# The Clam Before the Storm: A Meta-Analysis Showing the Effect of

#### **Combined Climate Change Stressors on Bivalves** 2

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#### 7 Abstract.

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8 Impacts of a range of climate change on individual marine organisms organisms taxa have been are increasingly

being analysed documented in laboratory and experimental studies. The use of different taxonomic groupings,

and assessment of different a range of processes, though, makes identifying overall trends challenging. Meta-

analysis -hashave been used to determine these general trends but their coarse taxonomic granularity, and may

mask phylogenetically different specific responses. Bivalve molluscs are are a data rich clade of -an-ecologically

and economically important calcifying marine important data rich eladetaxa, allowing for assessment of

individual species-specific vulnerability and across developmental stages. Drawing on the large body of

available literature, wWe conduct ause meta-analysis of 203 unique experimental setups, and to 10 climate

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16 change stressor combinations, to examine how bivalve growth rates respondssesd to increased water

temperature, acidity, deoxygenation, and changes to salinity in 10 climate change stressor combinations. This is

18 the , providing the most complete examination of bivalve sresponses to date, and, and combinations of these

19 drivers. Results shows that anthropogenic climate change will disproportionally affect different particularsome

families of bivalves disproportionally but almost unanimously negatively, suggesting taxonomic

21 granularitydifferentiation in what is considered a well understood group regarding in their climate change

response. Specifically Specifically, Mytilidae, Ostreidae, and Pectinidae (67% of experiments) respond with

23 negative effect sizes for all individual stressors while responses in Pinnidae-, Tellinidae and Veneridae are more

24 complex. HoweverO, our analysis suggests show past work confirming that earlier studies showing negative

25 impacts these resultson bivalves are driven by only 3-4 well studied commercially important bivalve families.

26 Despite the taxonomic differentiation, aAllmost all drivers and their combinations have significant negative

27 effects on growth, suggesting this is inherent to the group. The synergistic impacts of Combined

ddeoxygenation, acidification, and temperature shows results in the largest negative effect size. Eggs/larval

29 bivalves are more vulnerable overall than either juveniles or adults. Infaunal taxa, including Tellinidae and

Veneridae, appear more resistant to warming and oxygen reduction than epifaunal or free-swimming taxa but

31 this assessment is also based on a small number of datapoints. The current focus of experimental set-ups on

32 commercially important taxa and families within a small geographic range of habitats creates gaps in

understanding of global impacts on these economically important foundation organisms.

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#### 1 Introduction

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Predictions of Rrising levels of atmospheric carbon dioxide indicate will alter that the marine environment will 36 37 significantly alter over the coming decades. Sea surface temperatures are projected to rise 2-4°C globally by the 38 end of the century depending on region and emission scenario (IPCC, 2021) with some areas, such as the Gulf 39 of Mexico, already suffering frequent, severe deoxygenation events (Breitburg, et al., 2018). The heterogeneric 40 nature of change in each parameter will result in different combinations of stressors and varying extent of the 41 effect of each stressor on communities in different areas. It is increasingly important to identify how stressors 42 work both alone and in different combinations. Higher latitudes will be exposed to more severe warming than 43 the tropics (Meredith et al., 2019), resulting in sea ice and glacial melting, raising global sea levels, and 44 increasing runoff and freshwater influx into marine settings (Lu et al., 2022). Ocean pH will decline by between 45 0.3-1 units by the end of the 21st century, with with shallower waterscoastal regions expected to experience 46 greater pH decreases than the open ocean (IPCC, 2021). Oxygen levels in the ocean are projected to decrease by 47 up to 7% leading to an expansion of 'dead zones' (Breitburg, et al., 2018; Messié and Chavez, 2017; Schmidtko 48 et al., 2017). The heterogeneouserie nature of change in each environmental driver will result in location-49 specific combinations and extented of stressors. This complexity presents a significant challenging challenge for 50 decision--makersing infor fisheries and marine conservation.. Therefore, it is increasingly important to identify 51 how stressors arising from climate change work both individually and in different combinations on communities 52 and organisms -in different settingsregions, as interaction of stressors, though increasingly recognised in the 53 literature, are still underexplored.

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large spatiotemporal variations in physicochemical conditions such as pH, oxygen, and temperature (e.g., Hoffmann et al., 2011). This variability is exacerbated by anthropogenic climate change leading to more frequent extreme climate events, as well as redistribution of upwelling zones, circulation and currents, and alterations to both the quantity and quality of terrestrial runoff (Sydeman et al., 2014). Therefore, environmental changes are projected to especially impact shallow marine and coastal habitats, which harbour socially and economically important ecosystems. Up to 40% of the world's population lives within 200 km of the coastline (Neumann et al., 2015), and an estimated 775 million people globally have high dependence on these systems and their services (Selig et al., 2019). Costal ecosystems are estimated to contribute more than 60% of the total economic value of the biosphere (Martínez et al., 2007) but organisms adapted to live in these systems are predicted to suffer large alterations in their population fitness in response to future climate change (Kroeker et al., 2013; Sampaio et al., 2021; Hoppit and Schmidt, 2022).

At the intersection of the marine and terrestrial realms, shallow marine and coastal settings typically exhibit

Bivalve molluscs (Class Bivalvia) are cornerstones of coastal and shallow marine ecosystems, with representatives in all marine biomes where they provide provisioning and regulatory services (Olivier et al.,

2020; Carss et al., 2020; Vaughn and Hoellein, 2018). Bivalves are a key global food source, with production

69 for human consumption growing from 51 thousand tonnes in 1950 to more than 12.4 million tonnes today

(Smaal et al., 2019). As a result, bivalve aquaculture has an estimated global market value of \$17.1 billion (van

71 der Schatte Olivier et al., 2018).

Additionally, there is a growing awareness of the wider ecosystem benefits of bivalves as habitat formers. Their

73 biogenic three-dimensional reefs formed by sessile epifaunal taxa such as oysters increase surrounding

