range of phenotypes might pay off (Starrfelt and Kokko 2012; Franch-Gras *et al*. 2017). Potentially, variability itself could be heritable, which might allow these variants to keep up with rapidly changing environments via 'heritable bet-hedging' (Pal and Miklos 1999; O'Dea *et al*. 2016).

Novel environments could increase phenotypic variance by exposing previously hidden (cryptic) genetic variation, or by inducing new epigenetic changes. Under normal conditions the genotype slowly accumulates genetic changes that are not expressed. When the temperature changes, some of this variation can be revealed and exposed to selection (McGuigan and Sgrò 2009; Paaby and Rockman 2014; Wood and Brodie 2015). Any variants with a selective advantage could be preferentially inherited, and spread through the population. Alternatively, a change in temperature

can induce changes in gene expression via heritable epigenetic modifications. While these changes will only be heritable in the short term (if at all), they may still increase the likelihood that the phenotypes become genetically encoded, via genetic assimilation (Pal and Miklos 1999; Crispo 2007). Despite a theoretical basis behind the adaptive potential of increased phenotypic variance (Ghalambor *et al*. 2007), the effect of temperature on phenotypic variance is largely unexplored in empirical studies.

Fishes should reveal whether temperature changes do increase phenotypic variance because, as ectotherms, they are particularly sensitive to their external temperature (Neuheimer *et al*. 2011). Previous studies have shown the phenotypic average of many phenotypic traits is affected by the developmental environment (i.e. there is developmental plasticity) (Jonsson and Jonsson 2014). However, while phenotypic variance is at the heart of evolutionary theory, statistical analyses have historically focussed on testing for differences in phenotypic means. Few, if any, studies explicitly test whether the developmental temperature changes phenotypic variance, but the statistical tools now exist to approach this question using a meta-analysis.

Here we present the first meta-analysis on the phenotypic effects of developmental temperature in fish, and the first to test for the effects of developmental temperature on phenotypic variability in any species. We test 10 a-priori predictions, which we registered before data exploration and analysis (O'Dea et al. 2018). We predicted that: (1) Fish reared in warmer temperatures will have greater phenotypic variability than fish experiencing control temperatures, controlling for any effect of temperature on the phenotypic mean (Fig. 1C). (2) Changing the developmental temperature will

impact the mean of traits, according to the studies reviewed in Jonsson and Jonsson (2014). Warm temperatures will increase growth rate and metabolic rate, but reduce size, muscle fibre number, and heart volume (c.f. Hesse's rule; Müller *et al*. 2014). (3) Cool temperature treatments will cause differences in phenotypic means and variability that are similar in magnitude to warm temperature treatments, but with the same direction in variability and opposing directions in means. This prediction assumes that the developmental temperature and optimal phenotypic mean are linearly correlated, and fishes have evolved adaptive developmental plasticity. (4) Larger differences between control and treatment temperature will result in larger differences in phenotypic means and variability. (5) Longer treatment durations will cause a larger difference in phenotypic means and variability. (6) An earlier start in treatment will cause larger differences in phenotypic means and variability. (7) A permanent treatment will have a larger effect on phenotypic means and variability than a transient treatment. (8) Traits with more variation in the control temperature will show a larger plastic mean response to the treatment temperature. (9) Experimental populations with greater amounts of genetic diversity – as measured by the numbers of fish who contributed sperm or eggs to the experimental population – will show more phenotypic variability, and respond more to temperature treatments. (10) Temperature treatments that approach or exceed the optimal thermal limits of the species will elicit larger phenotypic effects than temperature treatments within the normal thermal range.

Methods

Availability of data, code, and materials

Data, analysis code, and list of screened studies is available to download from https://osf.io/e2tyw/ (O'Dea *et al*. 2018B).

Finding data

Protocol and registration

We reported details of a systematic meta-analysis following the PRISMA guidelines (Preferred Reporting Items for Systematic Reviews and Meta-Analyses; Moher *et al*. 2009). We registered our study protocol prior to data exploration and analysis. This registration includes details of our a-priori hypotheses, search methods, and planned analyses, and can be viewed on the Open Science Framework (osf.io/8ymh9; O'Dea *et al*. 2018A).

Eligibility criteria

Study Design

We included experimental studies that reared fish eggs or newly hatched fish embryos under at least two temperature conditions: (1) normal temperature (control treatment; defined below under *Data collection process*) and (2) warmer than normal temperature (warm treatment). If data were available for a cool temperature treatment, in addition to the warm treatment, we extracted those data too. Those data allowed us to test whether any phenotypic differences were simply caused by a temperature change, or whether the direction of the temperature changes mattered. When data on multiple temperature treatments were presented at increasing temperature differences from the control, we took each control-treatment pairwise comparison. We excluded

treatments that caused survival lower than 10%, so that we were testing for the effects of viable temperature changes, not extreme developmental stress. The cut-off value of 10% was chosen because all studies with very low survival fell below this value. The temperature treatments needed to commence on or before the day of hatching, and the treatments needed to be simultaneous (i.e. families or groups split between treatments; between-subject design). We included studies where the treatment was maintained for the duration of the experiment, and also studies where fish were brought back to a common, control temperature before being measured.

Phenotypic measurements

Studies needed to report means, sample sizes, and variance or a measure of dispersion (standard deviations, standard errors, interquartile ranges, or coefficient of variations) for ratio-scale phenotypic traits (i.e. traits measured on a continuous scale with a lower-bound at zero). Where sample sizes or variance were missing, we attempted to contact authors for this information. All contacted authors (n = 8) were asked if they could provide additional data (published or unpublished) that could be used in our meta-analysis. Five authors replied to requests for data, and two provided data used in analysis. We excluded proportion (binary) data (e.g., sex ratio), because these types of traits do not measure variance, and measurements taken before the day of hatching (e.g., egg mass). The minimum sample size for inclusion was three fish per treatment group. Genetic and molecular data were outside the scope of this meta-analysis.

Information sources

Search

We performed a systematic search using the Scopus and Web of Science online databases on 8th November 2017, removed duplicate results, and obtained 1,316

studies for screening. Both databases were accessed through the McGill Library subscription. The exact search strings were:

Scopus: TITLE-ABS-KEY ("*fish*" OR "bass" OR "carp" OR "char" OR "cod" OR "salmon*" OR "sole" OR "tetra" OR "*trout") AND TITLE-ABS-KEY ("high* temperature*" OR "elevated temperature*" OR "high* water temperature*" OR "elevated water temperature*" OR "rearing temperature*" OR "effects of temperature*" OR "temperature challenge*" OR "thermal stress*" OR "embr* temper*")

AND TITLE-ABS-KEY ("rear*" OR "incubat*" OR "developmental temperature*") AND LANGUAGE (english) AND NOT SRCTITLE ("Japanese Edition")

AND NOT TITLE-ABS-KEY ("cryo*" OR "triploidy" OR "jellyfish")

AND (LIMIT-TO (SUBJAREA , "AGRI") OR LIMIT-TO (SUBJAREA , "BIOC") OR LIMIT-TO (SUBJAREA , "ENVI") OR LIMIT-TO (SUBJAREA , "MEDI") OR LIMIT-TO (SUBJAREA , "VETE") OR LIMIT-TO (SUBJAREA , "IMMU"))

Web of Science: (TS=("*fish*" OR "bass" OR "carp" OR "char" OR "cod" OR "salmon*" OR "sole" OR "tetra" OR "*trout") AND TS=("high* temperature*" OR "elevated temperature*" OR "high* water temperature*" OR "elevated water temperature*" OR "rearing temperature*" OR "effects of temperature*" OR "temperature challenge*" OR "thermal stress*" OR "embr* temper*") AND TS=("rear*" OR "incubat*" OR "developmental temperature*") NOT SO=("Japanese Edition") NOT TS= ("cryo*" OR "triploidy" OR "jellyfish")) AND (SU=(Agriculture OR Behavioral Sciences OR Biochemistry & Molecular Biology OR Biodiversity & Conservation OR Developmental Biology OR Endocrinology & Metabolism OR Environmental Sciences & Ecology OR Evolutionary Biology OR Fisheries OR

Genetics & Heredity OR Marine & Freshwater Biology OR Reproductive Biology OR Research & Experimental Medicine OR Veterinary Sciences OR Zoology))

The first term in our search string – "*fish*" OR "bass" OR "carp" OR "char" OR "cod" OR "salmon*" OR "sole" OR "tetra" OR "*trout" – was designed to include studies on fish that do not necessarily mention fish in the title, abstract or keywords. To decide on the fish names to include, we compiled a list of the most common fish names from the "list of common fish names" page on Wikipedia. We then performed our search with the individual addition of each of these names, and recorded the number of hits. For the names that added >10 hits, we downloaded the titles of these papers, and scanned them to see which were suitable. We excluded names that generated many hits for studies that were not on fish, such as "ray".

In addition, on 31st January 2018 we performed a backward and forward search to find the studies cited in, and studies that subsequently cited, Jonsson & Jonsson 2014. This additional search yielded 294 results. All search results can be downloaded from osf.io/e2tyw.

Study selection

The exact numbers of screened and included studies are shown in Fig. S1, and the list of included studies is presented in Table S1.

We used Rayyan software to screen titles and abstracts (Ouzzani *et al*. 2016).

Three people (REO, ML, and SN) screened the abstracts, using a decision tree (Fig. S2). We had a partial overlap of decisions (36% abstracts screened by more than one person, among which 24% of abstracts had conflicting decisions). Conflicting decisions were discussed and resolved.

Nearly 85% of the 1610 abstracts were excluded after screening.

We performed full-text screening for the remaining 247 papers included after abstract screening, from which 62 papers were included for data extraction. The full list of screened studies is available from osf.io/e2tyw.

Extracting data

Data collection process

Data were extracted from text, tables, or figures. To extract data from figures we used the *metaDigitse* package (v.1.0; Pick *et al*.) in *R* (v. 3.4.3; R Development Core Team 2018). All data were extracted by one author (REO), but to verify these extractions half of the data (50% of papers) were checked by other authors. We extracted data as control-treatment pairwise comparisons. For laboratory fish strains, the control temperature was taken as the usual rearing conditions for the system. For wild-caught fish, the temperature used as control was either specified in the paper, or was inferred from other studies on the same species. The data were excluded if the 'control' temperature was outside the reported optimal temperature range for the species, as reported from the websites Fishbase (Froese and Pauly 2000) and Animal Diversity Web (University of Michigan Museum of Zoology 2018). Each pairwise comparison was given a unique ID (unit of analysis), a group ID (the group of eggs that had been split between temperatures), a paper ID (the paper reporting the data), and a species ID (the species that was measured). To minimise errors, data were entered into a relational database, built using Filemaker Pro software (v. 12). Data exported from this software are available from osf.io/e2tyw, and a copy of the relational database is available on request from REO.

Data items

For each pairwise comparison, we extracted information about the type, magnitude, and length of the temperature treatment. Phenotypic traits were divided into 11 fine categories, which we grouped into four broad categories: (1) behaviour (behaviour); (2) life-history (growth); (3) morphology (bone number, condition, morphology, scale number, size); and (4) physiology (heart, metabolism, muscle fibre, swim performance). In addition to recording information about the natural temperature range of the fish species represented in the dataset, we also extracted life-history information using the websites Fishbase (Froese and Pauly 2000) and Animal Diversity Web (University of Michigan Museum of Zoology 2018). For the full list of moderator variables, see Table S2.

Analysing data

Effect sizes

To test for phenotypic differences between a treatment and a control group of fish, we calculated two effect sizes for each pairwise comparison, along with their associated sampling variance: the log response ratio (*lnRR*; Hedges *et al*. 1999) and the log coefficient of variation ratio (*lnCVR*; Nakagawa *et al*. 2015). To test for mean phenotypic differences we used *lnRR*, which is the natural logarithm of the ratio between the mean phenotype in the treatment and control groups. To test for differences in phenotypic variance we used *lnCVR*, where the ratio represents the difference between the coefficients of variation (i.e. standard deviations divided by means) for the treatment and control. We used *lnCVR* because, as expected, our data showed a strong positive correlation between mean and variance. We calculated each effect size in *R*, using the *escalc* function in the *metafor* package (v. 2.1-0;

Viechtbauer 2010). For both logged ratios we specified the treatment group as the numerator and the control group as the denominator, so that positive values represented a trait value increase in the treatment, and negative values represented a trait value decrease in the treatment.

In addition to calculating the phenotypic differences between the treatment and control groups directly, we also estimated them from random-slope meta-regression models. This involved modelling logged standard deviations directly while controlling for corresponding logged mean values (*lnSD*; Raudenbush and Bryk 1987). This is an alternative method that has greater statistical power to test for differences in variability between a control and treatment (c.f. Nakagawa *et al*. 2015). More details are given below under *Sensitivity analyses*.

Meta-analysis

We fit meta-analytic and meta-regression multilevel linear mixed-effects models, using the *rma.mv* function in the *metafor* package (v. 2.1-0; Viechtbauer 2010) in *R* (v. 3.5.1; R Development Core Team 2008), specifying the Nelder-Mead method of optimization. Our data contained multiple levels and different types of non-independence (Noble *et al*. 2017). We partially accounted for this non-independence in two main ways: with random-effects, and with sampling variance-covariance matrices.

To decide on the random-effects structure we compared null models, which were run using the maximum likelihood method, with combinations of 5 random effects: unit ID, paper ID, group ID, species, and phylogeny (modelled with a phylogenetic relatedness correlation matrix; to generate the phylogeny (shown in Fig. 2) we searched for species names in the Open Tree Taxonomy (Hinchliff *et al*. 2015), using the *tnrs_match_names* function in the *R* package *rotl* (v. 3.0.4; Michonneau *et al*.

2016). We computed branch lengths using the default settings of the *compute.brlen* function in the *R* package *ape* (v. 5.1; Paradis and Schliep 2018)). The data were structured so that group ID and paper ID were roughly equivalent (as few papers presented data for multiple groups of fish), so only one of these random effects could be fit at a time. Subsequent model selection was based on comparing the model's variance components and AIC values, which are shown in Table S3. We chose a model with group ID and unit ID as random effects. Here the variance component for group ID represents between-group variance, and the variance component for unit ID represents residual (within-group) variance.

We specified sampling variance as variance-covariance matrices, with the sampling variance for each effect size on the diagonal, and the covariance between these measures as off-diagonal elements at appropriate locations. We ran two types of models: 'conservative', and 'non-conservative'. The conservative model assumed a 0.5 correlation between the effect size sample variances with the same group ID. The 'non-conservative' model assumed no correlation (i.e. independent sample variances). These two approaches yielded qualitatively similar results; here we present results from the non-conservative models, but the results for conservative models are presented in the SI.

Meta-regression

We estimated the amount of heterogeneity in our dataset (I^2_{total}) for the multilevel meta-analytic models, using the method described by Viechtbauer 2018. Most meta-analyses in ecology and evolution find high levels of heterogeneity (Senior *et al*. 2016), and ours were no exception (87% and ~100% for *lnRR* and *lnCVR* meta-analytic models, respectively). We therefore turned to meta-regression models to both explain some of this heterogeneity (the between-study variance and within-study

variance), and test our a-priori predictions. The 'full model' included all significant and marginally non-significant (i.e. p value <0.1) predictors, after first checking for multicollinearity between the predictors.

Transformations

All regression coefficients for continuous moderator variables were estimated at the average values of those predictors, by mean-centering continuous inputs (i.e. subtracting the means from each value of the input variable). Where both the type of treatment (cool or warm) and a continuous variable were fit in the same model, the continuous variable was mean-centered separately for each treatment type (Nakagawa *et al*. 2017). In addition, the amount of variation expressed by fish in the control group (*lnCV*) was *z*-scaled to be expressed in standard deviation units.

Sensitivity analysis

To determine the robustness of our results, we performed a number of sensitivity analyses.

(i) Bayesian meta-analysis

We re-ran all *lnCVR* and *lnRR* models with an alternative Bayesian approach, using the *MCMCglmm* package (v. 2.25; Hadfield 2010). We used a parameter expanded prior ($V = 1$, $nu = 0.002$, $alpha.mu = 0$, $alpha.V = 1000$) for the random effect of group ID and fixed the sampling variance for each effect size using an inverse-Wishart prior ($V = 1$, $fix = 1$). All MCMC chains were run for 100,000 iterations, with a 10,000 burn and 100 thinning interval, and we visually checked that these chains were mixing well. All results were very similar to those produced using *metafor*, and they are available in the SI.

(ii) lnSD instead of lnCVR

We used an alternative method to test for differences in variability between the control and treatment groups, where the logged standard deviation (*lnSD*) for each group of fish was the response variable. To account for the mean-variance relationship the logged mean was included as a fixed effect. We tested for the effect of the treatment by including the treatment factor (either 'control' or 'treatment') as a fixed effect. In addition to the random effects of unit ID and group ID, we also included a random slope for each control-treatment pairwise comparison. In order to include this random slope, we ran these models using *MCMCglmm* (this model specification is not currently supported in *metafor*). This Bayesian approach also allowed us to set 1 as the coefficient of the fixed effect of logged mean, which makes the coefficient for the fixed effect of treatment equivalent to *lnCVR* (Nakagawa *et al*. 2015). For the other fixed effects we set the prior at 0 with large uncertainty (variance of 10,000,000).

(iii) Publication bias

As none of our data originates from unpublished studies, the results are at risk of publication bias (a bias towards significant differences). This bias is likely to be a greater issue for mean differences than variance differences, because most studies did not explicitly test for differences in variability. We took three steps to explore whether publication bias was an issue in our dataset: first, we first plotted *lnRR* and *lnCVR* against their standard errors (square-root of sampling variances), to look for asymmetry in these funnel plots (Fig. S3). Next, we ran Egger's regression on the 'meta-analytic residuals' (*sensu* Nakagawa and Santos 2012) of effect-sizes and their sampling errors. These residuals were calculated from full Bayesian models, including the type of treatments and the interactions with trait type and treatment

magnitude for *lnCVR*, with the addition of the treatment condition and variability in the control group for *lnRR* (Table S18). Finally, we tested whether studies with larger effects tend to be published earlier (known as the time-lag effect), by including publication year as a moderator variable in meta-regression models (Jennions and Møller 2002) (Table S19).

(iv) Leave-one-out analyses

To test how robust our main results were to the exclusion of individual studies, we performed leave-out-one analyses, where we ran the same models multiple times, each time leaving out one subset of data. The subsets of data we left out were particular experimental groups of fish (i.e. group ID).

