



Coral adaptation to climate change: meta-analysis reveals high heritability across multiple traits

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	decreases under temperature stress, explicit tests of the heritability of thermal tolerance itself – such as coral thermal reaction norm shape – are lacking. Nevertheless, our findings overall reveal high trait heritability for the majority of coral traits, suggesting corals may have a greater potential to adapt to climate change than has been assumed in recent evolutionary models.

Coral adaptation to climate change: meta-analysis reveals high heritability across multiple traits

Running Title: Trait heritability in reef-building corals

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Abstract

Anthropogenic climate change is a rapidly intensifying selection pressure on biodiversity across the globe and, particularly, on the world's coral reefs. The rate of adaptation to climate change is proportional to the amount of phenotypic variation that can be inherited by subsequent generations (i.e., narrow-sense heritability, h^2). Thus, traits that have higher heritability (e.g., $h^2 > 0.5$) are likely to adapt to future conditions faster than traits with lower heritability (e.g., $h^2 < 0.1$). Here, we synthesize 95 heritability estimates across 19 species of reef-building corals. Our meta-analysis reveals low heritability ($h^2 < 0.25$) of gene expression metrics, intermediate heritability ($h^2 = 0.25$ – 0.50) of photochemistry, growth, and bleaching, and high heritability ($h^2 > 0.50$) for metrics related to survival and immune responses. Some of these values are higher than typically observed in other taxa, such as survival and growth, while others were more comparable, such as gene expression and photochemistry. There was no detectable effect of temperature on heritability, but narrow-sense heritability estimates were generally lower than broad-sense estimates, indicative of significant non-additive genetic variation across traits. Trait heritability also varied depending on coral life stage, with bleaching and growth in juveniles generally having lower heritability compared to bleaching and growth in larvae and adults. These differences may be the result of previous stabilizing selection on juveniles or may be due to constrained evolution resulting from genetic trade-offs or genetic correlations between growth and thermotolerance. While we find no evidence that heritability decreases under temperature stress, explicit tests of the heritability of thermal tolerance itself – such as coral thermal reaction norm shape – are lacking. Nevertheless, our findings overall reveal high trait heritability for the majority of coral traits, suggesting corals may have a greater potential to adapt to climate change than has been assumed in recent evolutionary models.

45 **Keywords:** adaptation, animal model, Breeder's equation, climate change, evolution, natural
46 selection, Scleractinia, thermal tolerance

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Introduction

Anthropogenic climate change is one of the greatest selective pressures on organisms worldwide (Davis et al. 2005; Hughes et al. 2018b; Nolan et al. 2018). To avoid extinction, species need to either acclimatize, move to new habitats, or adapt to new conditions (Davis et al. 2005; Jump and Peñuelas 2005; Gienapp et al. 2008). Acclimatization on its own may initially increase the duration of time that a population can persist in an altered environment, but is bounded by physiological thresholds that limit tolerance of long-term environmental change, and for populations living close to their extremes already (van Heerwaarden et al. 2016; Comte and Olden 2017; Sasaki and Dam 2019). Migration to new environments is similarly limited (Jump and Peñuelas 2005; Schloss et al. 2012; Walters and Berger 2019), especially for predominantly sessile organisms for which range extension depends upon long-distance dispersal of offspring (Hughes et al. 2003; Archambault et al. 2018; c.f. Kremer et al. 2012). Consequently, understanding whether and how species are likely to adapt to future conditions is crucial in predicting species persistence in the context of climate change (Logan et al. 2014a).

Adaptive evolution to a changing environment occurs when population genotype frequencies change to express traits or phenotypes that provide increased fitness (Falconer and Mackay 1996). However, adaptation of a trait can only occur at a rate proportional to the narrow-sense heritability coefficient, h^2 , calculated as the ratio between population variance attributable to additive genetic effects, V_a , and the total observed phenotypic variance, V_p (Box 1). The narrow-sense heritability coefficient is a key parameter in the univariate ‘Breeder’s equation’, which predicts the mean population response in trait values for a single trait undergoing selection.

Box 1. Heritability and the Breeder's equation

Heritability is the proportion of a trait's relative genetic variation compared to its total phenotypic variation (V_P). As a dimensionless quantity that describes population responses to selection, heritability is often calculated to compare across different traits, populations, or species (Visscher et al. 2008). There are two types of heritability: broad-sense heritability (H^2) and narrow-sense heritability (h^2).

$$\text{Broad-sense: } H^2 = \frac{V_A + V_D + V_I}{V_P} \quad \text{Narrow-sense: } h^2 = \frac{V_A}{V_P} \quad (1)$$

The former is 'broad' in that it includes all sources of genetic variation (V_G), including additive genetic variation (V_A), as well as non-additive sources such as dominance (V_D) and epistasis (V_I), which are genetic effects not (necessarily) inherited by offspring produced through sexual reproduction (Falconer and Mackay 1996), and thus broad-sense heritability is calculated using clones or genets. Narrow-sense heritability, h^2 , is the proportion of phenotypic variance that is due to additive genetic variance (V_A) alone, and thus is the strictly 'heritable' genetic component of the trait of interest in sexually-reproducing individuals. Narrow-sense heritability is thus calculated using pedigree information from genetically distinct individuals. Important caveats when estimating either narrow or broad-sense heritability include controlling for common environment across individuals as well as considering potential genotype-by-environment interactions, parental effects that may alter offspring phenotype, and the potential for epigenetic inheritance (Falconer and Mackay 1996; Visscher et al. 2008).

Narrow sense heritability can be used to predict and understand population responses to selection. Consider one population where the mean critical thermal maximum (CT_{max}) of the population is 30°C and CT_{max} is highly heritable, e.g. $h^2 =$

0.5. If a temperature anomaly occurs, resulting in the death of the more heat-susceptible individuals and shifting the mean population CT_{max} to 32°C, the univariate Breeder's equation predicts that the mean change in population response (R) in CT_{max} will be:

$$R = h^2 \cdot S = 0.5 \cdot (32^\circ\text{C} - 30^\circ\text{C}) = +1^\circ\text{C} \tag{2}$$

In other words, an increase in the mean selected population CT_{max} of +2°C (S , the 'selection differential') translates to an expected increase in the next generation's average CT_{max} of +1°C (Lush 1937; Lande 1979; Falconer and Mackay 1996). Now consider a second population experiencing the same selection event, but with a relatively low heritability in CT_{max} , e.g. $h^2 = 0.1$. The predicted change in CT_{max} in the next generation would be: $R = 0.1 \cdot (32^\circ\text{C} - 30^\circ\text{C}) = +0.2^\circ\text{C}$, or a five-fold lower response to the same selection pressure. Thus, the relative response of a trait in a population under selection is proportional to the value of the narrow-sense heritability coefficient for said trait, h^2 .

Different traits often have different heritability coefficients, and may also covary with one another (Wright et al. 2019). Counterintuitively, traits which are tied closely to biological fitness (e.g., life history traits, longevity/survival, fecundity) often have relatively low heritability compared to physiological and behavioural traits, and compared to morphological traits that often have higher heritability (Mousseau and Roff 1987; Price and Schluter 1991; Wheelwright et al. 2014; Martins et al. 2019). For example, when populations have previously undergone strong stabilizing selection for a trait tied closely to fitness, the narrower range and variance of trait values observed in the population translates to a reduction in the relative contribution of additive genetic effects to total phenotypic variation, and a decrease in the heritability coefficient (Charmantier and Garant 2005; Teplitsky et al.

2009; Wheelwright et al. 2014). Understanding the potential rate and limits to adaptive evolution will therefore require an understanding of heritability across different traits (Wheelwright et al. 2014).

Selective pressures differ not only in terms of the trait being examined, but also across life stages/ages, growth forms, and environments (e.g., genotype-by-environment interactions). Thus, heritability should vary across these factors as well (Charmantier and Garant 2005; Wilson et al. 2008; Wheelwright et al. 2014). Early life stages/ages can experience strong stabilizing selection for traits associated with early life fitness, and thus exhibit reduced h^2 for these traits. Increasing importance of environmental effects and acclimation to local environments can also reduce the relative importance of additive genetic variation and thus h^2 at intermediate stages/ages (Charmantier et al. 2006a). Finally, late-acting mutations can accumulate in older individuals to cause age-dependent increases in V_A , and thus h^2 , for traits tied closely with fitness (Charmantier et al. 2006a; Charmantier et al. 2006b; Wilson et al. 2008). Similar selective pressures can result in similar h^2 values for traits of species occupying similar ecological niches. For example, in reef-building corals, colony growth form directly influences individual growth rate, fecundity, and survival (Pratchett et al. 2015; Madin et al. 2020). Tabular coral species (which form large horizontal plates supported by a central stalk) exhibit increased adult mortality relative to other coral growth forms in the same habitat due to their increased mechanical vulnerability (Madin et al. 2014). However, it remains unknown whether and how heritability of traits varies among coral species with different growth forms.

In the context of climate change, decreasing environmental suitability and increasing selective pressure on traits tied closely to fitness can reduce trait heritability, resulting in a counter-intuitive reduction in the capacity for populations to evolve to environmental change (Charmantier and Garant 2005; Wilson et al. 2006; Wheelwright et al. 2014). Conversely,

other studies have found no distinguishable relationship between h^2 and environmental favourability (Rowinski and Rogell 2017), and others still identify positive correlations of h^2 with increasingly harsh environmental temperatures (Gunay et al. 2011). Clearly, further research is required to quantify how heritability may change across life stages and environments of the future, especially when attempting to project population outcomes in response to future conditions.