biodiversity (Fariñas-Franco and Roberts, 2014). Complex reef frameworks and individual bivalve shells in softsubstrate environments can act as microhabitats to other invertebrates through creation of new hard substrates and by altering local flow regimes or even temperature (McAfee et al., 2017). Filter-feeding bivalves can reduce pollution and clear large particulates out of the water column (Smyth et al., 2018). They enhance or change local marine productivity (Donnarumma et al., 2018; Strain et al., 2021) via selective removal of specific species of phytoplankton (Ward and Shumway, 2004). Deposition of bivalve faeces and pseudofaeces, along with burrowing activity of motile infaunal deposit or suspension feeders, can lead to changes in the local flux or enrichment of organic matter into the sediment and biogeochemical cycling (Smyth et al., 2013), and ultimately habitat suitability for other benthos. Anthropogenic pressures including coastal development, overfishing, and pollution have resulted in demonstrable decreases in global bivalve populations (e.g., De Groot, 1984; Baeta et al., 2014). Akin to other calcifying invertebrate organisms, it has been hypothesised that the physiochemical changes resulting from climate change will reduce bivalve growth, impair maintenance of shells (Maynou et al., 2020; Knights et al., 2020), and disrupt larval settlement patterns and spawning (Bascur et al., 2020; Figueirodo et al., 2022). In recognition of the environmental, social, and economic benefits bivalves produce, and the current and future pressures they face, the group is a focus for conservation efforts (zu Ermgassen et al., 2020; Buelow and Waltham, 2020, Gagnon et al., 2020). However, despite extensive study there remain significant important gaps in our understanding of their response to climate change across different bivalve families. Current understanding of how bivalves will respond to various climate change stressors is based on field studies and lab-derived experimental data focused largely on ocean acidification and response to warming, generally observing negative responses (e.g., Beukema et al., 2009; van Colen et al., 2012; Addino et al., 2019; Eymann et al., 2020). Synthesis work through meta-analysis supports the notion that bivalves overall will respond negatively to climate change (Kroeker et al., 2013; Harvey et al., 2013; Sampaio et al., 2021; Hoppit and Schmidt, 2022; Leung et al., 2022). These studies have shown that the synergistic effects of ocean acidification, ocean warming, and an increase in hypoxic events decrease the growth rates of calcifying marine organisms (Kroeker et al., 2010; Maynou et al., 2020; Knights et al., 2020; Sampaio et al., 2021). However, these analyses have been conducted at high taxonomic rankings, e.g., examining changes at phylum level, thereby they risking averaging differential outcomes at finer taxonomic resolution. Organisms experience though-disparate responses to environmental drivers based on local phenotypic expression (Dong et al., 2017) and environmental influences (Genner et al., 2010) resulting, for example, in species-specific mortality risk to extreme heat based on local microclimates and adaptation (Montalto et al., 2016). 'Clumping' these diverse responses make hiHigh level analyses and their generalized trends can be difficult to interpret due to clumping diverse responses into generalized trends (Helmuth et al., 2005). Organisms experience disparate responses to environmental drivers based on local phenotypic expression (Dong et al., 2017) and environmental influences (Genner et al., 2010) resulting, for example, in species-specific mortality risk to extreme heat based on local microclimates and adaptation (Montalto et al., 2016). Therefore, our current understanding of how bivalves respond to climate change based on broad scale synthesis work might not capture the granularity and diversity of responses this

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group exhibits.

We aimed to fill this gap by employing a meta-analysis methodology to explore the effects of marine climate stressors, and combinations thereof, on bivalve growth at both the whole-group and family levels. Our analysis explores 10 stressor combinations, greatly expanding earlier work examining only four stressors (Sampaio et al. 2021). For the first time in a meta-analysis of impacts of marine climate change, we explore taxonomic sensitivities within a family and identify large gaps in taxonomic understandings of how response to climate change in this very well-studied group. We address the question of Our aim is to determine whether a negative response to climate change is intrinsic to the group or driven by specific taxa. We focused on studies that emphasize bivalve growth rates; a commonly studied trait that offers insight into organism vulnerability to answer how these growth rates are impacted by climate stressors, and whether different families or developmental stages are more sensitive to climate stressors than others. Additionally, we examine the range of experimental work assessing bivalve sensitivity to climate change to understand which families are most represented taxonomic diversity of the experiments available in the published literature for meta-analysis. We We hypothesise that a focus on commercially important bivalve taxa may be creating a likely bias in current observations. Our findings encourage a new approach to meta-analysis by moving towards more differentiated taxonomic understandings of a group's responses to-the future conditions, while still providing a summative response above the individual species level needed for conservation decision making.

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129 2 Methods

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The data and code is accessible in the Github folder https://github.com/georgehoppit/Bivalve-meta-analysis.

1.12.1 Study selection criteria

132 Primary literature focusing on bivalve growth was identified using Web of Science Core collection. The 133 keywords used were "bivalve", "Bivalvia", "meta-analysis", "acidification", "pH", "hypercapnia", "ocean 134 change" "temperature", "salinity", "oxygen", "deoxygenation", "hypoxia", "anoxia", and combinations thereof. 135 Articles collected ranged from 1997-2020. Articles were screened initially through title relevance, then abstract 136 content, and finally full-text content (Fig. 1), from which individual experimental set-ups were extracted. Article 137 lists from previous meta-analyses with similar scope (Kroeker et al., 2013; Harvey et al., 2013; Sampaio et al., 138 2021) were additionally consulted to identify material missed from initial search strings. For a list of included 139 articles used for analysis please consult 'Data availability' section.

Core Collection using a series of keywords (see main text). Screening resulted in the identification of 79 relevant articles with 203 experimental set-ups that were included in our meta-analysis.

When extracting data from papers, we optedselected for experiments that fitted within what the authors of said experiments considered represented plausible elimate change values for end-of-century climate conditions conditions or their location/bivalve examined specific expression, and excluded physiological stress experiments which often subject animals to artificially unnatural conditions. Data were extracted from studies

[Figure 1] PRISMA flow diagram of screening process for the present study following recommended guidelines

(Page et al., 2021). Relevant articles on Bivalvia growth experiments were identified from the Web of Science

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148 which maintained constant experimental conditions, thereby also not exploring the natural diurnal variability 149 which is large in coastal settings (Dong et al., 2017; Hofmann et al., 2011 ref) especially for species which are 150 exposed to air at low tide. DataThe data overview for individual species is available in our accompanying data. 151 We used growth as a broad measure of organism physiological response to climate stressors (and not more 152 specific measures like shell thickness or organismsoft tissue mass) for two main reasons. DOne, disentangling 153 specific growth measurements would diluteweaken our analysis greatly due to the wide disparity in approaches 154 the experimental approaches for measuring growth responses to climate stressors. TwoAdditionally, using 155 growth in this manner keeps our study in line with previous meta-analyses (Krocker et al., 2013; Harvey et al., 156 2013; Sampaio et al., 2021), who all used growth and not more specific measurements), . As such, analysing 157 growth in this manner has become standardised in the synthesis literature for comparable research, and 158 allowings direct comparisons with past work with different regional foci. We opted against using survivorship 159 as death often recorded just as a percentagein culture is common also in control experiments. Furthermore, 160 recording of this information is not detailed enough and often limited to percentage which is not sufficient for 161 this type of analysis, as meta-analysis-which requires depends means, standard deviation, and sample size being 162 reported to calculate effect sizeon absolute numbers. -

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We included articles with lab-based studies that focused on direct measurements of Bivalvia growth including length, mass, condition index, or shell thickness. Proxies for growth were excluded, such as scope for growth or RNA production, as these introduce additional uncertainties and variability to the growth signal and were not directly comparable to absolute measures of growth. Only studies where the bivalves were fed and studies on larvae that develop without feeding were included, as nutrient intake has a significant strong impact on growth (Norkko et al., 2005; Thomsen et al., 2013; Ballesta-Artero et al., 2018). Study sample size, mean growth value of both control and treatment groups, and indication of the variation of growth values (confidence intervals, standard error, and standard deviation) were extracted from articles. Absolute values were used, as percentage data could not be combined with absolute measurements within the Metafor package. Data were extracted directly from result text, tables, or supplementary data when possible. Data from figures was collected using WebPlotDigitizer v. 4.4 (Rohatgi, 2022). Control values for climate stressors for each article were based on authors' determination of control conditions. Climate stressor values were based on realistic end of century projections based on author's determination for that experimental setup or study location. The phylogeny and column chart (Fig. 2) were plotted using R v. 4.1.0 (R Core Team, 2021) and the packages ggplot2 v. 3.3.5  $(Wickham, 2016), ggtree\ v.\ 3.2.1\ (Yu\ et\ al.,\ 2017), ape\ v.\ 5.6.1\ (Paradis\ and\ Schliep,\ 2019), and\ patchwork\ v.$ 1.1.1 (Pederson, 2020). The topology is taken from the time-scaled 'budding II' family-level phylogeny of Crouch et al. (2021).