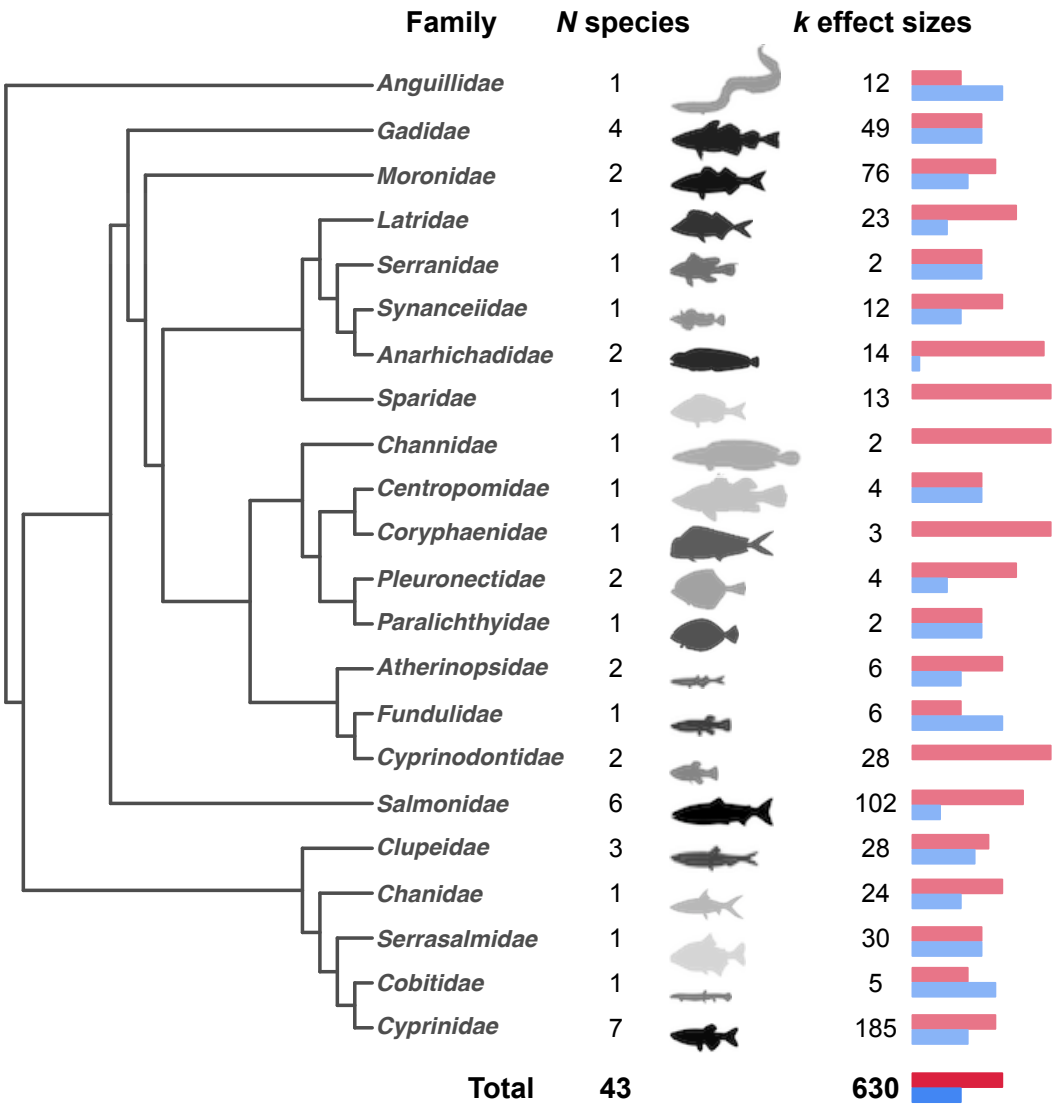

Figure 2

The number of effect sizes for each family of fish, and the number of species representing each family, shown alongside the estimated phylogeny from the Open Tree of Life (Michonneau *et al*. 2016). The size of fish silhouettes depicts the order of maximum length for the species in that family (range = 6 – 210 cm), and the silhouette shading level represents the total number of fish measured for species in that family (range = 10 – 1,960 fish; darker shades depict higher sample sizes). The lengths of horizontal bars correspond to the percentage of effect sizes that originate from warm treatments (red; top bar) and cool treatments (blue; bottom bar).

Results

Description of dataset

Our data set (available from osf.io/e2tyw) includes 62 papers reporting data on 43 species. We analysed 630 effect sizes for the difference between 84 groups of control and treatment fish. The median and mean sample size in each sample (control or treatment group of fish) was 30 and 41.4, respectively. Fig. 2 shows the spread of data across the phylogeny of species represented in the dataset. Warm treatments comprised 65.1% of the effect sizes, and the average increase in temperature for these treatments was 4.4 degrees Celsius. The magnitude of the temperature difference for the 34.9% of effect sizes for the cool treatment was 3.1 degrees Celsius. The vast majority of effect sizes represented the phenotypic difference for morphological and physiological traits (76.2% and 21%, respectively). The duration of the temperature treatment was very positively skewed: the median day that fish were measured was 12 days after the treatment started, whereas the average was 36 days. Similarly, the median and mean of the treatment start date was 0 and 1.6 days. In a minority of cases, the fish in the treatment group were brought back to the control temperature before they were measured (i.e. transient treatments: 16% of effect sizes). The median and average number of parents who contributed eggs or sperm to a given experimental group of fish was 10 and 15, based on information available for 70% of effect sizes.

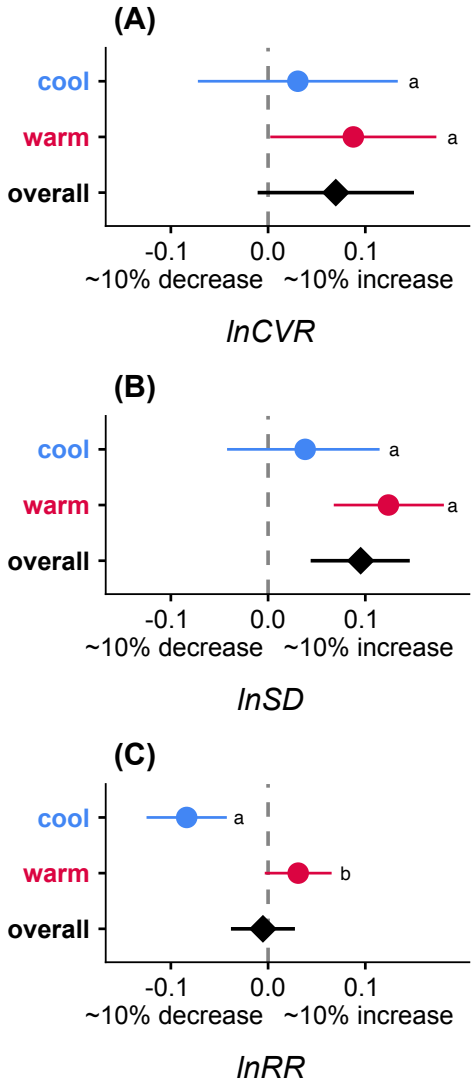

Figure 3

Main meta-analytic and meta-regression results for phenotypic differences between the control and treatment group in (A-B) variability, and (C) means within different trait categories. Whiskers denote 95% confidence intervals; estimates are statistically significant if the confidence intervals do not cross the dashed vertical line at zero. Black diamonds represent meta-analytic intercepts (n = 630). Blue and red circles represent meta-regression intercepts for cool and warm treatments, respectively (n = 220 and n = 410), and lowercase 'a' and 'b' symbols indicate whether these estimates are significantly difference from each other (using a significance threshold of alpha = 0.05). (A-B) Warm treatments tend to increase phenotypic variance, whereas variance in cool treatments is unchanged. Treatment differences in (A) are analysed with *lnCVR*, using a redistricted maximum likelihood model. Treatment differences in (B) are analysed in Bayesian random slope models using *lnSD*, with the log of phenotypic means fixed to 1. (C) Cool treatments tend to decrease phenotypic means, whereas warm treatments show a smaller and non-significant increase in means.

1. Did warm temperatures increase phenotypic variability?

Fish reared in warmer temperatures expressed 9.2% more variable phenotypes than fish reared in normal temperatures (*lnCVR*: 0.088, 95% confidence interval, CI: 0.002 to 0.173; Fig. 3A, Table S4). Using the alternative *lnSD* method of analysis, we estimated a 13.2% increase in phenotypic variability in warm temperature treatments ($lnSD_{\text{control-warm treatment slope}}$: 0.124, 95% confidence interval, CI: 0.068 to 0.181; Fig. 3B, Table S5).

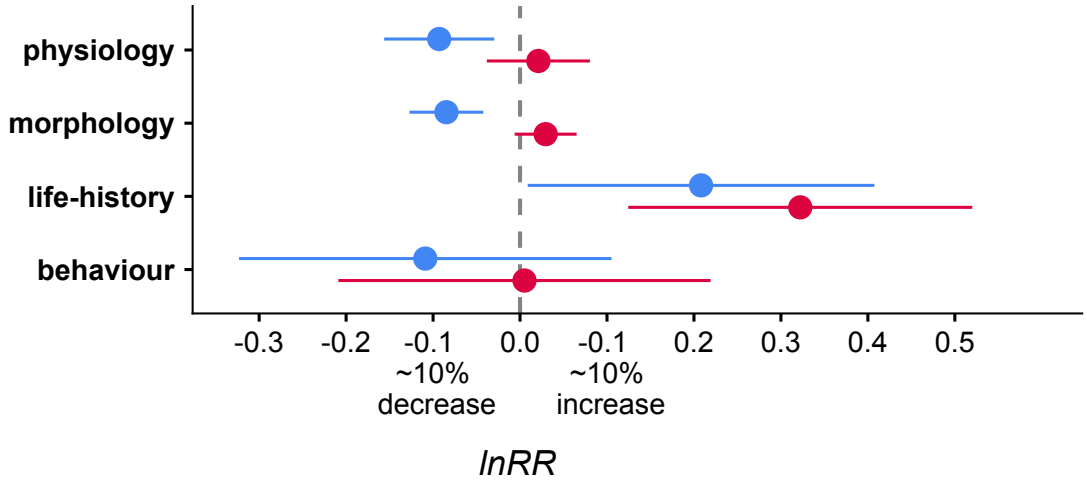

Figure 4
Effects of temperature treatments on phenotypic means, within different types of trait categories. Whiskers denote 95% confidence intervals; estimates are statistically significant if the confidence intervals do not cross the dashed vertical line. The confidence intervals for physiology and morphology are narrower than for life-history and behaviour, because they are estimated from more data.

2. Did changed developmental temperatures change phenotypic means?

Warm temperatures tended to show a statistically non-significant 3.1% increase in the means of phenotypic traits ($lnRR_{\text{warm intercept}}$: 0.031, CI: -0.003 to 0.065; Fig. 3C, Table S7). Among different types of phenotypic traits, only growth rate (which was classified as life-history) showed a statistically significant 38% increase in warmer

temperatures, but note that this estimate is based on very little data ($n = 4$; $lnRR_{\text{life-history warm intercept}}$: 0.322, CI: 0.124 to 0.520; Fig. 4, Table S9). Warm temperature treatments did not reduce mean values in any of the broad categories of phenotypic traits (Table S9).

Cool treatments showed a larger effect on phenotypic means than warm treatments and significantly reduced trait means by 8% ($lnRR_{\text{cool intercept}}$: -0.084, CI: -0.125 to -0.042; Fig. 4, Table S7).

Because cool and warm treatments had opposing effects on phenotypic means, in the combined meta-analysis these treatments effectively cancelled each other out. The overall meta-analytic mean therefore found no change in the mean phenotype as a result of changes in the developmental temperature ($lnRR_{\text{intercept}}$: -0.005, CI: -0.038 to 0.028; Fig. 3C, Table S7).

3. The differences between cool and warm treatments

In meta-regressions of mean phenotypic differences, the type of treatment (cool or warm temperatures) was an important moderator variable to account for heterogeneity in the size and magnitude of effects ($lnRR\ Q_m = 35.45$, $df = 1$, $p < 0.000$; Table S19). The estimate of the phenotypic mean for the warm treatment was 10.8% greater than the estimate for cool treatments ($lnRR_{\text{warm-cool slope}}$: -0.115 CI: -0.152 to -0.077; Fig. 3C, Fig. 4, Table S7).

In contrast to phenotypic differences in means, the type of treatment was less important for meta-regressions of phenotypic differences in variability ($lnCVR\ Q_m = 1.421$, $df = 1$, $p = 0.233$; Table S19). While the tendency for variability to increase was driven by warm temperature treatments, the 5.5% contrast between the treatment

types was non-significant ($lnCVR_{warm\text{-}cool\ slope}$: -0.057, CI: -0.151 to 0.037; Fig. 3A, Table S4).

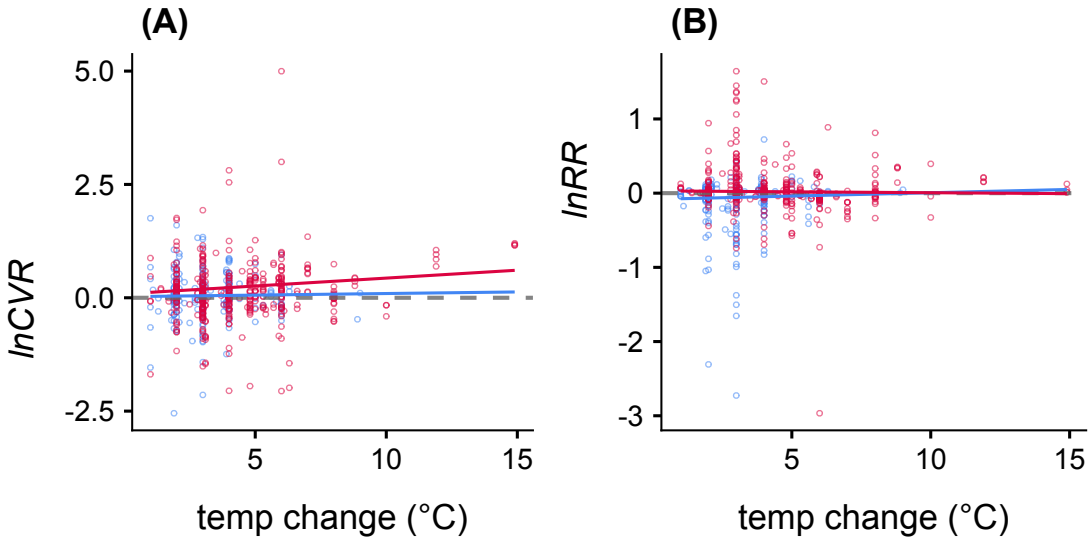

Figure 5

The relationship between the magnitude of temperature change (absolute values) and phenotypic effects for (**A**) differences in variability and (**B**) differences in means. Note the scale of the y-axis is wider than the x-axis in Fig. 1. Open circles are raw values, and solid lines show the intercept and slope estimates for meta-regression models. Cool treatments are shown in blue, and warm treatments are shown in red. (**A**) Warm treatments tended to increase phenotypic variability, and the magnitude of this effect significantly increases as the treatment moves further from the control temperature. Cool treatments did not affect phenotypic variability, regardless of the size of the temperature difference. (**B**) The magnitude of temperature change had no impact on the size of the phenotypic mean difference.

4. Do larger changes in temperature cause larger effects?

Larger temperature treatments caused greater variability increases in the warm temperature treatments, but not the cool temperature treatments. The slope of the meta-regression model indicated a 1-degree increase in warm temperatures caused a significant 3.5% increase in variability ($lnCVR_{warm\ degree\ difference\ slope}$: 0.035, CI: 0.009 to 0.061; Fig. 5A, Table S10). To illustrate this effect of the magnitude of the temperature change, we ran post-hoc meta-regression models where the intercept was

estimated at different distances from the control temperature (Fig. 6; Table S11). At the average magnitude of warm temperature treatments (4.4 degrees Celsius) the model predicted a 8.9% increase in variability. When we shifted the intercept to 3 degrees warmer, at 7.4 degrees Celsius, the phenotypic variability increased by 20.9% ($lnCVR_{\text{warm average magnitude + 3 degrees intercept}}$: 0.19, CI: 0.074 to 0.305; Fig. 6A; Table S11). A change in the developmental temperature caused a change in phenotypic means, but the magnitude of this difference did not increase as the temperature moved further away from the control ($lnRR_{\text{warm degree difference slope}}$: -0.002 CI: -0.014 to 0.009; $lnRR_{\text{cool degree difference slope}}$: 0.009 CI: -0.014 to 0.032; Fig. 5B, Table S12). Post-hoc meta-regression models confirmed that increasing the magnitude of temperature change did not increase the magnitude, or statistical significance, of the mean difference estimates (Fig. 6B; Table S13).

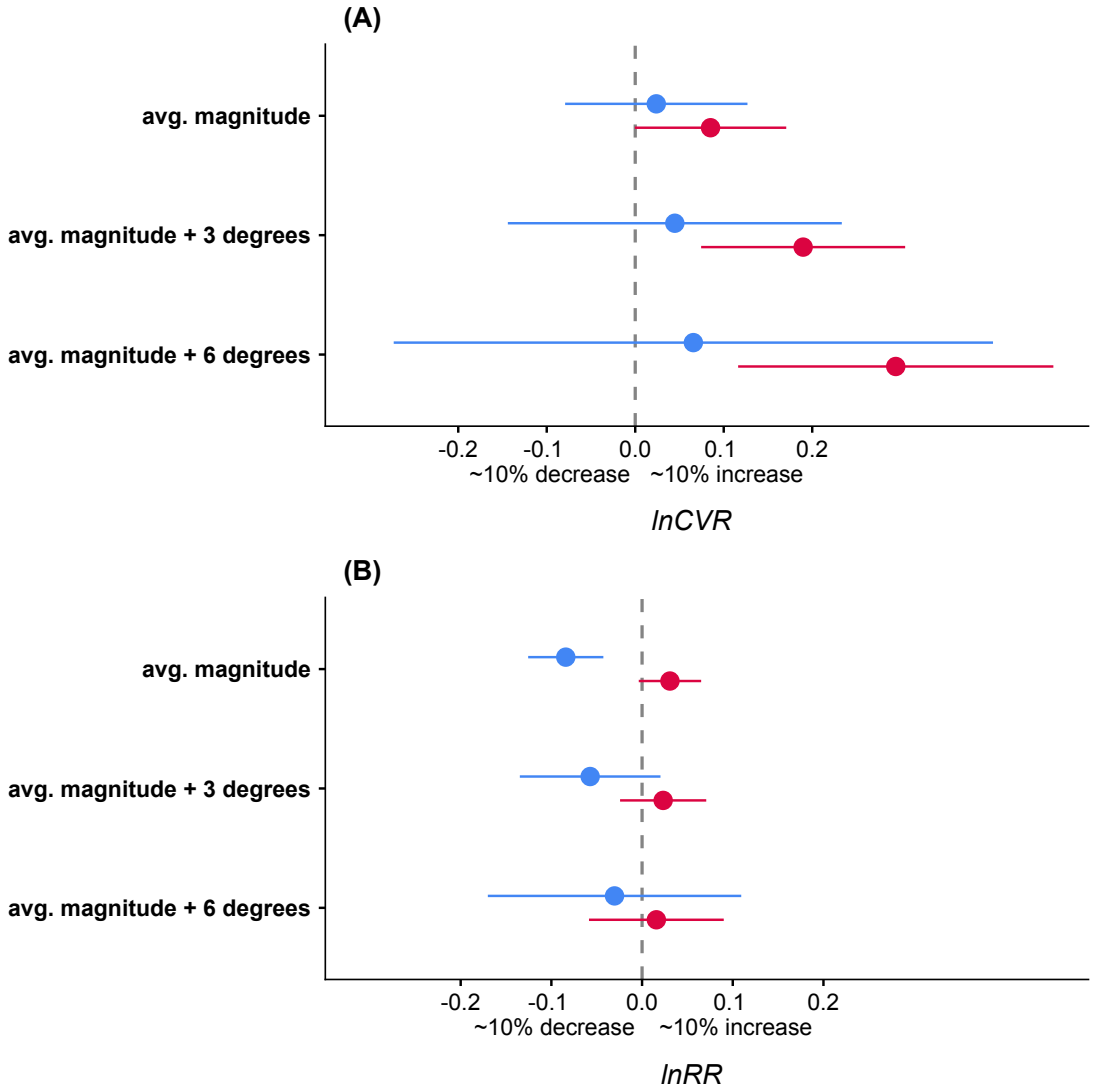

Figure 6

Estimates of the phenotypic differences in (A) means and (B) variability between control and treatment groups, estimated from the intercept of meta-regression models with the type of treatment – cool (blue) or warm (red) – and the magnitude of temperature change. Each model includes the interaction term, and the magnitude of temperature change is shifted separately for each type of treatment, to estimate the intercept at different magnitudes of temperature change. The "avg. magnitude" is 3.1 degrees for cool treatments, and 4.4 degrees for warm treatments. Whiskers denote 95% confidence intervals; estimates are statistically significant if the confidence intervals do not cross the dashed vertical line.

To illustrate the combined effects of temperature treatments on the mean and variance of phenotypic traits, we present simulated normal distributions of a phenotypic trait, based on our model estimates, in Fig. 7.