Reef-building scleractinian corals are particularly sensitive to climate stressors, as evidenced by coral bleaching during thermal anomalies. Reef diversity and coral cover have declined throughout the 21st century (Wulff 2006; Pratchett et al. 2011; Hughes et al. 2018b), with 75% of global reefs now being considered threatened (Burke et al. 2011). Widespread bleaching of coral communities now occurs at temperatures approximately 0.5°C higher than a decade ago, suggesting strong selection for increased thermotolerance worldwide (Maynard et al. 2008; Guest et al. 2012; Sully et al. 2019). However, given the rapid warming of sea surface temperatures and the increase in the frequency and severity of mass bleaching events on coral reefs worldwide (Hughes et al. 2018a; Lough et al. 2018), it remains unclear whether corals can adapt to the prolonged thermal stress they now experience with increasing regularity (Pandolfi et al. 2011; Hoegh-Guldberg et al. 2017). Models estimating long-term coral adaptation to climate change have assumed low to medium heritability of thermotolerance (e.g., $h^2 = 0.01$ – 0.50 ; Cropp and Norbury 2020; Matz et al. 2020; Logan et al. 2021), despite some evidence of model outcomes being sensitive to the rate of adaptation (Bay et al. 2017; Cropp and Norbury 2020), evidence of high heritability for coral survivorship in high temperatures (e.g., $h^2 = 0.75$: Kirk et al. 2018), and the potential for rapid symbiont evolution in response to thermal change (e.g., Chakravarti et al. 2017; Buerger et al. 2020). Therefore, our ability to project the future of coral populations in the

context of climate change is critically dependent upon the estimates of trait heritability used in eco-evolutionary models (Visser 2008; Logan et al. 2014a; Logan et al. 2014b).

Worldwide, reef-building corals are undergoing increasingly strong selection for temperature tolerance due to anthropogenic climate change. Here, we undertake a quantitative meta-analysis of published heritability estimates for reef-building corals to better understand which traits are likely to change most rapidly given increased environmental change. We examine the relative heritability of different trait types such as coral gene expression, bleaching, growth, symbiont community structure, and survival, and investigate potential interactions among life stages and, for experiments that manipulate temperature, to the magnitude of temperature stress to which corals are exposed. We also estimate the relative heterogeneity of heritability estimates, examine differences between narrow-sense vs. broad-sense heritability estimates, and identify how differences in coral growth forms influence estimates of h^2 .

Literature Analysis

Literature search

We undertook an exhaustive literature review to find all possible heritability point estimates and associated measures of sampling variance (e.g., standard errors, confidence or credibility intervals) for scleractinian corals by canvassing two major research databases: Google Scholar and Web of Science. Keyword searches were conducted in October 2020 to identify all studies reporting heritability estimates for corals, and/or their associated symbionts. We searched for studies using the keywords and Booleans: “heritability” AND “coral” OR “familial effects” AND “coral”. We found a total of 16 studies reporting heritability and one study with heritability estimates that could be extracted from the published data. We then mined the references cited within each paper from the initial search

to identify two additional studies reporting heritability estimates. We contacted some study authors when text alluded to heritability estimates, but values were not reported in the final manuscript, all of whom kindly contributed those heritability estimates to our analysis. Where possible, we selected single heritability estimates calculated using a fixed effect of temperature or other treatment, rather than taking multiple heritability estimates calculated by splitting the data by each treatment. Many of the studies report multiple heritability estimates for the same or similar traits. For five studies (Lohr and Patterson 2017; Kirk et al. 2018; Wright et al. 2019; Zhang et al. 2019; Manzello et al. 2019), we selected one representative heritability estimate when there were multiple and highly related h^2 estimates (e.g., Kaplan-Meier survival and percent survival; symbiont abundance and chlorophyll A content; total linear extension and net buoyant weight). Finally, we extracted both broad-sense (H^2) and narrow-sense (h^2) heritability estimates for the same trait where both were reported together in order to examine differences between H^2 vs. h^2 ; however, this occurred only for a single study (Carlon et al. 2011).

The above resulted in a total of 103 unique heritability values estimated using a number of methods (see Supplementary Text S1 for a description of the different methods used). Of the 103 total estimates, eight were further excluded on the basis of statistical issues for one of two reasons: (1) there was insufficient variation in relatedness among individuals to properly assess heritability (one study with one estimate), or (2) there was insufficient or expected null variation in the phenotype being examined (two studies, with one and six estimates each). The latter was the case when studies estimated heritabilities associated with coral mortality or bleaching while in ambient conditions, which results in little to no phenotypic variation from which to calculate narrow-sense heritability (i.e., none of the corals bleached or died). This left 95 unique and valid heritability estimates from 19 studies.

Pre-processing

Heritability is calculated as a proportion of total phenotypic variation, and thus is constrained to fall between zero and one (Falconer and Mackay 1996). Because most classical meta-analytical statistical models assume normally-distributed uncertainty, transformation of our estimates prior to meta-analysis was necessary (Viechtbauer 2010; Lin and Xu 2020). Thus, we converted point estimates of heritabilities and associated standard errors (SE) to 95% confidence intervals, then transformed both the point estimates as well as the upper and lower 95% confidence (or Bayesian credible) limits to the natural logarithmic scale using the transformation:

$$h_T^2 = \ln[h^2 + 0.2] \quad (1)$$

with a horizontal displacement of + 0.2 to avoid excluding lower h^2 CIs that had slightly negative values when the point estimate was close to zero (see Supplementary Text S2 and Supplementary Code Documentation A for details).

There were four estimates from two studies that did not report any associated SE or CI values, and another three estimates whose lower CI values (when calculated from the SE) were less than -0.2, which prevented their transformation to the \ln -scale. To include these data in the meta-analysis but down-weight their leverage on the overall analysis, we fit a quantile regression through the 95th quantile of transformed SE vs. transformed h^2 (Koenker and Hallock 2001; Koenker 2020) using only heritability estimates that were able to be transformed to the \ln -scale. value of the heritability on the transformed scale (h_T^2) to predict SE_T values. We then used this fitted equation ($SE_T = 0.255 - 0.452 \cdot h_T^2$) to interpolate missing SE_T values, making the conservative assumption that they would have values at the upper 95th quantile (i.e., among the most uncertain estimates).

Factors of interest

206 We identified five explanatory factors present in most studies: trait type, heritability
207 type, life stage, growth form, and temperature manipulation (Table 1). Differences in
208 heritability estimates among specific coral/symbiont species were also of interest; however,
209 most studies examined only a single species and there was little overlap in species across
210 studies, with the exception of a number of studies examining *Acropora millepora* heritability.
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Table 1. Explanatory factors and covariates examined in the meta-analysis of coral heritability estimates

Factor/Covariate	Levels	Definition
<i>Heritability type</i>	Broad-sense heritability, H^2	The proportion of phenotypic variation explained by all genetic effects, which includes sources of variance associated with additive, dominance, and epistatic effects
	Narrow-sense heritability, h^2	the proportion of phenotypic variation explained by additive genetic effects
<i>Trait type</i>	Gene expression	Up- or down-regulation of various genes involved in intracellular stress pathways
	Photochemistry	Measures of symbiont photochemistry, chromoprotein content
	Growth	Coral or corallite growth measures including calcification rates, buoyant weight change, larval areal expansion, linear extension, and new growth branches
	Nutrient content	Total protein or carbohydrate content present in hosts or whole holobiont tissues
	Bleaching	Symbiont cell densities or change in cell densities, bleaching index scores (a proxy for symbiont cell density), and Chlorophyll A content (correlated to symbiont cell density)
	Morphology	Static intraspecific corallite measurements and larval volumes upon birth

	Symbiont community	Symbiont community indices (Leinster and Cobbold's <i>D</i>) and proportion of symbionts that are more the thermally-tolerant species (<i>Durussdinium</i> spp.)
	Immune response	Catalase and phenoloxidase activity within holobiont tissues
	Survival	Measures of survival/mortality/settlement success, including counts of settlement success or survival, percent survival/mortality at the end of a fixed period, larval survival through high temperatures, or differences in survival between control and temperature treatments
	Gamete compatibility	π -value, the percent larval contribution of various sires to various dams. Excluded from meta-analysis due to the presence of only a single estimate
<i>Coral life stage</i>	larvae	Estimates for free-swimming gamete or planula larvae stages up to successful settlement
	juvenile	Estimates from post-settlement to sexually mature adult
	adult	Estimates from colonies after sexual maturity or using coral nubbins
<i>Coral growth forms</i>	branching	Arborescent form; tree-like branching extensions
	corymbose	Finger-like extensions
	massive	Ball- or boulder-shaped corals
	encrusting	Low-spreading corals often occurring on hard, rocky substrates

	columnar	Upwards-growing cylindrical corals
<i>Temperature</i>	covariate	Difference (in +°C) between the study's reported control or ambient temperature and the heat treatment
<i>difference</i>		temperature

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212 *Reported heritability estimates*