180 [Figure 2] Experimental representation of 18 Bivalvia families in 203 unique experimental setups from 79
181 relevant articles found in Web of Science Core Collection. **A**, time-scaled 'budding II' phylogeny of extant
182 Bivalvia from Crouch et al. (2021). The root age is 485.4 Ma. **B**, number of experiments representing each
183 extant family.

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### 1.22.2 Statistical analysis

We preformed meta-analysis on the impacts of climate stressors on the growth of Bivalvia at whole-class and family levels following methods described in Hoppit and Schmidt (2022). Stressors identified from the included experiments are water oxygen depletion (O<sub>2</sub>), increased acidity (decreased pH), salinity decrease change (S), and temperature increase (T), and combinations of these stressors (indicated as, e.g., O<sub>2</sub> + pH) (Figs 3–5; Table 2). Stressor effects could be synergistic (additive) or antagonistic (dampening reductive) (sensu Harvey et al., 2013), or dominated by one stressor (unaffected by changes in another stressor). Additionally, we separated out

191 the effect sizes of these stressors on different growth stages (egg/larva, juvenile, adult) for the entire class

192 Bivalvia.

Analyses used R v. 4.0.3 (R Core Team, 2020) and the package Metafor version 3.0-2 (Viechtbauer, 2010). Metafor function escalc was used to calculate effect size and sampling variance. We chose Log Response Ratio (LnRR; the natural log of the response ratio) as the measure of effect size to measure the proportion of change between the mean of the treatment and control responses to experimental intervention. An effect size of zero corresponds to a statistically insignificant effect. Multivariate meta-analytical models (function rma.mv) were used to calculate mean effect sizes of climate stressor impacts on bivalve growth rates for three subsets of data: all bivalves pooled, different developmental stages, and families with sufficient sample sizes ( $n \ge 7$ ). Significant results were identified when model 95% confidence intervals did not overlap zero effect size. Models used random intercepts for articles and species intercepts for each treatment to compensate for similarities introduced by studies, as data originating from the same experimental setup or from the same species are assumed to be more likely similar than data from different articles or species. Residual heterogeneity (QE), calculated as part of the meta-analytical models, was used to determine whether additional study moderators not considered might be influencing study results (Hedges and Olkin, 1985).

Publication bias was tested using Egger's regression test. Following Habeck and Schultz (2015), function rma.mv was extended using the square root of effect size variance in the model moderator variables to conduct a regression test. Egger's regression test looks at the symmetry of the data published and determines whether there are statistically 'missing' studies within the spread of the papers published (Egger et al., 1997). We used meta-regression to determine whether published results had changed over the 25 years from which studies had been collated, using study year as a moderator variable. This would indicate whether increasingly detailed knowledge has altered the overall picture with regards to the effect of each climate change stressor.

## 23 Results

Our literature search produced the most detailed examination of bivalve growth rates under multiple climate
stressors to date. We identified 79 studies with 203 unique experiments meeting the criteria, comprising 18
families and 37 species (Figs 1, 2; Table 1). Sampling of families was highly uneven: Mytilidae make up 36% of
the experiments and 81% of the experiments include just four families: Mytilidae, Ostreidae, Pectinidae, and
Veneridae; including Pinnidae and Tellinidae increases the total to 88% (Table 1).

We find consistent and significant negative effects of all single stressors and most combinations acting on the

entire class Bivalvia, in agreement with previous meta-analyses (Fig. 3; Table 2). At the class level, many

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221 combinations of stressors increase the negative effect on growth in a synergistic way (Fig. 3; Table 2). For 222 example, pH and O2 treatments are greater in combination than either alone, as were salinity + temperature and 223 pH + temperature. The effect of pH + salinity- is intermediate between that of the two single stressors, 224 dampening the salinity effect, while O2 + temperature causes a smaller effect than either single stressor. The 225 combination of three stressors, O2 + pH + temperature, causes the strongest negative effect size to both 226 individual stressors and any combinations. While low heterogeneity is preferable in terms of data validity it is 227 rarely achievable in environmental meta-analyses. Therefore, the significant heterogeneity in the data is 228 expected given it is drawn from so many disparate studies: QE = 300509.7155, df = 148, P < 0.0001. 229 [Figure 3] Effect size (log-response ratio, LnRR) for individual and combined effects of temperature (T), acidity 230 (pH), oxygenation (O2), and salinity (S) as stressors on bivalve growth rates for all Bivalvia. Points represent 231 mean effect size with error bars indicating 95% confidence intervals. Numbers indicate number of included experiments. Significance is indicated with asterisks: \* P < 0.05, \*\* P < 0.01, \*\*\* P < 0.001. 232 233 [Table 1] Representation of bivalve families across 203 experimental studies included in this meta-analysis. 234 [Table 2] Single and combined stressor effect sizes from a meta-analysis of 203 experimental set-ups (logresponse ratio, LnRR). Significance is indicated with asterisks: \* P < 0.05, \*\* P < 0.01, \*\*\* P < 0.001. 235 236 Thirty-one of the 203 experimental set-ups involve adult Bivalvia, 14 on unspecified ages/stages, 45 on eggs/ 237 larvae, and the remaining 113 focused on juvenile stages. Separating by growth stage shows that the 238 combination of pH and O2 stressors causes significantly negative effect size at all points in the life cycle (Fig. 239 4). Salinity is not an significant important stressor for larval or juvenile bivalves but causes a significant 240 reduction in growth in adults. Juveniles show responses to most stressors, whereas egg/larvae and adult bivalves 241 have much smaller sample sizes, and do not show significant effect size responses across the stressors. 242 Families do not all respond in the same way as the whole class Bivalvia, and stressors affect different families in 243 unexpected ways (Fig. 5). Mytilidae, Ostreidae, and Pectinidae (67% of experiments) respond with negative 244 effect sizes for all individual stressors (Fig. 5A-C). Pinnidae show positive responses for single stressors 245 temperature and pH, but negative when in combination combined (Fig. 5D). Tellinidae show positive responses 246 for oxygen and O2 + pH (Fig. 5E). Veneridae (14% of experiments) show mixed results with significant 247 negative effect sizes of salinity, pH + S, O<sub>2</sub> + pH, and O<sub>2</sub> + pH + T, but strong positive responses to temperature 248 and  $O_2 + T$  (Fig. 5F). 249 [Figure 4] Effect size (log-response ratio, LnRR) for individual and combined effects of oxygenation (O<sub>2</sub>), 250 acidity (pH), salinity (S), and temperature (T) as stressors on Bivalvia growth rates at different life stages 251 (egg/larval, juvenile, adult). Points represent mean effect size with error bars indicating 95% confidence 252 intervals. Numbers indicate number of included experiments. Significance is indicated with asterisks: \* P < 253 0.05, \*\* P < 0.01, \*\*\* P < 0.001. 254 [Figure 5] Effect size (log-response ratio, LnRR) for individual and combined effects of oxygenation (O2),

acidity (pH), salinity (S), and temperature (T) as stressors on Bivalvia growth rates separated by family. A,

Mytilidae. B, Ostreidae. C, Pectinidae. D, Pinnidae. E, Tellinidae. F, Veneridae. Points represent mean effect

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size with error bars indicating 95% confidence intervals. Numbers indicate number of included experiments.

258 Significance is indicated with asterisks: \* P < 0.05, \*\* P < 0.01, \*\*\* P < 0.001.

years (see Appendix B; Fig. B1 and Table B1).