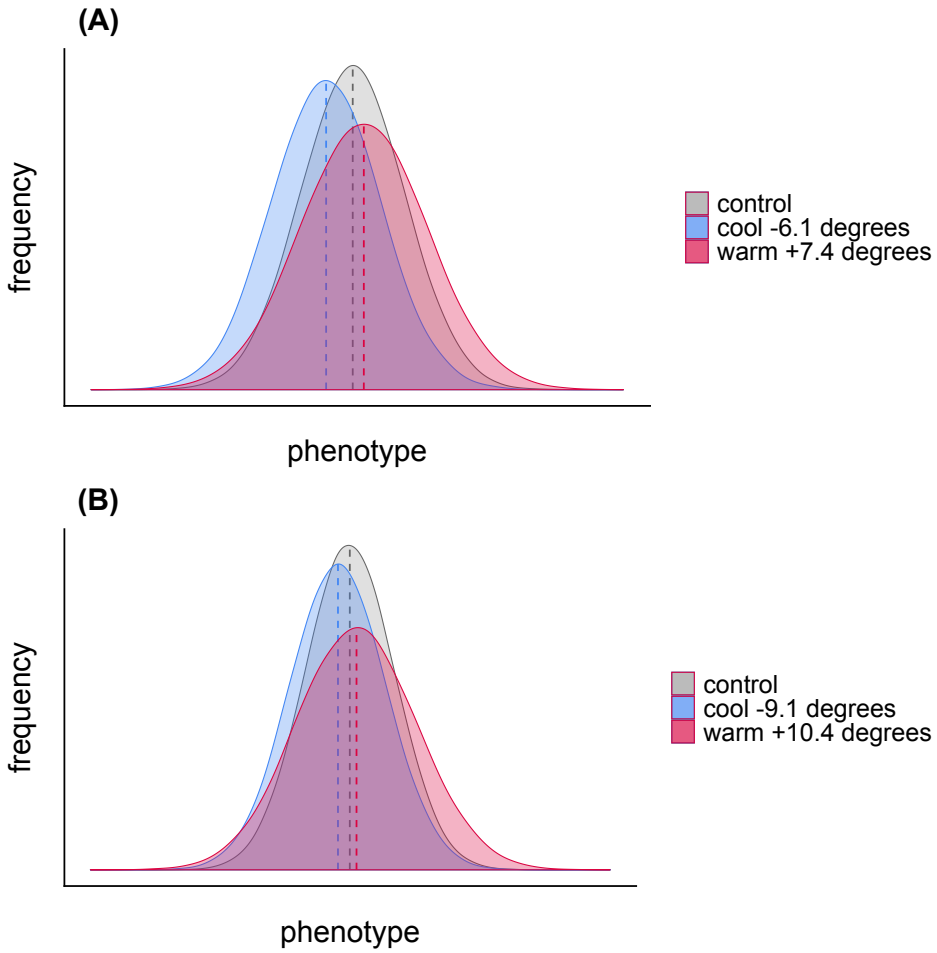

Figure 7
Phenotypic distributions for fish in the control and treatment groups when the temperature is changed beyond the average treatment magnitude (A) by 3 degrees and (B) by 6 degrees Celcius, based on simulations of model estimates. Control group = grey, cool treatment = blue, and warm treatment = red. Dashed vertical lines show the phenotypic means. (**A**) At 6.1 degrees below normal, cool treatments decrease trait means but cause no noticeable difference in variance. At 7.4 degrees above normal, warm treatments show a smaller increase in means, but show a noticeable increase in variance. (**B**) If the treatment moves 3 degrees further from the control then the differences in means do not increase (if anything, they decrease), but the warm treatment variability continues to increase.

5. Do longer treatment durations cause larger effects?

The length of the treatment (mean ± sd = 35.5 ± 44.9 days) had no effect on the magnitude of phenotypic differences between the treatment and control groups, in

either mean or variability (variance: $lnCVR_{\text{treatment duration slope}}$: 0, CI: -0.002 to 0.001; mean: $lnRR_{\text{treatment duration slope}}$: 0.000, CI: 0.000 to 0.001; Fig. S6, Table S14).

6. Did changing the temperature earlier cause larger effects?

In order to be included in our meta-analysis, the temperature treatment had to start before or on the day of hatching (i.e. the time between eggs being fertilized, and developing into larvae). Within this limited range of time for the treatment to start, we found little effect of the timing of the treatment on the magnitudes of phenotypic differences (variance: $lnCVR_{\text{treatment start slope}}$: -0.006, CI: -0.012 to 0.00; mean: $lnRR_{\text{treatment start slope}}$: 0, CI: -0.003 to 0.002; Fig. S7, Table S14).

7. Do permanent treatments cause larger effects than transient treatments?

The permanence of the treatment condition (permanent or transient) had no effect on phenotypic variability ($lnCVR_{\text{permanent-transient difference}}$: 0.045, CI: -0.120 to 0.210; Fig. S8, Table S15), and a significant effect on phenotypic means (7.4% difference between permanent and transient treatments; $lnRR_{\text{permanent-transient difference}}$: -0.077, CI: -0.142 to -0.013; Fig. S8, Table S15). Because transient treatments were only a small portion of our data set (16% of effect sizes), it is possible that this difference was not due to the treatment conditions *per se*, but rather due to uneven sampling of other moderator variables. For example, cool treatments were over-represented in the transient data subset (49% cool treatments in transient treatments compared to 32% in permanent treatments). We therefore included both treatment type and treatment condition as fixed effects in the 'full model' (which also included trait type and variability of the control group; Table S18). In the full model, both cool and warm treatments showed a reduction in mean phenotype in transient compared to permanent conditions. Because

cool treatments tended to decrease the phenotypic mean, this suggests that transient treatments had a larger phenotypic effect than permanent treatments. In contrast, warm treatments tended to increase phenotypic means (albeit not statistically significantly), suggesting that warm treatments had larger phenotypic effects when the treatment condition was permanent rather than transient.

8. Does having more variation allow for larger average plastic responses?

The amount of phenotypic variability in normal temperatures affected the amount of developmental plasticity expressed in abnormal temperatures. In warm temperature treatments, at the average magnitude of the temperature change (4.4 degrees Celsius), an increase in baseline variability of one standard deviation estimated a 10% increase in the phenotypic mean ($lnRR_{\text{warm control variability slope}}$: 0.095, CI: 0.068 to 0.122; Fig. S9, Table S16). The same increase in variation was associated with a 6.9% decrease in the phenotypic mean at the average magnitude of cool temperature treatments (3.1 degrees Celsius) ($lnRR_{\text{cool control variability slope}}$: -0.071, CI: -0.106 to -0.036; Fig. S9, Table S16). The relationship between the magnitude of variability of the control group and the magnitude of plasticity was particularly consistent for warm treatments, with the slope remaining statistically significant in all full models (Table 18).

9. Does the number of parents impact the plastic response of a population?

We predicted that groups of fish from greater numbers of parents would show greater plastic responses to changes in the developmental temperature, but this was not the case (Table 12). The basis for our prediction was that greater genetic diversity would lead to greater phenotypic diversity. This assumption was not statistically supported: a post-hoc meta-regression found no significant relationship between the number of

parents and the amount of phenotypic variability expressed in normal temperatures ($lnCV_{\text{number parents slope}}$: 0.160, CI: -0.031 to 0.351; Fig. S10C).

10. Does the distance of the treatment from the species' thermal limit matter?

The magnitude of the temperature change had no impact on mean phenotypic differences, regardless of the distance of the temperature change from the optimal thermal limit of the species (Tables S12 and S14). The magnitude of the temperature change did matter for variability: larger differences in temperature induced greater increases in variability (Table S10). However, pushing temperatures beyond the thermal limit of the species did not induce greater phenotypic variability. An increase in distance from the thermal limit of 1 degree tended to reduce the variability difference by 1.1% ($lnCVR_{\text{distance from thermal limit slope}}$: -0.011, CI: -0.022 to 0.000; Table S14).

Publication bias and sensitivity analyses

Funnel plots and leave-one-out

Visual inspection of funnel plots indicated some asymmetrical distribution of effect sizes around the meta-analytic mean (Fig. S3A and Fig. S3B). The usefulness of these funnel plots for multivariate meta-analyses is debatable, however, and when we average the effect sizes within groups of fish (the main random effect) the funnel plots look more symmetrical (Fig. S3C and Fig. S3D). To test the sensitivity of our meta-analytic and meta-regression means to exclusion of certain levels of the random effect, we ran 'leave one out' analyses. We re-ran the meta-analytic model and meta-regression of treatment type (cool and warm) after removing one experimental fish group (n = 84 models, for the 84 groups of fish in the data set), and compared the

estimates and confidence intervals to our overall results. The estimates for mean and variance differences overall, and in cool and warm treatments, appeared fairly robust (Fig. S4 and Fig. S5).

Publication bias

The results of Egger's regression on the meta-analytic residuals indicated the presence of publication bias in the data set for phenotypic differences in means, but not variability (Table S17). However we did not find evidence of a time-lag bias (larger effect sizes were not published earlier; Table S18).

Discussion

Changing fish's developmental temperature changed their average phenotype, but in opposing directions depending on whether the temperature was increased or decreased. These shifts in average phenotype could indicate adaptive plasticity (Fig. 1B), or maladaptive responses to thermal stress. Increases in temperature, but not decreases, also increased phenotypic variability, which suggests a reduction in genotype precision that causes a spreading in reaction norms (Hansen *et al*. 2006; Snell-Rood *et al*. 2018) (Fig. 1C,E). These effects were not significantly moderated by the starting date or duration of the temperature change, the distance of the new temperature from the thermal limit of the species, or the number of parents who contributed to the spawning. There were limits to directed plasticity: the average phenotype did not continue to change as the temperature changed, although warmer temperatures did induce more variation around this mean. Populations that expressed more variability in normal conditions showed larger plastic responses in both mean and variance. Combined, these results demonstrate warmer-than-standard

developmental temperatures can increase the frequency of rare phenotypes in fish populations, and potentially induce novel phenotypes.

Increased variability in novel environments

We found that warm environments increase phenotypic variability, despite no change in the phenotypic mean in all trait categories except growth rate, with larger changes in the environment causing greater expression of stochastic plasticity. The evolutionary consequences of phenotypic plasticity have long been debated (Crispo 2007). The extent to which stochastic plasticity will help fish populations adapt to a warming world depends on whether beneficial phenotypes are heritable. Hansen *et al*.'s 2006 literature survey suggests an underappreciated source of phenotypic variation is genotype imprecision (whereby genotypes do not precisely produce their target phenotype, so this variation is not heritable). A decrease in precision in challenging environments could improve the odds of some individuals thriving, and therefore help populations to ride out temporary warming periods even without a heritable change in phenotypes. But increases in phenotypic variation – the spreading of the reaction norms shown in Fig. 1E (Snell-Rood *et al*. 2018) – could be caused by interactions between the genotype and the environment, in which case the beneficial genotypes could quickly spread through the population. A permanent environmental change might eventually select for the plastic phenotype to be produced regardless of the developmental temperature (i.e. genetic assimilation; Crispo 2007). There is some evidence, based on genotype-by-environment interactions, for the adaptive potential of warm-induced variants in a coral reef fish and a salmon species (*Acanthochromis polyacanthus*: Munday *et al*. 2017), *Onchorhynchus nerka*: Burt *et al*. 2012). Warm temperatures in early life also cause epigenetic changes (e.g., sex determination; Piferrer *et al*. 2012), and these epigenetic effects could range from short-term

(Campos *et al*. 2014) to transgenerational (Burton and Metcalfe 2014). Of course, the beneficial effects of increased variability are entwined with population size, because small populations cannot afford to lose a large fraction of their population (e.g., Devils Hole pupfish Jones *et al*. 2016).

The direction of the temperature change matters

Compared to warm treatments, and contrary to our predictions, cool treatments had no significant effect on phenotypic variability and caused a larger shift in the phenotypic mean. An artificial explanation for this result is that the 'cool' and 'warm' categories in our data could have been inaccurate; perhaps the experimental fish represented in the meta-analyses were kept closer to their thermal maximum than their thermal minimum to accelerate development, as is common in aquaculture (Arguello-Guevara *et al*. 2017). If we accept the temperature categories, there are competing explanations for their differences, depending on whether directed plasticity in response to temperature change is interpreted as (1) an adaptive response to a shift in the optimal phenotype; or (2) a maladaptive response to thermal stress. Under the first scenario, assuming that the optimal phenotype is linearly correlated with the environmental temperature, fishes seemed to respond better to cool rather than warm temperature changes – perhaps in cool temperatures they are relieved of constraints that exist at warm temperatures (e.g., metabolic constraints; Hans O Pörtner 2009). More speculatively, the ancestral history of fishes might have occurred in more in cool than warm environments, so that cool temperatures represent a familiar change that fish can adaptively respond to (Fig. 1B), whereas warm temperatures are a novel stressor that triggers an increase in developmental noise (Fig. 1C) (Ghalambor *et al*. 2007). The second scenario leads to the opposite interpretation; cool temperatures are more

likely than warm temperatures to cause a slide in the population mean away from the adaptive optimum (i.e. fishes in warm temperatures show greater 'genetic compensation', *sensu* Grether 2005). Distinguishing between these scenarios is an area for future research; our meta-analysis tests for phenotypic changes, but it cannot determine whether those changes are adaptive.

Limited directed plasticity

Contrary to our expectations larger temperature changes did not cause larger shifts in the phenotypic mean (i.e. limited directed plasticity). Similar results have been found for thermal acclimation at later developmental stages in coral reef fishes (Grenchik *et al*. 2013; Donelson 2015). Again, alterative interpretations depend on whether a shift in average phenotype is considered adaptive. Adaptive plasticity might be constrained at more extreme temperatures. For example the oxygen and capacity limited thermal tolerance hypothesis predicts fishes growth and aerobic scope will be constrained in warm temperatures, as increases in basal metabolic demands outpace resource consumption and the availability of dissolved oxygen (Hans O Pörtner 2009; Donelson *et al*. 2011). Alternatively, plasticity is likely to be costly in novel environments (Snell-Rood *et al*. 2018), so the average phenotype might be 'fixed' in order to prevent a maladaptive slide in the population average in response to environmental perturbations. This canalization is seen in examples of genetic compensation and counter gradient variation (Grether 2005).

Average differences could be over-estimated

We found some evidence that studies reporting large average differences between treatment and control groups were over-represented in our dataset. This pattern could reflect publication bias and selective reporting within studies, whereby 'positive'

findings are more likely to be published and reported by authors than null results (Jennions *et al*. 2013). In contrast to mean differences, our effect sizes for variance differences did not show evidence of selective reporting and/or publication bias. This is not surprising, because studies typically do not test hypotheses based on variability differences (an exception in our dataset was Burt *et al*. 2012). Unfortunately, while there has been a recent push towards increasing transparency in scientific publications, our review found low uptake of these initiatives within this field (Nosek *et al*. 2015). Only two studies included in the dataset had data readily available to download online, and many studies were excluded due to low reporting standards of essential information. We therefore urge that future studies on the effects of developmental temperature make all data publicly available, to reduce the adverse effects of selective reporting in research synthesis (Parker *et al*. 2016).

Other limitations and future directions

Our data had limited coverage over some moderator variables for which we tested predictions, which highlights areas warranting future research. The vast majority of traits represented in our dataset were morphological (mostly length and mass). Future studies should focus on other types of traits, such as behaviour, for which little data was available (this gap was also identified by a more general review of the effects of fishes' rearing environments; Jonsson and Jonsson 2014). These data could facilitate better predictions of how fishes respond to climate change. Longer-term studies are also required to assess the lifelong implications (i.e. fitness) of different developmental environments; the majority of our dataset consists of phenotypic traits measured in juvenile fish. It is valuable to measure adult fish because the phenotypic response of fish to different temperatures can vary depending on the measured life stage, due to changes in both optimal temperature conditions (Arguello-Guevara *et al*.

2017) and different resource requirements (e.g., endogenous versus exogenous feeding; Baras *et al*. 2012). For example, the dominance of juvenile measurements in our dataset could account for why we found an overall increase in body size at warm temperatures, despite a decrease being generally expected in adult fishes (Burt *et al*. 2012; Kim *et al*. 2017; Munday *et al*. 2017). Another explanation would be the generally benign conditions experienced in laboratory settings, which could mask resource limitation trade-offs that would be expected in nature (Munday *et al*. 2008).

Practical implications

As the world warms, and temperature fluctuations become more frequent and severe (Bathiany *et al*. 2018), how will fishes respond? In the short term, our results suggest minimal responses of the average population phenotypes, but (as predicted by Ghalambor *et al*. 2007) an increase in phenotypic variants in the population. If the initial population size is large enough, then increased variability should increase the likelihood of that population surviving and adapting to the new environment. Importantly, the potential for increased variation in warm environments is predicted by a population's underlying amount of phenotypic variability. To reduce the economic impact of climate change on fisheries, therefore, it is important that harvested populations maintain phenotypic variation within a considerable population size. The importance of maintaining phenotypic variation could affect management strategies for harvested fish populations (Villegas-Ríos *et al*. 2016). Large and diverse populations will stand the best chance of adapting to environmental change. Additional sources of stress should be reduced as much as possible; for example, survival of hatchery-reared *Salmo salar* during a heatwave was improved through minimising larval stress by mimicking natural rearing conditions (Bamberger 2009).

Conclusions

We found proof-of-concept support for an increase in phenotypic variability in warm environments, especially for large changes in temperature. Unusual phenotypes that are induced by the environment could facilitate adaptation to novel environments. We encourage future studies to report and consider the implications of this variation. Further empirical research will be needed to determine whether variants induced by the environment are heritable and stable, whether the cause is underlying cryptic genetic variation or epigenetic modifications, and whether the propensity for variability is itself heritable (i.e., heritable bet hedging, *sensu* O'Dea *et al*. 2016). Future theoretical work should consider the implications of environmental effects on intraspecific variation for evolutionary and ecological models (Bolnick *et al*. 2011). As environmental conditions are becoming increasingly unpredictable, the capacity of species to produce and maintain phenotypic variability might be a crucial determinant of long-term population survival.

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Supporting Information for:

Developmental temperature affects phenotypic means and variability: a meta-analysis of fish data

Authors and affiliations

Rose E. O'Dea[1,2], *Malgorzata Lagisz*[1], *Andrew P. Hendry*[2] & *Shinichi Nakagawa*[1]

[1]Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia

[2]Department of Biology & Redpath Museum, McGill University, Montréal, Québec, H3A 0C4, Canada

Correspondence

Rose E. O'Dea

Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia

Tel: +61 2 9385 8865

Email: rose.eleanor.o.dea@gmail.com

Figures

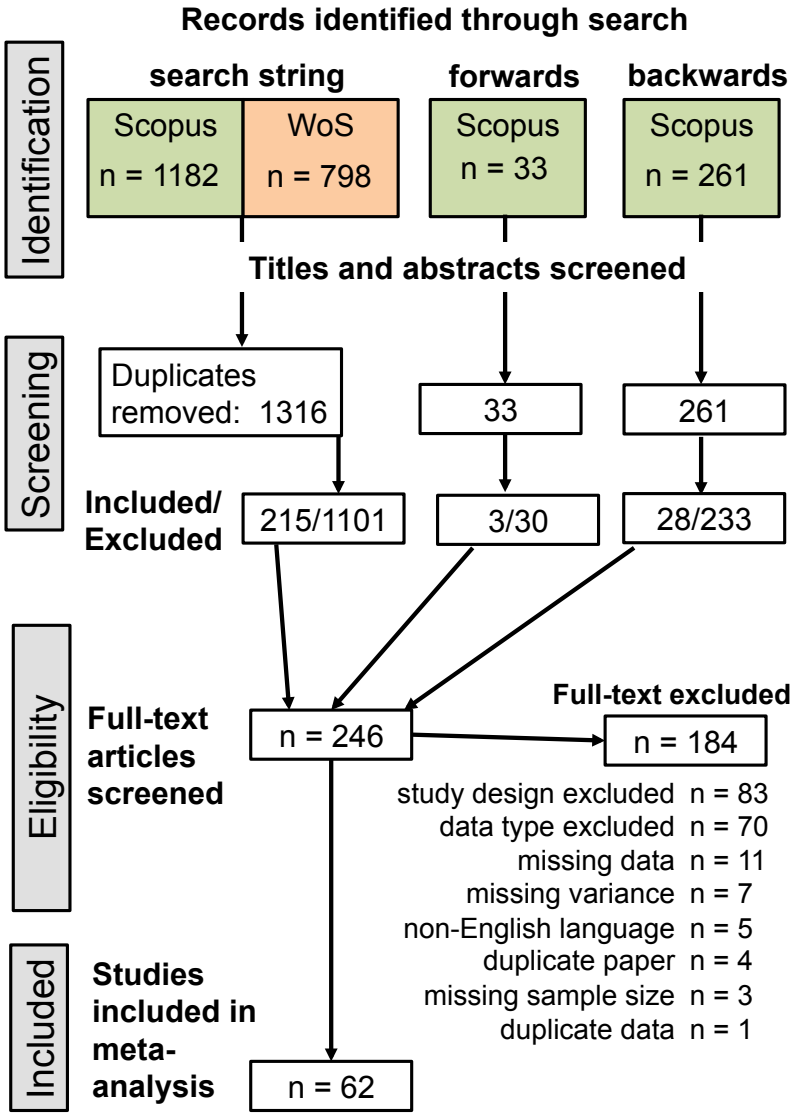


Figure S1

PRISMA diagram: the stages of searching and screening to find the studies included in this meta-analysis. The full list of included studies, and the list of studies excluded at the full-text stage, is available from osf.io/e2tyw.