213 We collected a total of 95 valid heritability estimates from 19 independent studies of
 214 scleractinian corals (Fig. 1). Three studies (Császár et al. 2010; Wright et al. 2019; Quigley et al.
 215 2020) each involving multiple trait types, provide 59% of all heritability estimates (Fig. 1-left).
 216 There was an even split of studies (9:9 studies) examining narrow-sense (h^2) and broad-sense (H^2)
 217 heritability, with one study (Carlon et al. 2011) reporting both heritability types. However, the
 218 number of raw estimates produced by each study differed markedly, with more broad-sense
 219 estimates ($n = 70$) than narrow-sense ($n = 25$). The studies also differed in terms of which trait type
 220 was reported, with most studies reporting only a single estimate (12 studies), and the other seven
 221 studies reporting on two to six distinct trait types. Survival was the most frequently studied trait
 222 type (nine studies, 15 estimates), while bleaching (six studies, 10 estimates) and growth (six studies,
 223 23 estimates) were also diversely studied. The latter often included comparisons of multiple species
 224 or symbionts within the same study, resulting in a large number of estimates. Most trait type
 225 estimates originated from least two independent studies estimates, save for immune response (four
 226 estimates from one study) and gamete contribution (one estimate). We therefore interpret the results
 227 for immune response with caution, given that they all belong to the same study, and excluded the
 228 single estimate for gamete compatibility from the subsequent meta-analysis. Notably, there were
 229 limited studies of the heritability of coral reproduction and fecundity, and there were no heritability
 230 estimates of thermal optimum (T_{opt}), measures of performance breadth (e.g., B80, B95), or critical
 231 thermal limits ($CT_{max/min}$). Only three studies reported the total phenotypic variation and/or the level
 232 of additive genetic variation, which would be particularly useful for calculating metrics of
 233 evolvability (Visscher et al. 2008; Ma et al. 2014). We therefore recommend that future studies
 234 report these estimates of variation.

235 For life stage, there were 63 estimates (from eight studies) for adults, 18 estimates for
 236 juveniles (from seven studies), and 14 for larvae (from five studies), with every study reporting on
 237 only a single life stage save for two reporting on two different life stages (Carlon et al. 2011;

238 Quigley et al. 2017). There was similar lack of overlap across heritability types (70 broad-sense vs.
239 25 narrow-sense heritability estimates across 10 vs. 10 studies, respectively), with only one study
240 having both valid broad-sense and narrow-sense heritabilities (Carlson et al. 2011). Across coral
241 growth forms, there were 61 estimates of corymbose corals (from seven studies), 21 estimates for
242 massive corals (from eight studies), nine estimates for branching/arborescent (from six studies), and
243 three and one estimates for encrusting and columnar corals, respectively (each from a single study).
244 Finally, 14/19 studies (83/95 estimates) recorded temperatures, and thus the effect of temperature
245 manipulation on heritability could be examined for these studies. However, the difference between
246 the manipulated vs. control/ambient temperatures varied substantially across each study, with all
247 temperature manipulation differences being positive (i.e., control/ambient conditions were always
248 less than the treatment temperatures) but positively skewed (a few experiments used temperatures
249 that differed by 10°C between control and high temperature treatments, but most used smaller
250 elevations of temperature). For example, 29 estimates of heritability originated from
251 control/ambient conditions (from seven separate studies), while 54 estimates were obtained from
252 above-ambient temperature treatments (from 12 studies). Additionally, there was limited overlap of
253 control and heated temperature differences for some trait types, making it difficult to compare the
254 effect of temperature for trait types such as symbiont community (two control estimates),
255 morphology (one control estimate) and gene expression (nine temperature differences, but no
256 control estimates).

257

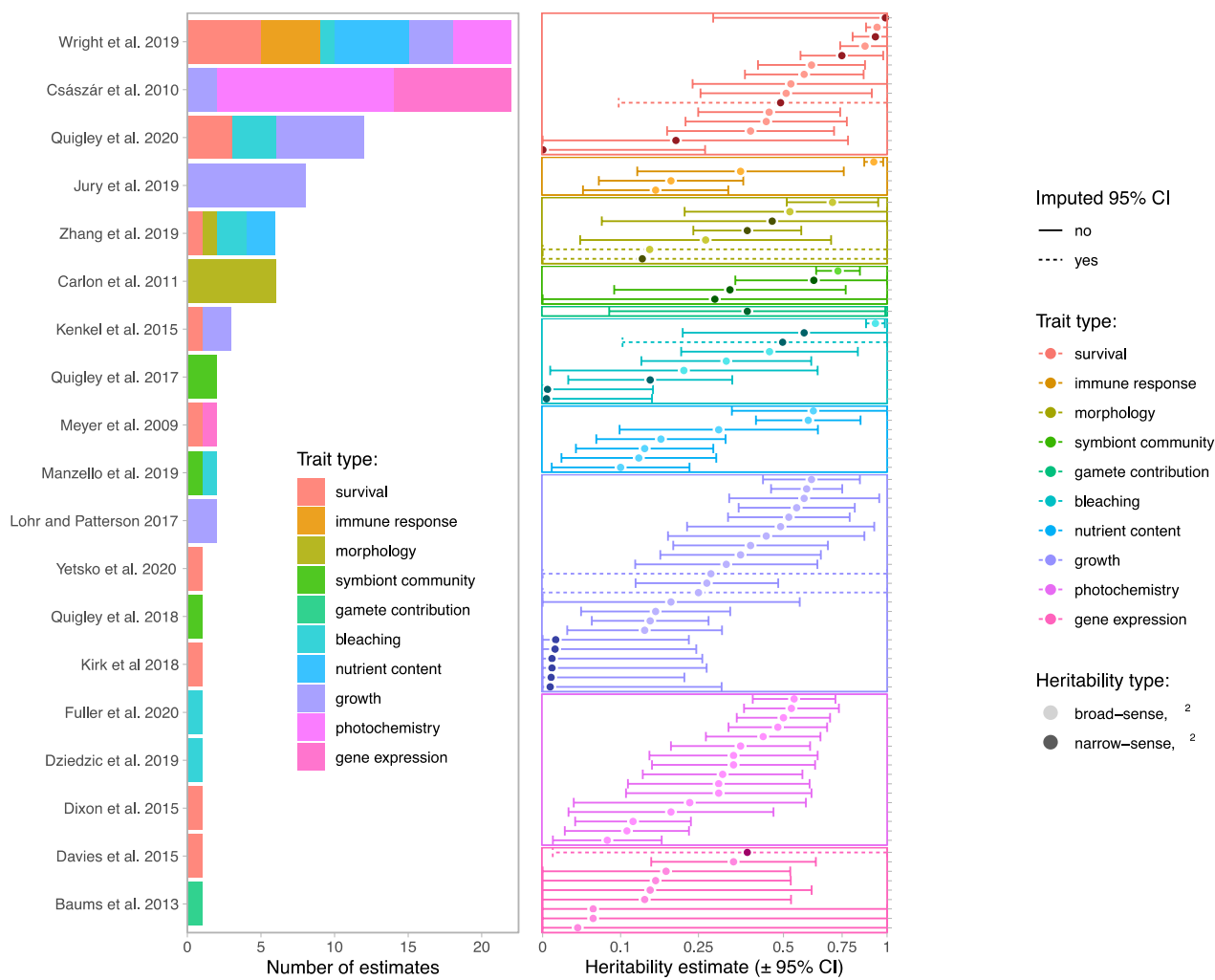


Fig. 1. Heritability estimates ($N = 95$) of various traits across 19 studies of reef-building corals. Colour indicates the specific trait type (hue) and heritability type (broad-sense H^2 as lighter tint circles, narrow-sense h^2 as darker shade). Left: Number of estimates reported in each study. Right: Point estimates of heritability and their associated 95% confidence/credible intervals (whiskers) on a logarithmic (\ln) scale. Heritability estimates closer to one indicate higher heritability and thus the potential for higher rates of trait adaptation within the population. Dashed lines represent heritability estimates where standard errors/confidence intervals were imputed.

Meta-analysis approach

We used the *R* package *metafor* (Viechtbauer 2010) to fit mixed-effects meta-analytic models to $\ln(h^2 + 0.2)$ transformed heritability estimates (h^2_T) and associated estimate sampling variance, while accounting for both fixed and random effects. Due to some missing combinations of

271 explanatory factors within the dataset (e.g., not all traits were measured for all life stages, or for all
272 coral growth forms), the complete dataset only allowed us to consider additive effects of trait type,
273 heritability type, life stage, and growth form in an overall analysis. Temperature was not controlled
274 for or measured in all studies, and thus was excluded as a covariate at this stage. To further assess
275 the robustness of this model and examine interactions, we then analyzed subsets of the complete
276 dataset to test for: (a) trait \times life stage interactions, (b) trait \times heritability interactions, and (c) main
277 effects and interactions involving growth form. Finally, we examined a subset of the complete data
278 that reported treatment temperature differences relative to ambient temperature, including trait \times
279 temperature difference interactions and additive effects of life stage, heritability type, and growth
280 form. All models were fit using more conservative t-distribution approximations of confidence
281 intervals in the case of multi-level random effect models, and final models fit using the more
282 conservative Knapp and Hartung (2003) adjustment for single-level random effect meta-models
283 when multi-level random effects structures were not selected during model selection (Viechtbauer
284 2010; VanAert and Jackson 2019).

