

Competitive interactions moderate the effects of elevated temperature and atmospheric CO₂ on the health and functioning of oysters

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Supplement 1. Summary of statistical models

We present the data for each response variable including mean ± standard error for each treatment level.

For each response variable, we started with an initial linear regression model of the form:

$$[Dependent\ variable] \sim Temp + CO_2 + Oyster + \\ Temp \times CO_2 + Temp \times Oyster + CO_2 \times Oyster + \\ Temp \times CO_2 \times Oyster$$

Abbreviations:

Temp = Temperature (2 levels; 12°C or 16°C)

CO₂ = atmospheric [CO₂] (2 levels; ambient [400ppm] versus elevated [1000ppm])

Oyster = species composition within each mesocosm (6 levels; two individuals of *C. gigas*; two individuals of *O. edulis*; one *C. gigas* with one *O. edulis*; one *O. edulis* with one *C. gigas*; a single *C. gigas*; a single *O. edulis*)

Where it was necessary to account for violation of homogeneity of variance, we used a linear regression with GLS estimation. All independent factors were treated as nominal and we carried out a manual backwards selection procedure to refine each model. The minimal adequate model is shown for each response variable.

Supplement 2. Model S1 | FILTRATION (N = 140)

Minimal adequate model:

Filtration ~ Oyster,

weights = varIdent(form = ~ 1|Oyster), method = "ML")

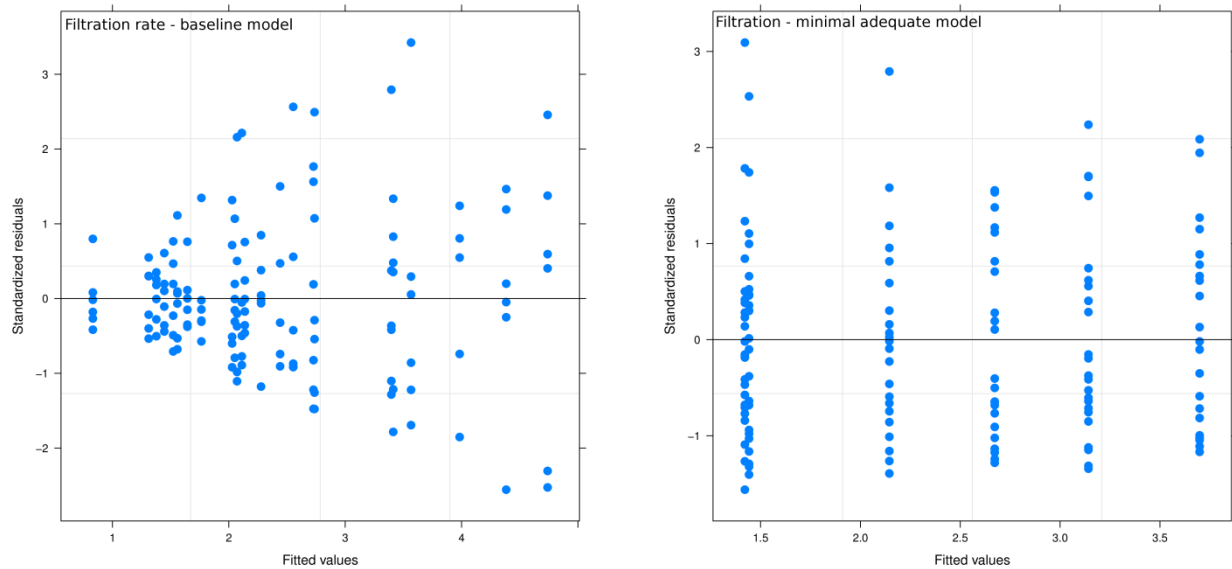


Figure S1. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms for response variable *Filtration*.