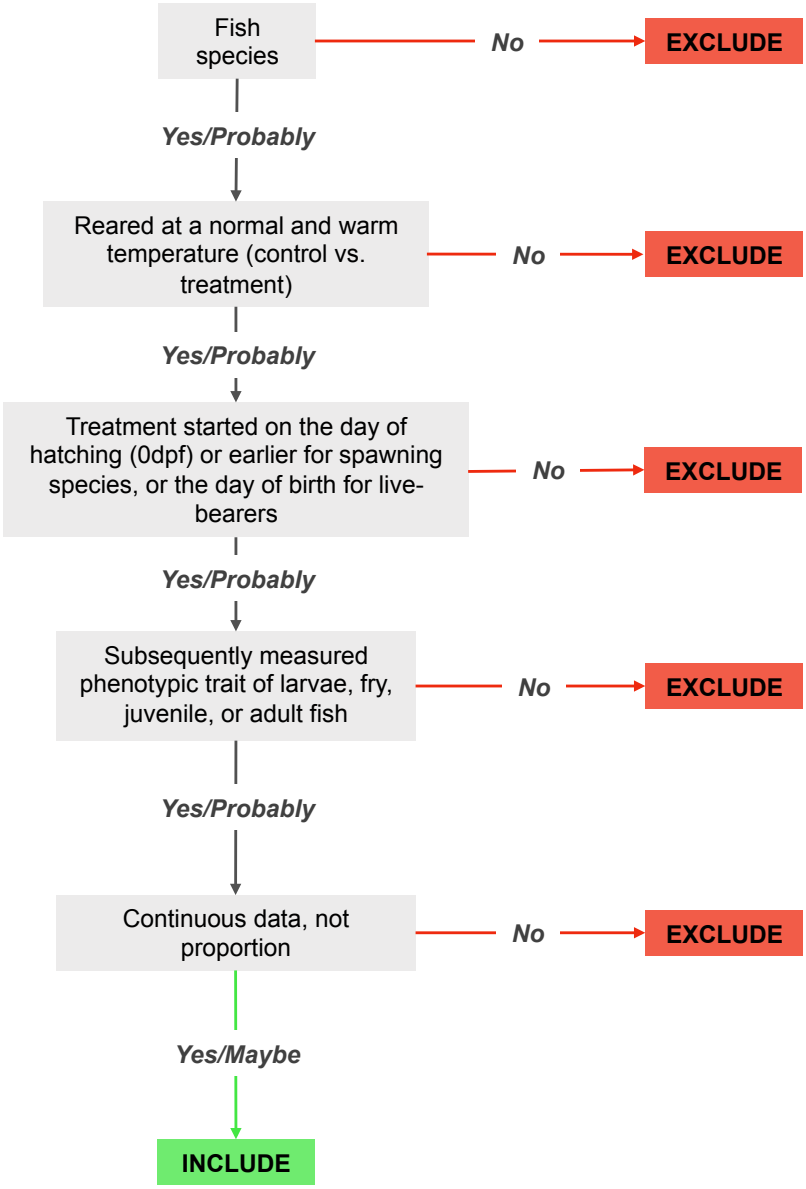


Figure S2

Decision tree used to evaluate studies for inclusion and exclusion at the stage of title and abstract screening.

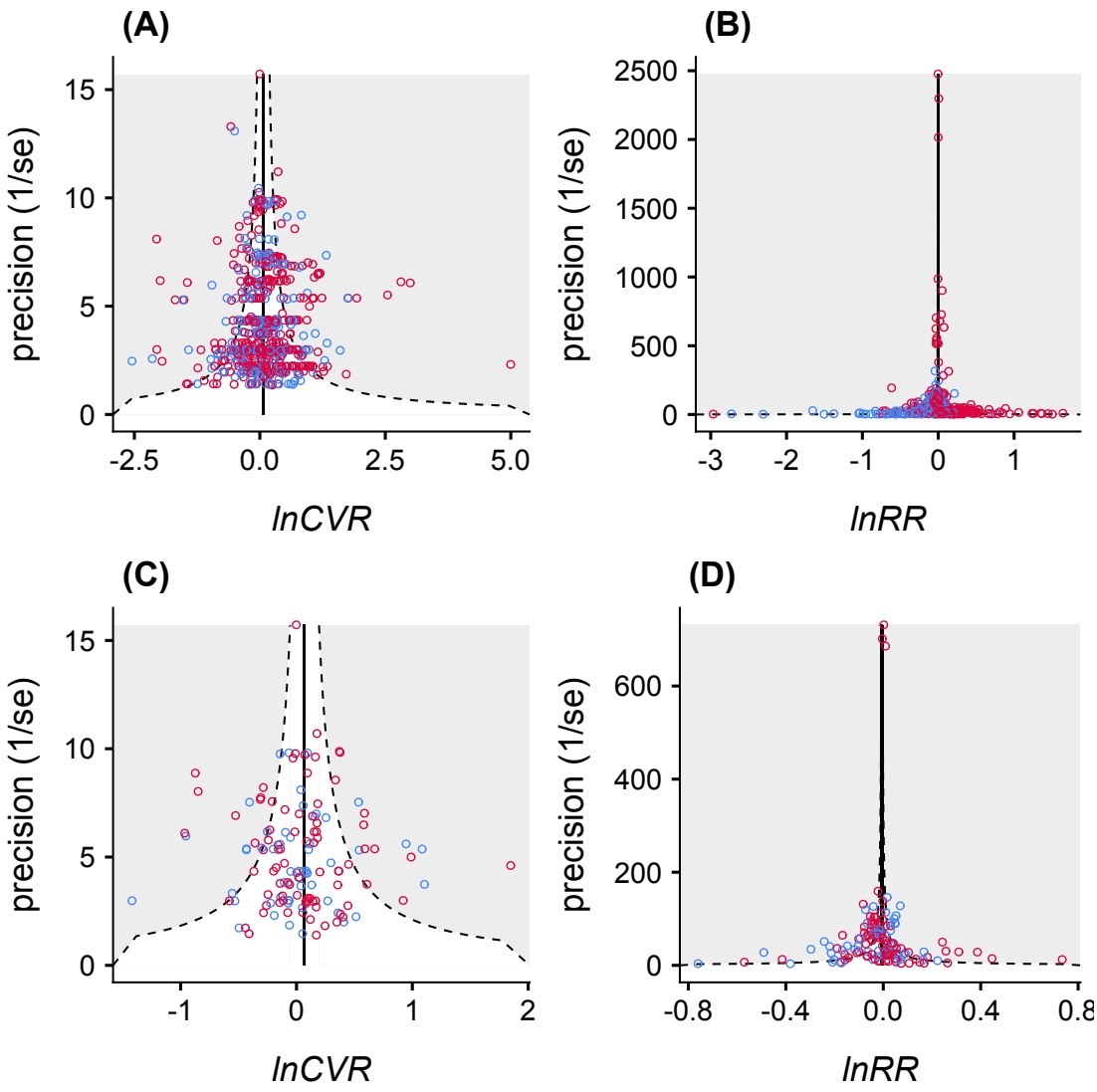
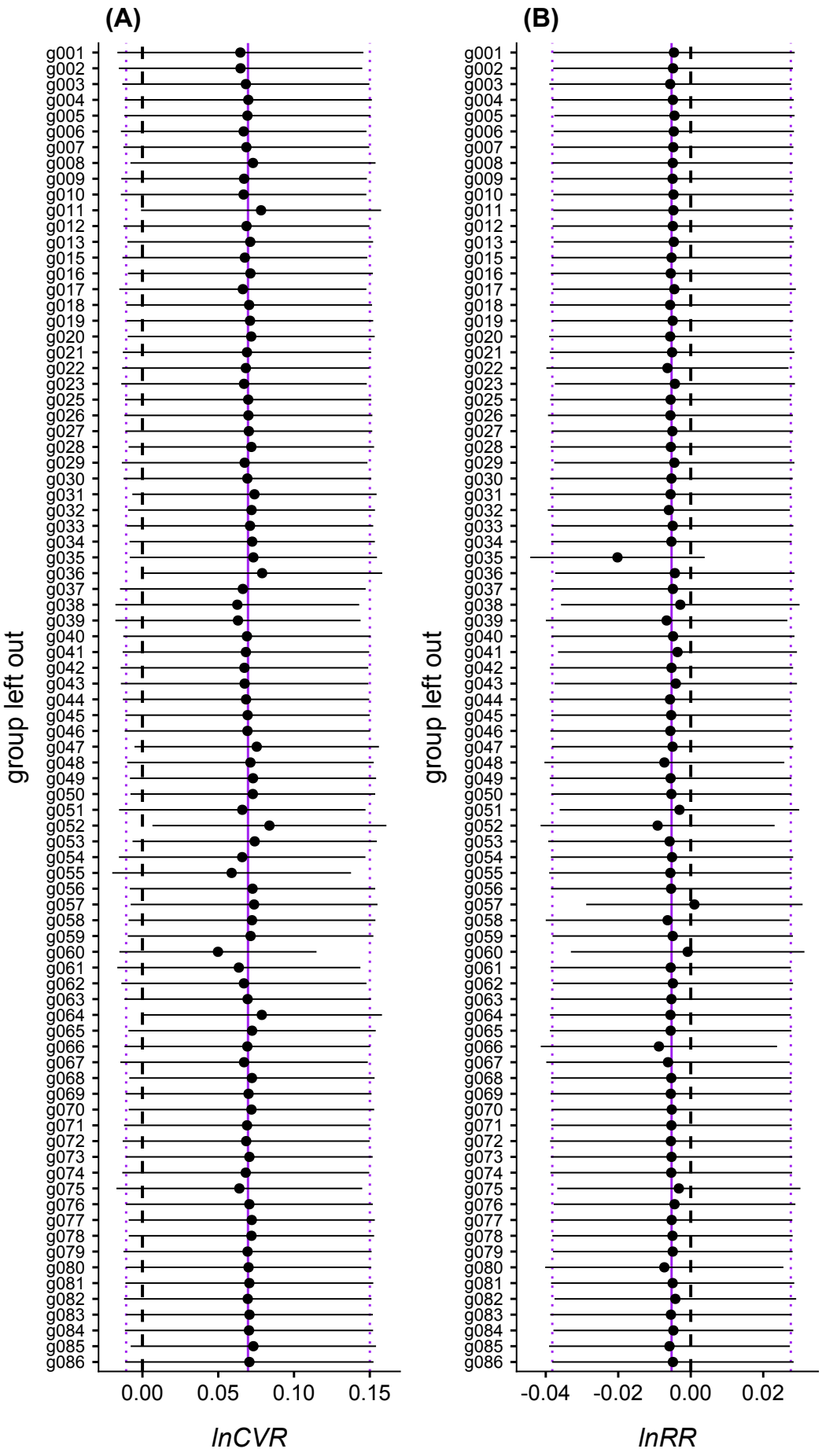


Figure S3

Funnel plots showing the distribution of effect sizes around the meta-analytic mean, for meta-analysis of variance differences (*lnCVR*, panels A and C) and mean differences (*lnRR*, panels B and D). The y-axis represents the precision of the estimates (inverse of the standard error, which is the square root of the sampling variance). Panels (A) and (B) show the raw values of effect sizes. Panels (C) and (D) show effect sizes that have been averaged for each group of fish in the data set (the main random effect in the analyses).


(A)
(B)
group left out
g001
g002
g003
g004
g005
g006
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g008
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g011
g012
g013
g015
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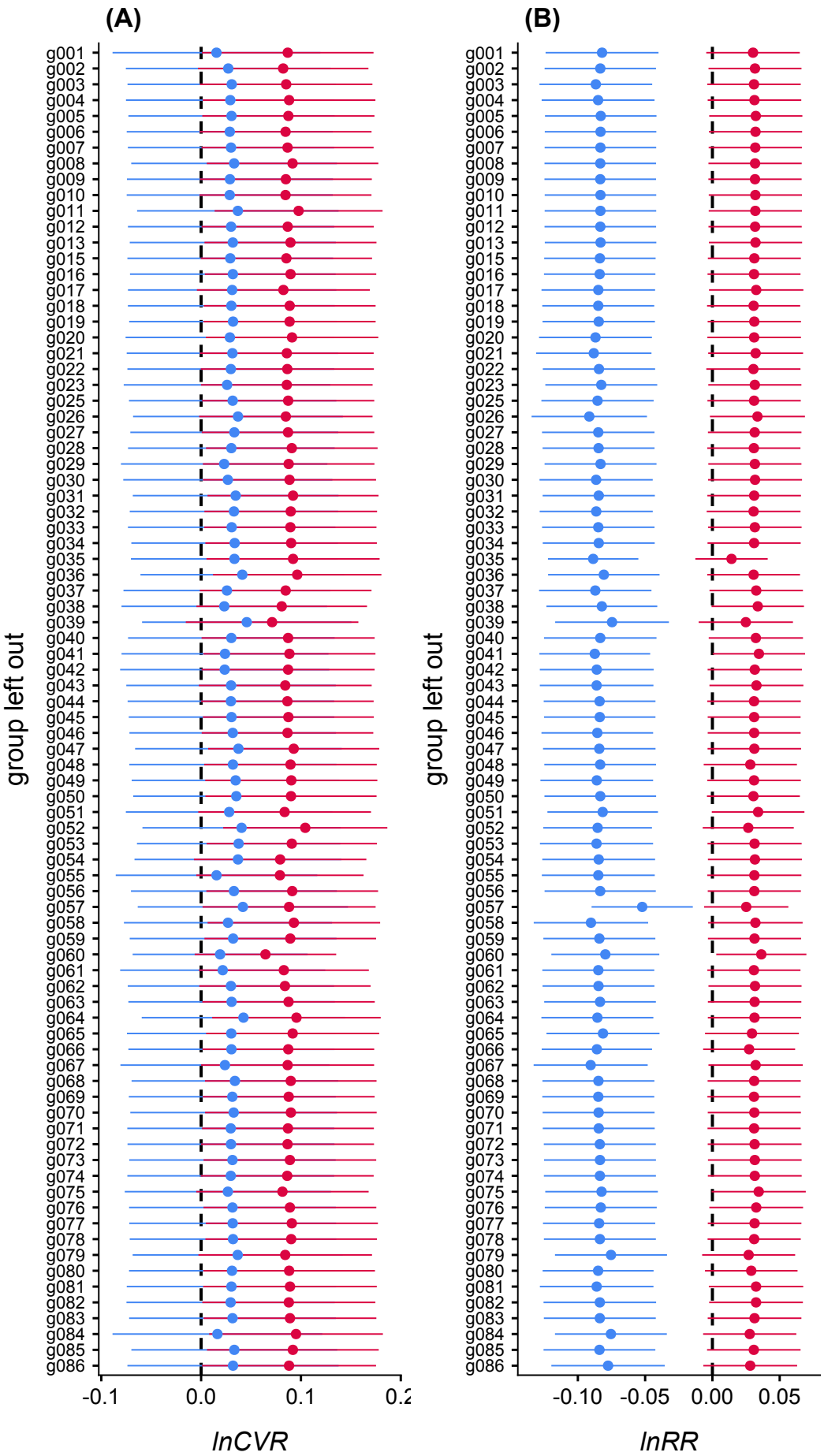
g079
g080
g081
g082
g083
g084
g085
g086
0.00
0.05
0.10
0.15
lnCVR
-0.04
-0.02
0.00
0.02
lnRR

Figure S4

Meta-analytic means from leave-one-out sensitivity analyses, where one fish group is iteratively left out of the data set for (A) variability differences, and (B) mean differences. Points and their whiskers are the meta-analytic means and their 95% confidence intervals. The dashed black vertical lines show the line of no effect – confidence intervals not crossing this line are statistically significant. The solid purple lines are the overall meta-analytic estimates (the black diamonds shown in Fig.1). The dotted purple lines are the upper and lower bounds of the confidence intervals for these overall meta-analytic estimates.


(A)
(B)
group left out
g001
g002
g003
g004
g005
g006
g007
g008
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g086
-0.1
0.0
0.1
0.2
-0.10
-0.05
0.00
0.05
lnCVR
lnRR

Figure S5

Meta-regression intercepts for the cool and warm treatment groups, estimated from leave-one-out sensitivity analyses for (A) variability differences, and (B) mean differences. Points and their whiskers are the meta-analytic means and their 95% confidence intervals; blue points are cool treatments, and red points are warm treatments. The dashed black vertical lines show the line of no effect – confidence intervals not crossing this line are statistically significant.

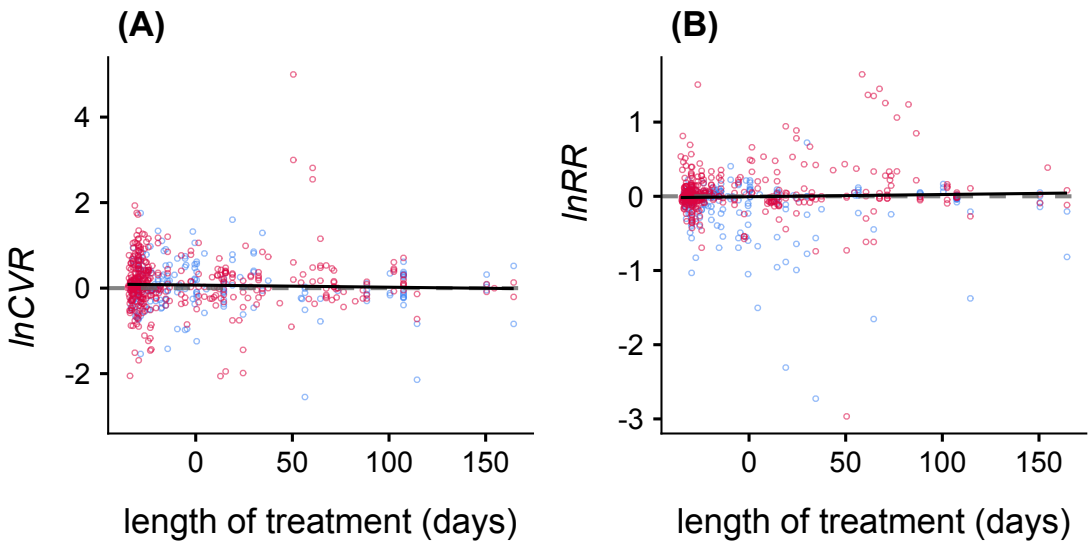

Figure S6

The length of the treatment in days, shown against the phenotypic effects of developmental temperature treatments on (A) variability and (B) means. The slope of the solid horizontal line is not significantly different from zero, indicating that longer treatments do not cause larger phenotypic differences. Red circles denote warm temperature treatments, and blue circles denote cool temperature treatments.