285 We considered the top model for each analysis as the model with the lowest Akaike's
286 Information Criterion, corrected for small sample sizes (AICc). We considered this model a
287 substantial improvement over other candidate models when the difference in AICc scores (ΔAICc)
288 was greater than two (Burnham and Anderson 2004). We followed the four-step model selection
289 strategy outlined in Zuur et al. (2007, 2009): (1) define the 'beyond optimal' fixed effects structure
290 – that is, the most conceivably complex yet biologically relevant fixed effects possible, (2) select
291 (via the lowest AICc value) the optimal random effects structure for models fit using restricted
292 maximum likelihood (REML), (3) select (via the lowest AICc value) the optimal fixed effects
293 structures for models fit using maximum likelihood, (4) re-fit the final model using REML. Study
294 and species were highly confounded and precluded the inclusion of both as random effects within
295 the same model. Thus, we fit models using one of the following random effects structures: estimate
296 ID only (1|estimate ID), study ID only (1|study ID), species only (1|species), estimate ID nested

within its respective study ID (1|study ID/estimate ID), estimate ID nested within species (1|species/estimate ID), or a random effect variance fixed at zero.

After fitting models for each analysis, we examined the level of among-study heterogeneity (τ^2) using the I^2 index (Higgins and Thompson 2002), which provides an estimate of the among-study variance relative to the total variance not explained by the fixed effects. We used the Q_E statistic to test for significant residual heterogeneity after accounting for fixed effects (Viechtbauer et al. 2015). Higher proportions of heterogeneity indicate that variation in true effect size of heritability is a distribution of study effects (i.e. due to methodological or other study differences), whereas lower heterogeneity indicates that any among-study heterogeneity is likely small relative to measurement error, so studies are measuring a common heritability value (Higgins and Thompson 2002; Ban et al. 2014). We report the pseudo- R^2 for meta-analytical models, computed by comparing the difference in $\hat{\tau}^2$ estimated using models including fixed effects ($\hat{\tau}_{ME}^2$) vs. a model with the same random-effects structure, but with no fixed effects ($\hat{\tau}_{RE}^2$): $R^2 = (\hat{\tau}_{RE}^2 - \hat{\tau}_{ME}^2) / \hat{\tau}_{RE}^2$ (Raudenbush 2009). Where significant interactions were found between factors with more than two levels, we employed simultaneous tests for testing multiple general linear hypotheses determined by visual inspection of marginal estimates, and report p-values adjusted using the single-step method.

Model standardized residuals were plotted against fitted values to look for strong deviations from normality, and data were simulated using the fitted model and plotted with the true data to assess model performance. We assessed the presence of publication bias by plotting the model residuals by their precision (inverse of standard error) to produce a funnel plot (Møller and Jennions 2001). We also calculated the Rosenberg fail-safe number, which indicates if model findings are robust to any apparent publication bias if the number is greater than five times the number of studies plus ten (Rosenthal 1991; Rosenberg 2005). Finally, we used Cook's distances to determine highly influential points for each model (Cook and Weisberg 1982).

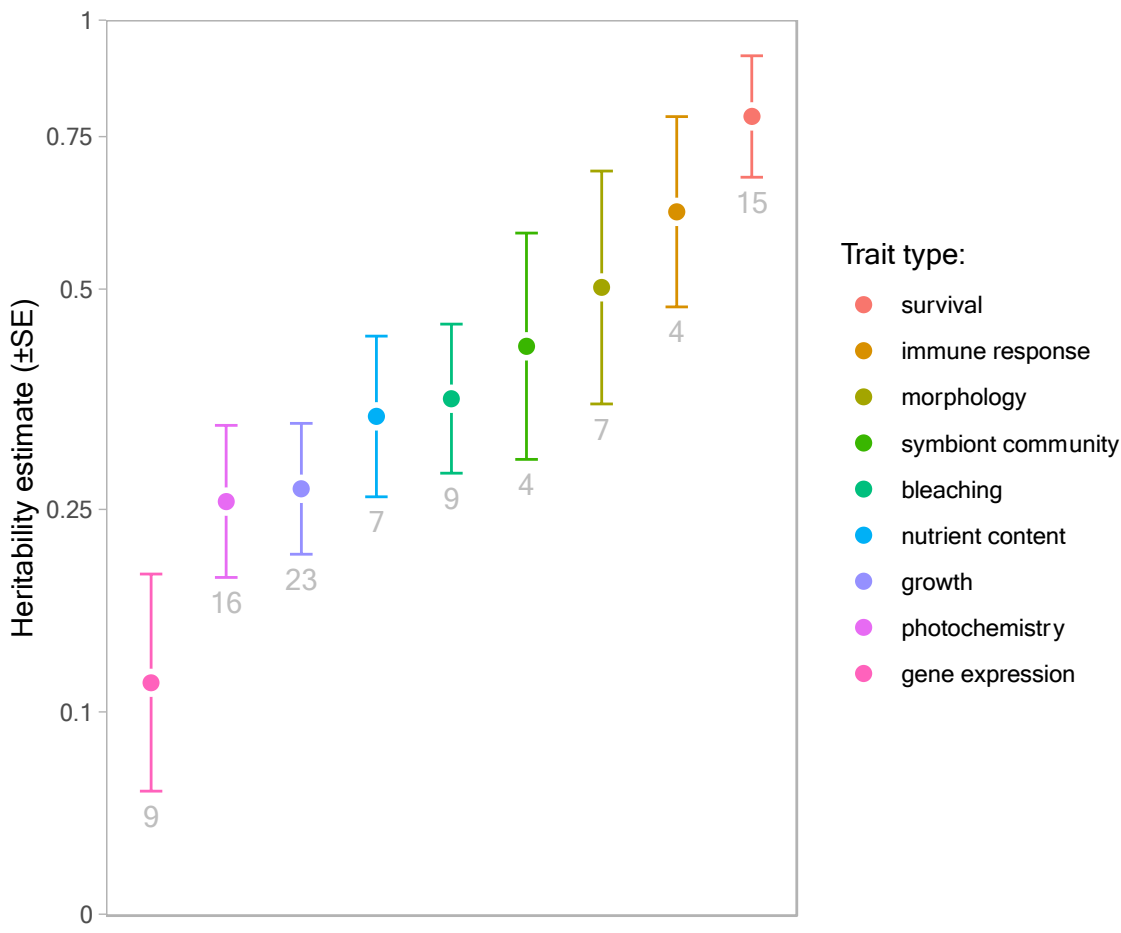
323 **High heritability of coral traits**

324 The results of the overall analysis reveal that the heritability of coral traits has considerable
 325 heterogeneity that can be explained by trait type. The final selected model used trait type as the sole
 326 explanatory factor, and had substantial residual heterogeneity ($QE_{85} = 478$, $p < 0.0001$), with the
 327 total percent of variance not attributable to sampling error, $I^2_{total} = 91\%$, composed of
 328 predominantly between-study variance ($I^2_{study} = 57\%$ of total), but with substantial within-study
 329 variance ($I^2_{estimate} = 34\%$ of total) as well. In all models, random effects involving estimate ID, study
 330 ID, or estimate ID nested in study ID were always selected, with no support for random effects
 331 involving species.

332 Trait type was by far the most important predictor of heritability across all studies (Table
 333 S1), with traits such as gene expression having low heritability ($h^2 < 0.25$); photochemistry, growth,
 334 nutrient content, symbiont abundance, morphology, and symbiont community having moderate
 335 heritability ($h^2 = 0.25\text{--}0.5$); and immune response and survival/larval settlement success having the
 336 highest heritability estimates ($h^2 > 0.5$; Fig. 2). However, models that included additive effects of
 337 trait type + heritability type and trait type + life stage were supported by model selection (i.e., they
 338 fit almost as well as the model with trait type alone). However, the effect sizes of both were small
 339 relative to the effect of different trait types (Table S2; Fig. S2). For example, broad-sense
 340 heritabilities were 1.4–2.1 times higher than narrow-sense heritability and varied by a factor of 1.1
 341 to 2.1 across different life stages (within the same trait type), whereas trait type differences were
 342 much larger, being up to 6.7 times larger in the case of survival vs. gene expression. Estimates for
 343 the mean heritability of different traits ranged from low to high, but most traits were moderately
 344 heritable (Fig. 2). Gene expression traits had the lowest estimated mean heritability ($h^2=0.12$), while
 345 survival had the highest ($h^2=0.79$), followed by immune response ($h^2=0.62$), with the other
 346 estimated trait mean heritabilities falling between 0.26–0.50 (Fig. 2). One estimate in particular, a
 347 value of 0.92 for *Acropora millepora* (Wright et al. 2019), drove the high heritability of immune

348 response (Cook’s distance = 5.2), while all other Cook’s distances were relatively low (< 2). Thus,
349 the estimated high heritability of immune response should be interpreted cautiously.

350 The final model’s funnel plot exhibited no signs of publication bias (Fig. S1), and the fail-
351 safe number (i.e. the number of null-result studies required to overturn a significant result) was an
352 order of magnitude above five times the number of studies plus ten (1,285 >> 100), indicating that
353 the model findings are robust to any underlying publication bias.



354
355 **Fig. 2.** Heritability estimates \pm SE for the trait type-only model, not accounting for differences due
356 to (i.e., pooled across) life stage and heritability type. Traits are sorted along the spectrum according
357 to their overall relative heritability, with heritability closer to one indicating more heritable traits.
358 The number of estimates included in the meta-analysis for each trait type are indicated below each
359 error bar in grey. The gamete compatibility trait type is excluded due to its reliance on only a single
360 study/estimate.

