Reduced plasticity and variance in physiological rates for ectotherm populations under climate change

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## Abstract

Climate change is expected to result in warmer and more variable thermal environments globally. Greater thermal variability is expected to result in strong selection pressures leading to genetic adaptation and/or the evolution of adaptive phenotypic plasticity. Such responses depend on genetic and phenotypic variability, yet most work has focused on plastic changes in mean phenotypic responses to climate warming ignore how temperature may change phenotypic variability. Using a large database of physiological rate data from marine, freshwater and terrestrial ectotherms we quantify the capacity for temperature acclimation and the extent to which relative variance (i.e., coefficient of variation) in physiological rates change at high temperatures. Using new effect size estimates and meta-analysis, we show that across habitats relative variance in physiological rates decreased at higher temperatures. Freshwater ectotherms are capable of acclimating and have the smallest reductions in relative variance. Marine organisms also showed a capacity to acclimate to higher temperatures but they coincide with a reduction in relative variance in physiological rates. Relative variance reductions were particularly pronounced for terrestrial ectotherms, and this coincides with a lack of capacity for acclimation highlighting the vulnerability of terrestrial ectotherms to climate change. Neither life-history stage nor past climate explained effect variability. Our results emphasise how beneficial acclimation responses may trade-off with reductions in physiological rate variance that could have important evolutionary and ecological ramifications that affect our understanding of how climate change will impact populations in the future.

## Main

Climate change is expected to result in warmer but also more variable thermal environments for many organisms globally1–3. Greater thermal variability in the past should result in strong selection pressures that lead to genetic adaptation and/or the evolution of adaptive phenotypic plasticity – both of which are considered important for population resilience to contemporary human-induced climate change4–11. Without plasticity or adaptation, high extinction rates are predicted unless organisms can migrate to track suitable habitats9,12. Phenotypic plasticity is expected to be the ‘first line of defence’ against changing climates, thereby buying time for genetic adaptation to take place (i.e., the ‘plasticity first hypothesis’)13, 14. Phenotypic plasticity is predicted to evolve when environmental variability is high but predictable and the costs of plasticity are low7,9,15–17. Despite this theoretical expectation, empirical support is scant (but see 18), likely because many organisms can behaviorally adjust micro-habitat selection to offset thermal stress, the costs of plasticity are high6,16, or the prediction is only supported for specific life-history stages.

Reversible phenotypic plasticity, such as acclimation, is expected to provide greater potential to buffer populations from climate impacts as responses are relatively rapid and can therefore be fine-tuned to proximate environmental conditions (assuming the costs of plasticity are low)15,16. Acclimation is driven by endocrine and epigenetic processes that change the underlying physiology to facilitate a rapid response to the environment19–21. However, the focus up to now has been primarily on mean physiological responses. For example, mean thermal tolerances or acclimation abilities in a population are likely to shift in response to thermal environments4,22–24. However, it is possible that intrapopulation variability might also be impacted in addition to the mean. Understanding how variability in physiological rates – traits thought to be closely linked to fitness – are affected by climate change is important because lack of physiological variation can limit responses to selection (i.e., the ‘opportunity for selection on a trait’)25. Higher physiological variance in a population may also indicate greater niche breadth which can buffer populations against environmental change26–29. Decreases in phenotypic variance also suggests strong stabilising selection or reflect constraints on performance15,16. Changes in physiological trait variation may also have important ecological consequences by promoting population productivity and stability30,31, species coexistence and ecosystem processes26,32,33. The implications of changes in variance could, therefore, have wide-reaching consequences for understanding the capacity of populations to persist in and adapt to novel environments but to date have been largely ignored15.

Periods of past climatic change have had disproportionate impacts on some ecosystems over others raising the question of which ecosystems will be most vulnerable to contemporary climate change. Species occupying terrestrial ecosystems are thought to be particularly vulnerable given their weak acclimation abilities and greater probability of experiencing thermal extremes that overwhelm physiological homeostasis4,22,34, whereas greater proximity to upper thermal limits in marine systems have questioned such conclusions35. Marine and freshwater ecosystems appear to have greater physiological acclimation capacitye.g., 4,24. However, it is unclear if the magnitude of physiological adjustment is sufficient to compensate for potentially negative environmental effects, particularly when temperature interacts with other abiotic changes. Low oxygen availability may be a major factor influencing the vulnerability of aquatic ecosystems, whereas remaining close to thermal limits and greater water loss is expected to be a stronger constraint on physiological processes in terrestrial ectotherms36. Given that terrestrial ectotherms are expected to be closer to their thermal limits, an increase in temperature may have a stronger impact on variation in physiological rates within populations compared to aquatic ectotherms which may have important cascading effects on energy transfer and productivity across different ecosystems10,37.

Here, we use new effect sizes and meta-analysis to re-evaluate the degree to which aquatic and terrestrial ectotherms are capable of physiological plasticity. We then expand these effect sizes to allow for comparisons of variance in physiological rates to ask the following questions: 1) How much is variance in physiological rates expected to change, if at all, as temperatures rise? 2) Are temperature effects on plastic adjustments in physiological rates larger than changes in variance across aquatic and terrestrial ectotherms? 3) Are changes in plasticity or variance in physiological rates impacted by past climate history? 4) How are means and variances in physiological rates expected to change under climate change?

## Results

Using a large database on physiolgical rates4 for marine, freshwater and terrestrial ectotherms we apply new effect size estimates38 that capture changes in mean physiological rates (), and changes in their relative variance (), standardised to a 10C temperature difference. These standardised effects sizes can be converted to percentage differences allowing us to compare the relative magnitude of rate changes resulting from acclimation and relative variance change at high temperatures. Acclimation responses can be measured by comparing acclimation () to acute () from ectotherms acclimated to different temperatures. The difference in compared to measures the extent of acclimation (i.e., plasticity).

The final dataset included a total of 91 freshwater (fishes = 48, molluscs = 4, amphibians = 19, reptiles = 8, arthropods = 10, and a single crustacean and nematode species), 90 marine (fishes = 47, annelids = 2, molluscs = 21, echinoderms = 7, reptiles = 1, arthropods = 10, and a single crustacean and cnidarian species), and 45 terrestrial species (annelids = 1, molluscs = 5, arthropods = 14, reptiles = 12 and amphibians = 12 along with a single tardigrade species) ([Figure 1](#fig-1) A). We had more data on acute thermal responses (n = 1115) compared to thermal responses after an acclimation period (n = 798) because both acclimation temperatures had separate acute responses ([Figure 1](#fig-1)). While the two acute effect sizes did differ significantly from each other, on average (acute responses were greater for animals acclimated to high temperatures – = 0.07, 95% CI: 0.04 to 0.1, = < 0.0001), they were in the same direction and only differed by ~10%. As such, we averaged the two acute effect sizes in subsequent analyses.

Most of the effect size estimates came from measurements of metabolic rates (both resting and maximal – = 190, = 3069, considering acute and acclimation effects together), metabolic enzymes rates ( = 61, = 2394) and whole-organism performance traits (i.e., measures of speed and endurance – = 73, = 963).