Table S1a. Contribution of factors from the minimal adequate model to *Filtration* rates.

	d.f. ¹	AIC ²	L- Ratio ³	P-value
Full model	30	533.5		
Oyster	5	538.7	34.47	<0.001

¹ Degrees of freedom

² Akaike information criterion

³ Likelihood ratio

Table S1b. Pairwise comparisons of *Filtration* for all levels in “Oyster”. Data are coefficients \pm standard error (in italics) and underneath the t-values with superscript P-values in parentheses comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Intra <i>C. gigas</i>	Intra <i>O. edulis</i>	Inter <i>C. gigas</i>	Inter <i>O. edulis</i>	Single <i>C. gigas</i>	Single <i>O. edulis</i>
Intra <i>C. gigas</i> ¹	-					
Intra <i>O. edulis</i> ²	<i>2.227 \pm 0.566</i> (4.03 ^{<0.001})	-				
Inter <i>C. gigas</i> ³	<i>0.557 \pm 0.695</i> (0.80 ^{0.424})	<i>-1.721 \pm 0.467</i> (-3.68 ^{<0.001})	-			
Inter <i>O. edulis</i> ⁴	<i>2.256 \pm 0.562</i> (4.01 ^{<0.001})	<i>-0.021 \pm 0.228</i> (-0.09 ^{0.927})	<i>1.700 \pm 0.463</i> (3.67 ^{<0.001})	-		
Single <i>C. gigas</i> ⁵	<i>1.026 \pm 0.668</i> (1.54 ^{0.127})	<i>-1.251 \pm 0.426</i> (-2.94 ^{0.004})	<i>0.469 \pm 0.586</i> (0.80 ^{0.425})	<i>-1.230 \pm 0.421</i> (-2.92 ^{0.004})	-	
Single <i>O. edulis</i> ⁶	<i>1.554 \pm 0.605</i> (2.57 ^{0.011})	<i>-0.724 \pm 0.319</i> (-2.27 ^{0.025})	<i>0.997 \pm 0.514</i> (1.94 ^{0.054})	<i>-0.703 \pm 0.312</i> (-2.25 ^{0.026})	<i>0.528 \pm 0.476</i> (1.11 ^{0.270})	-

¹ *Crassostrea gigas* in intraspecific competition (i.e. with other *C. gigas*).

² *Ostrea edulis* in intraspecific competition (i.e. with other *O. edulis*).

³ *C. gigas* in interspecific competition (i.e. with *O. edulis*).

⁴ *O. edulis* in interspecific competition (i.e. with *C. gigas*).

⁵ *C. gigas* with no competition.

⁶ *O. edulis* with no competition.

Supplement 3. Model S2 | RESPIRATION (N = 108)

Minimal adequate model:

Respiration ~ Oyster,
 weights = varIdent(form=~1|CO₂×Oyster), method = "ML")

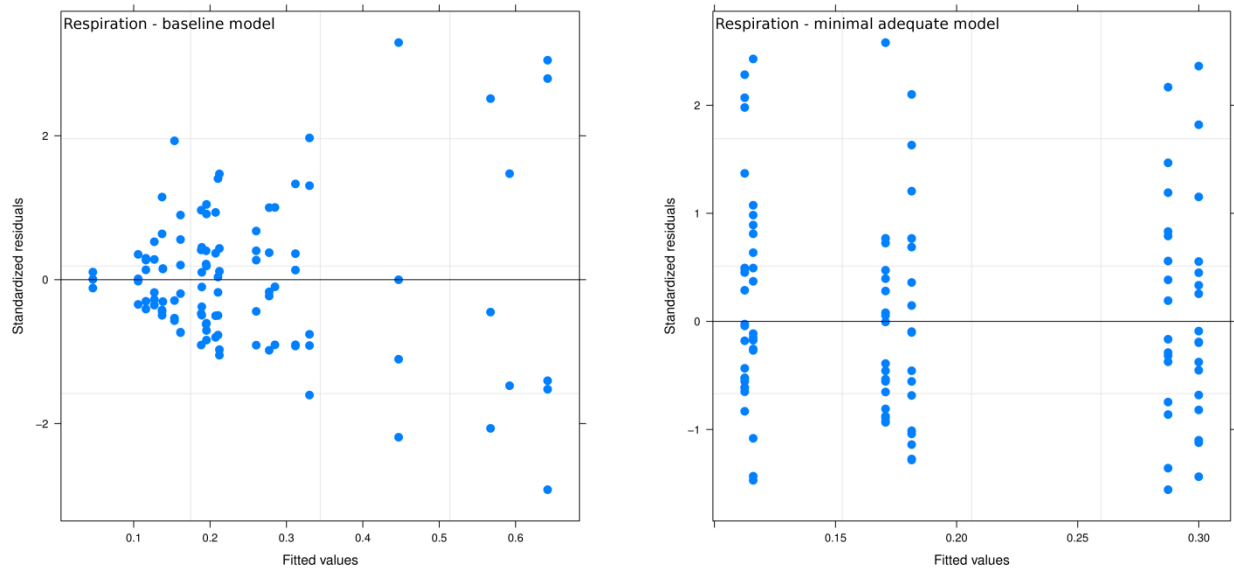


Figure S2. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms response variable *Respiration*.