Publications with significant results are published more often than would be expected by chance, suggesting negative observations are less frequently reported (see Appendix A; Table A1), as shown by highly significant Egger's regression test (P < 0.001) results for every stressor. Egger's regression test showed highly significant (P < 0.001) results for every stressor, indicating publications with significant results are published more often than would be expected by chance, suggesting negative observations are less frequently reported (see Appendix A; Table A1). Meta-regression analysis of publication by year and stressor showed that no individual stressor is changing in effect size signal through time, showing supporting consistency in publication findings over the

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#### 34 Discussion

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292 293 Our analysis explores a much greater combination of climate change stressors then past work, exploring 10 stressor combinations, while the largest known previous work Sampaio et al. (2021) explored 4. We also present the first known meta analysis for marine climate change which explores a taxon in its entirety and identify that even a very well-studied group has large gaps in taxonomic understandings of how its organisms respond to climate change. The impact of individual and combined climate stressors on growth rates of all bivalve molluscs in our study concurs with previous meta-analyses on marine calcifying invertebrates. The findings re-iterate that as a group, bivalves are highly vulnerable to conditions projected to occur under future climate change. Our analysis demonstrates that increased incidences of deoxygenation, pH decrease, as well as changes to temperature and salinity in nearshore marine environments in the future will inhibit the growth of bivalves. However, by focusing specifically on bivalves and separating out both bivalve family-level response and different life stages, we build upon previous synthesis work by revealing previously to date previously unappreciated complexity in responses. Effects of climate change for this group bivalves will in additionally to the physico-chemical environment, depend on the varied ecological and taxonomic makeup of specific habitats and will also vary across growth stages which exploit the marine habitat differently as plankton to settling as benthosy. We also also highlight that numerous biases that exist in currently available studies (taxonomic, ecological, geographic) which <del>currently</del> hinder upscaling of individual bivalve responses to a true global picture. Furthermore, our analysis hopes to move synthesis literature studies towards higher taxonomic understandings of an individual group's responses to the future ocean conditions, by showing the level of variability that can be present once taxonomic distinctions within a group are teased out.

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## 3.14.1 Climate change stressors will negatively impact bivalve growth

Our findings clearly show that growth rates in Bivalvia are negatively affected by climate stressors (Fig. 3). By exploring bivalves responses at a family level, we confirm our hypothesis that negative growth responses to climate change are likely inherent to this taxonomic group as a whole, despite the experimental bias in the published literature towards key families. Previous meta-analyses that incorporated bivalves did not focus on the group specifically but include them alongside numerous other taxa (i.e., categorizing bivalves within phylum Molluscathe group molluse) (Harvey et al., 2013; Kroeker et al., 2013; Sampaio et al., 2021). These analyses

294 which average over a wide range of taxa found little evidence for significant effect sizes except in a few single 295 stressors (pH and temperature: Harvey et al., 2013; hypoxia: Sampaio et al., 2021). 296 Unsurprisingly, the effect of temperature on bivalve growth is the most studied stressor in the experiments 297 included in our meta-analysis (35 experiments: Fig. 3) - a feature seen in other studies of the effects of marine 298 climate change (Borges et al., 2022). This bias is likely because temperature-altering experiments require less 299 complex equipment and sensors than pH or oxygen manipulation, have been performed over decades, and target 300 the most obvious effect of climatic change i.e., global warming. Inclusion of a substantially greater number of previous experiments within our meta-analysis (over 200 specific bivalve growth observations versus 45, 46, 301 302 and 34 Mollusca for Kroker et al. (2013), Harvey et al. (2013), and Sampaio et al. (2021) respectively) confirms 303 that all single climate stressors show significant negative effect sizes in bivalves (Fig. 3). Our analysis also 304 shows that in many cases this effect prevails when individual growth stages (Fig. 4) and the families containing 305 the largest number of experiments or observational data (Table 1; Fig. 5) are examined separately. 306 An important result is the identification of synergistic, additive, and antagonistic effects between different 307 stressors which in all cases in our analysis increase the negative response (Gobler et al., 2014; Stevens and 308 Gobler, 2018) (Table 2). For example, we identify significant negative effect sizes for O2 + pH, and temperature 309 + salinity when analysing overall bivalve responses (Fig. 3). The combination O<sub>2</sub> + pH has a stronger negative 310 synergistic effect size than compared to either oxygen or pH individually in all analyses (Figs. 3-5). Decreases 311 in pH restrict growth via restricting availability of CO<sub>3</sub><sup>2-</sup> and increasing HCO<sup>3-</sup> ions making shell building more 312 metabolically expensive and increasing shell dissolution (Ivanina et al., 2013; Byrne and Fitzer, 2019). Internal 313 tissues also require buffering against pH changes, incurring a further metabolic cost (Byrne and Fitzer, 2019). 314 Marine deoxygenation impacts metabolism, reducing an organism's ability to respond to these increased 315 metabolic requirements of shell generation and tissue buffering under a more acidic environment. Therefore, the 316 increased impact from combining these two stressors confirms our physiological understanding of the organism 317 (Pörtner and Farrell, 2008). 318 Mean effect sizes for each climate stressor differ between families within Bivalvia. Consequently, the effects of 319 climate change on this group will be habitat dependant and alter the taxonomic composition of coastal 320 ecosystems. The four most investigated families in our dataset (Mytilidae, Osteridae, Pectinidae, and Veneridae) 321 exhibit consistent negative growth responses to climate stressors (Fig. 5).-Exceptions exist for oxygen and 322 temperature changes for Mytilidae and Veneridae and temperature increase for Veneridae where we find mixed 323 responses which are discussed in more detail below (section 4.3). However, pH causes antagonistic decreases in 324 growth rate across these main families (Fig. 5), suggesting that any temperature-driven growth increases are 325 unlikely to occur under future projected conditions. These bivalve families are largely commercial species, 326 suggesting these families create a bias in the wider synthesis literature exploring bivalve response to climate 327 change. Additionally, this confirms our hypothesis that even though bivalves are considered a well studies 328 group, the signals detected in the literature are driven by a small subset of the taxa.

discussion, following rewriting to address reviewer comments

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### 3.24.2 Different bivalve life stages and ecologies show distinct responses to climate stressors

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Climate change will be acting on each part of the development of an organism. In bivalves, these different life stages have different habitats and mobility from free swimming larvae to sessile adults. Our results on how