### *Terrestrial and aquatic ectotherms differ in their capacity to acclimate but acclimation does not depend on life-history stage*

Overall, was 8.72% lower than across all habitats (95%CI: -15.14 to -2.45%). Ectotherms in marine and freshwater environments showed partial compensation of physiological rates ([Figure 1](#fig-1)B) amounting to reduced of 17.08% (95% CI: -24.32 to -10.19) in freshwater and 15.7% (95% CI: -25.96 to -4.79) in marine environments. In contrast, terrestrial ectotherms showed no acclimation (possibly even inverse acclimation) – showing a 6.6% increase in (95% CI: -6.56 to 21.19, [Figure 1](#fig-1)B).

Nonetheless, effect heterogeneity was high (only 2.85% of the variance was the result of sampling variability, 95% CI: 2.38 to 3.32%), and most variance was explained by the specific study and type of trait (Study: 29.41% , 95% CI: 20.78 to 38.49%; Trait Type: 29.35% , 95% CI: 19.97 to 39.53%). Evolutionary relationships among taxa and species ecology (i.e., species random effect) explained little variation in acute and acclimation responses (Species: 2.39% , 95% CI: 0.01 to 8.1%; Phylogeny: 2.89% , 95% CI: 0 to 12.94%).

Different trait categories showed different acclimation responses across habitat types, however, they mirrored overall patterns (see Supplement; [Figure 7](#fig-2)). Acclimation capacity also did not vary by life-history stage given there were no differences between and between adult and juveniles ([Figure 2](#fig-cvrlh) A-C) (Adult-Juvenile (Acute): 0, 95% CI: -0.21 to 0.2, = 0.96; Adult-Juvenile (Acclimation): 0.05, 95% CI: -0.16 to 0.38, = 0.83).

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| Figure 1- Taxonomic distribution of acute and acclimation estimates across major habitats. **A)** Phylogenetic distribution of taxa contained within the data. The total number of acute and acclimation type Q10 effect sizes are highlighted as well as whether the taxa is marine, freshwater or terrestrial. Silhouettes are representative taxa of major clades within the tree. **B)** Mean acute and acclimation across marine, freshwater, and terrestrial systems. **C)** Mean across traits for marine, freshwater and terrestrial systems. Note there were no differences between acute and acclimation types. k = total number of effect size estimates while the numbers in brackets indicate the number of species. Thick bars are 95% confidence intervals (CI) and thin bars 95% prediction intervals (PI). |

### *Reduced variation in physiological rates in terrestrial and marine ectotherms*

Relative variance in physiological rates, as captured by , showed a decrease across all habitat types but was especially pronouced in terrestrial and marine ectotherms. Overall, there was a 27.87% (95% CI: 10.77 to 40.91, = 0.01) reduction in relative physiologcial rate variance for terrestrial ectotherms and a 14.94% (95% CI: 1.87 to 29.97, = 0.07) reduction in relative variation for marine ectotherms when temperatures increased by 10C. In contrast, freshwater ectotherms exhibited a much smaller reduction in relative physiological rate variance at high temperatures (8.62%, 95% CI: 0.41 to 21.78, = 0.33).

The total proportion of heterogeneity in was lower compared to ( = 23.96, 95% CI: 20.36 to 27.27), with most variation being driven by between study and trait differences (see Supplement; [Figure 10](#fig-s3)). Each life-history stage exhibited the same pattern of variance change in each of the habitats ([Figure 2](#fig-cvrlh)). Reduced relative variance was particularly prominent for resting metabolic rates and sprint speed although traits differed in whether they exhibited a reduction in variation in physiological rates at high temperatures ([Figure 8](#fig-cvrtrait)).

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| Figure 2- Estimated mean acclimation and acute (A-C) and (D-F) for adult and juvenile life-history stages for Marine (A & D), Freshwater (B & E) and Terrestrial (C & F) ectotherms. k = total number of effect size estimates while the numbers in brackets indicate the number of species. Thick bars indicate 95% confidence intervals and thin bars indicate 95% prediction intervals. Raw data for both adult and juvenile life-history stages also presented but point are not separated by type for ease of presentation. |

### *Past climate does not influence acclimation capacity or expected change in variance*

Using the ERA5 climate model, we extracted a 30-year period (1950-2022) of either surface air temperature (0.01 resolution) for both terrestrial and freshwater taxa, or sea surface temperature for the marine taxa (at 0.25 resolution). We used the historical temperature data for each geographical location to calculate a measure of thermal variability and predcitability (see *Methods*). Thermal variability (i.e., ) and predictability experienced by a population in the past did not explain acclimation capacity or changes in physiological rate variance among terrestrial, marine or freshwater populations ([Figure 3](#fig-4); [Figure 4](#fig-5)).

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| Figure 3- Predicted mean (thick black line) as a function of the Thermal Coefficient of Variation (CV) (A) and thermal predictability (B) for wild populations across marine, freshwater and terrestrial habitats. Dashed lines indicate 95% confidence intervals and dotted lines indicate 95% prediction intervals. Model slope () along with the 95% CI and value is shown for each habitat. |

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| Figure 4- Predicted mean (thick black line) as a function of the Thermal Coefficient of Variation (CV) (A) and thermal predictability (B) for wild populations across marine, freshwater and terrestrial habitats. Dashed lines indicate 95% confidence intervals and dotted lines indicate 95% prediction intervals. Model slope () along with the 95% CI and value is shown for each habitat. |

### Changes in physiological rate variance under climate change

Acute and acclimation responses for wild ectotherms were much less common than studies on captive populations ( = 134, from 188 populations). Globally, there was a clear bias towards species in the Northern Hemisphere ([Figure 5](#fig-fig6) A-C). Projected changes in physiological rate variance were highly variable across the globe, with some regions showing a decrease in physiological rate variance, while others showing an increase ([Figure 5](#fig-fig6) D). However, out of the 188 populations, relative variance was predicted to decrease in 96.28% of the locations.

Using the ERA5 climate model, predictions of current global changes in physiological rate variance were generally conservative with our model explaining ~ 50% of the variation in the observed data ( = 0.48, 95% CI: 0.31 to 0.6). Across habitat types climate change is predicted to result in a only a 0.06% change in variance for freshwater systems (95% CI: -6.64 to 6.19%, = 0.95), whereas we expect a 2.72% reduction in relative variance for marine systems (95% CI: -6.12 to 1.39%, = 0.37) and a 12.88% reduction in relative variance for terrestrial systems (95% CI: -20.3 to -6.63%, = < 0.0001) under a RCP8.5 climate scenerio.

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| Figure 5- Model predictions for the expected change in acclimation across the globe for terrestrial, marine and freshwater ecthotherms. Predictions consider the uncertainty in random effects (i.e., species, phylogeny, study). Predicted change in physiological rate variance (relative variance) for each population based on current temperatures (average from 2018-2022; A-C) as well as the expected change from current temperatures based on future temperature predictions (average from 2096-2100, D). Future climate predictions are the reduction in relative variance expected under a RCP8.5 climate scenario relative to current climate conditions (% change). |

## Discussion

Understanding acclimation capacity and how variation in physiological rates change across populations and species is important for predicting the ecological and evolutionary consequences of climate change7,8,10,26,39. Here, we show that the relative variance () in physiological rates for ectotherms is expected to decrease to varying extents across terrestrial, marine and freshwater ecosystems as temperatures increase, with the decrease being particularly pronouced in terrestrial ectotherms (~28%). Such effects are expected to result in a decrease in the variability in physiological rates for marine and terrestrial ectotherms between ~4-13% under future climate change projections. Our results provide insight into the multifaceted ways in which climate warming will impact ectotherm populations that require further empirical and theoretical attention. We discuss our findings in the context of the current literature and highlight key areas for future research.