Table S2a. Contribution of factors from the minimal adequate model to *Respiration*.

	d.f.	AIC	L- Ratio	P-value
Full model	36	-36.6		
Oyster	5	-35.8	21.44	<0.001

Table S2b. Pairwise comparisons of *Respiration* for all levels in “Oyster”. Data are coefficients \pm standard error (in italics) with underneath the t-values and superscript P-values in parentheses, comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Intra <i>C. gigas</i>	Intra <i>O. edulis</i>	Inter <i>C. gigas</i>	Inter <i>O. edulis</i>	Single <i>C. gigas</i>	Single <i>O. edulis</i>
Intra <i>C. gigas</i>	-					
Intra <i>O. edulis</i>	<i>-0.055 \pm 0.033</i> (-1.63 ^{0.105})	-				
Inter <i>C. gigas</i>	<i>-0.004 \pm 0.038</i> (-0.09 ^{0.927})	<i>0.058 \pm 0.044</i> (1.32 ^{0.191})	-			
Inter <i>O. edulis</i>	<i>-0.184 \pm 0.048</i> (-3.87 ^{<0.001})	<i>-0.129 \pm 0.052</i> (-2.47 ^{0.015})	<i>-0.187 \pm 0.056</i> (-3.37 ^{0.001})	-		
Single <i>C. gigas</i>	<i>-0.171 \pm 0.047</i> (-3.64 ^{<0.001})	<i>-0.117 \pm 0.052</i> (-2.24 ^{0.027})	<i>-0.175 \pm 0.055</i> (-3.17 ^{0.002})	<i>0.013 \pm 0.062</i> (0.20 ^{0.839})	-	
Single <i>O. edulis</i>	<i>-0.065 \pm 0.037</i> (-1.78 ^{0.078})	<i>-0.011 \pm 0.043</i> (-0.25 ^{0.802})	<i>-0.069 \pm 0.047</i> (-1.47 ^{0.144})	<i>0.119 \pm 0.555</i> (2.17 ^{0.032})	<i>0.106 \pm 0.054</i> (1.95 ^{0.054})	-

SUPPLEMENT 4. MODEL S3 | HAEMOCYTES (N = 140)

Minimal adequate model:

Haemocytes ~ Temp + CO₂ + Oyster +
 Temp×CO₂ + CO₂×Oyster,
 weights = varIdent(form = ~ 1|CO₂×Oyster), method = "ML")