332 different bivalve life stages are affected by a range of climate stressors generally confirm previous meta-333 analyses across calcifying organsimsorganisms. Egg/larval bivalve growth rates display the largest number of 334 negative responses to single climate stressors, followed by juveniles, with adults showing more mixed responses 335 (Fig. 4). This Our results suggests early life stages are the most vulnerable to a specific set of stressors and that 336 the threat diminishes as organisms mature, supporting analyses by Sampaio et al. (2021) and Kroeker et al. 337 (2013) which focused primarily on the impacts of ocean acidification. It is important to note, though, that the 338 earlier developmental stages are more mobile and hence more able to relocate their niche to track their 339 environmental needs. 340 Combined climate stressors (e.g. pH + temperature, O<sub>2</sub> + pH, salinity + temperature) showed negative responses 341 across all growth stages-impacts on growth throughout ontogeny and different stages of life history. Our 342 findings oppose those of Harvey et al. (2013) who suggested limited variation in organism growth responses 343 exists-between life stages exposed to individual and synergistic ocean acidification and warming. In contrast to 344 our analysis, tTheir data were pooled from multiple phyla not specific taxonomic groups reiterating the need to 345 avoid too- much pooling and averaging in meta-analysis. 346 Most studies in our dataset, especially those on the families that dominate our meta-analysis (Fig. 4), are 347 focused on larval or juvenile stages. This likely explains some of the negative impacts on growth as for example shell mineralogy influences the impact of pH changes. Amorphous calcium carbonate secreted by larval 348 349 bivalves is 50-times more susceptible to dissolution than either calcite or aragonite (Bressan et al., 2014). 350 Changes to body size or decreased shell thickness could increase vulnerability to predation (Sadler et al., 2018). 351 Non-significant effects of lowered pH alone in adult bivalves likely result from more diverse shell mineralogy 352 (Weiss et al., 2002), the effects of a more robust adult shell (Beadman et al., 2003), or shelf formation of adults 353 from a high pCO<sub>2</sub> low pH micro-environment quite different to the surrounding seawater (Thomsen et al., 2010; 354 Hiebenthal et al., 2013). The adult's lifestyle, which includes for some taxa exposure to air and/or closed valves 355 while respiring naturally results in high variability of pH in the calcifying fluid and therefore the pH changes in 356 the experiments may be resulted in relatively less stress compared to earlier developmental stages. Most of the 357 adult experiments included in our meta-analysis were on aragonitic individuals or on mixed aragonitic-calcitic 358 Mytilidae and Pectinidae. Only one study (Lemasson et al., 2018) included two genera of adult oysters (Family 359 Ostreidae) which construct their shells primarily from calcite (Stenzel, 1963), a more stable carbonate 360 polymorph. 361 Our results suggest-indicate that adults have an increased susceptibility to salinity changes when compared to 362 juvenile and egg/larval stages, suggesting habitats projected to experience decreased salinity due to increased 363 seasonal runoff or enhanced evaporation in a restricted setting (Robins et al., 2016) will-may become 364 challenging for adult bivalves. It is important to note though that fewer experiments were conducted exploring 365 salinity, resulting in a low number of experimental studies and a greater need for determining the interaction 366 with other drivers such as pH, temperaturetemperature, and oxygen. 367 Increased sensitivity to climate stressors at different life stages has implications for bivalve aquaculture and

conservation effort (Smaal et al., 2019) with the potential to .- Hence an increased frequency of these conditions

will be disruptive to lifecycles in some taxa. Decreased growth rates in larval and juvenile stages might impact

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373 impacts of climate change. 374 Efforts to restore historical bivalve populations such as oysters in Chesapeake Bay (Bersoza Hernández et al., 375 2018) and Europe (Sas et al., 2020) will need to consider how climate stressors will impact population 376 dynamics. Restoration projects often transplant adult or juvenile species into new environments (Johnson et al., 377 2019); and our findings suggest transplanting adults might be a preferable strategy given the lower impact of 378 climate stressors at this developmental stage. 3.34.3 Consideration of habitat and ecology in the context of climate change 379 380 Many species belonging to the families Mytilidae, Osteridae, and Veneridae occur in intertidal habitats which 381 experience frequent fluctuations in oxygen, acidity, and temperature and has been hypothesised to provide some 382 species with an innate ability to resist or mitigate the effects of future environmental change (Gazeau et al., 383 2013; Zhang et al., 2020). Furthermore, this high variability may include environments overlapping with those 384 replicated in some of the experimental setups. Species can in natural environments evade some stressors vaia 385 behavioural thermoregulation, for example mobile infaunal bivalves have been shown to migrate to more 386 offshore habitats, or burrowing deeper into the sediment (Domínguez et al., 2020; Dominguez et al., 2021). 387 Negative growth responses though generally repeat across the taxa in our dataset irrespective of habitat. An 388 intertidal habitat or preference for marine or brackish water does not appear to alter observed growth responses 389 in the experimental setting to accumulated climate stressors. We as we find consistent decreases in growth rates 390 across taxa, withand commonly subtidal, epifaunal bivalves (such as many Pectinidae) also exhibitinging 391 significant negative responses (Aguirre-Velarde et al., 2019; Maynou et al., 2020). Interpreting the effects of 392 ecology on our results is complicated by the previously mentioned dominance of studies focused on juvenile and 393 early growth stages; many bivalves feature a veliger or early larval stage that live in and can tolerate quite 394 different environmental conditions to those of later stages of life history (i.e., pelagic, free-swimming larvae vs 395 infaunal or benthic attached lifestyles for juveniles and adults) (Waldbusser et al., 2013). 396 Examining the effect of other aspects of bivalve mode of life on our results also reveals complexities in 397 response. The ability to evade stress will depend on the lifestyle and habitat. Negative growth responses 398 generally repeat across taxa irrespective of habitat. Most experiments in our dataset are conducted on are 399 suspension feeding taxa with an epifaunal habitat. The investigated bivalves are free swimming (Pectinidae), 400 cemented to substrates or form biogenic reefs (Ostreidae), or use byssal threads to anchor in sediments or attach 401 to hard substrates (Pinnidae, Mytilidae, some Pectinidae). There is much lower representation in our dataset of 402 infaunal or burrowing taxa which may also include deposit feeders (e.g., families Tellinidae, Veneridae). Our 403 data suggest overwhelmingly negative impacts on growth of all stressors for epifaunal or free-swimming 404 suspension feeding taxa (families Mytilidae, Ostreidae, Pectinidae in Fig. 5). 405 Tellinidae and Veneridae show more varied responses to temperature, pH, and O2 depletion. These taxa are 406 active infaunal burrowers in soft sediment, which can often be undersaturated with respect to calcium carbonate

population recruitment by limiting the number of individuals surviving to adulthood. Settlement efficacy will

affect repopulation success, following disturbance (Gagnon, et al., 2021). Aquaculture and fisheries will need to

account for these increased vulnerabilities and adapt culturing strategies to compensate for the negative growth

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as well as oxygen-limited (Green et al., 2013; Stevens and Gobler, 2018) suggesting some resilience to these conditions.\_Both semi-infaunal Pinnidae and infaunal Veneridae also show significant positive effect sizes in response to warming (Fig. 5). It has been hypothesised that an infaunal habitat may reduce immediate susceptibility of bivalves to warming, as the substrate may act as a thermal refugia (Zhou et al., 2022). Taken together, these results suggests that lifestyle and habitat will control the ability of bivalves to evade climate stressors. However, interpreting the general role of tieringecology in providing resilience is complicated by the currently small number of experiments or observations on infaunal taxa, further highlighting the need for additional data on the effects of environmental stressors on the growth of burrowing bivalves and those from a wider range of specific shallow marine habitats.