### *Potential consequences of reduced plasticity and variance in physiological rates across ectotherms*

Understanding the interplay between plasticity and genetic adaptation has important implications for predicting a populations resilience to climate change8,10,11,39–42. For example, incorperating phenotypic plasticity and adaptation into species distribution models has been shown to dampen the predicted contraction of distributions in the face of climate changee.g., 39. In addition, it may be expected that reductions in variance impact the ‘opportunity for selection’ by reducing the strength of selection and/or the genetic variance exposed to selection, impacting a population’s capacity to evolve under climate change40,41. Quntifying the degree of plasticity and genetic/phenotypic variation in key physiolgical responses is therefore recognised as being critical to informing projections for organisms threatened by climate change11.

We show that plastic adjustments in physiological rates and changes in their relative variance differ across habitats. In freshwater habitats, acclimation responses will likely be beneficial and this coincides with relatively little reduction in the relative variance in physiological rates providing more raw material for selection to operate. In contrast, acclimation responses of marine organisms are associated with a nearly equal reduction in relative variance in physiological rates, which may trade-off with the beneficial effects that acclimation provides at high temperatures. In terrestrial ectotherms, relative variance reductions are particularly pronounced and this coincides with a general inability to acclimate. Considering acute physiological rates of animals acclimated to high temperatures are generally still elevated compared to cold-acclimated animals (~7% increase), acclimatization may not always provide adaptive benefits under climate change, particularly when considering changes in relative variance.

Our findings highlight the potential vulnerability of terrestrial and marine ectotherms to climate change. Our meta-analytic results provide opportunities to parameterise predictive models in ways that capture the percentage changes in relative variances and acclimation responses when predicting species distributions or modelling population resilience in the face of climate warming. Our results also define the range of biological responses observed across diverse taxa (e.g., through prediction intervals) providing opportunities to incorperate realistic biological variation into the modelling process. Incorperating relavant variation in models is needed fully appreciate the biological consequences such changes in variation and plasticity have on ecological and evolutionary dynamics39,43 and are yet to be explored.

### *Plasticity and variance in physiological rates do not differ between life-stages*

Life-history stages often occupy different ecological niches and exhibit different physiological responses, levels of plasticity, and patterns of mortality in response to temperature. As such, it is becoming increasingly important to understand how climate change will impact different life-history stages so that more realistic predictive models can be developed44,45. Greater plasticity for early life-stages of development is expected to be important to increase resilience to the effects of climate change because early life-stages are often particularly vulnerable periods in development46,47. Across a diversity of taxa, we show that there were generally similar patterns between early and late life stages – both in terms of variance changes and the capacity for plasticity. Our results highlight that early life stages are not likely to be protected from the impacts of climate change. Evidence across the literature is equivocal with respect to the extent to which one life-stage is more or less plastic than another48,49. For example, Moghadam *et al.*49 showed that larval *Drosophila* were more plastic in their heat hardening responses compared to adults. In contrast, Carter *et al.* 48 showed greater thermal plasticity in metabolism for adults but little in pupae of *Onthophagus taurus*. Unsurprisingly, there is much variation in the literature and our findings suggest that patterns will depend on the species and traits in question. However, very few studies measure multiple life-history stages within the same population. In future research, there needs to be more studies that explicitly compare differences in plasticity among life stages across multiple traits within the same population.

### *Ecological consequences of reduced variation in physiological rates*

Variance reductions in metabolism and performance (e.g., sprint speed) were key traits most strongly impacted by increased temperature. Changes in variability in physiological rates, particularly traits governing energy demand, could have important consequences on the flow of energy within and between populations, communities, and ecosystems10,37,50. More variable populations, genetically and/or phenotypically, are predicted to be associated with broader niches, reduced intraspecific competition, increased growth rate, decreased vulnerability to environmental change and lower extinction risk26,33,50–52. Maintaining intrapopulation variability in physiological rates in a warmer world may therefore be important for population resilience to climate change. For example, Kooijman *et al.* 31 integrated individual variation in dynamic energy budget (DEB) models developed for *Daphnia magna*. They showed that greater between-individual variation in DEB parameters led to less extreme population fluctuations compared to scenarios with no variation31. The differences in variance change across major habitat types suggest that terrestrial ectotherms will likely face greater challenges to adapting to climate change22,24,34, leading to greater rates of extinction and reduced productivity in terrestrial ecosystems. However, data testing the impacts of changes in variance on populations are limited to very few taxa. We need creative experimentation across broader taxa that manipulate levels of variance to understand their ecological outcomes. Our meta-analytic findings can be integrated into theoretical models by permitting model parameters to capture biologically relevant changes in variation. Such predictive models can then be integrated with experimental approaches to better understand the consequences of changes in variation on ecological dynamics.

### *No signature of past climate on capacity for physiological plasticity*

Theoretical evolutionary models predict that plasticity should evolve in populations experiencing greater environmental variability (spatial or temporal), particularly if oscillations are predictable over time, making environmental cues more reliable7–9,14,17,50,53. Higher spatial and temporal heterogeneity in terrestrial ecosystems54 suggests that plasticity should be more likely to evolve in terrestrial environments. However, we did not find evidence to this effect. This finding is consistent with other meta-analyses22,55 with thermal tolerance. The lack of relationship between physiological plasticity and environmental variability and predictability could be due to the challenges in estimating realistic microthermal environments given that air temperatures may not represent thermal enviroments many taxa actually experience in nature. Therefore, it is possible that more fine-scale resolution of the habitats that organisms occupy will elucidate expected patterns. Randomly fluctuating environments have been suggested to select for reduced plasticity, particularly if plastic responses are costly and this has been demonstrated by a number of empirical studies18,56,57. For example, using seed beetles (*Callosobruchus maculatus*), Hallsson *et al.*58 showed that experimentally evolving populations under randomly fluctuating thermal conditions did not show any increase in plasticity, but had reduced plasticity. Leung *et al.*18 also showed reduced plasticity in morphological traits of experimentally evolving algae populations (*Dunaliella salina*) when environments were less predictablesee also 57. These findings, in combination with our results, suggest that there are costs to being plastic or that the environmental signals are insufficient to trigger endocrine and epigenetic mechanisms that lead to plasticity when environments are not predictable 18,50. The fact that aquatic ectotherms did show a capacity to acclimate suggests that environmental predictability, which is expected to be higher in aquatic environments, may be more important than environmental variability in driving the evolution of plasticity.