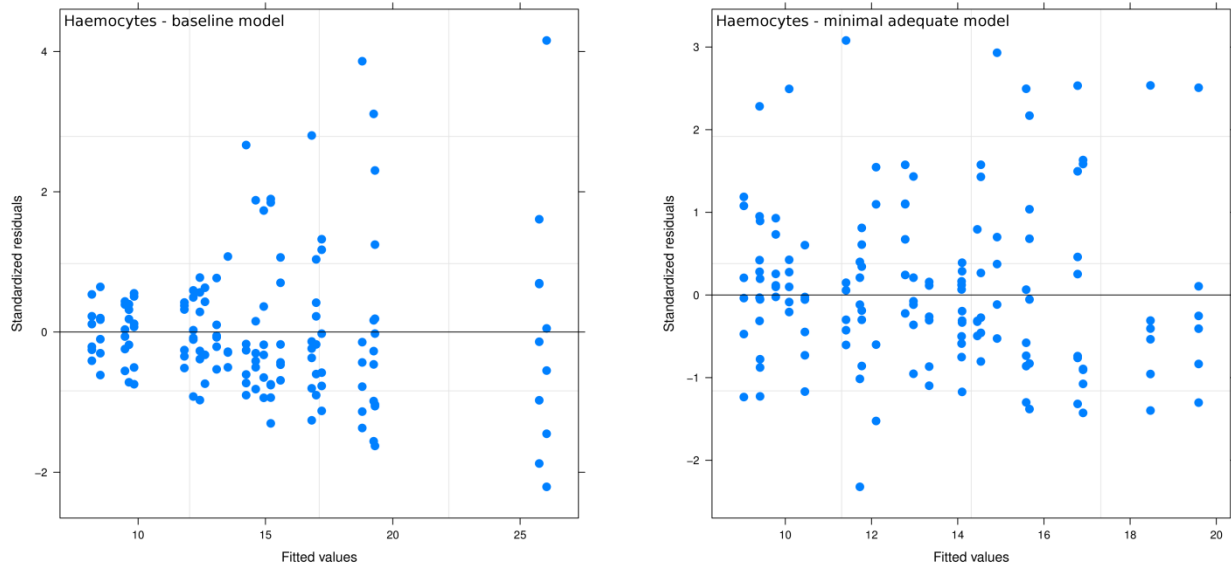


Figure S3. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S3a. Contribution of factors from the minimal adequate model to *Haemocytes*.

	d.f.	AIC	L- Ratio	P-value
Full model	36	1034.3		
Temp	2	1095.9	9.14	0.010
CO ₂	5	1029.3	23.58	0.001
Oyster	10	1021.9	22.28	0.014
Temp×CO ₂	5	1023.9	14.22	0.014
CO ₂ ×Oyster	1	1026.7	9.04	0.003

Table S3b. Pairwise comparisons of *Haemocytes* for all levels in “Temp×CO₂”. Data are coefficients ± standard error (in italics) with underneath the t-values with superscript P-values in parentheses, comparing row to column levels.

Temp		12°C		16°C	
Temp	CO ₂	400 ppm	1000 ppm	400 ppm	1000 ppm
12°C	400 ppm	-			
	1000 ppm	<i>-2.003 ± 1.925</i> (-1.04 ^{0.300})	-		
16°C	400 ppm	<i>-5.188 ± 2.211</i> (-2.35 ^{0.020})	<i>-3.184 ± 1.907</i> (-1.67 ^{0.097})	-	
	1000 ppm	<i>1.039 ± 1.875</i> (0.55 ^{0.580})	<i>3.043 ± 1.505</i> (2.02 ^{0.045})	<i>6.277 ± 1.857</i> (3.35 ^{0.001})	-

Supplement 5. Model S4 | PHAGOCYTOSIS (N = 140)

Minimal adequate model:

$Phagocytosis \sim CO_2$,
 weights = varIdent(form = ~ 1|CO₂) , method = "ML")

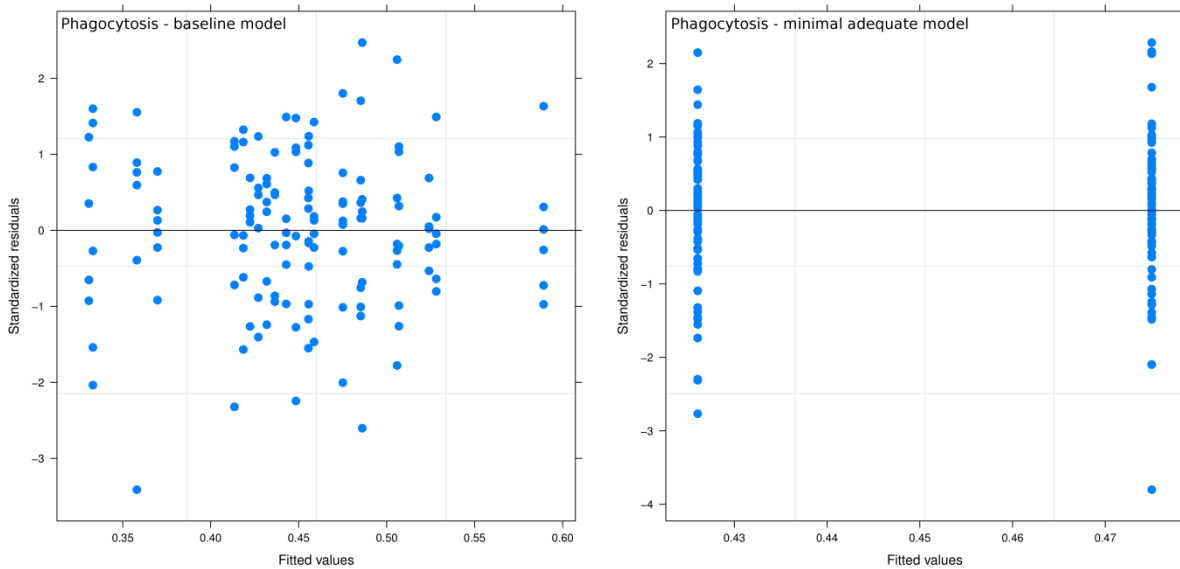


Figure S4. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S4. Contribution of factors from the minimal adequate model to *Phagocytosis*.