362 *Heritability across trait types in other organisms*

363 Heritability differences across trait types have been widely reported in other taxa (Mousseau
364 and Roff 1987; Wheelwright et al. 2014; Polderman et al. 2015; Flood et al. 2016). Life history
365 traits closely tied to fitness (e.g., longevity, fecundity) are often maintained due to strong stabilizing
366 selection and thus exhibit lower heritability compared to morphological, physiological, and
367 behavioural traits (Mousseau and Roff 1987; Price and Schluter 1991; Teplitsky et al. 2009;
368 Wheelwright et al. 2014). However, traits may also have low heritability due to a large contribution
369 to total variance by non-additive genetic variation, environmental variation, or through maternal
370 effects (the latter likely to be less pronounced in broadcast spawning corals than in organisms with
371 higher levels of parental care). In our analysis, gene expression had the lowest heritability, which is
372 consistent with many other studies noting the low heritability of mRNA (i.e., the ‘missing
373 heritability’ problem, Zuk et al. 2012; Yang et al. 2014). While the exact cause of missing
374 heritability for gene expression measures has yet to be determined, it may be due to highly variable
375 gene expression both within (i.e. low repeatability) and among individuals, or to epistatic gene
376 interactions, or some combination of both (Zuk et al. 2012; Yang et al. 2014). The heritability of
377 symbiont community composition was much higher than heritabilities estimated for the diversity of
378 human gut microbes ($h^2 = 0.019$), which is predominantly environmentally rather than genetically-
379 determined (Rothschild et al. 2018). However, beneficial microbes that are related to metabolic
380 health, such as gut bacteria of the family Christensenellaceae, and microbiomes of mice in
381 controlled laboratory environments (Org et al. 2015), show much higher heritabilities of $h^2=0.3-0.6$,
382 more consistent with our findings. Photochemical traits were estimated to have modest heritability
383 in our analysis; however, only two studies which included only broad-sense estimates were
384 available ($H^2 = 0.26$). In plants, broad-sense heritability of photosynthetic traits is variable but can
385 be very high (e.g., $H^2 = 0.87$, $0.5 - 0.99$, and 0.99 ; Geber and Dawson 1997, Flood et al. 2016, and
386 Tuhina-Khatun et al. 2015, respectively). Moderate narrow-sense heritability estimates, similar to
387 those reported here, have been reported for narrow-sense heritability of maximum quantum yield in

plants ($h^2 = 0.12\text{--}0.34$) (Qu et al. 2017). Heritability associated with bleaching and symbiont abundance in corals (often using chlorophyll content as a proxy) was estimated overall as $h^2 = 0.36$, which is similar to estimates of broad-sense heritability of chlorophyll content in plants (e.g., $h^2 = 0.44\text{--}0.49$ in *Oryza sativa* L., Tuhina-Khatun et al. 2015).

Life stage and heritability type, but not growth form, mediate trait heritability

Using a data subset to examine trait type and life stage interactions, a model of trait type \times life stage + heritability type with a random effect of estimate ID only was preferred under model selection (Table S3). Other analyses of trait type versus heritability type interaction and trait type and growth form interaction found further support for a trait type \times life stage interaction (see Supplementary Text S3). The final meta-model had moderate levels of heterogeneity among estimates ($QE_{55} = 96$, $p = 0.0005$; $I^2_{total} = 47\%$) and fixed effects helped explain much of the variation in heritability estimates (pseudo $R^2 = 78\%$). Parameter estimates for all trait types were similar to the previous overall model estimates (Fig. 3; Fig. S3; Table S4), but there were significant interactions for growth and bleaching in juveniles relative to other life stages as well as a for nutrient content in adults (Fig. 3; Table S4). Cook's distances for the trait type \times life stage + heritability type model were low overall (≤ 2), but three points had moderate leverage on the analysis (Cook's distance = 2.9–3.9), but the growth:juvenile interaction term remained important when any or all were excluded from the analysis. Coral growth form was never an important predictor of heritability, and species was never selected as an important random effect, suggesting that taxonomic differences may be too small or variable to detect, given the data currently available.

Life stage had a strong effect for certain trait type–heritability type combinations (Fig. 3; Table S4). For example, the estimated narrow-sense h^2 for bleaching metrics in adults was 9.1 times the same h^2 for juveniles, and two times the bleaching H^2 value in adults versus larvae. Growth and nutrient content broad-sense heritability also differed across life stage, with adult growth H^2 being 3.1 times that of juveniles and nutrient content H^2 being 3.9 times greater in larvae vs. adults. In

414 contrast, the effect of heritability type was relatively weak (1.4 to 2.5–fold higher for broad-sense
415 heritabilities vs. narrow-sense when controlling for trait type and life stage) compared to the effect
416 of trait type on heritability, which was up to 13.2 times higher heritability when comparing h^2
417 between juvenile bleaching vs. survival (Fig. 3; Table S4). However, this difference in broad- vs.
418 narrow-sense heritability type indicates the presence of substantial but not overwhelming non-
419 additive genetic variation as a portion of the total genetic variation present in broad-sense
420 heritability.

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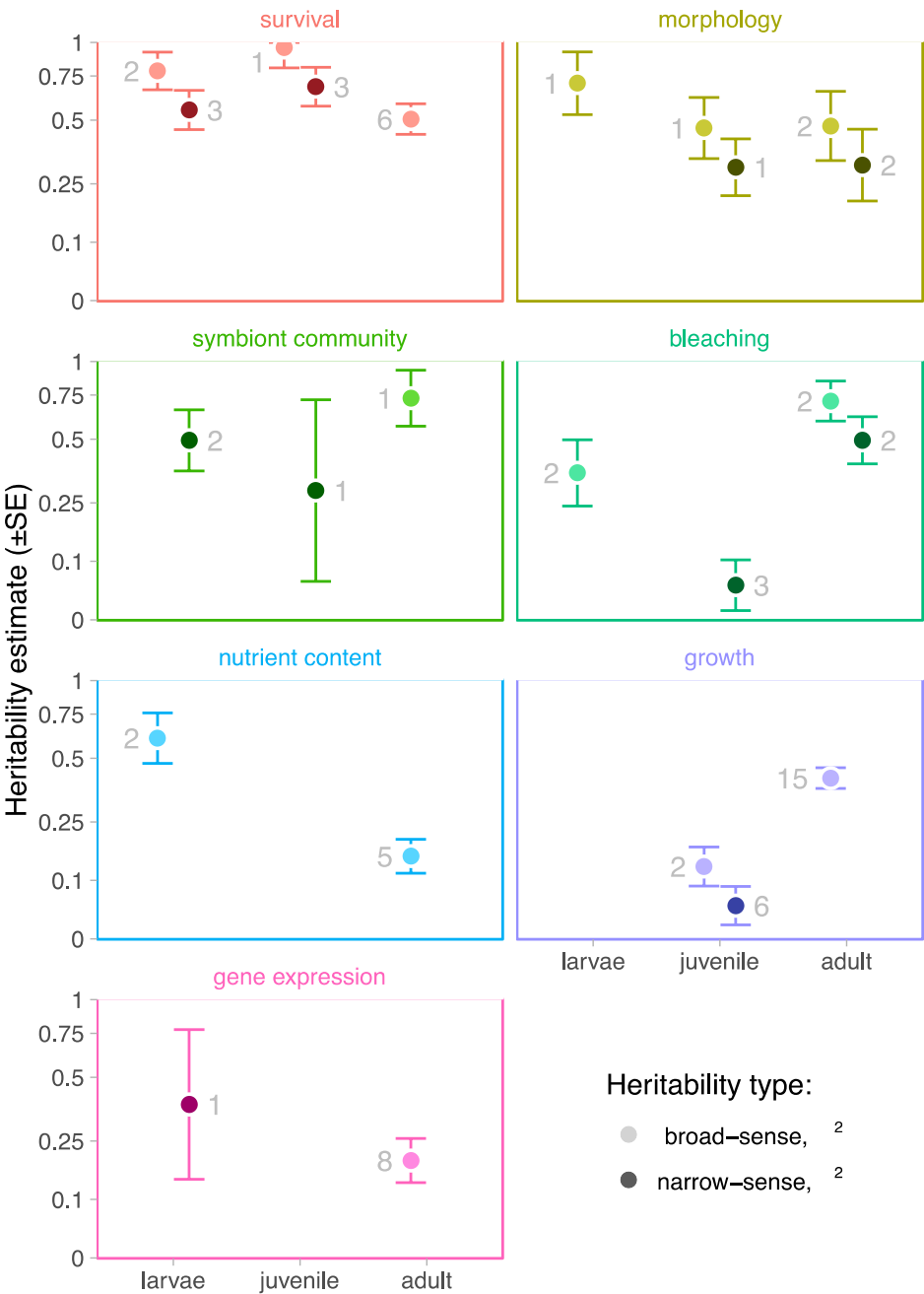


Fig. 3. Heritability estimates \pm SE across trait types with multiple life stages (x-axis) and different heritability types (lighter points: broad-sense heritability; darker points: narrow-sense heritability). Associated sample sizes (number of original estimates) are adjacent to each point in grey.