### *Conclusions and future directions*

Enhanced knowledge of how variation in physiological rates vary across populations and species and the degree to which they can be adjusted in response to the environment may increase our ability to make more informed predictions about the ecological and evolutionary dynamics of natural populations10,11,51. While we show general patterns across taxa and habitats it is important to recognise that this does not mean such patterns apply to all populations. Substantial variation in acclimation responses and changes in variance exist among populations as evidenced by wide prediction intervals. Nonetheless, changes in the relative variance in physiological rates could be better incorporated into physiological and ecological models to provide more nuanced and possibly more realistic predictions about the impacts of climate change on natural populations. While we do not yet understand the relative contribution of environmental and genetic factors to variances changes, models could better decouple how different levels of heritability with different total variance impact evolutionary and ecological predictions. Our meta-analysis allows for realistic models to be parameterised and ensure they are better aligned with empirical findings. Nonetheless, many fascinating questions remain unanswered that will require greater focus on the consequences of changes in variance (rather than just the mean). Particularly interesting questions include: How does a reduction in physiological rate variance change energy flow across tropic levels within communities? What are the biochemical, cellular and physiological mechanisms that underly reduced variance in physiological rates? Are reductions in variance in one trait associated with reductions in correlated traits, or do some traits increase while others decrease? How much of the reduction in variance is driven by lower levels of genetic variance? Answers to these questions will require integrative approaches that combine empirical and theoretical work across multiple levels of biological organisation but will likely provide useful advances in understanding the full consequences that climate change will have on ectotherms across all major ecosystems.

## Materials and Methods

### *Literature collection*

We compiled literature on ectothermic animals that measured physiological rates (e.g., metabolic rate) at two or more temperatures after having been acclimated (or acclimatized) at these temperatures. We used data from a previous meta-analysis4 and updated4’s data by extracting data from suitable studies from our own searches that followed the same search protocol. More specifically, we performed a literature search using the Web of Science database for articles or proceedings papers published in English from 2013 to 2017the date after 4 searches were conducted using the following topic search string: *“(acclimat* AND (therm\* OR temp*) NOT (plant* OR tree\* OR forest\* OR fung\* OR mammal\* OR marsup\* OR bird\* OR human OR exercis\* OR train\* OR hypoxi*))“*. We further limited to the following research areas: Anatomy Morphology; Biodiversity Conservation; Biology; Ecology; Endocrinology Metabolism; Entomology; Evolutionary Biology; Marine Freshwater Biology; Physiology; Respiratory System, Reproductive Biology, Zoology.

Our search resulted in 1,321 papers for screening in Rayyan59. We also cross-checked papers we found in our searches with a recent paper by23, which also updates the dataset of4’s. We included any papers that were missed between our searches and those of23.23 added 7 new studies (mainly because they were focused on metabolic rates), and our searches differed from theirs by only a single paperi.e., 60. Given the physiological traits we included were broader, we had a substantial increase in additional papers that we added to4’s dataset. More specifically, in addition to the 191 papers we included from the4 dataset, we extracted data from an extra 65 papers (with a total of 238 effects; a 34.03% increase in the number of published articles). Note that4 included a total of 205 publications, however, not all these contained the necessary statistics we needed to derive effect sizes and associated sampling variances (see below). While we may have missed papers, our goal was to obtain a large representative (and unbiased) sample of acclimation research rather than a comprehensive dataset. As such, our database represents the most up-to-date dataset used by4 to answer questions on physiological rates across ectotherms.

We split the screening of titles and abstracts for the 1,321 papers found in our search among DWAN, FK, FS, and SN evenly. To ensure consistency among authors in title and abstract inclusion, relevant authors went through a randomly selected set of papers together before the formal screening to calibrate selection of papers based on our inclusion criteria (see below). In cases of disagreement regarding inclusion, we conservatively included the paper for full text screening and discussed uncertain papers among authors to come to a decision. After title and abstract screening, there was a total of 149 papers for full text screening. Papers were included only if they: 1) measured a physiological rate acutely at two temperatures on a sample of animals chronically exposed to the same two temperatures for at least 1 week; and 2) where physiological rates measured were burst and sustained locomotion, metabolic rates (standard, resting, routine and maximal), heart rates, and/or enzyme activities. We provide a PRISMA flow diagram of our extraction process in the *Supplement* (see [Figure 6](#fig-prisma)).

### *Data Compilation*

We extracted means, standard deviations, and sample sizes for physiological rates at the two test temperatures. If there were more than two test temperatures, we chose only the test temperatures that fell within the most likely natural range of temperatures experienced by the species in question. We extracted these data from text, tables or figures of a given paper. Data were extracted from figures using the R package *metaDigitise*61. We also recorded the phylum, class, order, genus and species, and the latitude and longitude from where the experimental animals were sourced. For studies that did not provide latitude and longitude for the population, we searched for similar studies by the same lab group to identify where the population was likely to have been sourced. If the experimental animals were derived from the wild, we recorded the nearest latitude and longitude of the field collection site. If the animals were sourced from a commercial supplier, we took the latitude and longitude of the supplier. When it was not possible to find latitude and longitude using these methods, we looked up the distribution of the species in question and took the latitude and longitude of the centroid of the species’ distributional range.

### *Based Effect Sizes and Sampling Variances for Means and Variances*

Following38 we calculated a series of temperature-corrected effect sizes that compared mean physiological rates () as well as the variability in physiological rates ( and ). These effect sizes are similar to the traditional temperature coefficient (), but with formal analytical approximations of their sampling variances. Sampling variances for effect sizes allowed us to make use of traditional meta-analytic modelling approaches.

#### *Comparing changes in mean physiological rates*

To compare mean physiological rates, we calculated the log response ratio, 38 as follows:

Where, and are mean physiological rates and and are the temperatures at which these rates are measured. Log transformation of this ratio makes the effect size normally distributed. [Equation 1](#eq-lnq10) is essentially a temperature corrected equivalent to the log response ratio (lnRR)62,63 when the numerator and denominator are measured at different temperatures. This allows comparisons of the means from two temperature treatments directly regardless of the absolute measurement temperatures. The sampling variance for [Equation 1](#eq-lnq10) can be computed as follows (as described in38):

Here, and are the standard deviations and and are the sample sizes in group 1 and 2, respectively.

#### *Comparing variance in physiological rates*

64 proposed analogous effect size estimates to *lnRR* that allow for comparisons of changes in variance between two groups, the log variance ratio (*lnVR*) and the log coefficient of variation (*lnCVR*). *lnVR* and *lnCVR* are ratios that describe the relative difference in trait variability between two groups. We refer readers to64 for the equations describing *lnVR* and *lnCVR*, but these can easily be extended to their analogues (and associated sampling variance) as follows:

[Equation 3](#eq-lnq10VR) and [Equation 4](#eq-slnq10VR) describe the change in physiological rate variance ([Equation 3](#eq-lnq10VR)) across a 10°C temperature change along with its sampling variance ([Equation 4](#eq-slnq10VR)). While this is a useful metric, as discussed by64 there is often a strong mean-variance relationship that needs to be accounted for in analysing changes in variance. As such, we calculated the coefficient of variation, which standardizes changes in variance for changes in means as follows:

where is the coefficient of variation defined as . We refer to as relative variance because variance changes are relative to the mean.