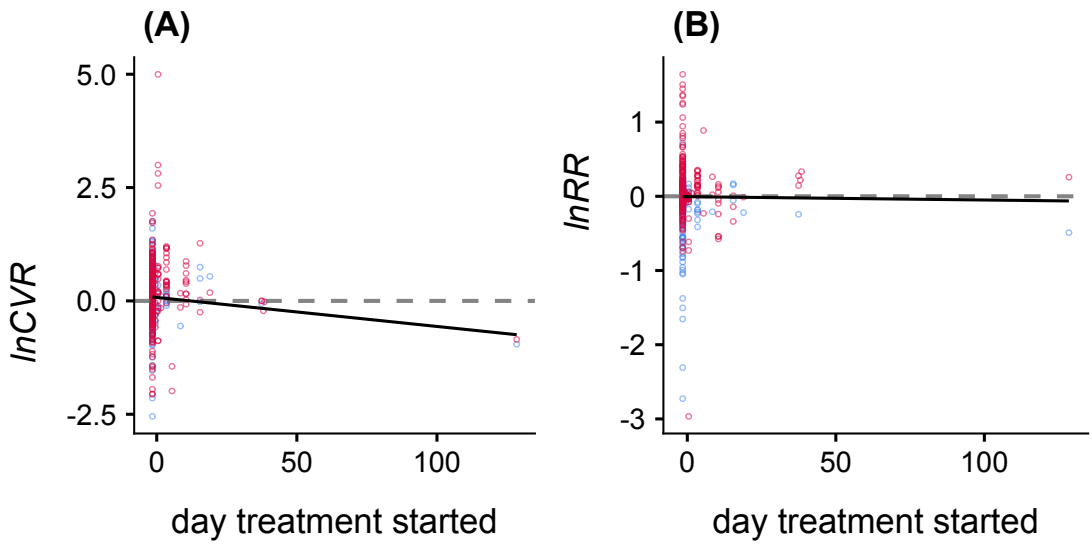

Figure S7

Effect sizes for the phenotypic effects of developmental temperature treatments on (A) variability and (B) means, shown against the day the treatment started (day 0 = day of fertilization). Note the distribution of starting days is very positively skewed. The dashed vertical line is the line of no effect – estimates towards the right of that line indicate an increase, and estimates towards the left indicate a decrease. The solid black line is a regression line, showing the intercept and slope estimate from meta-regression models. (A) There is a non-significant trend for the increase in variability to decrease over starting time, which is driven by estimates from one influential study. (B) There is no relationship between mean phenotypic differences and the day the treatment started.

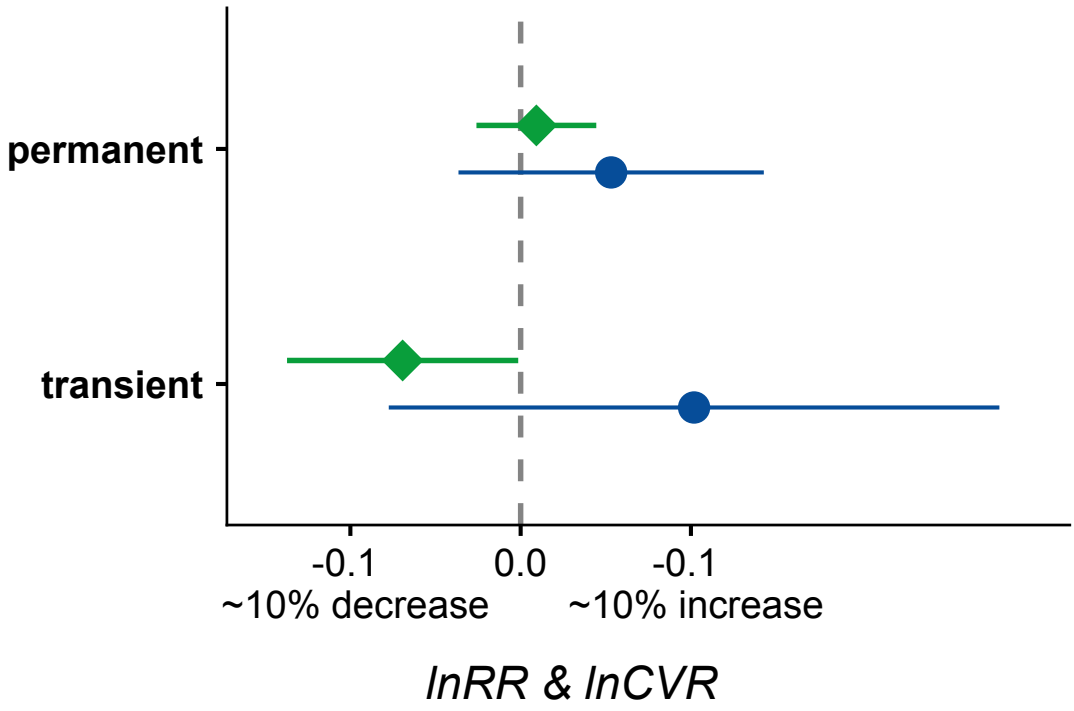

Figure S8

Meta-regression results for differences in phenotypic means and variability split by treatment condition (transient treatments are treatments that ended before the fish were measured). The dashed vertical line is the line of no phenotypic effect. Green diamonds are the estimates for *lnRR*; transient treatments result in significant decreases in trait means. Blue circles are the estimates for *lnCVR*; both treatment conditions show non-significant tendencies to increase difference in variability.

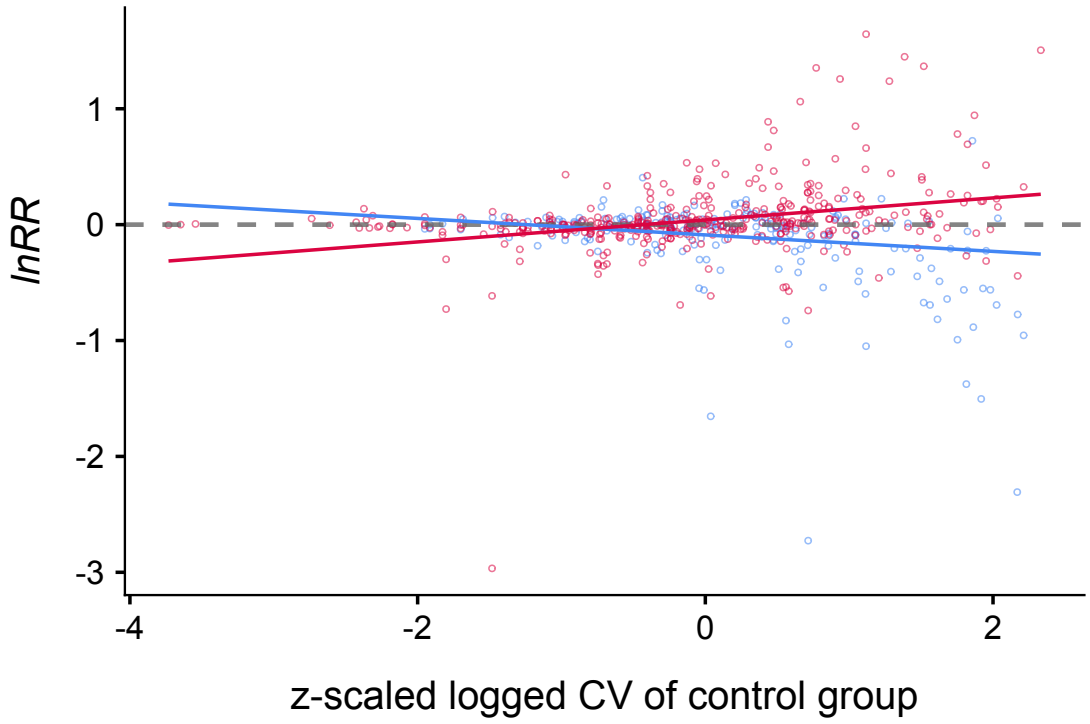

Figure S9

The amount of variability in the control group affects the mean phenotypic difference in the treatment group, for both cool and warm treatments (blue and red, respectively). Open circles are the raw values. The dashed vertical line is the line of no phenotypic difference; values to the right indicate a mean increase, and values to the left indicate a mean decrease.

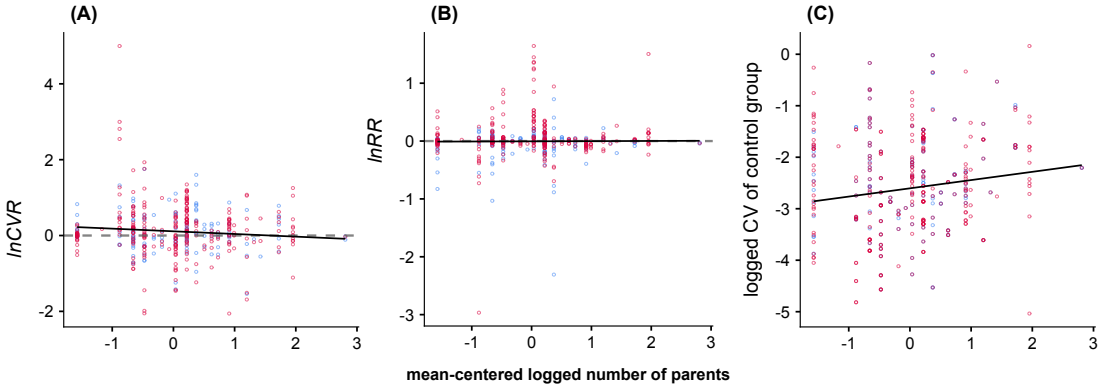

Figure S10

The relationship between the number of parents who spawn a group of fish, and the effect of developmental temperature treatments on phenotypes of those fish. (A) and (B): Groups of fish from more diverse sets of parents did not show greater plastic responses in either means or variance. (C) Control fish from more diverse sets of parents do not show greater amount of phenotypic variability.

Table S1

List of studies included in the meta-analysis.

Authors	Title	Journal	Volume	Pages	Year	DOI
Abdel I., Abellán E., López-Albors O., Valdés P., Nortes M.J., García-Alcázar A.	Abnormalities in the juvenile stage of sea bass (*Dicentrarchus labrax* L.) reared at different temperatures: types, prevalence and effect on growth	Aquaculture International	12	523-538	2004	10.1007/s10499-004-0349-9
Ackerly K.L., Ward A.B.	How temperature-induced variation in musculoskeletal anatomy affects escape performance and survival of zebrafish (*Danio rerio*)	Journal of Experimental Zoology Part A: Ecological Genetics and Physiology	325	25-40	2016	10.1002/jez.1993
Alami-Durante H., Rouel M., Kentouri M.	New insights into temperature-induced white muscle growth plasticity during *Dicentrarchus labrax* early life: a developmental and allometric study	Marine Biology	149	1551-1565	2006	10.1007/s00227-006-0304-6
Albokhadaim I., Hammond C.L., Ashton C., Simbi B.H., Bayol S., Farrington S., Stickl and , N.	Larval programming of post-hatch muscle growth and activity in Atlantic salmon (*Salmo salar*)	Journal of Experimental Biology	210	1735-1741	2007	10.1242/jeb.003194
Anastasiadi D., DÃaz N., Piferrer F.	Small ocean temperature increases elicit stage-dependent changes in DNA methylation and gene expression in a fish, the European sea bass	Scientific Reports	7		2017	10.1038/s41598-017-10861-6
Arul, V.	Effect of temperature on yolk utilization of *Channa striatus*	Journal of Thermal Biology	16	1-5	1991	10.1016/0306-4565(91)90043-2
Aydın İ., Küçük E., Şahin T., Kumlu M.	Effect of temperature on reversed asymmetry in hatchery-reared flounder (*Platichthys flesus luscus* Pallas, 1811)	Turkish Journal of Fisheries and Aquatic Sciences	15	737-740	2015	10.4194/1303-2712-v15_3_17
Barrionuevo W.R., Burggren W.W.	O2 consumption and heart rate in developing zebrafish (*Danio rerio*): influence of temperature and ambient O2	American Journal of Physiology	276	R505-R513	1999	10.1152/ajpregu.1999.276.2.R505
Berlinsky D.L., Taylor J.C., Howell R.A., Bradley T.M., Smith T.I.J.	The effects of temperature and salinity on early life stages of Black Sea Bass *Centropristis striata*	Journal of the World Aquaculture Society	35	335-344	2004	10.1111/j.1749-7345.2004.tb00097.x

Brooks S., Johnston I.A.	Influence of development and rearing temperature on the distribution, ultrastructure and myosin sub-unit composition of myotomal muscle-fibre types in the plaice *Pleuronectes platessa*	Marine Biology	117	501-513	1993	10.1007/BF00349326
Brown C.A., Gothreaux C.T., Green C.C.	Effects of temperature and salinity during incubation on hatching and yolk utilization of gulf killifish *Fundulus grandis* embryos	Aquaculture	315	335-339	2011	10.1016/j.aquaculture.2011.02.041
Burt J.M., Hinch S.G., Patterson D.A.	Parental identity influences progeny responses to incubation thermal stress in sockeye salmon *Onchorhynchus nerka*	Journal of Fish Biology	80	444-462	2012	10.1111/j.1095-8649.2011.03190.x
Canino, M.F.	Effects of temperature and food availability on growth and RNA/DNA ratios of walleye pollock *Theragra chalcogramma* (Pallas) eggs and larvae	Journal of Experimental Marine Biology and Ecology	175	1-16	1994	10.1016/0022-0981(94)90173-2
Carey G.R., Franklin C.E.	Effect of incubation and rearing temperature on locomotor ability in barramundi, *Lates calcarifer* Bloch, 1790	Marine and Freshwater Research	60	203-210	2009	10.1071/MF07250
Carmichael, G.J.	Scale-number differences of central stonerollers incubated and reared at different temperatures	Transactions of the American Fisheries Society	112	441-444	1983	10.1577/1548-8659(1983)112[441:SDOCSI]2.0.CO;2
Colchen T., Teletchea F., Fontaine P., Pasquet A.	Temperature modifies activity, inter-individual relationships and group structure in a fish	Current Zoology	63	175-183	2017	10.1093/cz/zow048
de Assis, JMF and Carvalho, RF and Barbosa, L and Agostinho, CA and Dal Pal-Silva, M	Effects of incubation temperature on muscle morphology and growth in the pacu (*Piaractus mesopotamicus*)	Aquaculture	237	251-267	2004	10.1016/j.aquaculture.2004.04.022
DiMaria R.A., Miller J.A., Hurst T.P.	Temperature and growth effects on otolith elemental chemistry of larval Pacific cod, *Gadus macrocephalus*	Environmental Biology of Fishes	89	453-462	2010	10.1007/s10641-010-9665-2
Dou S.Z., Masuda R., Tanaka M., Tsukamoto K.	Effects of temperature and delayed initial feeding on the survival and growth of Japanese flounder larvae	Journal of Fish Biology	66	362-377	2005	10.1111/j.1095-8649.2004.00601.x
Drozd B., Kouril J., Blaha M., Hamackova J.	Effect of temperature on early life history in weatherfish, *Misgurnus fossilis* (L. 1758)	Knowledge and Management of Aquatic Ecosystems	392	-	2009	10.1051/kmae/2009010

Galloway T.F., Kjørsvik E., Kryvi H.	Effect of temperature on viability and axial muscle development in embryos and yolk sac larvae of the Northeast Arctic Cod (*Gadus morhua*)	Marine Biology	132	559-567	1998	10.1007/s00227005042 1
Georga I., Koumoundouros G.	Thermally induced plasticity of body shape in adult zebrafish *Danio rerio* (Hamilton, 1822)	Journal of Morphology	271	1319-1327	2010	10.1002/jmor.10874
Hall T.E., Johnston I.A.	Temperature and developmental plasticity during embryogenesis in the Atlantic cod *Gadus morhua* L.	Marine Biology	142	833-840	2003	10.1007/s00227-003-1030-y
Hernández-Rubio M. C. and G. Figueroa-Lucero	Effects of temperature and salinity during the embryonic period of *Chirostoom humboldtainum* and *Chirostoma riojai* (Atherinopsidae) until hatching	Hidrobiologica	23	365-373	2013	
Jeuthe H., Brännäs E., Nilsson J.	Effects of variable egg incubation temperatures on the embryonic development in Arctic charr *Salvelinus alpinus*	Aquaculture Research	47	3753-3764	2016	10.1111/are.12825
Johnston I.A., Cole N.J., Abercromby M., Vieira V.L.A.	Embryonic temperature modulates muscle growth characteristics in larval and juvenile herring	Journal of Experimental Biology	201	623-646	1998	
Jones A.C., Lim D., Wayne-Thompson J.J., Urbina N., Puentedura G., Hillyard S., Breukelen F.V.	Oxygen consumption is limited at an ecologically relevant rearing temperature in pupfish eggs	Journal of Experimental Zoology Part A: Ecological Genetics and Physiology	325	539-547	2016	10.1002/jez.2048
Kamler E., Keckeis H., Bauer-Nemeschkal E.	Temperature-induced changes of survival, development and yolk partitioning in *Chondrostoma nasus*	Journal of Fish Biology	53	658-682	1998	10.1006/jfbi.1998.0733
Korwin-Kossakowski M.	The influence of temperature during the embryonic period on larval growth and development in carp, *Cyprinus carpio* L., and grass carp, *Ctenopharyngodon idella* (Val.): Theoretical and practical aspects	Archives of Polish Fisheries	16	231-314	2008	10.2478/s10086-008-0020-6
Koumoundouros G., Divanach P., Anezaki L., Kentouri M.	Temperature-induced ontogenetic plasticity in sea bass (*Dicentrarchus labrax*)	Marine Biology	139	817-830	2001	10.1007/s00227010063 5
Kucharczyk D., Luczynski M., Kujawa	Effect of temperature on embryonic and larval development of bream (*Abramis brama* L.)	Aquatic Sciences	59	214-224	1997	10.1007/s00270050009

R., Czerkies P.						
Lõhmus M., Fredrik Sundström L., Björklund M., Devlin R.H.	Genotype-temperature interaction in the regulation of development, growth, and morphometrics in wild-type, and growth hormone transgenic coho salmon	PLoS ONE	5	-	2010	10.1371/journal.pone.0009980
MacGregor R.B., MacCrimmon H.R.	Evidence of genetic and environmental influences on meristic variation in the rainbow trout, *Salmo gairdneri* Richardson	Environmental Biology of Fishes	2	25-33	1977	10.1007/BF00001413
Mari L., Garaud L., Evanno G., Lasne E.	Higher temperature exacerbates the impact of sediments on embryo performances in a salmonid	Biology Letters	12	-	2016	10.1098/rsbl.2016.0745
Martell D.J., Kieffer J.D., Trippel E.A.	Effects of temperature during early life history on embryonic and larval development and growth in haddock	Journal of Fish Biology	66	1558-1575	2005	10.1111/j.0022-1112.2005.00699.x
Matschak T.W., Hopcroft T., Mason P.S., Crook A.R., Stickl and , N.C.	Temperature and oxygen tension influence the development of muscle cellularity in embryonic rainbow trout	Journal of Fish Biology	53	581-590	1998	10.1006/jfbi.1998.0726
McCarthy I., Moksness E., Pavlov D.A.	The effects of temperature on growth rate and growth efficiency of juvenile common wolffish	Aquaculture International	6	207-218	1998	10.1023/A:1009202710566
McGurk, M.D.	Effects of delayed feeding and temperature on the age of irreversible starvation and on the rates of growth and mortality of pacific herring larvae	Marine Biology	84	13-26	1984	10.1007/BF00394522
Morehead D.T., Hart P.R.	Effect of temperature on hatching success and size of striped trumpeter (*Latris lineata*) larvae	Aquaculture	220	595-606	2003	10.1016/S0044-8486(02)00636-1
Nissling, A.	Effects of temperature on egg and larval survival of cod (*Gadus morhua*) and sprat (*Sprattus sprattus*) in the Baltic Sea - implications for stock development	Hydrobiologia	514	115-123	2004	10.1023/B:hydr.0000018212.88053.aa
Pan, T.C.F., von Herbing, I.H.	Metabolic plasticity in development: synergistic responses to high temperature and hypoxia in zebrafish, *Danio rerio*	Journal Of Experimental Zoology Part A-ecological Genetics And Physiology	327	189-199	2017	10.1002/jez.2092
Pavlidis M., Koumoundouros G., Sterioti A., Somarakis S., Divanach P.,	Evidence of temperature-dependent sex determination in the European sea bass (*Dicentrarchus labrax* L.)	Journal of Experimental Zoology	287	225-232	2000	10.1002/1097-010X(20000801)287:3<225::AID-JEZ4>3.0.