Low adaptive potential of juvenile growth and bleaching

Juvenile growth was much less heritable relative to adult growth, while bleaching was less heritable in juveniles relative to both larvae and adults, highlighting the differential adaptive

430 potential of coral life stage to selection for some trait types. This reduced bleaching heritability
431 from larvae to juveniles may be the result of previous strong stabilizing selection on growth and
432 bleaching traits in juveniles, thus driving reduced additive genetic variance through the fixation of
433 alleles and resulting in lower heritabilities compared to other traits (Fisher 1930; Teplitsky et al.
434 2009). Indeed, bleaching events likely represent a strong selective pressure for juvenile corals
435 (Dajka et al. 2019; Hughes et al. 2019). Similarly, reductions in growth may result in increased
436 mortality due to overgrowth competition and size-dependent predation (Vermeij and Sandin 2008;
437 Doropoulos et al. 2012; Madin et al. 2014). There is also evidence that increases in additive genetic
438 variance (V_A) may occur via mutation accumulation across an organism's lifetime (Wilson et al.
439 2008b). Moreover, reduced importance of local environment with age can result in reduced relative
440 total variation, V_P (e.g., the Wilson effect, Bouchard Jr. 2013). Both of these processes can therefore
441 result in older life stages having higher heritability estimates. Making the distinction between these
442 processes requires examining changes in V_A and V_P across an organism's lifetime, which no coral
443 studies have done to date.

444 Increased disturbances related to anthropogenic climate change are likely to select for
445 different species traits and communities (Herben et al. 2018; Pratchett et al. 2020), but little is
446 known regarding selection on life stages within the same trait. With increased frequency of
447 bleaching events resulting in more free space being made available to coral recruits, the adaptive
448 potential of juvenile coral growth rates may determine which corals become predominant in future
449 communities. However, negative trade-offs between bleaching and growth have been observed for
450 coral symbionts (Little et al. 2004; Berkelmans and Van Oppen 2006; Cunning et al. 2015) and
451 juvenile coral hosts (Kenkel et al. 2015a; Morikawa and Palumbi 2019), such that more thermally-
452 specialized holobionts may exhibit reduced growth rates in ambient conditions. If these phenotypic
453 trade-offs are genetically based, the genetic correlation between the two may constrain their
454 evolution to climate change and thus would explain why the estimated heritabilities for juvenile
455 bleaching and growth are lower compared to other life stages. More study of genetic correlations in

juveniles is required to understand how juveniles are likely to respond to selection due to climate change; however, one laboratory selection experiment on adult fragments from *Acropora millepora* did find a significant positive genetic correlation ($r_g = 0.19$) between bleaching and growth (Wright et al. 2019). With increased study of narrow-sense heritabilities and especially genetic correlations among traits and at different life stages, the constraints on corals' responses to environmental change will come into sharper focus.

Confounding sources of variation

Our review of the literature highlights some potential sources of bias in heritability estimates that are not well-controlled in coral studies to date. Studies that do not use shared common environments may overestimate heritability by confounding environment-driven phenotypic variation with additive genetic variation, such as when related individuals occur in the same environment and thus acclimatize similarly. Importantly, no studies examining adult corals raised corals to adulthood in a shared common environment, and thus do not control for preconditioning or canalization differences among colonies (Putnam and Gates 2015). However, coral larvae and juveniles were almost always raised in shared common environments during spawning and fertilization, thus larvae and juvenile heritability estimates are less likely to be overestimated due to this phenomenon. Despite this, there are a number of traits with higher heritability for larvae and/or juveniles relative to adults, such as survival, gene expression, nutrient content, and morphology (Fig. 3). This suggests that, at least for these traits, the variation associated with preconditioning and plasticity is unlikely to be particularly large relative to the additive genetic variance. Moreover, visual inspection of residuals suggested no additional unexplained variation that might be associated with whether or not a shared common environment was used (Fig. S9 in Supplementary Code C).

Our results are also affected by other sources of phenotypic variation not accounted for in present studies, such as parental and epigenetic effects. Parental effects may have a larger influence on heritability than previously assumed (Noble et al. 2014; Kenkel et al. 2015b), and may be

482 especially important for brooding corals in which the offspring develops within the parent colony as
483 well as for species inheriting their symbiont communities directly from parents (i.e. vertical
484 transmission) (Kenkel et al. 2015b; Quigley et al. 2017). Vertically-transmitting brooders and
485 broadcast spawning species make up a minority of species examined (3/19 and 9/19, respectively),
486 with the remaining being horizontally-transmitting spawners. Similarly, the number of heritability
487 estimates from vertical transmitters made up only 9/95 and 16/95 heritability estimates,
488 respectively, and thus parental effects via brooding and/or vertical transmission would have
489 impacted a minority of estimates. Epigenetic effects may also inflate heritability estimates (Putnam
490 and Gates 2015). In studies of multicellular animals, there has been little support for epigenetic
491 inheritance via CgP methylation (Torda et al. 2017), although at least one recent study in corals has
492 found such evidence (Liew et al. 2020). Further evidence is needed to determine if epigenetic
493 changes confer fitness benefits similar to additive genetic effects (Torda et al. 2017), thus future
494 studies aiming to separate phenotypic variation specific to parental effects, symbiont composition,
495 epigenome, and additive genetic effects would be especially valuable.

497 **Manipulated temperature has negligible effect on heritability**

498 When examining only studies that controlled for temperature, the magnitude of the
499 experiment temperature difference relative to ambient or control conditions had only a marginal
500 effect on the recorded heritability estimate (Fig. 4). The temperature difference values were all
501 positive and positively skewed, thus we square-root transformed the temperature difference data in
502 order to reduce the leverage of estimates obtained from studies using these large temperature
503 differences. After subsetting the data to exclude studies that did not report the temperature treatment
504 used relative to ambient conditions, we examined whether an interaction between trait type and
505 temperature difference was supported. Model selection favored a model of trait + heritability type,
506 with some support for alternative models of trait type only and trait type \times temperature difference
507 (Table S9; $\Delta AICc = 0.50$ and 1.89 , respectively) using random effects of estimate ID nested in

study ID. The trait + heritability type model had similar effect sizes compared to those in our analyses presented above (Fig. S6; Table S10). The effect of trait type in the trait type \times temperature model (3rd-optimal model) saw heritability differences up to 3.4–4.6 when the temperature was increased +1°C to +3°C above ambient. However, within the same trait type, temperature alone had a reduced effect, with heritability differences between 0–2.1 and 0–1.6 for +1°C and +3°C, respectively. More specifically, temperatures +1°C above ambient resulted in immune response heritability increasing by a factor of 2.1, while an increase of +3°C above ambient would increase heritability by a factor of 1.6. This interaction was primarily driven by a single estimate of immune response (Cook's distance = 7.6), and when removed, resulted in no strong interactions between trait type and temperature. Within other traits, the effect of temperature was even less pronounced. Bleaching traits were decreased by 28–33% for an increase in temperature of +1–3°C (though this was not significant). Other traits such as growth, photochemistry, and survival all showed marginal declines in heritability with increasing temperature difference (~3–5% decrease in heritability with +1–3°C). Separate analyses examining temperature as a categorical variable (ambient vs elevated), as well as analyses omitting ambient treatments all resulted in similar weak to non-existent effects of temperature on heritability (Fig. S7-8; Tables S11-14), suggesting a limited effect of manipulated temperature on heritability across studies. Since a model of trait type + heritability type was preferred over the model of trait type \times temperature manipulation (Table S9), and with the inclusion of heritability type precluding the ability to model a trait \times temperature interaction, we fit an additive model of trait type, heritability type, and temperature difference to estimate the marginal effect of temperature and found evidence for, at most, a very weak effect of temperature (Fig. 4).

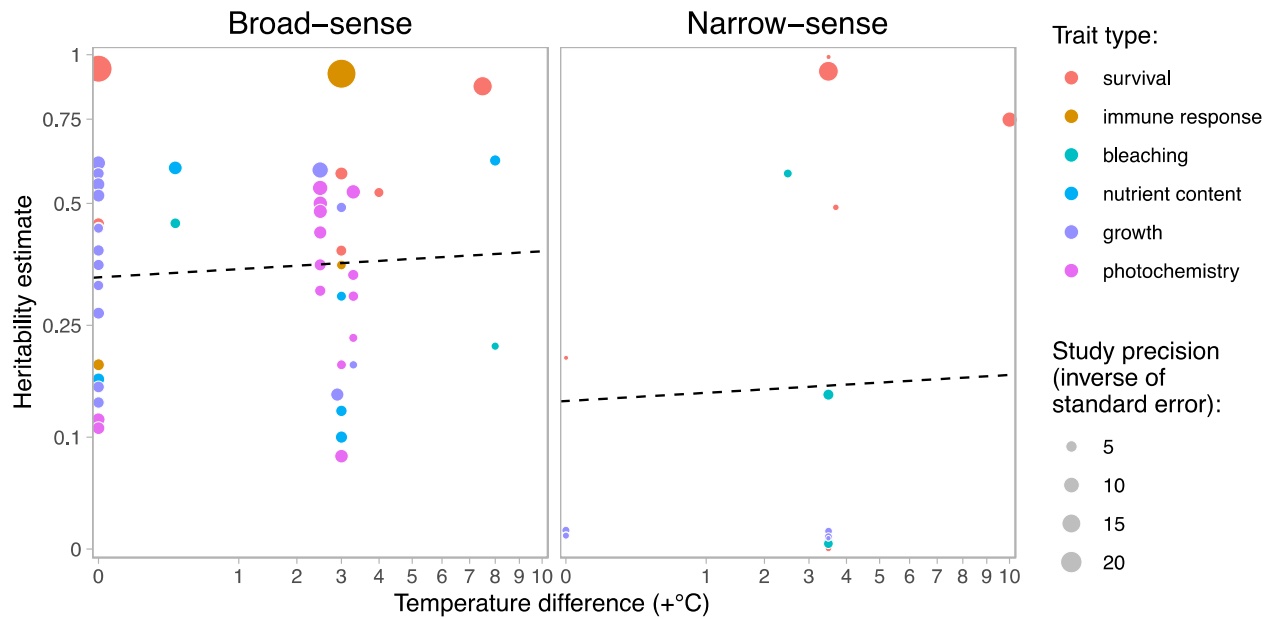


Fig. 4. Heritability vs. study temperature difference (treatment temperature relative to ambient/control temperature) for each trait type and heritability type, with the size of each point represents its relative precision. Dashed lines indicate the estimated marginal mean effect of temperature difference, while accounting for trait type and heritability type effects. One square-root degree difference ($+1\sqrt{^\circ\text{C}}$) translates to a mean increase in $\ln[h^2+0.2]$ heritability of 0.03 ± 0.05 SE.