#### *Calculating acute and acclimation , and estimates*

Using the mean, standard deviation, and sample size for all acute and acclimation treatments of studies in our databases we derived acute and acclimation , and estimates. For all effect sizes the higher acute or acclimation temperature was in the numerator and the lower of the two temperatures in the denominator. As such, positive effect sizes suggest that the mean or variance is larger at the higher of the two temperatures, standardized to 10°C.

### *Moderator Variables*

We recorded or derived a series of moderator variables from each study that are expected to have an impact on our effect size estimates. These included the duration of acclimation in days and acclimation type (“acclimation” or “acclimatization”) given that acclimation responses are expected to depend on how long chronic temperature exposure occurs (longer exposure = better acclimation response)4. We also recorded if the sample of animals were derived from captive or wild stocks, the life-history stage of the animals used (“adult” or “juvenile”) and the habitat type (“freshwater”, “marine” or “terrestrial”) given that4 show that these factors can impact estimates. Physiological rate measures varied widely across the studies but could generally be grouped into discrete trait categories4. As such, using the detailed information on the trait type, and its associated units from a given study, we categorized each effect size into one of 12 trait categories. These categories included measures of whole organism performance measures including cardiac (i.e., ‘cardiac’) and muscle (‘muscle’) function, sprint speed (‘sprint’) and endurance (‘endurance’) and metabolic rates (i.e., maximal and resting metabolic rate; max MR’, ‘rest MR’, respectively). Studies also quantified various enzymatic reaction rates, including enzymes involved in general metabolic responses (categorized as ‘metabolic enzyme’), various parts of the electron transport chain, including ATPase activity (‘ATPase’), mitochondrial leak (‘mito\_leak’) and oxidation (‘mito\_oxidation’) as well as antioxidant enzymes (‘antiox’). All other traits not falling within these categories were placed into ‘other’.

### *Climate Data*

To understand how climate has impacted species’ physiological acclimation abilities we used the coordinates reported by each study to extract temperature data from terrestrial and aquatic environments. It was unclear whether climate at the locations of captive reared organisms would be representative of a population’s climate history - particularly for species reared under captive condition for many generations. Given that we were interested in understanding climate driven effects on acclimation capacity we only used studies on wild populations for climate analyses.

Monthly average temperature data were extracted from the ERA5 climate model, available from the Copernicus climate data store65. For each population and species in the dataset we extracted a 30-year period (1950-2022) of either surface air temperature (0.01 resolution) for both terrestrial and freshwater taxa, or sea surface temperature for the marine taxa (at 0.25 resolution) using the *ncdf4* R packagevers. 1.22, 66. We chose surface temperature because we believed that it was more likely to reflect the micro-thermal environment experienced by terrestrial and freshwater ectotherms at those locations. For terrestrial species we estimated soil temperatures as this maybe more representative of microhabitat choice compared to air temperature. We fit models using both air and soil temperature and found that the results were qualitatively similar. We therefore only present results for air temperature.

Using the thermal time-series data for each location we calculated metrics of thermal variability across months and years as well as estimates of thermal predictability (i.e., autocorrelation). To estimate thermal variability, we calculated the coefficient of variation (, where SD = standard deviation in temperature and M = the mean temperature for each year). To estimate thermal predictability, we calculated the auto-regressive time lag across the entire dataset. Theoretical and empirical studies of plasticity evolution have emphasised the importance of both climate variability and predictability in plasticity evolution.

Lastly, to illustrate the effects that climate warming could have on physiological rate variance we also extracted climate projections and calculated thermal variability and predictability for the future. We used the CanESM2 climate model (2005-2100) under a high emissions scenerio (RCP8.5).

### *Meta-Analysis*

We analysed our data using multilevel meta-analytic (MLMA) and meta-regression (MLMR) models in R (vers. 4.3.1) using *brms*vers. 2.20.4 67,68,69 and *metafor*vers. 4.4.0 70. We fit both Bayesian and frequentist approaches to ensure that our results were consistent, and to create orchard plots more easilyvers. 2.0, 71,72. In addition, Bayesian methods better protect against type I errors in the presence of complex sources of non-independence73–75. For our Bayesian models, we ran 4 MCMC chains, each with a warm-up of 1000 followed by 4000 sampling iterations keeping every 5 iterations for a total of 3200 samples from the posterior distribution. We used flat Gaussian priors for ‘fixed’ effects (i.e., ) and a student t-distribution for ‘random’ effects (i.e., ). We checked that all MCMC chains were mixing and had converged (i.e., ). We compared any competing models using Akaike’s Information Criteria (AIC) (if frequentist) or Wantabe Information Criteria (WIC) (if Bayesian). We deemed models with the lowest IC value to be best supported if there was a between the competing models of 2 or more. If two models were within 2 units we went with the most parsimonious model.

#### *Multi-level Meta-analysis (MLMA) Models*

We first fit multi-level meta-analysis (MLMA) models (i.e., intercept-only models) for both and , that included study, species, and phylogeny as random effects to account for non-independence. We also included trait as a random effect to account for trait variation within the data. Our MLMA models allowed us to partition the variation in and among these key sources while accounting for total sampling variance in each. This allowed us to calculate the proportion of total heterogeneity [i.e., ; *sensu*76;38] along with various metrics describing the proportion of variance explained by each random effect level76. We also present 95% prediction intervals which describe the expected distribution of effects from future studies38,71.

A phylogeny was derived using the Open Tree of Life (OTL) with the *rotl* package in Rvers. 3.1.0, 77, and plotted using *ggtree*vers. 3.9.0, 78. We resolved all polytomies in the tree. Any missing taxa were replaced with closely related species and branch lengths were computed using Grafen’s methodusing power = 0.7, 79. We used the R packages *ape*vers. 5.7.1, 80 and *phytools*vers. 1.9.16, 81 to prune the tree for individual analyses and calculate phylogenetic covariance (or correlation) matrices used in meta-analytic models.

#### *Multi-level Meta-regression (MLMR) Models*

After quantifying levels of heterogeneity, we fit a series of multi-level meta-regression (MLMR) models to test our key questions. In all models, we included the same random effects as we used in our MLMA models. Acclimation time varied from 4 to 408 days (mean (SD) = 37.98 45.19 days), and terrestrial ectotherms were acclimated for a much shorter duration (mean (SD) = 23.53 15.56, n = 125) than both freshwater (mean (SD) = 36.81 28.71, n = 430) and marine species (mean (SD) = 46.18 67.21, n = 313). Rates of acclimation have been shown to be faster for many terrestrial groups compared to aquatic organisms [e.g., amphibians and reptiles have faster rates of acclimation than fishes; See82], which would make it more likely that terrestrial ectotherms would show lower post acclimation . To control for these possible differences, acclimation time was mean-centered (mean = 0) and included in all our models. As such, all estimates can be interpreted as values for an average level of acclimation time (i.e., 37.98 days).