Kentouri M.						CO;2-D
Pavlov D.A., Moksness E.	Development of the axial skeleton in wolffish, *Anarchichas lupus* (Pisces, Anarchichadidae), at different temperatures	Environmental Biology of Fishes	49	401-416	1997	10.1023/A:1007352802352
Peck M.A., Buckley L.J.	Measurements of larval Atlantic cod (*Gadus morhua*) routine metabolism: temperature effects, diel differences and individual-based modeling	Journal of Applied Ichthyology	24	144-149	2008	10.1111/j.1439-0426.2007.01004.x
Perrichon P., Pasparakis C., Mager E.M., Stieglitz J.D., Benetti D.D., Grosell M., Burggren W.W.	Morphology and cardiac physiology are differentially affected by temperature in developing larvae of the marine fish mahi-mahi (*Coryphaena hippurus*)	Biology Open	6	800-809	2017	10.1242/bio.025692
Peterson R.H., Martin-Robichaud D.J., Berge Å.	Influence of temperature and salinity on length and yolk utilization of striped bass larvae	Aquaculture International	4	89-103	1996	10.1007/BF00140591
Politis S.N., Mazurais D., Servili A., Zambonino-Infante J.-L., Miest J.J., Sørensen S.R., Tomkiewicz J., Butts I.A.E.	Temperature effects on gene expression and morphological development of european eel, *Anguilla anguilla* larvae	PLoS ONE	12		2017	10.1371/journal.pone.0182726
Raine J.C., Leatherl and , J.F.	Ontogeny of thyroid tissue and tissue thyroid hormone clearance in rainbow trout embryos reared at two temperatures	Fish Physiology and Biochemistry	20	209-217	1999	10.1023/A:1007775807438
Réalis-Doyelle E., Pasquet A., Fontaine P., Teletchea F.	How climate change may affect the early life stages of one of the most common freshwater fish species worldwide: the common carp (*Cyprinus carpio*)	Hydrobiologia		1-11	2017	10.1007/s10750-017-3324-y
Savoie A., Le François N.R., Cahu C., Blier P.U., Andreassen I.	Do protein hydrolysates improve survival and growth of newly-hatched spotted wolffish (*Anarhichas minor*), a non-metamorphic aquaculture fish species?	Aquaculture	261	782-788	2006	10.1016/j.aquaculture.2006.08.047
Schnurr M.E., Yin Y., Scott G.R.	Temperature during embryonic development has persistent effects on metabolic enzymes in the muscle of zebrafish	Journal of Experimental Biology	217	1370-1380	2014	10.1242/jeb.094037

Schönweger G., Schwerte T., Pelster B.	Temperature-dependent development of cardiac activity in unrestrained larvae of the minnow *Phoxinus phoxinus*	American Journal of Physiology - Regulatory Integrative and Comparative Physiology	279	R1634-R1640	2000	10.1152/ajpregu.2000.279.5.R1634
Sfakianakis D.G., Leris I., Kentouri M.	Effect of developmental temperature on swimming performance of zebrafish (*Danio rerio*) juveniles	Environmental Biology of Fishes	90	421-427	2011	10.1007/s10641-010-9751-5
Sfakianakis D.G., Leris I., Laggis A., Kentouri M.	The effect of rearing temperature on body shape and meristic characters in zebrafish (*Danio rerio*) juveniles	Environmental Biology of Fishes	92	197-205	2011	10.1007/s10641-011-9833-z
Sfakianakis D.G., Papadakis I.E., Papadaki M., Sigelaki I., Mylonas C.C.	Influence of rearing temperature during early life on sex differentiation, haemal lordosis and subsequent growth during the whole production cycle in European sea bass *Dicentrarchus labrax*	Aquaculture	412	179-185	2013	10.1016/j.aquaculture.2013.07.033
Silva P., Valente L.M.P., Olmedo M., ALvarez-BlaZquez B., Galante M.H., Monteiro R.A.F., Rocha E.	Influence of temperature on muscle fibre hyperplasia and hypertrophy in larvae of blackspot seabream, *Pagellus bogaraveo*	Aquaculture Research	42	331-340	2011	10.1111/j.1365-2109.2010.02627.x
Sweet J.G., Kinne O.	The effects of various temperature-salinity combinations on the body form of newly hatched *Cyprinodon macularius* (Teleostei)	Helgoländer Wissenschaftliche Meeresuntersuchungen	11	49-69	1964	10.1007/BF01611131
Usher M.L., Stickl and N.C., Thorpe J.E.	Muscle development in Atlantic salmon (*Salmo salar*) embryos and the effect of temperature on muscle cellularity	Journal of Fish Biology	44	953-964	1994	10.1111/j.1095-8649.1994.tb01267.x
Walsh W.A., Swanson C., Lee C.S.	Effects of development, temperature and salinity on metabolism in eggs and yolk-sac larvae of milkfish, *Chanos chanos* (Forsskål)	Journal of Fish Biology	39	115-125	1991	10.1111/j.1095-8649.1991.tb04346.x
Wen W., Huang X., Chen Q., Feng L., Wei L.	Temperature effects on early development and biochemical dynamics of a marine fish, *Inimicus japonicus*	Journal of Experimental Marine Biology and Ecology	442	22-29	2013	10.1016/j.jembe.2013.01.025
Whitney C.K., Hinch S.G., Patterson D.A.	Population origin and water temperature affect development timing in embryonic sockeye salmon	Transactions of the American Fisheries Society	143	1316-1329	2014	10.1080/00028487.2014.935481

Zummo G., Farina F., Tota B., Johnston I.A.	Influence of temperature on the development of the heart ventricle in herring (*Clupea harengus*) larvae	Journal of Experimental Zoology	275	196-203	1996	10.1002/(SICI)1097-010X(19960601/15)275:2/3<196::AID-JEZ11>3.0.CO;2-I

Table S2

Meta-data: full list of extracted moderator variables and their description

Field Name	Description
es_ID	unique ID for each row of data (i.e. each effect size)
species_ID	unique ID for each species
paper_ID	unique ID for each paper
group_ID	unique ID for each group of fish. The group is the clutch or pooled clutches of eggs that are split between incubator treatments
include	whether to include in analysis (yes/no)
exclusion_reason	reason why effect size is excluded (e.g. variance presented as zero)
notes	general comments
experimental_design	three options. (1) split pooled families = fertilized egg from multiple males/females mixed together and split between temperature treatments; split individual families = fertilized eggs from multiple males/females split and incubated separately; or split single family = fertilized eggs from one male/female pairing split between temperature treatments
cont_condition	whether the control temperature treatment was "controlled" or "ambient". Controlled = temperature maintained within a limited range (e.g. with incubator or thermostat). Ambient = temperature allowed to fluctuate with ambient conditions
temp_cont	temperature of the control group
temp_treat	temperature of the treatment group
deg_dif	degree difference between the control and treatment group
temp_common	if the treatment was transient, then the temperature that all fish were kept at after the manipulation period
treat_start_days	day post-fertilization that the treatment started (day of fertilization = day 0)
treat_end_days	day post-fertilization that the treatment ended (or the day the fish were measured)
treat_start_prop_maturity	time when the treatment started as a proportion of the average number of days the species takes to reach sexual maturity (treat_start_days/days_sexual_maturity)
treat_end_prop_maturity	time when the treatment ended as a proportion of the average number of days the species takes to reach sexual maturity (treat_end_days/days_sexual_maturity)
data_location	where in the paper the data is location
data_presentation	text or figure
variance_stat	original variance statistic presented in paper (sd = standard deviation, se = standard error, cv = coefficient of variation, cv100 = coefficient of variation*100, v = variance, IQR = interquartile range). For statistics other than sd, sd is calculated automatically in the database
measure_type	type of trait measured (12 options: behaviour, morphology, growth, metabolism, reproduction, size, swim performance, muscle fibre, condition, heart, bone number, scale number)
measure_description	longer description of the type of treatment measured
time_controlled	either absolute or developmental. Absolute = control and treatment fish measured on the same day post-fertilization. Developmental = control and treatment fish measured on different days, but the same developmental stage

control_time_measured_days	day fish in the control group were measured (days post-fertilization)
treat_time_measured_days	day fish in the treatment group were measured (days post-fertilization)
control_measured_prop_maturity	time fish in the control group were measured as a proportion of time taken to reach sexual maturity (control_time_measured_days/days_sexual_maturity)
treat_measured_prop_maturity	time fish in the treatment group were measured as a proportion of time taken to reach sexual maturity (treatment_time_measured_days/days_sexual_maturity)
n_control	sample size of fish in the control group
n_treat	sample size of fish in the treatment group
mean_control	mean of the control group
mean_treat	mean of the treatment group
sd_control	standard deviation of the control group
sd_treat	standard deviation of the treatment group
control_temp_difference	difference between the control temperature and the "optimal" temperature for the species (temp_cont - temp_optimal_mid)
number_mothers	number of female fish who contributed eggs to the fish group
number_fathers	number of male fish who contributed sperm to the fish group
number_parents	total number of parents (number_mothers + number_fathers)
species_notes	general notes on the species
common_name	common name for the species of fish
species_name	species name for the fish
NCBI_tax_ID	ID of the species on the NCBI Taxonomy Browser (https://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/), for finding taxonomic information about the species
AnAge_ID	ID of the species on AnAge: The Animal Ageing and Longevity Database (http://genomics.senescence.info/species/), for finding life-history information about the species
fishbase_ID	ID of the species on fishbase (https://www.fishbase.de/)
fishbase_URL	URL for the species page on fishbase (for use in web scraping information), for finding life-history and temperature information about the species
genus	species genus
family	species family
order	species order
average_lifespan_years	average lifespan of the fish species
maximum_lifespan_years	maximum lifespan of the fish species
days_sexual_maturity	average days taken to reach sexual maturiy
max_adult_weight_g	maximum adult weight of the species (grams)
average_adult_weight_g	average adult weight of the species (grams)
max_length_cm	maximum length of the species (cm)
average_length_cm	average length of the species (cm)
temp_crit_min	minimum critical temperature of the species
temp_optimal_min	lower limit of the optimal temperature range of the species
temp_optimal_mid	midpoint of the optimal temperature range of the species
temp_optimal_max	upper limit of the optimal temperature range of the species
temp_crit_max	maximum critical temperature of the species
temp_optimal_range	range of optimal temperatures (temp_optimal_max - temp_optimal_min)

references	references of additional sources of information for the species
fishbase_environment	preferred environment, according to fishbase
fishbase_size	size according to fishbase
fishbase_mating	mating system according to fishbase
ad_number_of_offspring	number of offspring, according to the website "Animal Diversity Web"
ad_male_age_maturity	time taken for males of the species to reach sexual maturity, according to the website "Animal Diversity Web"
ad_female_age_maturity	time taken for females of the species to reach sexual maturity, according to the website "Animal Diversity Web"
ad_wild_lifespan	lifespan of the species in the wild, according to the website "Animal Diversity Web"
ad_captive_lifespan	lifespan of the species in captivity, according to the website "Animal Diversity Web"
ad_temperature	information about temperature preferences of the species, according to the website "Animal Diversity Web"
multiple_ages_measured	whether or not the fish were measured at multiple timepoints
multiple_temperatures_measured	whether or not multiple warm or multiple cool treatments were measured
extreme_treatment_not_extracted	whether or not a temperature group was excluded due to very low survival (<10%)
extreme_treatment_survival	survival rates in the excluded temperature group
source_obtained	whether the paper was obtained from the search string, forwards, or backwards search
treat_type	type of treatment: cool (colder than the control temperature) or warm (warmer than the control temperature)
treat_length_days	length of the treatment in days (treat_time_measured_days - treat_start_days)
treat_length_maturity	length of the treatment as a fraction of days to reach sexual maturity (treat_length_days/days_sexual_maturity)
time_since_treat_ended_days	number of days between the fish being held at the temperature treatment and being measured (treat_time_measured_days - treat_end_days; 0 days for permanent treatments)
time_since_treat_ended_maturity	time between the fish being held at the temperature treatment and being measured, expressed as a propotion of time taken to reach sexual maturity (time_since_treat_ended_days/days_sexual_maturity)
treat_condition	two options: permanent (treatment maintained until fish measured) or transient (treatment fish brought back to control temperature before being measured)
treat_dist_limit	distance of treatment from the upper limit of the optimal thermal range for the species
trait.type	four options: (1) behaviour (behaviour); (2) life-history (growth); (3) morphology (bone number, condition, morphology, scale number, size); and (4) physiology (heart, metabolism, muscle fibre, swim performance)
deg_dif.C	mean-centered degree difference (mean = 0)
deg_dif.Ctreat	within-treatment mean-centered degree difference (mean = 0 for each treatment group)
deg_dif.Z	z-scaled degree difference (mean = 0 and sd = 1)
deg_dif.Ztreat	within-treatment z-scaled degree difference (mean = 0 and sd = 1 for each treatment group)
deg_dif.abs	absolute value of degree difference (so that cool treatments are no longer negative values)
deg_dif.C.abs	mean-centered absolute degree difference (mean = 0)

deg_dif.Ctreat.abs	within-treatment mean-centered absolute degree difference (mean = 0 for each treatment group)
deg_dif.Z.abs	z-scaled absolute degree difference (mean = 0 and sd = 1)
deg_dif.Ztreat.abs	within-treatment z-scaled absolute degree difference (mean = 0 and sd = 1 for each treatment group)
deg_dif.3.C.abs	treatment (mean+3)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (3 degrees above mean = 0)
deg_dif.6.C.abs	treatment (mean+6)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (6 degrees above mean = 0)
deg_dif.9.C.abs	treatment (mean+9)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (3 degrees above mean = 0)
deg_dif.3.Ctreat.abs	within-treatment (mean+3)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (3 degrees above mean = 0 for each treatment group)
deg_dif.6.Ctreat.abs	within-treatment (mean+6)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (6 degrees above mean = 0 for each treatment group)
deg_dif.9.Ctreat.abs	within-treatment (mean+9)-centered absolute degree difference, with an additional 3 degrees subtracted from each value (9 degrees above mean = 0 for each treatment group)
treat_length_days.C	mean-centered length of the treatment (mean = 0 days)
treat_length_days.Ctreat	within-treatment mean-centered length of the treatment (mean = 0 days for each treatment group)
treat_length_days.Z	z-scaled length of the treatment (mean = 0 and sd = 1 days)
treat_length_days.Ztreat	within-treatment z-scaled length of the treatment (mean = 0 and sd = 1 days for each treatment group)
treat_length_maturity.C	mean-centered length of treatment as a proportion of days to sexual maturity (mean = 0)
treat_length_maturity.Ctreat	within-treatment mean-centered length of treatment as a proportion of days to sexual maturity (mean = 0 for each treatment group)
treat_length_maturity.Z	z-scaled length of treatment as a proportion of days to sexual maturity (mean = 0 and sd = 1)
treat_length_maturity.Ztreat	within-treatment z-scaled length of treatment as a proportion of days to sexual maturity (mean = 0 and sd = 1 for each treatment group)
log.treat_length_days	natural logarithm of the length of treatment
log.treat_length_days.C	mean-centered natural logarithm of the length of treatment
log.treat_length_days.Ctreat	within-treatment mean-centered natural logarithm of the length of treatment
log.treat_length_days.Z	z-scaled natural logarithm of the length of treatment
log.treat_length_days.Ztreat	within-treatment z-scaled natural logarithm of the length of treatment
log.treat_length_maturity	natural logarithm of the length of treatment as a proportion of time to reach sexual maturity
log.treat_length_maturity.C	mean-centered natural logarithm of the length of treatment as a proportion of time to reach sexual maturity
log.treat_length_maturity.Ctreat	within-treatment mean-centered natural logarithm of the length of treatment as a proportion of time to reach sexual maturity
log.treat_length_maturity.Z	z-scaled natural logarithm of the length of treatment as a proportion of time to reach sexual maturity
log.treat_length_maturity.Ztreat	within-treatment z-scaled natural logarithm of the length of treatment as a proportion of time to reach sexual maturity
treat_start_days.C	mean-centered day the treatment started

treat_start_days.Ctreat	within-treatment mean-centered day the treatment started
treat_start_days.Z	z-scaled day the treatment started
treat_start_days.Ztreat	within-treatment z-scaled day the treatment started
treat_start_prop_maturity.C	mean-centered day the treatment started as a proportion of days taken to reach sexual maturity
treat_start_prop_maturity.Ctreat	within-treatment mean-centered day the treatment started as a proportion of days taken to reach sexual maturity
treat_start_prop_maturity.Z	z-scaled day the treatment started as a proportion of days taken to reach sexual maturity
treat_start_prop_maturity.Ztreat	within-treatment z-scaled day the treatment started as a proportion of days taken to reach sexual maturity
ln_number_parents	natural logarithm of the number of male and female fish who spawned the fish group
C.ln_number_parents	mean-centered natural logarithm of the number of male and female fish who spawned the fish group
Z.ln_number_parents	z-scaled natural logarithm of the number of male and female fish who spawned the fish group
C.treat_dist_limit	mean-centered distance of the temperature treatment from the upper limit of the optimal temperature range for the species
Z.treat_dist_limit	z-scaled distance of the temperature treatment from the upper limit of the optimal temperature range for the species
CVR	logged coefficient of variation (lnCVR)
VCVR	sampling variance for the logged coefficient of variation (lnCVR)
RR	logged response ratio (lnRR)
VRR	sampling variance for the logged respond ratio (lnRR)
SMD	standardised mean difference (Hedge's g)
VSMD	sampling variance for the standardised mean difference (Hedge's g)
CV_control	logged coefficient of variation for the control group (lnCV)
ZCV_control	sampling variance for the logged coefficient of variation for the control group (lnCV)
Ztreat.CV_control	within-treatment z-scaled logged coefficient of variation for the control group (lnCV)

Table S3

Model diagnostics for difference combinations of 0, 1 or 2 random effects from 5 possible options: unit ID, group ID, paper ID, species, and phylogeny (modelled with a phylogenetic relatedness correlation matrix). All models assume no covariance between effect sizes from the same group of fish.