Trait adaptation to warming temperatures

Our meta-analysis suggests that the capacity for corals to adapt to warming temperatures may be relatively consistent over short periods of moderately high temperature (e.g., $+1$ – 3°C , the temperature increases used in most of the studies we analyzed). However, this is contingent on the assumption that coral responses to temperature conditions in the lab are similar to their responses to temperatures in the field. Previous studies have found that many traits are expected to respond differently to climate change (Ahrens et al. 2020), that heritability measurements may change with temperature (Bubliy and Loeschke 2002), and that the rate of temperature increase employed in each study can also affect heritability (Chown et al. 2009). Similarly, previous heritability studies in insects report trait-specific interactions with temperature (Bubliy and Loeschke 2002; Gunay et al. 2011). Current theory suggests that more extreme environments should produce increased selective

pressures that may reduce heritability (Falconer and Mackay 1996; Charmantier and Garant 2005; Wilson et al. 2006). However, despite expectations based on theory and empirical results like those described above, differences in the temperature gradients used in each study did not predict the among-treatment differences in heritability estimates for corals. Specifically, temperature had negligible effect on the estimation of trait heritability, such that an increase of +1°C may increase high vs. low trait heritability by 4 to 9%, respectively, while an increase of +3°C results in an increase in heritability of 7 to 16% (changes that, if real, would be opposite of the predicted direction). These findings indicate that populations with sufficient genetic diversity are unlikely to experience a reduction in heritability associated with warmer temperatures, in turn suggesting substantial retention of the capacity to adapt in the face of ongoing temperature change.

Coral thermal performance and challenges to predicting future adaptation to climate change

The absence of an effect of temperature on trait heritability observed here could reflect differences among studies in the way temperature treatments were applied, and/or differences in how temperature effects were statistically modelled. Many traits of organisms are non-linearly related to temperature, and these relationships are captured by measuring thermal performance curves (TPCs). TPCs are quantified by subjecting individuals to increasing temperatures at a standardized rate while repeatedly measuring performance (Angilletta 2009; Chown et al. 2009), to identify: (1) the value of maximal performance (P_{max}), (2) the temperature at which maximum performance occurs i.e., the thermal optimum (T_{opt}); (3) the performance breadth (e.g., B80, B95), and, somewhat related to the latter, (4) the limits of thermal performance (e.g., CT_{max}) (Angilletta 2009; Logan et al. 2014b; Bodensteiner et al. 2020). Measuring limits to thermal tolerance involves either static assays of survival time in a constant high temperature, such as heat knockdown time (Ma et al. 2014; Castañeda et al. 2019), or dynamic assays involving gradually increasing temperature until failure, such as temperature-at-death and CT_{max} (Doyle et al. 2011; Castañeda et al. 2019).

575 The way in which temperature was modelled in each of the studies analyzed herein – and
576 consequently, which component of thermal performance was captured – is likely to affect the
577 heritability estimated. For example, studies incorporating temperature treatment as a fixed effect
578 and estimating heritability using a single model (Meyer et al. 2009; Dixon et al. 2015; Lohr and
579 Patterson 2017; Manzello et al. 2019), or studies that calculate heritability from the difference in
580 trait values between low vs. high temperature treatments (Császár et al. 2010; Dziedzic et al. 2019;
581 Yetsko et al. 2020) likely estimated the heritability of thermal sensitivity (i.e., how performance
582 changes as temperature changes). Conversely, studies that used separate models for low-
583 temperature and high-temperature treatments (Kirk et al. 2018; Wright et al. 2019; Zhang et al.
584 2019; Quigley et al. 2020) produced separate estimates of the heritability of performance under the
585 two temperatures. One inherent problem with such an approach arises if there is little or no
586 variation in the trait value for one of the treatment levels (e.g., no mortality of bleaching observed
587 under control conditions or no observable growth when corals are placed in extreme heat). The
588 absence of among-individual variation in performance in these cases means that the estimated
589 heritability will always be near zero, regardless of any underlying additive genetic variation
590 associated with the trait in question. For studies of thermotolerance, obtaining heritability estimates
591 via differenced treatment values or as a fixed treatment effect (and thereby providing heritability
592 estimates indicative of the trait's thermal sensitivity) is likely preferable, but ideally future studies
593 would characterize responses based on many temperature points along the TPC to obtain CT_{max} ,
594 T_{opt} , and P_{max} .

595 In this review, we were unable to assess whether heritabilities associated with thermal
596 sensitivity in performance were different from heritabilities of performance itself (Fig. S10).
597 However, the evolution of both maximal performance and the thermal sensitivity are inherently
598 linked by the shape of the TPC (e.g., a higher peak in the TPC would result in higher trait values
599 and greater trait thermal sensitivity), and thus their relationship may be correlated (Janhunen et al.
600 2016). For example, with the evolution of higher upper thermotolerance (e.g., increasing CT_{max}),

organisms may face reduced thermal performance breadth and thermal plasticity (Hoffmann et al. 2013; Comte and Olden 2017; Baker et al. 2018). Growth and the thermal sensitivity of growth are negatively correlated for one-year-old rainbow trout (*Oncorhynchus mykiss*) at low temperatures, but not at higher temperatures, thus while there is moderate heritability for both growth ($h^2 = 0.46$) and thermal sensitivity of growth ($h^2 = 0.24$), selection for higher growth is predicted to result in increased thermal sensitivity in future generations held at low temperatures, but unlikely to affect thermal sensitivity at higher temperatures (Janhunen et al. 2016). Similar trade-offs of growth vs. sensitivity have been observed as well in adult rainbow trout (Sae-Lim et al. 2015). Further complicating the matter, some genetic correlations among life history traits may be temperature-specific (reviewed in Sgrò and Hoffmann 2004), including cases where negative genetic correlations can become positive at higher temperatures and vice-versa. Thus, coral trait evolution may further be complicated by (currently unmeasured) genetic correlations across TPC metrics.

Conclusion

Our meta-analysis estimates relatively high heritability for some traits, such as survival and growth. This, coupled with the fact that heritability does not appreciably decline with increasing temperature manipulation, suggests the potential for coral adaptation to future conditions of weak to moderate climate change. Nevertheless, potential confounding factors that could bias some of our heritability estimates upwards remain to be explored, including the effects of preconditioning and canalization in adults, parental and symbiont effects, and transgenerational inheritance of CgP methylation. Recent evolutionary models of corals consider the heritability of the thermal optimum for corals, T_{opt} , to be anywhere from negligible (e.g., $h^2 = 0.01$) to low/medium (e.g., $h^2 = 0.16$ – 0.50) (Cropp and Norbury 2020; Matz et al. 2020; Logan et al. 2021). However, there are no available estimates for coral thermal performance traits such as T_{opt} , CT_{min} , CT_{max} , and $B80$, and our knowledge of how TPC parameters co-evolve remains very limited. For example, the evolution of higher thermal optima (T_{opt}) may result in reduced maximal performance (P_{max}) or performance

627 breadth (CT_{min} , CT_{max} , and $B80$). Other genetic trade-offs such as growth vs. thermotolerance for
628 both corals and symbionts may exist, further constraining coral evolution to climate change. Future
629 studies would ideally construct TPCs using multiple temperatures across a known pedigree of
630 individuals in order to calculate heritabilities and associated trade-offs for TPC parameters across
631 one or multiple traits. Combined with our current knowledge of trait heritabilities, this would allow
632 better predictions regarding thermal evolution of corals in response to climate change. Nevertheless,
633 our findings suggest that corals may be capable of adapting more rapidly to the thermal challenges
634 imposed by climate change than previously thought.

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642

643 **Data accessibility statement**

644 All extracted heritability estimates and supplementary code are available at
645 <https://github.com/ecology/heritability-meta> (pending article acceptance).