We first tested the degree to which acute and acclimation and effects varied by habitat type (i.e., terrestrial, freshwater, and marine ecosystems). Models included an interaction between effect type (i.e., acute or acclimation) and habitat. Reduced mean relative to indicates that acclimation to thermal environments results in partial compensation of physiological rates (i.e., phenotypic plasticity), whereas no differences between and suggests organisms are not capable of physiological plasticity4,23. In contrast, a difference in relative to would imply that changes in between individual variation in physiological rates across 10C differ depending on whether acute or acclimation responses are measured. If the interaction between effect type and habitat was not supported, then we fit a model that only contained additive effects of effect type and habitat. Following on from these models, we subset each habitat type and explored how mean changed across traits. Within each habitat (marine, freshwater, and terrestrial) we fit a series of models that included an interaction between effect type (acute / acclimation) and trait category (as defined above). Variance in effects within trait categories appeared to vary depending on the trait type in question. Comparison of a model with and without heteroscedastic residual variance favored a model with heteroscedastic residual variance across trait categories (; marine = 58, freshwater = 120, and terrestrial = 12). To ensure models converged we limited to trait categories for each habitat with six or more effect sizes.

Second, we tested whether different life-stages are more or less likely to acclimate by fitting a model for each habitat type and including an interaction between life-stage (‘adult’ or ‘juvenile’) and effect type. We predicted that acclimation responses would be more likely early in development compared to later in development as this pattern has been shown in previous studiese.g., 49, but that this should depend on the habitat type given the different constraints faced by different early life stages across major habitat types.

#### *Modelling how climate change will impact on opportunity for selection*

To understand the consequences of human-induced climate change on the potential to impact the opportunity for selection on physiological traits we fit a model that included an interaction between acclimation type, habitat type, latitude and longitude. We assumed that any change in across latitude and longitude could vary by habitat type (i.e., an interaction between habitat). We used non-linear tensors for latitude and longitude as any response could be complicated by local factors (e.g., altitude). Our model included random effects of species, trait, phylogeny and study. We predicted the expected change in for each wild population in our dataset at the specific populations latitude and longitude. To do this, we first converted the predicted to a 1C change as opoosed to 10C as follows:

[Equation 7](#eq-lCVRpred) turned the expected change across 10C to 1C. We then multiplied this predicted change by the change in air and sea surface temperatures at the locations of each population (and species) that is expected under high emissions scenerios in 2080.

### *Publication Bias*

We explored the possibility for publication bias graphically, using funnel plots, and more formally by including in our meta-regression models sampling variance (or sampling standard error)83. Funnel plot asymmetry may suggest a form of publication bias called the ‘file-drawer’ effect whereby low-powered studies are less likely to be published. To test whether sampling variance covaried with effect size we included it in a multi-level meta-regression model that accounted for all the random effects (study, species, trait) and fixed effects (acclimation time, type of effect, habitat, trait category and the interaction between habitat type and trait category).

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## References

1. Suarez-Gutierrez, L., Müller, W. A. & Marotzke, J. Extreme heat and drought typical of an end-of-century climate could occur over europe soon and repeatedly. *Communications Earth & Environment* **4**, 415, https://doi.org/10.1038/s43247-023-01075-y (2023).

2. Easterling, D. R. *et al.* Climate extremes: Observations, modelling and impacts. *Science* **289**, 2068–2074 (2000).

3. Ummenhofer, C. C. & Meehl, G. A. Extreme weather and climate events with ecological relevance: A review. *Philosophical Transactions of the Royal Society of London, Series B: Biological Sciences* **372**, 20160135, http://doi.org/10.1098/rstb.2016.0135 (2017).

4. Seebacher, F., White, C. R. & Franklin, C. E. Physiological plasticity increases resilience of ectothermic animals to climate change. *Nat. Clim. Chang.* **5**, 61 (2015).

5. Merila, J. & Hendry, A. P. Climate change, adaptation, and phenotypic plasticity: The problem and the evidence. *Evolutionary Applications* **7**, 1–14., doi:10. 1111/eva.12137 (2014).

6. Chevin, L. M. & Lande, R. Evolution of environmental cues for phenotypic plasticity. *Evolution* **69**, 2767–2775, https:// doi.org/10.1111/evo.12755 (2015).

7. Chevin, L.-M. & Hoffmann, A. A. Evolution of phenotypic plasticity in extreme environments. *Philosophical Transactions of the Royal Society of London, Series B: Biological Sciences* **372**, 20160138, https://doi.org/10.1098/rstb.2016.0138 (2017).

8. Chevin, L.-M., Lande, R. & Mace, G. M. Adaptation, plasticity, and extinction in a changing environment: Towards a predictive theory. *PLoS Biology* **8**, e1000357, https://doi.org/10.1371/journal.pbio.1000357 (2010).

9. Nunney, L. Adapting to a changing environment: Modeling the interaction of directional selection and plasticity. *Journal of Heredity* **107**, 15–24 (2016).

10. Seebacher, F., Narayan, E., Rummer, J. L., Tomlinson, S. & Cooke, S. J. How can physiology best contribute to wildlife conservation in a warming world? *Conservation Physiology* **11**, coad038 (2023).

11. Cooke, S. J. *et al.* One hundred research questions in conservation physiology for generating actionable evidence to inform conservation policy and practice. *Conservation Physiology* **9**, coab009 (2021).

12. Cahill, A. E. *et al.* How does climate change cause extinction? *Proceedings of the Royal Society B: Biological Sciences* **280**, 20121890 (2012).

13. West-Eberhard, M. J. *Developmental plasticity and evolution.* (Oxford University Press, New York., 2003).

14. Lande, R. Adaptation to an extraordinary environment by evolution of phenotypic plasticity and genetic assimilation. *Journal of Evolutionary Biology* **22**, 1435–1446 (2009).

15. Scheiner, S. M., Barfield, M. & Holt, R. D. The genetics of phenotypic plasticity. XVII. Response to climate change. *Evolutionary Applications* **13**, 388–399 (2020).

16. Dewitt, T. J., Sih, A. & Wilson, D. S. Costs and limits of phenotypic plasticity. *Trends in Ecology and Evolution* **13**, 77–81 (1998).

17. Reed, T. E., Waples, R. S., Schindler, D. E., Hard, J. J. & Kinnison, M. T. Phenotypic plasticity and population viability: The importance of environmental predictability. *Proceedings of the Royal Society B: Biological Sciences* **277**, 3391–3400 (2010).

18. Leung, C., Rescan, M., Grulois, D. & Chevin, L. 2020. *Ecology Letters* **23**, 1664–1672 (2020).

19. Seebacher, F. & Simmonds, A. I. Histone deacetylase activity mediates thermal plasticity in zebrafish (danio rerio). *Scientific Reports* **9**, 8216 (2019).

20. Little, A. G., Kunisue, T., Kannan, K. & Seebacher, F. Thyroid hormone actions are temperature-specific and regulate thermal acclimation in zebrafish (danio rerio). *Bmc Biology* **11**, 1–15 (2013).

21. Taff, C. C. & Vitousek, M. N. Endocrine flexibility: Optimizing phenotypes in a dynamic world? *Trends in ecology & evolution* **31**, 476–488 (2016).

22. Gunderson, A. R. & Stillman, J. H. Plasticity in thermal tolerance has limited potential to buffer ectotherms from global warming. *Proceedings of the Royal Society B: Biological Sciences* **282**, 20150401 (2015).

23. Havird, J. C. *et al.* Distinguishing between active plasticity due to thermal acclimation and passive plasticity due to Q10 effects: Why methodology matters. *Funct. Ecol.* **0**, 1–14 (2020).