	d.f	AIC	L Ratio	P-value
Full model	26	-188.4		
CO ₂	1	-193.8	6.07	0.014

Supplement 6. Model S5 | PROTEINS (N = 140)

Minimal adequate model:

Proteins ~ Temp + Oyster +
 Temp×Oyster
 weights = NULL , method = "ML")

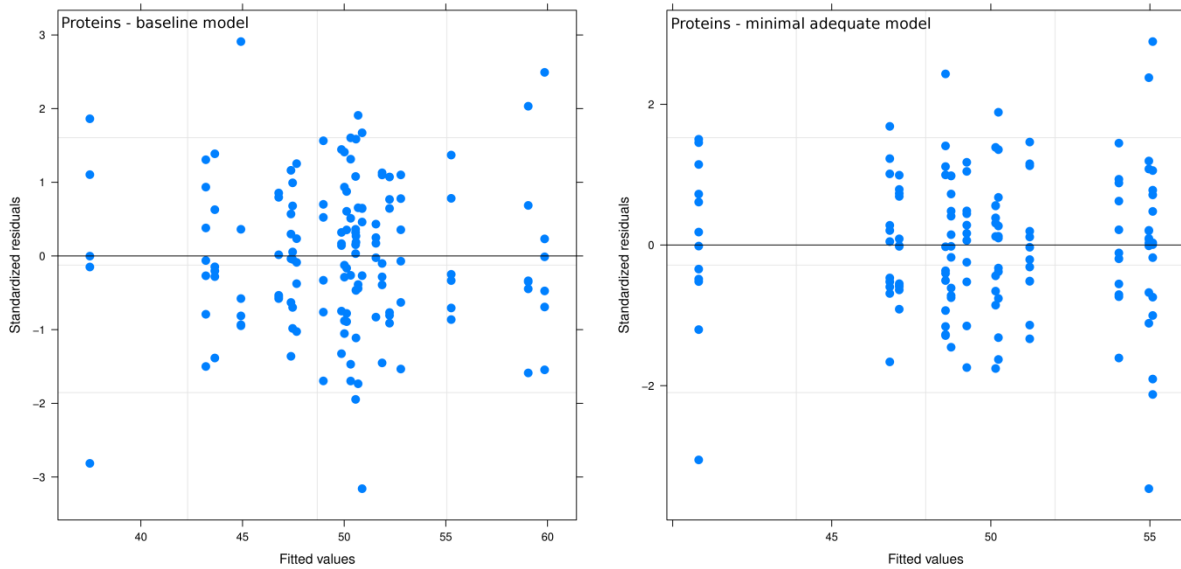


Figure S5. Variance plots of the baseline model (full factorial) and the minimal adequate linear regression model after weighting among variance covariates and backwards step-wise elimination of insignificant terms.

Table S5a. Contribution of factors from the minimal adequate model to *Proteins*.

	d.f.	AIC	<i>L</i> - Ratio	<i>P</i> -value
Full model	25	1082.2		
Temp	6	1072.8	16.03	0.014
Oyster	10	1065.9	17.16	0.071
Temp×Oyster	5	1073.6	12.77	0.025

Table S5b. Pairwise comparisons of *Proteins* for all levels in “Temp×Oyster”. Data are coefficients ± standard error (in italics) with underneath the t-values and superscript P-values in parentheses, comparing row to column levels. The relevant species composition comparisons are highlighted in bold.