3.44.4 Experimental studies of bivalve response are biased by commercially important taxa, and have disparate protocols

Our meta-analysis clearly reveals that available data on bivalve growth responses to climate stressors contain a number of biases, likely due to the commercial importance of certain families (e.g., Mytilidae, Ostreidae, Pectinidae, Veneridae) and individual species within them for aquaculture and common ecosystem services (e.g., van der Schatte Olivier et al., 2020), as well as ease of access to specimens. Our meta analysis clearly reveals that available data on bivalve growth responses to climate stressors contain a number of biases. The majority of experimental set-ups are limited to a few families (e.g. Mytilidae [73], Ostreidae [31], Pectinidae [32], Veneridae [28]) (Fig. 2; Table 1), with a focus on epifaunal (Mytilidae, Pectinidae) or reef-building taxa (Ostreidae) that inhabit both intertidal and subtidal zones, and limited number of infaunal (Veneridae) or semiinfaunal (Pinnidae) taxa. This bias is likely due to the commercial importance of these families and individual species within them for aquaculture and common ecosystem services (e.g., van der Schatte Olivier et al., 2020), as well as ease of access to specimens. Many experiments document that bivalve specimens were sourced from commercial aquaculture facilities. A number of families included in our meta-analysis are represented only by individual experiments: for example, Dreissenidae, Hitellidae, Mesodesmatidae, Myidae and Pharidae. Comparison of the number of experiments vs. bivalve phylogeny shows that entire families have no documented experimental or observational work investigating climate stressor impacts on growth (Fig. 2). This confirms our hypothesis that even though bivalves are considered a well-studied group, the signals detected in the literature are often driven by a subset of taxa.

While our results are based on studies with varying experimental protocols, this is unavoidable when conducting synthesis analyses due to the vast range of labs and researchers gathering data, and our approach is consistent with other meta-analyses of similar nature (e.g., Hoppit and Schmidt 2022; Harvey et al., 2013; Kroeker et al., 2013; Sampaio et al., 2021). WhileAs we are using studies with disparate protocols and experimental measurements (e.g., some studies measuring soft tissue weight and others shell length) can introduce variability, the meta-regression analyses we conducted (Appendix B; Fig. B1) -shows that effect sizes across studies and experimental setups have not significantly changed across time. This result is, suggesting suggests that variability in research practices consistently observes similar results does not impact our results. While we acknowledge that sSome stressor combinations have low sample sizes, as multi-f-factor experiments are notoriously work intensive and difficult to perform. These lower numbers decreases which lowers-confidence in

**Commented [GH25]:** Section heading expanded to show we discuss and highlight Reviewer 2's point about the variability in experimental protocol that our data were extracted from

**Commented [GH26]:** Reworded to better indicate our studies novelty, and shortened for brevity

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**Commented [GH28R27]:** Sentence added to also link back to our hypothesis

**Commented [GH29]:** Added to better highlight a short coming of the available data used for meta-analysis

those specific observations and conclusion, this is a reflection of the available literature for synthesis, and highlightss the stressor combinations in greater need of experimental study the importance ofto considering a wider range of drivers than the most frequently often assesseds combination of warming and acidification alone.

**Commented [GH30]:** Added this section to better justify our use of disparate experimental setups, as it is consistent with comparable literature

Our findings are also geographically biased towards the global north. Most studies clearly gathered organisms and data from the coasts of the USA, Europe, or China, resulting in <a href="mailto:significant-important">significant-important</a> portions of the global ocean like the Caribbean or African coasts being unrepresented in these data. While our meta-analysis focused specifically on bivalve growth, this result emphasizes the unevenness of experimental research into this group. If this disparity of understanding is not rectified then implementing effective climate change adaptation and mitigation strategies and upscaling these results to ecosystem-scale changes are challenging.

While our experimental sample is larger than previous meta-analyses, these biases also leave much uncertainty about how responses will scale up from commercially important species to other, rarely studied groups of bivalves, which while of lesser importance for aquaculture or commercial exploitation, may act as keystone species within fragile marine ecosystems. This further limits the quality and quantity of available information that conservationists and stakeholders need to develop strategies to safeguard marine social-ecological systems. Given our findings overwhelmingly suggest that bivalves as a group (Figs 3, 4) and common, well-studied families (Fig. 5) will likely experience decreased growth rates under protected projected end-of-century conditions, how likely is it that families or species with no current experimental observations will also follow this trend? Additional experimental and observational work on specific bivalve species and families is urgently required which would greatly assist in developing conservation strategies for this important group of marine calcifiers.

## 45 Conclusions

- Regardless of these biasesO, our results suggest that climate change will greatly affect marine bivalves, interacting with other stresses these organisms already face, show that gReduced growth rates predicted by our meta-analysis have important implications for population stability in these commercially important keystone marine taxa, as well as for guiding future conservation and mitigation efforts. Our meta-analysis concludes that growth rates of bivalve molluses significantly decrease when exposed to climate stressors by exploring the largest and most diverse grouping of climate stressor impacts on bivalve growth to date. We demonstrate thawitht synergistic combinations factors of stressors (e.g., effects of combined temperature + O<sub>2</sub> + pH change) causinge greater reductions in bivalve growth then individual stressors. This result is true for bivalves overall, and when separating out by growth stage in the most commonly studied bivalve families (Ostreidae, Mytilidae, Pectinidae, Veneridae). Reduced growth rates predicted by our meta-analysis have important implications for population stability in these commercially important keystone marine taxa, as well as for guiding future conservation and mitigation efforts.
- This result is true for bivalves overall, and when separating out by growth stage in the most commonly
  studied bivalve families (Ostreidae, Mytilidae, Pectinidae, Veneridae). We show that the signal of
  negative bivalve growth responses to climate change observed in the wider literature is likely driven by

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these commonly studied families, confirming our hypothesis that commercial species are creating a bias in the literature, and that most of the taxa has no known experimental observations.

- 2. Eggs/larval stages are significantly more susceptible to reduced growth then other developmental stages. The potential effects on recruitment, as well as settlement and recovery after disturbance, has important implications for conservation or transplant efforts, suggesting a renewed focus on transplanting adult specimens rather than larvae/juveniles should be examined.
- 3-2. Epifaunal filter feeders, such as Ostreidae and Mytilidae, had mostly negative growth responses to environmental stressors. In contrast, infaunal and semi-infaunal suspension or deposit feeding bivalves, Veneridae, Tellinidae, and Pinnidae showed more mixed or even positive growth response under higher temperatures, suggesting that burrowing or buried taxa may be buffered from or resilient to some predicted changes. However, these data are based on a small number of studies, and these families still showed-providing less confidence in the negative growth effects with other stressors and combinations of stressors
- 4-3. By focusing on a few commercially relevant taxa, these commonly studied families are creating a bias in the literature. A large proportion of bivalve families lack any rigorous experimental or observational data resulting in large knowledge gaps hampering conservation efforts. We highlight that A available data on bivalve response to climate stressors also contain has large biases towards early or juvenile growth stages and, commercially important species from the global north, and that a large proportion of bivalve families lack any rigorous experimental or observational data. Regardless of these biases, our results suggest that climate change will greatly affect marine bivalves, interacting with other stresses these organisms already face. Further, based on the consistently negative growth responses to different climate stressors we document, it is likely novel experiments on unexplored bivalve species will also experience negative growth responses to climate shange. Our results should be replicated for other commonly studied marine organisms like seaweeds or echinoderms to see assess if taxonomic bias drives commonly assumed physiological responses to climate change.

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**Commented [DS33]:** Deleted to remove repetition from earlier in conclusions

**Commented [GH34]:** Added this as we think negative growth responses are inherent to the group based on our results

**Commented [GH35]:** This adds how our work can influence the wider field, not just for bivalves

Appendices

Appendix A

Table A1. Publication bias results of Egger's regression test.