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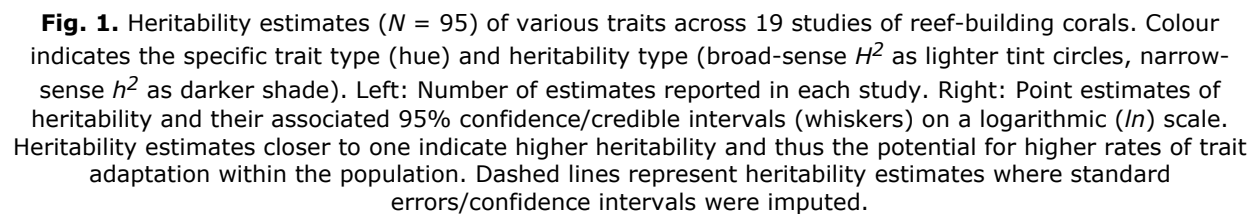
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254x203mm (300 x 300 DPI)

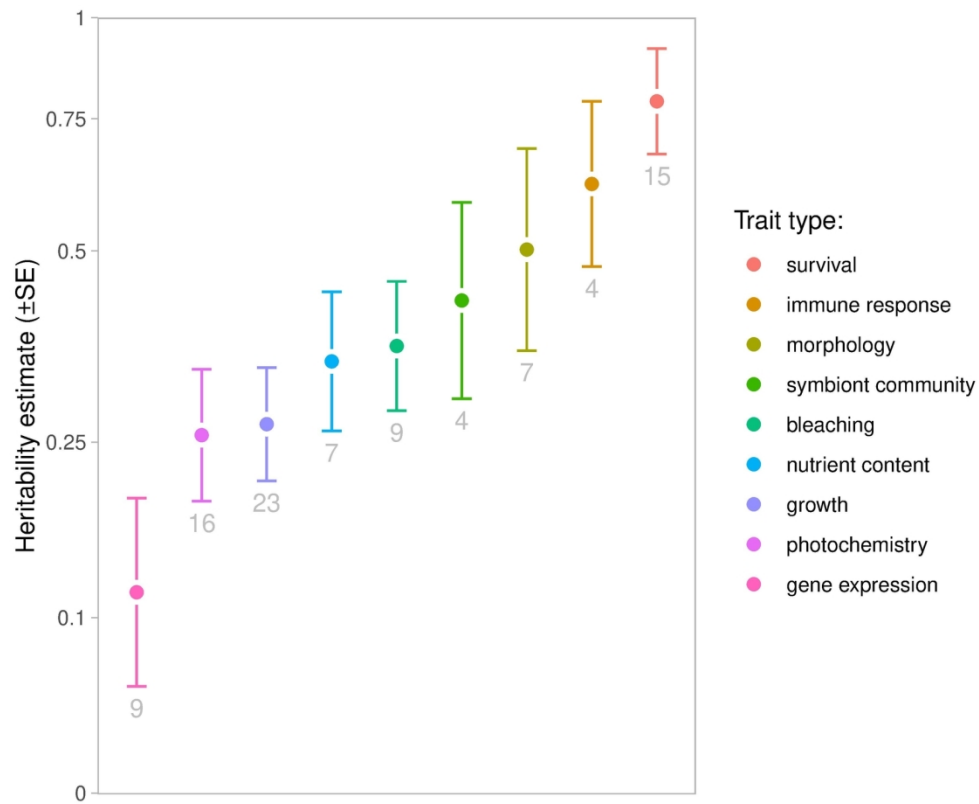


Fig. 2. Heritability estimates \pm SE for the trait type-only model, not accounting for differences due to (i.e., pooled across) life stage and heritability type. Traits are sorted along the spectrum according to their overall relative heritability, with heritability closer to one indicating more heritable traits. The number of estimates included in the meta-analysis for each trait type are indicated below each error bar in grey. The gamete compatibility trait type is excluded due to its reliance on only a single study/estimate.

152x127mm (300 x 300 DPI)

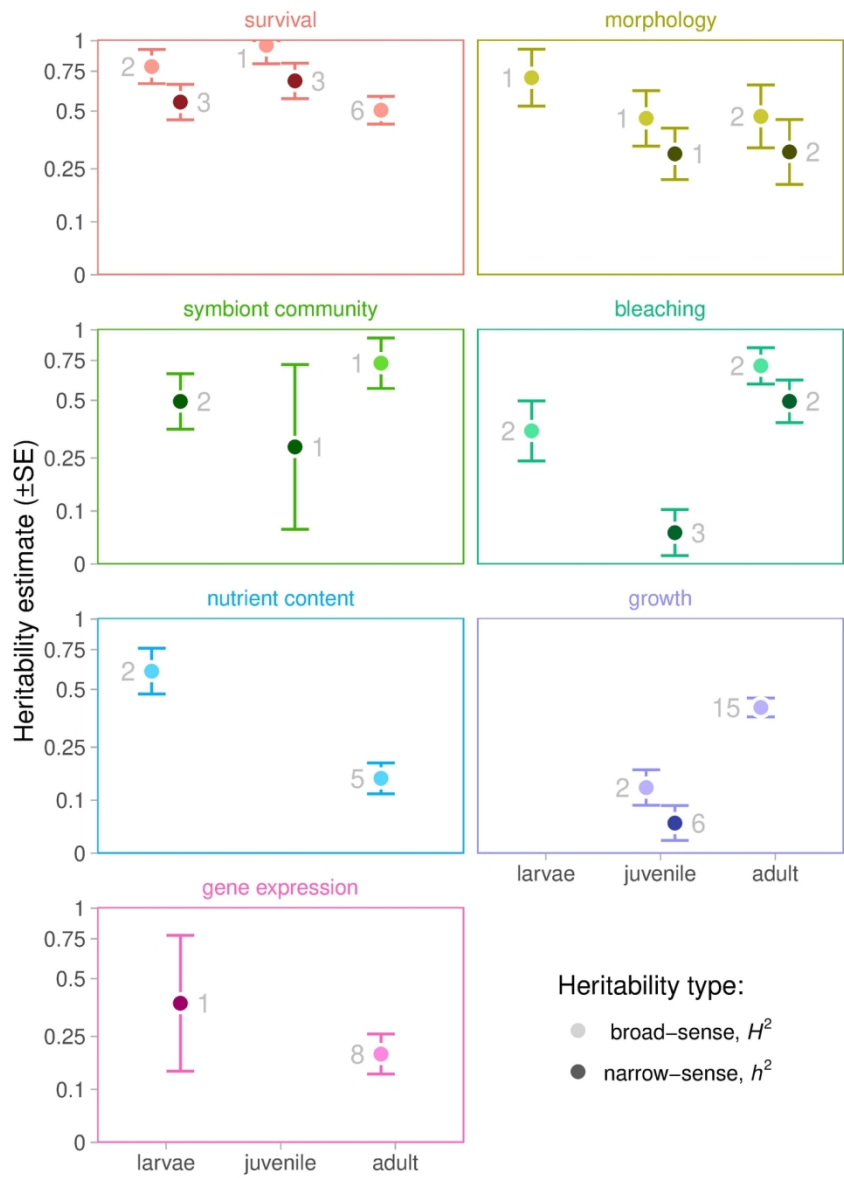


Fig. 3. Heritability estimates \pm SE across trait types with multiple life stages (x-axis) and different heritability types (lighter points: broad-sense heritability; darker points: narrow-sense heritability). Associated sample sizes (number of original estimates) are adjacent to each point in grey.

127x177mm (300 x 300 DPI)

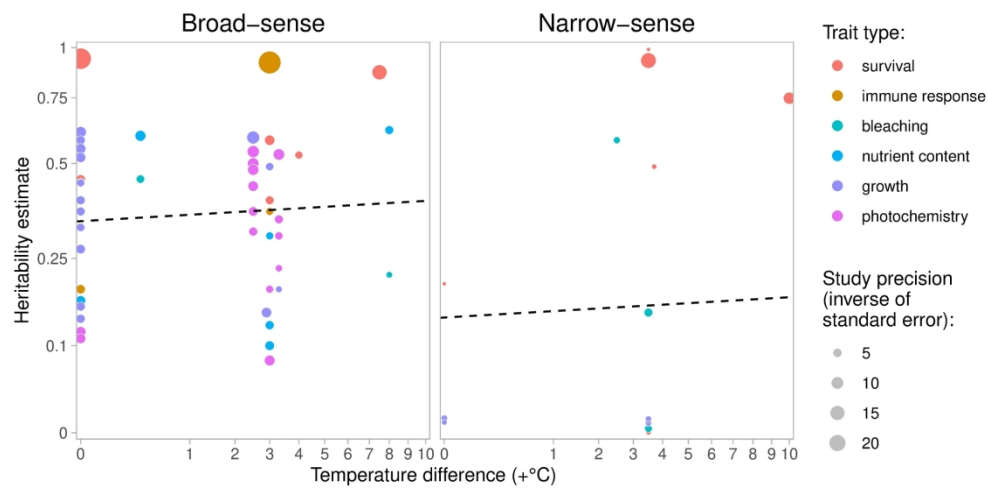


Fig. 4. Heritability vs. study temperature difference (treatment temperature relative to ambient/control temperature) for each trait type and heritability type, with the size of each point represents its relative precision. Dashed lines indicate the estimated marginal mean effect of temperature difference, while accounting for trait type and heritability type effects. One square-root degree difference ($+1\sqrt{^{\circ}\text{C}}$) translates to a mean increase in $\ln[h^2+0.2]$ heritability of 0.03 ± 0.05 SE.

203x101mm (300 x 300 DPI)