	Temp	12°C						16°C					
Temp	Oyster	Intra <i>C. gigas</i>	Intra <i>O. edulis</i>	Inter <i>C. gigas</i>	Inter <i>O. edulis</i>	Single <i>C. gigas</i>	Single <i>O. edulis</i>	Intra <i>C. gigas</i>	Intra <i>O. edulis</i>	Inter <i>C. gigas</i>	Inter <i>O. edulis</i>	Single <i>C. gigas</i>	Single <i>O. edulis</i>
12°C	Intra <i>C. gigas</i>	-											
	Intra <i>O. edulis</i>	<i>-6.006 ± 4.169</i> (-1.44 ^{0.153})	-										
	Inter <i>C. gigas</i>	<i>-14.15 ± 4.169</i> (-3.39 ^{0.001})	<i>-8.143 ± 4.169</i> (-1.95 ^{0.053})	-									
	Inter <i>O. edulis</i>	<i>-6.303 ± 4.169</i> (-1.51 ^{0.133})	<i>-0.297 ± 4.169</i> (-0.07 ^{0.943})	<i>7.846 ± 4.169</i> (1.88 ^{0.062})	-								
	Single <i>C. gigas</i>	<i>-8.426 ± 4.263</i> (-1.98 ^{0.050})	<i>-2.419 ± 4.263</i> (-0.57 ^{0.571})	<i>5.724 ± 4.263</i> (1.34 ^{0.182})	<i>-2.122 ± 4.263</i> (-0.50 ^{0.619})	-							
	Single <i>O. edulis</i>	<i>-9.420 ± 4.263</i> (-2.21 ^{0.029})	<i>-3.414 ± 4.263</i> (-0.80 ^{0.425})	<i>4.729 ± 4.263</i> (1.11 ^{0.269})	<i>-3.117 ± 4.263</i> (-0.73 ^{0.466})	<i>-0.995 ± 4.263</i> (0.23 ^{0.820})	-						
16°C	Intra <i>C. gigas</i>	<i>-13.21 ± 4.169</i> (-3.17 ^{0.002})	<i>-7.201 ± 4.169</i> (-1.73 ^{0.087})	<i>0.943 ± 4.169</i> (0.23 ^{0.821})	<i>-6.904 ± 4.169</i> (-1.66 ^{0.100})	<i>-4.781 ± 4.263</i> (-1.12 ^{0.264})	<i>-3.786 ± 4.263</i> (-0.89 ^{0.376})	-					
	Intra <i>O. edulis</i>	<i>-10.40 ± 4.169</i> (-2.50 ^{0.014})	<i>-4.398 ± 4.169</i> (-1.05 ^{0.293})	<i>3.745 ± 4.169</i> (0.90 ^{0.371})	<i>-4.101 ± 4.169</i> (-0.98 ^{0.327})	<i>-1.979 ± 4.263</i> (-0.46 ^{0.643})	<i>-0.984 ± 4.263</i> (-0.23 ^{0.818})	<i>2.803 ± 4.169</i> (0.67 ^{0.503})	-				
	Inter <i>C. gigas</i>	<i>-7.758 ± 4.169</i> (-1.86 ^{0.065})	<i>-1.752 ± 4.169</i> (-0.42 ^{0.675})	<i>6.391 ± 4.169</i> (1.53 ^{0.128})	<i>-1.455 ± 4.169</i> (-0.35 ^{0.728})	<i>0.667 ± 4.263</i> (0.16 ^{0.876})	<i>1.662 ± 4.263</i> (0.39 ^{0.697})	<i>5.449 ± 4.169</i> (1.31 ^{0.194})	<i>2.646 ± 4.169</i> (0.63 ^{0.527})	-			
	Inter <i>O. edulis</i>	<i>-7.934 ± 4.169</i> (-1.90 ^{0.059})	<i>-1.928 ± 4.269</i> (-0.46 ^{0.645})	<i>6.216 ± 4.169</i> (-0.39 ^{0.696})	<i>-1.630 ± 4.169</i> (-0.39 ^{0.696})	<i>0.492 ± 4.263</i> (0.12 ^{0.908})	<i>1.487 ± 4.263</i> (0.35 ^{0.728})	<i>5.273 ± 4.169</i> (1.26 ^{0.208})	<i>2.471 ± 4.169</i> (0.59 ^{0.554})	<i>-0.176 ± 4.169</i> (-0.04 ^{0.966})	-		
	Single <i>C. gigas</i>	<i>-14.27 ± 4.169</i> (-3.42 ^{0.001})	<i>-8.264 ± 4.169</i> (-1.98 ^{0.050})	<i>-0.121 ± 4.169</i> (-0.03 ^{0.977})	<i>-7.967 ± 4.169</i> (-1.91 ^{0.058})	<i>-5.845 ± 4.263</i> (-1.37 ^{0.173})	<i>-4.850 ± 4.263</i> (-1.14 ^{0.257})	<i>-1.064 ± 4.169</i> (-0.26 ^{0.799})	<i>-3.866 ± 4.169</i> (-0.93 ^{0.355})	<i>-6.512 ± 4.169</i> (-1.56 ^{0.121})	<i>-6.337 ± 4.169</i> (-1.52 ^{0.131})	-	
	Single <i>O. edulis</i>	<i>-9.332 ± 4.263</i> (-2.19 ^{0.030})	<i>-3.326 ± 4.263</i> (-0.78 ^{0.437})	<i>4.817 ± 4.263</i> (1.13 ^{0.261})	<i>-3.029 ± 4.263</i> (-0.71 ^{0.479})	<i>-0.907 ± 4.354</i> (-0.21 ^{0.835})	<i>0.088 ± 4.354</i> (0.02 ^{0.984})	<i>3.875 ± 4.263</i> (0.91 ^{0.365})	<i>1.072 ± 4.263</i> (0.25 ^{0.802})	<i>-1.574 ± 4.263</i> (-0.37 ^{0.713})	<i>-1.398 ± 4.263</i> (-0.33 ^{0.743})	<i>-4.938 ± 4.263</i> (1.16 ^{0.249})	-