516 For all stressors: df=195

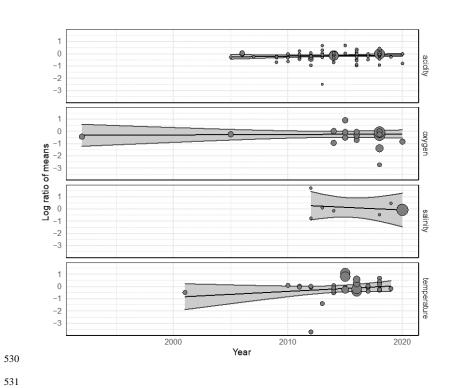
	estimate	se	pval	tval	<del>ci.lb</del> ◀	ci.u Formatted Table
sqrt(vi):StressorO2	-5.5054	0.367	<.0001	-15.0026	-6.2292	<del>-4.7816</del>
sqrt(vi):StressorpH	-1.5811	0.3003	<.0001	-5.2654	-2.1733	-0.9888
sqrt(vi):StressorpH and O2	-10.929	0.3705	<.0001	<del>-29.4969</del>	<del>-11.6597</del>	<del>-10.1982</del>
sqrt(vi).Suessorpri and 02	10.727	0.5705	<.0001	25.1505	11.0557	10.1702
sqrt(vi):StressorpH and	<del>-7.2009</del>	0.3165	<.0001	-22.7541	<del>-7.8251</del>	<del>-6.5767</del>
	<del>-1.2003</del>	0.3103	₹.0001	-22.1341	-7.0231	<del>-0.5707</del>
temperature						
cart(vi) Ctroscorcolinity	-1.5428	0.7805	0.0495	<del>-1.9765</del>	-3.0823	-0.0033
sqrt(vi):Stressorsalinity						
sqrt(vi):Stressorsalinity and pH	<del>-10.1106</del>	0.9205	<.0001	-10.9841	<del>-11.9261</del>	<del>-8.2951</del>
sqrt(vi):Stressortemperature	-0.8807	0.3563	0.0143	-2.4717	-1.5834	<del>-0.1779</del>
sqrt(vi):Stressortemperature and	-1.0071	0.5775	0.0828	<del>-1.7439</del>	<del>-2.1462</del>	0.1319
<del>02</del>						
sqrt(vi):Stressortemperature and	<del>-9.7482</del>	0.5994	<.0001	-16.2629	-10.9304	<del>-8.5659</del>
<del>pH and O2</del>						
	estimate	<u>se</u>	<u>pval</u>	tval	<u>ci.lb</u>	<u>ci.ub</u>
sqrt(vi):Stressortemperature and	estimate	<b>₹869</b>	200001	<u>tvak</u> 344	<u>cislb</u> 153	city 872
salinity						
sqrt(vi):StressorO <sub>2</sub>	<u>-5.5054</u>	0.367	<.0001	-15.0026	-6.2292	Formatted: Subscript
sqrt(vi):StressorpH						
<u>sqrt(17)stressorpri</u>	<u>-1.5811</u>	0.3003	<.0001	<u>-5.2654</u>	-2.1733	-0.9888
<u> </u>	<u>-1.5811</u>	0.3003	<.0001	-5.2654	-2.1733	-0.9888
						-0.9888
sqrt(vi):StressorpH and O <sub>2</sub>	<u>-1.5811</u> <u>-10.929</u>	<u>0.3003</u> <u>0.3705</u>	<.0001 <.0001	<u>-5.2654</u> <u>-29.4969</u>	-2.1733 -11.6597	-0.9888 -10: Formatted: Subscript
sqrt(vi):StressorpH and O <sub>2</sub>	-10.929	0.3705	<.0001	-29.4969	-11.6597	Formatted: Subscript
sqrt(vi):StressorpH and O <sub>2</sub>	-10.929	0.3705	<.0001	-29.4969	-11.6597	Formatted: Subscript
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature	-10.929 -7.2009	0.3705	<.0001 <.0001	-29.4969 -22.7541	-11.6597 -7.8251	Formatted: Subscript  -6.5767
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and	-10.929	0.3705	<.0001	-29.4969	-11.6597	Formatted: Subscript
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature	-10.929 -7.2009	0.3705	<.0001 <.0001	-29.4969 -22.7541	-11.6597 -7.8251	Formatted: Subscript  -6.5767
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature  sqrt(vi):Stressorsalinity	-10.929 -7.2009	0.3705 0.3165 0.7805	<.0001 <.0001 0.0495	-29.4969 -22.7541 -1.9765	-11.6597 -7.8251 -3.0823	-10: Formatted: Subscript  -6.5767
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature  sqrt(vi):Stressorsalinity	-10.929 -7.2009	0.3705 0.3165 0.7805	<.0001 <.0001 0.0495	-29.4969 -22.7541 -1.9765	-11.6597 -7.8251 -3.0823	-10: Formatted: Subscript  -6.5767
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature  sqrt(vi):Stressorsalinity	-10.929 -7.2009	0.3705 0.3165 0.7805	<.0001 <.0001 0.0495	-29.4969 -22.7541 -1.9765	-11.6597 -7.8251 -3.0823	-10: Formatted: Subscript  -6.5767
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature  sqrt(vi):Stressorsalinity  sqrt(vi):Stressorsalinity and pH	-10.929 -7.2009 -1.5428 -10.1106	0.3705 0.3165 0.7805 0.9205	<.0001 <.0001  0.0495 <.0001	-29.4969 -22.7541 -1.9765 -10.9841	-11.6597 -7.8251 -3.0823 -11.9261	-10- Formatted: Subscript  -6.5767  -0.0033 -8.2951
sqrt(vi):StressorpH and O <sub>2</sub> sqrt(vi):StressorpH and temperature  sqrt(vi):Stressorsalinity sqrt(vi):Stressorsalinity and pH	-10.929  -7.2009  -1.5428  -10.1106  -0.8807	0.3705 0.3165 0.7805 0.9205	<.0001 <.0001 <.0001  0.0495 <.0001  0.0143	-29.4969  -22.7541  -1.9765  -10.9841  -2.4717	-11.6597 -7.8251 -3.0823 -11.9261	-10- (Formatted: Subscript  -6.5767  -0.0033 -8.2951

sqrt(vi):Stressortemperature and	<u>-9.7482</u>	0.5994	<.0001	<u>-16.2629</u>	<u>-10.9304</u>	<u>-8.5659</u>
pH and O <sub>2</sub>						Formatted: Subscript
sqrt(vi):Stressortemperature and	<u>-4.2012</u>	0.869	<.0001	<u>-4.8344</u>	<u>-5.9153</u>	<u>-2.4872</u>
salinity			ĺ			
			1			

523524 Appendix B.

Fig. B1 Meta-regression Change of effect sizes of 203 experimental setups on Bivalvia growth through time from 1997 to 2020. A, acidity (pH). B, temperature. C, deoxygenation. D, salinity. Each point shows the effect size against the data set publication year. Point size indicates the experiment contribution weight to the linear model. Each plot shows the regression of effect size against publication year with the 95% confidence interval shaded. All regression analyses show no significant change during this period.