24. Pottier, P. *et al.* Developmental plasticity in thermal tolerance: Ontogenetic variation, persistence, and future directions. *Ecology Letters* **25**, 2245–2268 (2022).

25. Pelletier, F. & Coulson, T. A new metric to calculate the opportunity for selection on quantitative characters. *Evolutionary Ecology Research* **14**, 729–742 (2012).

26. Bolnick, D. I. *et al.* Why intraspecific trait variation matters in community ecology. *Trends in Ecology and Evolution* **26**, 183–192 (2011).

27. Schindler, D. E. *et al.* Population diversity and the portfolio effect in an exploited species. *Nature* **465**, 609–613 (2010).

28. Zheng, S., Hu, J., Ma, Z., Lindenmayer, D. & Liu, J. Increases in intraspecific body size variation are common among north american mammals and birds between 1880 and 2020. *Nature Ecology and Evolution* **7**, 347–354, https://doi.org/10.1038/s41559-022-01967-w (2023).

29. Slatyer, R. A., Hirst, M. & Sexton, J. P. Niche breadth predicts geographical range size: A general ecological pattern. *Ecology Letters* **16**, 1104–1114 (2013).

30. Agashe, D. The stabilizing effect of intraspecific genetic variation on population dynamics in novel and ancestral habitats. *The American Naturalist* **174**, 255–267 (2009).

31. Kooijman, S., Van der Hoeven, N. & Van der Werf, D. Population consequences of a physiological model for individuals. *Functional Ecology* 325–336 (1989).

32. Imura, D., Toquenaga, Y. & Fujii, K. Genetic variation can promote system persistence in an experimental host-parasitoid system. *Population Ecology* **45**, 205–212 (2003).

33. Hart, S. P., Schreiber, S. J. & Levine, J. M. How variation between individuals affects species coexistence. *Ecology letters* **19**, 825–838 (2016).

34. Hoffmann, A. A., Chown, S. L. & Clusella-Trullas, S. Upper thermal limits in terrestrial ectotherms: How constrained are they? *Functional Ecology* **27**, 934–949 (2013).

35. Pinsky, M. L., Eikeset, A. M., McCauley, D. J., Payne, J. L. & Sunday, J. M. Greater vulnerability to warming of marine versus terrestrial ectotherms. *Nature* **569**, 108–111 (2019).

36. Verberk, W. C. E. P. *et al.* Can respiratory physiology predict thermal niches? *Annals of the New York Academy of Sciences* **1365**, 73–88 (2016).

37. Barneche, D. R. *et al.* Warming impairs trophic transfer efficiency in a long-term field experiment. *Nature* **592**, 76–79 (2021).

38. Noble, D. W. A. *et al.* Meta-analytic approaches and effect sizes to account for ‘nuisance heterogeneity’ in comparative physiology. *J. Exp. Biol.* **225**, jeb243225 (2022).

39. Bush, A. *et al.* Incorporating evolutionary adaptation in species distribution modelling reduces projected vulnerability to climate change. *Ecology letters* **19**, 1468–1478 (2016).

40. Urban, M. C. *et al.* When and how can we predict adaptive responses to climate change? *Evolution Letters* (2023).

41. Hoffmann, A. A. & Sgrò, C. M. Climate change and evolutionary adaptation. *Nature* **470**, 479–485 (2011).

42. Merilä, J. & Hendry, A. P. Climate change, adaptation, and phenotypic plasticity: The problem and the evidence. *Evolutionary applications* **7**, 1–14 (2014).

43. DeMarche, M. L., Doak, D. F. & Morris, W. F. Incorporating local adaptation into forecasts of species’ distribution and abundance under climate change. *Global Change Biology* **25**, 775–793 (2019).

44. Levy, O. *et al.* Resolving the life cycle alters expected impacts of climate change. *Proceedings of the Royal Society B: Biological Sciences* **282**, 20150837 (2015).

45. Petitgas, P. *et al.* Impacts of climate change on the complex life cycles of fish. *Fisheries Oceanography* **22**, 121–139 (2013).

46. Martin, T. E. Age-related mortality explains life history strategies of tropical and temperate songbirds. *Science* **349**, 966–970 (2015).

47. Stearns, S. C. Life-history tactics: A review of the ideas. *The Quarterly review of biology* **51**, 3–47 (1976).

48. Carter, A. W. & Sheldon, K. S. Life stages differ in plasticity to temperature fluctuations and uniquely contribute to adult phenotype in onthophagus taurus dung beetles. *Journal of Experimental Biology* **223**, jeb227884 (2020).

49. Moghadam, N. N., Ketola, T., Pertoldi, C., Bahrndorff, S. & Kristensen, T. N. Heat hardening capacity in drosophila melanogaster is life stage-specific and juveniles show the highest plasticity. *Biology letters* **15**, 20180628 (2019).

50. Hendry, A. P. Key questions on the role of phenotypic plasticity in eco-evolutionary dynamics. *Journal of Heredity* **107**, 25–41 (2016).

51. Forsman, A. Rethinking phenotypic plasticity and its consequences for individuals, populations and species. *Heredity* **115**, 276–284 (2015).

52. Forsman, A. Effects of genotypic and phenotypic variation on establishment are important for conservation, invasion, and infection biology. *Proceedings of the National Academy of Sciences* **111**, 302–307 (2014).

53. Murren, C. *et al.* Constraints on the evolution of phenotypic plasticity: Limits and costs of phenotype and plasticity. *Heredity* **115**, 293–301 (2015).

54. Steele, J. H., Brink, K. H. & Scott, B. E. Comparison of marine and terrestrial ecosystems: Suggestions of an evolutionary perspective influenced by environmental variation. *ICES Journal of Marine Science* **76**, 50–59 (2019).

55. Barley, J. M. *et al.* Limited plasticity in thermally tolerant ectotherm populations: Evidence for a trade-off. *Proceedings of the Royal Society B* **288**, 20210765 (2021).

56. Rescan, M., Leurs, N., Grulois, D. & Chevin, L.-M. Experimental evolution of environmental tolerance, acclimation, and physiological plasticity in a randomly fluctuating environment. *Evolution Letters* **6**, 522–536 (2022).

57. Leung, C., Grulois, D., Quadrana, L. & Chevin, L.-M. Phenotypic plasticity evolves at multiple biological levels in response to environmental predictability in a long-term experiment with a halotolerant microalga. *Plos Biology* **21**, e3001895 (2023).

58. Hallsson, L. R. & Björklund, M. Selection in a fluctuating environment leads to decreased genetic variation and facilitates the evolution of phenotypic plasticity. *Journal of evolutionary biology* **25**, 1275–1290 (2012).

59. Ouzzani, M., Hammady, H., Fedorowicz, Z. & Elmagarmid, A. Rayyan—a web and mobile app for systematic reviews. *Syst. Rev.* **5**, 210–220 (2016).

60. Bulgarella, M., Trewick, S. A., Godfrey, A. J. R., Sinclair, B. J. & Morgan-Richards, M. Elevational variation in adult body size and growth rate but not in metabolic rate in the tree weta hemideina crassidens. *J. Insect Physiol.* **75**, 30–38 (2015).