Measure	Random Effect	N levels	Variance	AIC
lnCVR	none			3845
lnRR				47309
lnCVR	group ID	84	0.114	2512
lnRR		84	0.021	33193
lnCVR	paper ID	62	0.122	2746
lnRR		62	0.028	33940
lnCVR	species	43	0.090	3188
lnRR		43	0.013	39456
lnCVR	phylogeny	43	2.051	3237
lnRR		43	0.270	39502
lnCVR	group ID	84	0.081	1081
	unit ID	630	0.188	
lnRR	group ID	84	0.013	107
	unit ID	630	0.041	
lnCVR	paper ID	62	0.084	1090
	unit ID	630	0.199	
lnRR	paper ID	62	0.017	94
	unit ID	630	0.040	
lnCVR	species	43	0.060	1112
	unit ID	630	0.222	
lnRR	species	43	0.008	189
	unit ID	630	0.052	
lnCVR	phylogeny	43	0.093	1141
	unit ID	630	0.245	
lnRR	phylogeny	43	0.060	217
	unit ID	630	0.054	

Table S4

Results of meta-analytic and meta-regression models for variances differences (*lnCVR*) between treatment and control groups, fit using *rma.mv*. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Model**	**Treatment**	**Coefficient**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnCVR								
	meta-analytic	all	intercept	0	0.070	-0.011	0.150	630
				0.5	0.086	-0.011	0.182	
	meta-regression	warm	intercept	0	**0.088**	**0.002**	**0.173**	410
				0.5	**0.106**	**0.005**	**0.207**	
		cool	intercept	0	0.031	-0.072	0.133	220
				0.5	0.043	-0.074	0.161	
		warm-cool difference	slope	0	-0.057	-0.151	0.037	
				0.5	-0.062	-0.162	0.037	

Measure	**Model**	**Covariance**		**Random effects**		**Heterogeneity**		
				N levels	Sigma 2	I^2_{Total}	$I^2_{group\_ID}$	$I^2_{unit\_ID}$
lnCVR	meta-analytic							
		0	group_ID	84	0.083	86.7	26.5	60.2
			unit_ID	630	0.188			
		0.5	group_ID	84	0.084	88.8	22.5	66.3
			unit_ID	630	0.246			

Table S5

Results of meta-analytic and meta-regression models for the slope of the difference in variability (*lnSD*) between treatment and control groups, fit using *MCMCglmm*. Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Treatment**	**Coefficient**	**Fixed effects**					
			Mode	Mean	SD	HPD.lb	HPD.ub	*k*
lnSD								
	all	control-treatment difference	**0.102**	**0.095**	**0.026**	**0.044**	**0.146**	1260
	warm	control-treatment difference	**0.120**	**0.124**	**0.030**	**0.068**	**0.181**	820
	cool	control-treatment difference	0.037	0.038	0.041	-0.042	0.115	440
	warm-cool slope difference	interaction	-0.080	-0.087	0.050	-0.180	0.013	

Table S6

Results of meta-analytic and meta-regression models for variances differences (*lnCVR*) between treatment and control groups, fit using *MCMCglmm*. All models assume sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Model**	**Treatment**	**Coefficient**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR								
	meta-analytic	all	intercept	0.070	0.071	0.045	-0.026	0.153
	meta-regression	warm	intercept	**0.077**	**0.089**	**0.045**	**0.001**	**0.170**
		cool	intercept	0.058	0.032	0.053	-0.072	0.130
		warm-cool difference	slope	-0.068	-0.052	0.047	-0.140	0.042
Measure	**Model**	**Variable**	**N levels**	**Random effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	meta-analytic							
		group_ID	84	0.054	0.064	0.022	0.026	0.110
		unit_ID	630	0.225	0.221	0.016	0.188	0.252
Measure	**Model**		**Heterogeneity**				**DIC**	**R^2**
			Mode	Mean	SD			
lnCVR	meta-analytic						995.03	0.831
		I^2_{Total}	0.968	0.969	0.001			
		$I^2_{group\_ID}$	0.047	0.048	0.016			
		$I^2_{unit\_ID}$	0.758	0.754	0.015			

Table S7

Results of meta-analytic and meta-regression models for mean differences (*lnRR*) between treatment and control groups, fit using *rma.mv*. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Model**	**Treatment**	**Coefficient**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnRR								
	meta-analytic	all	intercept	0	-0.005	-0.038	0.028	630
				0.5	-0.019	-0.061	0.024	
	meta-regression	warm	intercept	0	0.031	-0.003	0.065	410
				0.5	0.035	-0.01	0.08	
		cool	intercept	0	**-0.084**	**-0.125**	**-0.042**	220
				0.5	**-0.133**	**-0.188**	**-0.078**	
		warm-cool difference	slope	0	**-0.115**	**-0.152**	**-0.077**	
				0.5	**-0.169**	**-0.222**	**-0.115**	

Measure	**Model**	**Covariance**		**Random effects**		**Heterogeneity**		
				N levels	Sigma^2	I^2_{Total}	$I^2_{group\_ID}$	$I^2_{unit\_ID}$
lnRR	meta-analytic							
		0	group_ID	84	0.014	99.9	25	75
			unit_ID	630	0.041			
		0.5	group_ID	84	0.017	100	15.5	84.5
			unit_ID	630	0.091			

Table S8

Results of meta-analytic and meta-regression models for mean differences (*lnRR*) between treatment and control groups, fit using *MCMCglmm*. All models assume sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Model**	**Treatment**	**Coefficient**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnRR								
	meta-analytic	all	intercept	-0.010	-0.009	0.016	-0.040	0.022
	meta-regression	warm	intercept	**0.032**	**0.034**	**0.017**	**0.000**	**0.067**
		cool	intercept	**-0.094**	**-0.094**	**0.021**	**-0.134**	**-0.055**
		warm-cool difference	slope	**-0.118**	**-0.128**	**0.020**	**-0.169**	**-0.094**
Measure	**Model**	**Variable**	**N levels**	**Random effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnRR	meta-analytic							
		group_ID	84	0.008	0.009	0.003	0.004	0.014
		unit_ID	630	0.047	0.048	0.004	0.041	0.055
Measure	**Model**		**Heterogeneity**				**DIC**	**R^2**
			Mode	Mean	SD			
lnRR	meta-analytic						-42.875	0.955
		I^2_{Total}	1.000	1.000	0.000			
		$I^2_{group\_ID}$	0.008	0.008	0.003			
		$I^2_{unit\_ID}$	0.947	0.946	0.004			

Table S9

Results of meta-regression models with treatment type and trait type as fixed effects, for mean differences (*lnRR*) between treatment and control groups, fit using rma.mv and *MCMCglmm*. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Method	**Treatment**	**Coefficient**	**Trait**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
rma.mv								
	warm	intercept						
			behaviour	0	0.005	-0.209	0.219	4
				0.5	-0.239	-0.519	0.04	
			life-history	0	**0.322**	**0.124**	**0.52**	4
				0.5	**0.504**	**0.243**	**0.765**	
			morphology	0	0.029	-0.006	0.065	323
				0.5	0.036	-0.011	0.082	
			physiology	0	0.021	-0.038	0.080	79
				0.5	0.021	-0.058	0.099	
	cool	intercept						
			behaviour	0	-0.109	-0.323	0.105	8
				0.5	**-0.405**	**-0.684**	**-0.127**	
			life-history	0	**0.208**	**0.009**	**0.407**	2
				0.5	**0.338**	**0.075**	**0.602**	
			morphology	0	**-0.085**	**-0.127**	**-0.042**	157
				0.5	**-0.130**	**-0.187**	**-0.073**	
			physiology	0	**-0.093**	**-0.156**	**-0.030**	53
				0.5	**-0.145**	**-0.229**	**-0.061**	
	warm-cool difference	slope						
			behaviour	0	**-0.114**	**-0.152**	**-0.076**	
				0.5	**-0.166**	**-0.218**	**-0.113**	
			life-history	0	**-0.114**	**-0.152**	**-0.076**	
				0.5	**-0.166**	**-0.218**	**-0.113**	
			morphology	0	**-0.114**	**-0.152**	**-0.076**	
				0.5	**-0.166**	**-0.218**	**-0.113**	
			physiology	0	**-0.114**	**-0.152**	**-0.076**	
				0.5	**-0.166**	**-0.218**	**-0.113**	

Method	**Treatment**	**Coefficient**	**Trait**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
MCMCglmm								
	warm	intercept						

		behaviour	0.086	0.109	0.117	-0.124	0.332
		life-history	**0.342**	**0.343**	**0.101**	**0.166**	**0.551**
		morphology	**0.037**	**0.032**	**0.017**	**-0.001**	**0.065**
		physiology	0.030	0.020	0.031	-0.041	0.078
cool	intercept						
		behaviour	-0.001	-0.016	0.115	-0.242	0.210
		life-history	**0.190**	**0.216**	**0.106**	**0.014**	**0.429**
		morphology	**-0.096**	**-0.097**	**0.021**	**-0.139**	**-0.057**
		physiology	**-0.114**	**-0.108**	**0.033**	**-0.172**	**-0.040**
warm-cool difference	slope						
		behaviour	**-0.132**	**-0.129**	**0.020**	**-0.170**	**-0.094**
		life-history	**-0.129**	**-0.127**	**0.021**	**-0.168**	**-0.089**
		morphology	**-0.123**	**-0.129**	**0.020**	**-0.170**	**-0.092**
		physiology	**-0.129**	**-0.128**	**0.020**	**-0.167**	**-0.089**

Table S10

Slope results of meta-regression models with treatment type and mean-centered magnitude as fixed effects, for variance differences *(lnCVR*) between treatment and control groups, fit using rma.mv and *MCMCglmm*. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Method**	**Treatment**	**Slope**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnCVR	*rma.mv*							
		warm	degree difference					410
				0	**0.035**	**0.009**	**0.061**	
				0.5	**0.031**	**0.000**	**0.061**	
		cool	degree difference					220
				0	0.007	-0.048	0.062	
				0.5	0.012	-0.049	0.073	
		warm-cool difference	degree difference					
				0	-0.028	-0.086	0.031	
				0.5	-0.018	-0.084	0.047	

Measure	**Method**	**Treatment**	**Slope**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	*MCMCglmm*							
		warm	degree difference	**0.033**	**0.033**	**0.015**	**0.004**	**0.062**
		cool	degree difference	0.000	0.007	0.028	-0.055	0.058
		warm-cool difference	degree difference	-0.032	-0.024	0.030	-0.085	0.032

Table S11

Intercept results of meta-regression models with treatment type and magnitude as fixed effects, for variance differences (*lnCVR*) between treatment and control groups, fit using *rma.mv* and *MCMCglmm*. Intercepts are estimated at the average treatment magnitude, 3 degrees, 6 degrees, and 9 degrees above the mean, where the mean = 3.9 overall, 4.4 for warm treatments, and 3.1 for cool treatments. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Method**	**Treatment**	**Intercept**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnCVR	*rma.mv*							
		overall						630
			mean degree difference	0	0.063	-0.018	0.144	
				0.5	0.079	-0.018	0.175	
			mean + 3 degree difference	0	**0.159**	**0.055**	**0.263**	
				0.5	**0.169**	**0.046**	**0.291**	
			mean + 6 degree difference	0	**0.255**	**0.096**	**0.414**	
				0.5	**0.258**	**0.073**	**0.444**	
			mean + 9 degree difference	0	**0.351**	**0.129**	**0.574**	
				0.5	**0.348**	**0.089**	**0.607**	
		warm						410
			mean degree difference	0	**0.085**	**0.000**	**0.171**	
				0.5	**0.104**	**0.003**	**0.205**	
			mean + 3 degree difference	0	**0.190**	**0.074**	**0.305**	
				0.5	**0.195**	**0.060**	**0.331**	

			mean + 6 degree difference	0	**0.294**	**0.116**	**0.472**	
				0.5	**0.287**	**0.078**	**0.496**	
			mean + 9 degree difference	0	**0.399**	**0.149**	**0.649**	
				0.5	**0.379**	**0.086**	**0.672**	
		cool						220
			mean degree difference	0	0.024	-0.079	0.127	
				0.5	0.031	-0.087	0.149	
			mean + 3 degree difference	0	0.045	-0.144	0.233	
				0.5	0.067	-0.147	0.282	
			mean + 6 degree difference	0	0.066	-0.273	0.404	
				0.5	0.104	-0.277	0.484	
			mean + 9 degree difference	0	0.087	-0.411	0.584	
				0.5	0.140	-0.418	0.697	

Measure	**Method**	**Treatment**	**Intercept**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	*MCMCglmm*							
		overall						
			mean degree difference	0.065	0.061	0.045	-0.033	0.143
			mean + 3 degree difference	**0.159**	**0.155**	**0.055**	**0.045**	**0.256**
			mean + 6 degree difference	**0.248**	**0.251**	**0.084**	**0.093**	**0.410**
			mean + 9 degree difference	**0.352**	**0.347**	**0.115**	**0.120**	**0.555**
		warm						
			mean degree difference	0.064	0.085	0.046	-0.010	0.174
			mean + 3 degree difference	**0.168**	**0.186**	**0.061**	**0.076**	**0.313**
			mean + 6 degree difference	**0.289**	**0.289**	**0.092**	**0.105**	**0.456**

	mean + 9 degree difference	**0.445**	**0.385**	**0.129**	**0.160**	**0.644**
cool						
	mean degree difference	0.048	0.023	0.054	-0.081	0.134
	mean + 3 degree difference	0.097	0.053	0.096	-0.145	0.224
	mean + 6 degree difference	0.035	0.076	0.182	-0.269	0.395
	mean + 9 degree difference	0.147	0.094	0.268	-0.436	0.606

Table S12

Slope results of meta-regression models with treatment type and mean-centered magnitude as fixed effects, for mean differences (*lnRR*) between treatment and control groups, fit using rma.mv and *MCMCglmm*. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Method**	**Treatment**	**Slope**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnRR	*rma.mv*							
		warm	degree difference					410
				0	-0.002	-0.014	0.009	
				0.5	-0.010	-0.026	0.005	
		cool	degree difference					220
				0	0.009	-0.014	0.032	
				0.5	0.023	-0.010	0.055	
		warm-cool difference	degree difference					
				0	0.011	-0.013	0.036	
				0.5	0.033	-0.002	0.068	

Measure	**Method**	**Treatment**	**Slope**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnRR	*MCMCglmm*							
		warm	degree difference	-0.005	-0.005	0.006	-0.016	0.007
		cool	degree difference	0.011	0.012	0.012	-0.012	0.035
		warm-cool difference	degree difference	0.012	0.017	0.013	-0.008	0.042

Table S13

Intercept results of meta-regression models with treatment type and magnitude as fixed effects, for variance differences (*lnRR*) between treatment and control groups, fit using rma.mv and *MCMCglmm*. Intercepts are estimated at the average treatment magnitude, 3 degrees, 6 degrees, and 9 degrees above the mean, where the mean = 3.9 overall, 4.4 for warm treatments, and 3.1 for cool treatments. Covariance = 0 assumes no correlation between sampling variances from the same fish group. Covariance = 0.5 assumes sampling variances for the same group have a 0.5 correlation (i.e. more conservative model). Effects with 95% confidence intervals (CI) not crossing zero are indicated in bold. *k* - number of effect sizes included in the analysis

Measure	**Method**	**Treatment**	**Intercept**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnRR	*rma.mv*							
		overall						630
			mean degree difference	0	-0.007	-0.040	0.026	
				0.5	-0.020	-0.062	0.023	
			mean + 3 degree difference	0	0.016	-0.027	0.060	
				0.5	0.002	-0.057	0.062	
			mean + 6 degree difference	0	0.039	-0.028	0.106	
				0.5	0.025	-0.070	0.119	
			mean + 9 degree difference	0	0.062	-0.033	0.157	
				0.5	0.047	-0.088	0.181	
		warm						410
			mean degree difference	0	0.031	-0.004	0.065	
				0.5	0.034	-0.011	0.079	
			mean + 3 degree difference	0	0.023	-0.024	0.071	
				0.5	0.004	-0.061	0.068	

			mean + 6 degree difference	0	0.016	-0.059	0.090	
				0.5	-0.027	-0.131	0.077	
			mean + 9 degree difference	0	0.008	-0.096	0.113	
				0.5	-0.057	-0.205	0.090	
		cool						220
			mean degree difference	0	**-0.084**	**-0.126**	**-0.043**	
				0.5	**-0.132**	**-0.187**	**-0.077**	
			mean + 3 degree difference	0	-0.057	-0.135	0.020	
				0.5	-0.064	-0.175	0.046	
			mean + 6 degree difference	0	-0.030	-0.170	0.109	
				0.5	0.003	-0.198	0.205	
			mean + 9 degree difference	0	-0.003	-0.209	0.202	
				0.5	0.071	-0.226	0.368	

Measure	**Method**	**Treatment**	**Intercept**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnRR	*MCMCglmm*							
		overall						
			mean degree difference	-0.006	-0.008	0.016	-0.040	0.022
			mean + 3 degree difference	0.016	0.014	0.022	-0.029	0.055
			mean + 6 degree difference	0.023	0.034	0.035	-0.032	0.100
			mean + 9 degree difference	0.041	0.056	0.052	-0.043	0.155
		warm						
			mean degree difference	**0.032**	**0.033**	**0.017**	**0.000**	**0.064**
			mean + 3 degree difference	0.008	0.018	0.025	-0.028	0.066
			mean + 6 degree difference	0.017	0.003	0.037	-0.067	0.076

	mean + 9 degree difference	-0.004	-0.013	0.055	-0.125	0.089
cool						
	mean degree difference	**-0.085**	**-0.095**	**0.021**	**-0.135**	**-0.055**
	mean + 3 degree difference	-0.045	-0.060	0.040	-0.136	0.017
	mean + 6 degree difference	-0.035	-0.023	0.076	-0.156	0.133
	mean + 9 degree difference	0.003	0.011	0.114	-0.195	0.244

Table S14

Meta-regression results for the effects of treatment duration in days (logged days), the day the treatment started, and the distance of the treatment from the upper limit of the thermal optimum, and the number of parents on mean and variance difference (*lnRR* and *lnCVR*). *k* - number of effect sizes included in the analysis

Measure	**Method**	**Coefficient**	**Covariance**	**Fixed effects**			
				Mean	CI.lb	CI.ub	*k*
lnCVR	*rma.mv*						
		treatment duration					630
			0	**0.000**	**-0.002**	**0.001**	
			0.5	**-0.001**	**-0.002**	**0.001**	
		treatment start date					630
			0	**-0.006**	**-0.012**	**0.000**	
			0.5	-0.006	-0.014	0.001	
		logged number of parents					440
			0	-0.070	-0.180	0.039	
			0.5	-0.088	-0.204	0.029	
		distance from thermal limit					628
			0	**-0.011**	**-0.022**	**0.000**	
			0.5	-0.015	-0.027	-0.003	
lnRR	*rma.mv*						
		treatment duration					630
			0	**0.000**	**0.000**	**0.001**	
			0.5	0.000	-0.001	0.001	
		treatment start date					630
			0	0.000	-0.003	0.002	

		0.5	0.000	-0.004	0.004	
	logged number of parents					440
		0	0.003	-0.037	0.043	
		0.5	0.011	-0.040	0.061	
	distance from thermal limit					628
		0	**-0.006**	**-0.010**	**-0.001**	
		0.5	-0.003	-0.010	0.003	

Measure	**Method**	**Coefficient**	**Fixed effects**				
			Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	*MCMCglmm*						
		treatment duration	-0.001	-0.001	0.001	-0.002	0.001
		treatment start date	**-0.006**	**-0.007**	**0.003**	**-0.013**	**-0.001**
		logged number of parents	-0.091	-0.065	0.057	-0.179	0.043
		distance from upper limit	**-0.012**	**-0.012**	**0.006**	**-0.023**	**-0.001**
lnRR	*MCMCglmm*						
		treatment duration	**0.000**	**0.000**	**0.000**	**0.000**	**0.001**
		treatment start date	**-0.007**	**-0.006**	**0.003**	**-0.012**	**0.000**
		logged number of parents	0.006	0.001	0.018	-0.031	0.039
		distance from upper limit	-0.007	-0.006	0.003	-0.011	-0.001

Table S15

Meta-regression results for the effect of whether or not the treatment was permanent or transient (transient = all fish brought back to the same temperature before being measured), on differences in mean and variance *(lnRR* and *lnCVR*). *k* - number of effect sizes included in the analysis

Measure	Method	Treatment Type	Coefficient	Covariance	Fixed effects			
					Mean	CI.lb	CI.ub	*k*
lnCVR	*rma.mv*							
		permanent	intercept	0	0.064	-0.021	0.148	530
				0.5	0.072	-0.029	0.173	
		transient	intercept	0	0.109	-0.055	0.272	100
				0.5	0.160	-0.016	0.335	
		permanent-transient difference	slope	0	0.045	-0.120	0.210	
				0.5	0.088	-0.085	0.261	
lnRR	*rma.mv*							
		permanent	intercept	0	0.005	-0.029	0.039	530
				0.5	-0.002	-0.047	0.043	
		transient	intercept	0	**-0.072**	**-0.137**	**-0.007**	100
				0.5	**-0.109**	**-0.195**	**-0.022**	
		permanent-transient difference	slope	0	**-0.077**	**-0.142**	**-0.013**	
				0.5	**-0.106**	**-0.195**	**-0.018**	