Supplement 7. Model S6 | GLUCOSE (N = 140)

Intercept only model. Data are shown for information only, as no significant terms were found.

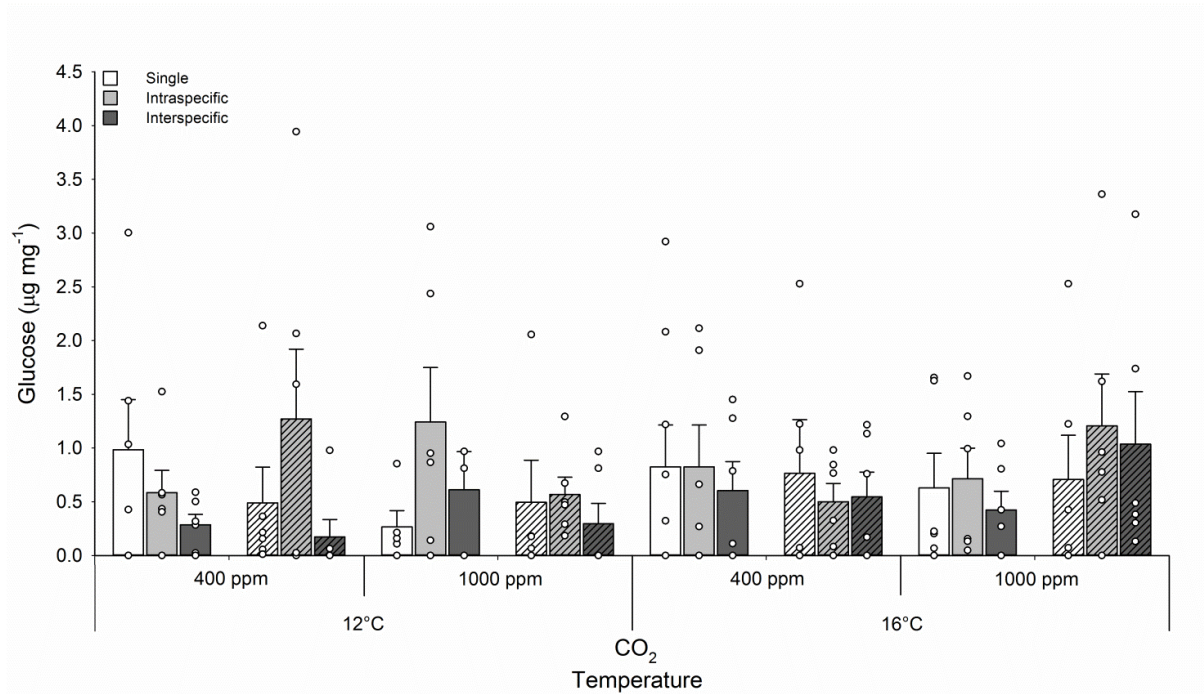


Figure S6. Glucose concentration in haemolymph of *C. gigas* (no hashed bars) and *O. edulis* (hashed bars) maintained alone and in intra- and inter-specific mixtures under elevated temperature and concentration of CO_2 . Bars indicate mean (\pm SEM) and dots are raw data values.