**Commented [GH36]:** Updated to better show this is a meta-regression



**Table B1.** Regression analysis of publications by stressor per year.

Acid	estimate	se	tval	df	pval	ci.lb	ci.ub
intrcpt	-21.2396	19.6612	-1.0803	88	0.2830	-60.3120	17.8328
Year	0.0105	0.0098	1.0725	88	0.2864	-0.0089	0.0299
Temp							
intrcpt	-96.5465	74.7711	-1.2912	33	0.2056	-248.6695	55.5764
Year	0.0478	0.0371	1.2888	33	0.2064	-0.0277	0.1233
Oxygen							
intrcpt	-7.5967	36.9562	-0.2056	16	0.8397	-85.9404	70.7470
Year	0.0037	0.0183	0.1990	16	0.8447	-0.0352	0.0425
Salinity							
intrcpt	87.7248	203.0242	0.4321	6	0.6808	-409.0574	584.5071
Year	-0.0435	0.1007	-0.4315	6	0.6812	-0.2900	0.2030

Signif. codes: 0 '\*\*\* 0.001 '\*\* 0.01 '\* 0.05 '.' 0.1 ' '1 Code availability  $Code\ used\ for\ analyses\ available\ at\ https://github.com/georgehoppit/Bivalve-meta-analysis$ Data used for analyses available at https://github.com/georgehoppit/Bivalve-meta-analysis 

Commented [DS37]: Can we make the datafile also available via Pangaea to increase visibility? If you give it to me I will also link it at our data archive on data.bris so that people can find it with the paper

561	Author contributions
562 563 564 565	Conceptualization: GH, BCM; data curation, formal analysis, investigation, methodology: RKW, GH; resources software, validation: RKW, GH, BCM, JDW; supervision: GH, JDW, BCM; visualization: RKW, GH, BCM; writing – original draft: RKW; writing – review & editing: RKW, GH, DNS, BCM, JDW. (https://credit.niso.org)
566	
567	Competing interests
568	The authors declare that they have no conflict of interest.
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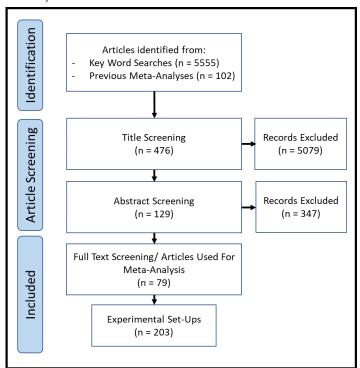
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Figure 1. PRISMA flow diagram of screening process for the present study following recommended guidelines (Page et al., 2021). Relevant articles on Bivalvia growth experiments were identified from the Web of Science Core Collection using a series of keywords (see main text). Screening resulted in the identification of 79 relevant articles with 203 experimental set-ups that were included in our meta-analysis.



**Figure 2.** Experimental representation of 18 Bivalvia families in 203 unique experimental setups from 79 relevant articles found in Web of Science Core Collection. **A**, time-scaled 'budding II' phylogeny of extant Bivalvia from Crouch et al. (2021). The root age is 485.4 **Ma**. **B**, number of experiments representing each extant family.

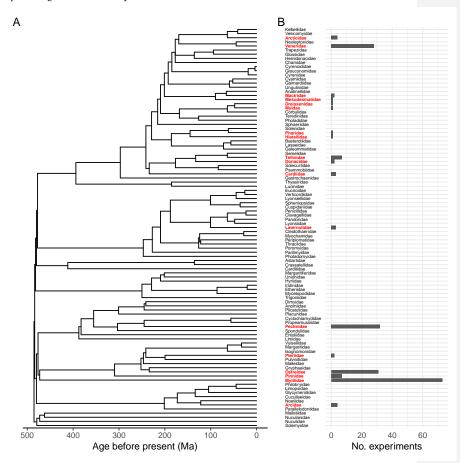


Figure 3. Effect size (log-response ratio, LnRR) for individual and combined effects of temperature (T), acidity (pH), oxygenation ( $O_2$ ), and salinity (S) as stressors on bivalve growth rates. **A**, for all Bivalvia. **B**, for Bivalvia excluding Veneridae. Points represent mean effect size with error bars indicating 95% confidence intervals. Numbers indicate number of included experiments. Significance is indicated with asterisks: \*P < 0.05, \*P < 0.01, \*P < 0.001.

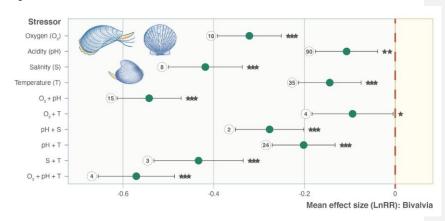


Figure 4. Effect size (log-response ratio, LnRR) for individual and combined effects of oxygenation  $(O_2)$ , acidity (pH), salinity (S), and temperature (T) as stressors on Bivalvia growth rates at different life stages (egg/larval, juvenile, adult). Points represent mean effect size with error bars indicating 95% confidence intervals. Numbers indicate number of included experiments. Significance is indicated with asterisks: \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.

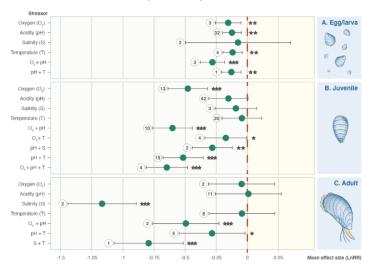
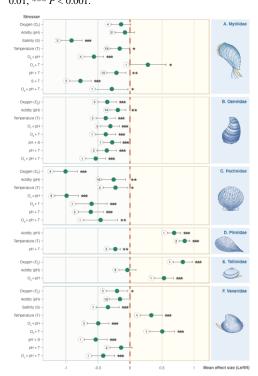


Figure 5. Effect size (log-response ratio, LnRR) for individual and combined effects of oxygenation (O<sub>2</sub>), acidity (pH), salinity (S), and temperature (T) as stressors on Bivalvia growth rates separated by family. A, Mytilidae. B, Ostreidae. C, Pectinidae. D, Pinnidae. E, Tellinidae. F, Veneridae. Points represent mean effect size with error bars indicating 95% confidence intervals. Numbers indicate number of included experiments. Significance is indicated with asterisks: \* P < 0.05, \*\* P < 0.01, \*\*\* P < 0.001.



**Table 1.** Representation of bivalve families across 203 experimental studies included in this meta-analysis.

Family	Number of experimental set-ups
Arcidae	4
Arcticidae	4
Cardiidae	3
Dinacidae	2
Dreissenidae	1
Hiatellidae	1
Laternulidae	3
Mactridae	2
Mesodesmatidae	1
Myidae	1
Mytilidae	73
Ostreidae	31
Pectinidae	32
Pharidae	1
Pinnidae	7
Pteriidae	2
Tellinidae	7
Veneridae	28

**Table 2.** Single and combined stressor effect sizes from a meta-analysis of 203 experimental set-ups <u>for</u> <u>bivalves</u> (log-response ratio, LnRR). Significance is indicated with asterisks: \*P < 0.05, \*\*P < 0.01, \*\*\* P < 0.001.

		Mean effect size	95% confidence interval		
Stressor	Sample size	(R)	lower	upper	P-value
Oxygenation (O <sub>2</sub> )	18	-0.3214	-0.3916	-0.2513	<.0001
Acidity (pH)	90	-0.1077	-0.1762	-0.0392	0.0022
Salinity (S)	8	-0.4184	-0.4997	-0.3372	<.0001
Temperature (T)	35	-0.1445	-0.2135	-0.0756	<.0001
$O_2 + pH$	15	-0.5421	-0.6126	-0.4716	<.0001
$O_2 + T$	4	-0.0944	-0.1836	-0.0052	0.0382
pH + S	2	-0.2771	-0.3522	-0.2019	<.0001
pH + T	24	-0.2021	-0.2712	-0.1330	<.0001
S + T	3	-0.4335	-0.5316	-0.3354	<.0001
$O_2+pH+T$	4	-0.5703	-0.6542	-0.4864	<.0001