61. Pick, J. L., Nakagawa, S. & Noble, D. W. A. Reproducible, flexible and high throughput data extraction from primary literature: The metaDigitise R package. *Methods Ecol. Evol.* **10**, 426–431 (2019).

62. Hedges, L. V., Gurevitch, J. & Curtis, P. S. The meta-analysis of response ratios in experimental ecology. *Ecology* **80**, 1150–1156 (1999).

63. Lajeunesse, M. J. On the meta-analysis of response ratios for studies with correlated and multi-group designs. *Ecology* **92**, 2049–2055 (2011).

64. Nakagawa, S. *et al.* Meta-analysis of variation: Ecological and evolutionary applications and beyond. *Methods Ecol. Evol.* **6**, 143–152 (2015).

65. Hersbach, H. *et al.* The ERA5 global reanalysis. *Quart. J. Roy. Meteor. Soc.* **146**, 1999–2049 (2020).

66. Pierce, D. ncdf4: Interface to unidata netCDF (version 4 or earlier) format data files. (2021).

67. Bürkner, P.-C. Brms: An R package for bayesian multilevel models using stan. *J. Stat. Softw.* **80**, 1–28., doi:10.18637/jss.v080.i01 (2017).

68. Bürkner, P.-C. Advanced bayesian multilevel modeling with the R package brms. *R J.* **10**, 395–411 (2018).

69. Stan development team. RStan: The R interface to stan. *R package version 2. 21. 3. https://mc-stan. org/.* (2021).

70. Viechtbauer, W. Conducting meta-analyses in R with the metafor package. *J. Stat. Softw.* **36**, 1–48. URL: https://www.jstatsoft.org/v36/i03/ (2010).

71. Nakagawa, S. *et al.* The orchard plot: Cultivating forest plots for use in ecology, evolution and beyond. *Research Synthesis Methods* **12**, 4–12 (2021).

72. Nakagawa, S. *et al.* orchaRd 2.0: An r package for visualising meta-analyses with orchard plots. *Methods in Ecology and Evolution* **14**, 2003–2010.

73. Nakagawa, S., Senior, A. M., Viechtbauer, W. & Noble, D. W. A. An assessment of statistical methods for non-independent data in ecological meta-analyses: comment. *Ecology* **in press.**, https://doi.org/10.1002/ecy.3490 (2021).

74. Song, C., Peacor, S. D., Osenberg, C. W. & Bence, J. R. An assessment of statistical methods for nonindependent data in ecological meta-analyses. *Ecology* **e03184**, (2021).

75. Noble, D. W. A., Lagisz, M., O’Dea, R. E. & Nakagawa, S. Non‐independence and sensitivity analyses in ecological and evolutionary meta‐analyses. *Molecular Ecology* **26**, 2410–2425 (2017).

76. Nakagawa, S. & Santos, E. S. A. Methodological issues and advances in biological meta-analysis. *Evol. Ecol.* **26**, 1253–1274 (2012).

77. Michonneau, F., Brown, J. W. & Winter, D. J. Rotl: An R package to interact with the open tree of life data. *Methods Ecol. Evol.* **7**, 1476-1481. doi:10.1111/2041-210X.12593 (2016).

78. Yu, G., Smith, D., Zhu, H., Guan, Y. & Lam, T. T.-Y. Ggtree: An R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods Ecol. Evol.* **8**, 28–36, doi:10.1111/2041–210X.12628 (2017).

79. Grafen, A. The phylogenetic regression. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* **326**, 119–157 (1989).

80. Paradis, E. & Schliep, K. Ape 5.0: An environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* **35**, 526–528 (2019).

81. Revell, L. J. Phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.* **3**, 217–223 (2012).

82. Einum, S. & Burton, T. Divergence in rates of phenotypic plasticty among ectotherms. *Ecol. Lett.* **26**, 147–156 (2023).

83. Nakagawa, S. *et al.* Methods for testing publication bias in ecological and evolutionary meta-analyses. *Methods in Ecology and Evolution* **13**, 4–21 (2022).

## Supplemental Results and Figures

#### PRISMA Flow Diagram

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| Figure 6- PRISMA flow diagram of the literature search and screening process. |

#### Acute and acclimation for different trait categories across marine, freshwater and terrestrial taxa

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| Figure 7- Acute and Acclimation across traits for A) marine, B) freshwater and C) terrestrial systems. k = total number of effect size estimates while the numbers in brackets indicate the number of species. Thick bars indicate 95% confidence intervals and thin bars indicate 95% prediction intervals. The x-axis is truncated for ease of visualisation. |

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| Figure 8- Acute and Acclimation across traits for A) marine, B) freshwater and C) terrestrial systems. k = total number of effect size estimates while the numbers in brackets indicate the number of species. Thick bars indicate 95% confidence intervals and thin bars indicate 95% prediction intervals. The x-axis is truncated for ease of visualisation. |

#### Comparing raw variance changes using

Analysis of suggested that variance increases with higher temperatures across all habitat types, with terrestrial ectotherms having the smallest increase in variance ([Figure 9](#fig-s1)). **?@tbl-s1**

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| --- |
| Figure 9- Estimated mean for marine, freshwater and terrestrial systems. Note there were no differences between acute and acclimation types so they were averaged. Thick black bars are 95% confidence intervals (CI’s) and thin bars 95% prediction intervals (PI’s). The percentage change in variance is also back calculated. Note that these are raw variances and do not account for changes in mean physiological rates. k = total number of effect size estimates while the numbers in brackets indicate the number of species. |

| **Parameter** | **Estimate** | **Est.Error** | **l-95% CI** | **u-95% CI** |
| --- | --- | --- | --- | --- |
| **Fixed Effects** | | | | |
| Intercept | 0.4932 | 0.10684 | 0.2984 | 0.7281 |
| Acclimation Time (z scaled) | -0.0001 | 0.00071 | -0.0015 | 0.0013 |
| Acclimation Effect | -0.0247 | 0.04247 | -0.1097 | 0.0593 |
| Habitat (Marine) | -0.0024 | 0.09890 | -0.1957 | 0.1968 |
| Habitat (Terrestrial) | -0.2032 | 0.10196 | -0.3956 | -0.0049 |
| Acclimation\*Marine | -0.0857 | 0.07817 | -0.2389 | 0.0700 |
| **Random Effects** |  |  |  |  |
| Study | 0.3647 | 0.03944 | 0.2910 | 0.4434 |
| Phylogeny | 0.1194 | 0.09729 | 0.0043 | 0.3630 |
| Species | 0.0821 | 0.05471 | 0.0041 | 0.2017 |
| Trait | 0.3134 | 0.04159 | 0.2386 | 0.3975 |

#### Plots of for multi-level models

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| Figure 10- estimates. A) B) and C) . |

#### Publicaton Bias Analysis

Funnel plots did not show any noticable deviation from the typical funnel shape for any of the effect size estimates ([Figure 11](#fig-s2)).

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| --- |
| Figure 11- Funnel plot of precision (1/sampling standard error) against effect size for A) log response ratio (), B)log coefficient of variance ratio () and C) log variance ratio (). Both acute (‘green’) and acclimation (‘orange’) effect sizes are plotted. |