Measure	Method	Treatment Type	Coefficient	Fixed effects				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	*MCMCglmm*							
		permanent	intercept	0.061	0.061	0.044	-0.023	0.145
		transient	intercept	0.093	0.128	0.081	-0.035	0.276
		permanent-transient difference	slope	0.077	0.069	0.082	-0.104	0.218
lnRR	*MCMCglmm*							
		permanent	intercept	0.001	0.003	0.017	-0.030	0.036
		transient	intercept	**-0.068**	**-0.076**	**0.033**	**-0.144**	**-0.014**
		permanent-transient difference	slope	**-0.078**	**-0.079**	**0.033**	**-0.143**	**-0.017**

Table S16

Slope results bivariate meta-regression Results for the effects of the amount of variation in the control group on the mean phenotypic response to a temperature treatment *(lnRR*), for cool and warm treatments. *k* - number of effect sizes included in the analysis

Measure	**Method**	**Slope**	**Treatment**	**Covariance**	**Fixed effects**			
					Mean	CI.lb	CI.ub	*k*
lnRR	*rma.mv*	z-scaled control *lnCV*						
			warm	0	**0.095**	**0.068**	**0.122**	410
				0.5	**0.109**	**0.074**	**0.143**	
			cool	0	**-0.071**	**-0.106**	**-0.036**	220
				0.5	**-0.124**	**-0.167**	**-0.080**	
			warm-cool difference	0	**-0.166**	**-0.205**	**-0.127**	
				0.5	**-0.232**	**-0.281**	**-0.184**	

Measure	**Method**	**Slope**	**Treatment**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
lnRR	*MCMCglmm*	z-scaled control *lnCV*						
			warm	**0.100**	**0.095**	**0.015**	**0.064**	**0.122**
			cool	**0.091**	**0.093**	**0.015**	**0.063**	**0.120**
			warm-cool difference	**-0.175**	**-0.171**	**0.020**	**-0.211**	**-0.133**

Table S17

Results of full model for the differences in variance (*lnCVR*) between control and treatment groups, for the effects of treatment type and the interactions with trait type and treatment magnitude (mean-centered absolute value of degree difference). *k* - number of effect sizes included in the analysis

Method	Treatment	Trait	Coefficient	Covariance	Fixed effects			
					Mean	CI.lb	CI.ub	*k*
rma.mv								
	warm							
		behaviour	intercept	0	0.006	-0.709	0.721	4
				0.5	-0.024	-0.773	0.725	
		behaviour	treatment magnitude (slope)	0	**0.033**	**0.006**	**0.059**	
				0.5	0.028	-0.003	0.058	
		life-history	intercept	0	-0.505	-1.076	0.066	4
				0.5	-0.604	-1.211	0.003	
		life-history	treatment magnitude (slope)	0	**0.033**	**0.006**	**0.059**	
				0.5	0.028	-0.003	0.058	
		morphology	intercept	0	**0.093**	**0.004**	**0.181**	323
				0.5	**0.113**	**0.008**	**0.218**	
		morphology	treatment magnitude (slope)	0	**0.033**	**0.006**	**0.059**	
				0.5	0.028	-0.003	0.058	
		physiology	intercept	0	0.091	-0.078	0.260	79
				0.5	0.089	-0.086	0.265	
		physiology	treatment magnitude (slope)	0	**0.033**	**0.006**	**0.059**	
				0.5	0.028	-0.003	0.058	
	cool							
		behaviour	intercept	0	0.549	-0.039	1.136	8
				0.5	0.485	-0.117	1.087	
		behaviour	treatment magnitude (slope)	0	0.003	-0.052	0.058	

			0.5	0.008	-0.054	0.069	
	life-history	intercept	0	0.339	-0.422	1.099	2
			0.5	0.351	-0.448	1.151	
	life-history	treatment magnitude (slope)	0	0.003	-0.052	0.058	
			0.5	0.008	-0.054	0.069	
	morphology	intercept	0	0.033	-0.076	0.142	157
			0.5	0.036	-0.090	0.162	
	morphology	treatment magnitude (slope)	0	0.003	-0.052	0.058	
			0.5	0.008	-0.054	0.069	
	physiology	intercept	0	-0.081	-0.283	0.120	53
			0.5	-0.048	-0.251	0.155	
	physiology	treatment magnitude (slope)	0	0.003	-0.052	0.058	
			0.5	0.008	-0.054	0.069	
warm-cool difference							
	behaviour	intercept	0	0.543	-0.181	1.266	
			0.5	0.509	-0.215	1.234	
	behaviour	treatment magnitude (slope)	0	-0.030	-0.089	0.030	
			0.5	-0.020	-0.086	0.047	
	life-history	intercept	0	0.844	-0.079	1.767	
			0.5	0.956	-0.016	1.927	
	life-history	treatment magnitude (slope)	0	-0.030	-0.089	0.030	
			0.5	-0.020	-0.086	0.047	
	morphology	intercept	0	-0.060	-0.164	0.045	
			0.5	-0.077	-0.192	0.038	
	morphology	treatment magnitude (slope)	0	-0.030	-0.089	0.030	
			0.5	-0.020	-0.086	0.047	
	physiology	intercept	0	-0.173	-0.390	0.045	
			0.5	-0.138	-0.337	0.062	

		physiology	treatment magnitude (slope)	0	-0.030	-0.089	0.030	
				0.5	-0.020	-0.086	0.047	

Method	**Treatment**	**Trait**	**Coefficient**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
MCMCglmm								
	warm							
		behaviour	intercept	0.036	0.008	0.375	-0.712	0.705
		behaviour	treatment magnitude (slope)	**0.035**	**0.031**	**0.014**	**0.003**	**0.058**
		life-history	intercept	-0.599	-0.553	0.299	-1.126	0.050
		life-history	treatment magnitude (slope)	**0.030**	**0.030**	**0.014**	**0.002**	**0.056**
		morphology	intercept	**0.106**	**0.096**	**0.048**	**0.006**	**0.192**
		morphology	treatment magnitude (slope)	**0.031**	**0.031**	**0.014**	**0.003**	**0.056**
		physiology	intercept	0.056	0.084	0.093	-0.113	0.247
		physiology	treatment magnitude (slope)	**0.036**	**0.031**	**0.013**	**0.006**	**0.058**
	cool							
		behaviour	intercept	0.471	0.571	0.326	-0.065	1.230
		behaviour	treatment magnitude (slope)	0.000	0.003	0.028	-0.049	0.056
		life-history	intercept	0.179	0.331	0.388	-0.471	1.038
		life-history	treatment magnitude (slope)	-0.002	0.003	0.029	-0.051	0.060
		morphology	intercept	0.050	0.032	0.057	-0.083	0.142
		morphology	treatment magnitude (slope)	0.010	0.004	0.030	-0.054	0.062

	physiology	intercept	-0.054	-0.085	0.105	-0.293	0.106
	physiology	treatment magnitude (slope)	0.003	0.003	0.029	-0.054	0.059
warm-cool difference							
	behaviour	intercept	0.619	0.542	0.333	-0.105	1.188
	behaviour	treatment magnitude (slope)	-0.018	-0.028	0.031	-0.088	0.034
	life-history	intercept	1.182	0.879	0.473	-0.063	1.784
	life-history	treatment magnitude (slope)	-0.022	-0.027	0.031	-0.082	0.038
	morphology	intercept	-0.050	-0.060	0.054	-0.160	0.053
	morphology	treatment magnitude (slope)	-0.036	-0.027	0.031	-0.089	0.028
	physiology	intercept	-0.142	-0.160	0.107	-0.370	0.049
	physiology	treatment magnitude (slope)	-0.019	-0.029	0.030	-0.094	0.023

Table S18

Results of full model for the differences in means (*lnRR*) between control and treatment groups, for the effects of treatment type and the interactions with trait type, treatment condition, and variation in the control group (within-treatment *Z*-scaled). *k* - number of effect sizes included in the analysis

Method	Treatment	Trait	Coefficient	Covariance	Fixed effects			
					Mean	CI.lb	CI.ub	*k*
rma.mv								
	warm	behaviour						4
			permanent treatment (intercept)	0	0.146	-0.126	0.418	
				0.5	0.092	-0.269	0.453	
			permanent-transient difference	0	**-0.086**	**-0.159**	**-0.013**	
				0.5	-0.089	-0.188	0.009	
			control variance (slope)	0	**0.107**	**0.079**	**0.135**	
				0.5	**0.120**	**0.084**	**0.156**	
	warm	life-history						4
			permanent treatment (intercept)	0	**0.576**	**0.346**	**0.807**	
				0.5	**0.721**	**0.429**	**1.014**	
			permanent-transient difference	0	**-0.086**	**-0.159**	**-0.013**	
				0.5	-0.089	-0.188	0.009	
			control variance (slope)	0	**0.107**	**0.079**	**0.135**	
				0.5	**0.120**	**0.084**	**0.156**	
	warm	morphology						291
			permanent treatment (intercept)	0	**0.061**	**0.024**	**0.097**	
				0.5	**0.058**	**0.011**	**0.106**	
			permanent-transient difference	0	**-0.086**	**-0.159**	**-0.013**	
				0.5	-0.089	-0.188	0.009	
			control variance (slope)	0	**0.107**	**0.079**	**0.135**	
				0.5	**0.120**	**0.084**	**0.156**	
	warm	physiology						60

		permanent treatment (intercept)	0	-0.017	-0.081	0.046	
			0.5	-0.039	-0.122	0.044	
		permanent-transient difference	0	**-0.086**	**-0.159**	**-0.013**	
			0.5	-0.089	-0.188	0.009	
		control variance (slope)	0	**0.107**	**0.079**	**0.135**	
			0.5	**0.120**	**0.084**	**0.156**	
cool	behaviour						4
		permanent treatment (intercept)	0	-0.125	-0.354	0.103	
			0.5	**-0.406**	**-0.696**	**-0.115**	
		permanent-transient difference	0	**-0.082**	**-0.161**	**-0.004**	
			0.5	-0.090	-0.197	0.016	
		control variance (slope)	0	**-0.073**	**-0.110**	**-0.036**	
			0.5	**-0.123**	**-0.168**	**-0.078**	
cool	life-history						2
		permanent treatment (intercept)	0	-0.201	-0.482	0.080	
			0.5	-0.214	-0.605	0.176	
		permanent-transient difference	0	**-0.082**	**-0.161**	**-0.004**	
			0.5	-0.090	-0.197	0.016	
		control variance (slope)	0	**-0.073**	**-0.110**	**-0.036**	
			0.5	**-0.123**	**-0.168**	**-0.078**	
cool	morphology						128
		permanent treatment (intercept)	0	**-0.085**	**-0.132**	**-0.038**	
			0.5	**-0.123**	**-0.184**	**-0.062**	
		permanent-transient difference	0	**-0.082**	**-0.161**	**-0.004**	
			0.5	-0.090	-0.197	0.016	
		control variance (slope)	0	**-0.073**	**-0.110**	**-0.036**	
			0.5	**-0.123**	**-0.168**	**-0.078**	
cool	physiology						37
		permanent treatment (intercept)	0	-0.039	-0.114	0.036	
			0.5	-0.030	-0.129	0.070	

		permanent-transient difference	0	**-0.082**	**-0.161**	**-0.004**
			0.5	-0.090	-0.197	0.016
		control variance (slope)	0	**-0.073**	**-0.110**	**-0.036**
			0.5	**-0.123**	**-0.168**	**-0.078**
warm-cool difference	behaviour					
		permanent treatment (intercept)	0	-0.272	-0.554	0.011
			0.5	**-0.498**	**-0.861**	**-0.134**
		permanent-transient difference	0	0.003	-0.087	0.094
			0.5	-0.001	-0.125	0.124
		control variance (slope)	0	**-0.180**	**-0.220**	**-0.139**
			0.5	**-0.243**	**-0.292**	**-0.194**
warm-cool difference	life-history					
		permanent treatment (intercept)	0	**-0.777**	**-1.128**	**-0.426**
			0.5	**-0.935**	**-1.411**	**-0.460**
		permanent-transient difference	0	0.003	-0.087	0.094
			0.5	-0.001	-0.125	0.124
		control variance (slope)	0	**-0.180**	**-0.220**	**-0.139**
			0.5	**-0.243**	**-0.292**	**-0.194**
warm-cool difference	morphology					
		permanent treatment (intercept)	0	**-0.145**	**-0.190**	**-0.101**
			0.5	**-0.181**	**-0.241**	**-0.122**
		permanent-transient difference	0	0.003	-0.087	0.094
			0.5	-0.001	-0.125	0.124
		control variance (slope)	0	**-0.180**	**-0.220**	**-0.139**
			0.5	**-0.243**	**-0.292**	**-0.194**
warm-cool difference	physiology					
		permanent treatment (intercept)	0	-0.022	-0.100	0.057
			0.5	0.010	-0.097	0.116

			permanent-transient difference	0		0.003	-0.087	0.094
				0.5		-0.001	-0.125	0.124
			control variance (slope)	0		**-0.180**	**-0.220**	**-0.139**
				0.5		**-0.243**	**-0.292**	**-0.194**

Method	**Treatment**	**Trait**	**Treatment Magnitude**	**Fixed effects**				
				Mode	Mean	SD	HPD.lb	HPD.ub
MCMCglmm								
	warm	behaviour						
			permanent treatment (intercept)	0.176	0.222	0.147	-0.053	0.513
			permanent-transient difference	**-0.094**	**-0.089**	**0.038**	**-0.157**	**-0.007**
			control variance (slope)	0.103	0.104	0.015	0.077	-0.046
	warm	life-history						
			permanent treatment (intercept)	**0.560**	**0.587**	**0.126**	**0.328**	**0.826**
			permanent-transient difference	**-0.099**	**-0.088**	**0.036**	**-0.153**	**-0.014**
			control variance (slope)	**0.111**	**0.105**	**0.015**	**0.075**	**0.927**
	warm	morphology						
			permanent treatment (intercept)	**0.063**	**0.062**	**0.019**	**0.029**	**0.103**
			permanent-transient difference	**-0.097**	**-0.090**	**0.037**	**-0.163**	**-0.018**
			control variance (slope)	**0.098**	**0.104**	**0.015**	**0.074**	**0.174**
	warm	physiology						
			permanent treatment (intercept)	-0.005	-0.014	0.034	-0.081	0.050
			permanent-transient difference	**-0.087**	**-0.088**	**0.038**	**-0.170**	**-0.018**
			control variance (slope)	**0.102**	**0.104**	**0.015**	**0.078**	**0.027**
	cool	behaviour						

		permanent treatment (intercept)	-0.074	-0.060	0.125	-0.344	0.156
		permanent-transient difference	-0.086	-0.080	0.042	-0.157	0.002
		control variance (slope)	-0.079	-0.081	0.020	-0.119	0.924
cool	life-history						
		permanent treatment (intercept)	-0.184	-0.204	0.158	-0.519	0.104
		permanent-transient difference	**-0.082**	**-0.081**	**0.040**	**-0.154**	**-0.001**
		control variance (slope)	**-0.072**	**-0.080**	**0.020**	**-0.123**	**-0.028**
cool	morphology						
		permanent treatment (intercept)	**-0.093**	**-0.093**	**0.023**	**-0.137**	**-0.049**
		permanent-transient difference	-0.085	-0.083	0.042	-0.161	0.002
		control variance (slope)	-0.084	-0.080	0.020	-0.118	0.395
cool	physiology						
		permanent treatment (intercept)	-0.056	-0.042	0.039	-0.123	0.031
		permanent-transient difference	**-0.092**	**-0.083**	**0.041**	**-0.164**	**-0.002**
		control variance (slope)	-0.091	-0.083	0.019	-0.119	0.585
warm-cool difference	behaviour						
		permanent treatment (intercept)	**-0.235**	**-0.285**	**0.142**	**-0.551**	**-0.002**
		permanent-transient difference	0.010	0.006	0.048	-0.100	0.092
		control variance (slope)	**-0.190**	**-0.184**	**0.020**	**-0.220**	**-0.141**
warm-cool difference	life-history						

		permanent treatment (intercept)	**-0.719**	**-0.789**	**0.187**	**-1.158**	**-0.426**
		permanent-transient difference	0.015	0.006	0.047	-0.080	0.103
		control variance (slope)	**-0.187**	**-0.187**	**0.020**	**-0.227**	**-0.147**
warm-cool difference	morphology						
		permanent treatment (intercept)	**-0.157**	**-0.155**	**0.024**	**-0.204**	**-0.111**
		permanent-transient difference	0.002	0.006	0.049	-0.093	0.099
		control variance (slope)	**-0.195**	**-0.185**	**0.021**	**-0.224**	**-0.144**
warm-cool difference	physiology						
		permanent treatment (intercept)	-0.031	-0.027	0.041	-0.110	0.053
		permanent-transient difference	0.000	0.008	0.049	-0.092	0.102
		control variance (slope)	**-0.185**	**-0.185**	**0.021**	**-0.228**	**-0.149**

Table S19

Test of moderators (coefficients) based on the omnibus Wald-type test of all linear combinations, for *metafor* models

N parameters	Moderators	Measure	QM statistic	p-value	QM/Qtotal
2	type of treatment	*lnCVR*	1.421	0.233	0.000
		lnRR	**35.452**	**0.000**	0.001
5	type of treatment * type of trait	*lnRR*	**44.299**	**0.000**	0.001
4	type of treatment * treatment magnitude	*lnCVR*	**8.179**	**0.042**	0.002
		lnRR	**36.213**	**0.000**	0.001
2	treatment duration	*lnCVR*	0.454	0.500	0.000
		lnRR	0.929	0.335	0.000
2	treatment start date	*lnCVR*	**4.340**	**0.037**	0.001
		lnRR	0.117	0.732	0.000
2	number of parents	*lnCVR*	1.586	0.208	0.000
		lnRR	0.022	0.881	0.000
2	distance from thermal limit	*lnCVR*	**4.160**	**0.041**	0.001
		lnRR	**6.103**	**0.013**	0.000
2	treatment condition (permanent or transient)	*lnCVR*	0.286	0.593	0.000
		lnRR	**5.479**	**0.019**	0.000
4	type of treatment * control variability	*lnRR*	**117.332**	**0.000**	0.002
10	type of treatment * (type of trait + treatment magnitude)	*lnCVR*	**18.594**	**0.029**	0.005
14	type of treatment * (type of trait + treatment magnitude + condition + control variability)	*lnRR*	**161.745**	**0.000**	0.003

Table S20

Intercept estimates from Bayesian Egger's regressions, performed on the full meta-regression model residuals and measurement errors. Intercepts with Highest Posterior Density intervals (HPD) not crossing zero (in bold) indicate publication bias in the data.

Test	**Method**	**Measure**	**Intercept**		
			Mean	CI.lb	CI.ub
Egger's regression	*MCMCglmm*	*lnCVR*	0.173	-0.171	0.516
		lnRR	**-7.964**	**-9.119**	**-6.664**

Table S21

Meta-regression results for the effects of publication year on mean and variance differences *(lnRR* and *lnCVR*). *k* - number of effect sizes included in the analysis

Measure	**Method**	**Slope**	**Covariance**	**Fixed effects**			
				Mean	CI.lb	CI.ub	*k*
lnCVR	*rma.mv*	Publication year					630
			0	-0.002	-0.009	0.005	
			0.5	-0.003	-0.010	0.005	
lnRR	*rma.mv*	Publication year					630
			0	0.000	-0.003	0.002	
			0.5	0.000	-0.004	0.003	

Measure	**Method**	**Slope**	**Fixed effects**				
			Mode	Mean	SD	HPD.lb	HPD.ub
lnCVR	*MCMCglmm*	Publication year	-0.005	-0.002	0.004	-0.010	0.005
lnRR	*MCMCglmm*	Publication year	0.000	0.000	0.001	-0.003	0.002