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Relative enrichment of ammonium and its impacts on open-ocean phytoplankton community composition under a high-emissions scenario

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Section S1.

Nitrification in PISCES-v2 was previously treated as a one-step conversion of NH_4^+ to NO_3^- but was split into its two component steps (ammonia and nitrite oxidation) for the purposes of this study. Both steps were simulated implicitly by multiplying a maximum growth rate μ^{max} (day^{-1}) by the concentration of substrate (µM) to return a maximum potential rate (µM day^{-1}). This was then multiplied by limitation terms (L^X) representing the effect of environmental conditions to return the realized rate.

For ammonia oxidation ($[NH_4^+]\rightarrow[NO_2^-]$),

$$[NH_4^+]\rightarrow[NO_2^-] = \mu_{AO}^{max} \cdot [NH_4^+] \cdot L_{AO}^{NH_4^+} \cdot L_{AO}^{PAR} \cdot L_{AO}^{pH} \qquad S1$$

$$\mu_{AO}^{max} = \max(0.2, 0.029 \cdot T - 0.147) \qquad S2$$

$$L_{AO}^{NH_4^+} = \frac{NH_4^+}{NH_4^+ + K_{AO}^{NH_4^+}} \qquad S3$$

$$L_{AO}^{PAR} = 1 - \frac{PAR}{PAR + K_{AO}^{PAR}} \qquad S4$$

$$L_{AO}^{pH} = \min\left(1, \frac{10^{(pH - pK_a)}}{10^{(R_{pH} - pK_a)}}\right) \qquad S5$$

In the above, μ_{AO}^{max} is estimated by a linear model with a floor of 0.2 day^{-1} (Eqn. S2). This model was fit to the growth curves of three ecotypes of ammonia-oxidizing archaea (Qin et al., 2015) and returns rates of 0.8 day^{-1} near 30°C (Fig. S16). A floor of 0.2 day^{-1} was justified by relatively high rates observed in near-freezing waters (Tolar et al., 2016). The limitation term for NH_4^+ uptake ($L_{AO}^{NH_4^+}$, Eqn. S3) assumes a constant half-saturation coefficient $K_{AO}^{NH_4^+}$ of 0.1 µM, which is well reflective of both natural marine assemblages of archaea (Horak et al., 2013; Newell et al., 2013; Olson, 1981; Peng et al., 2016; Wan et al., 2018) and the cultivated archaea *Nitrosopumilus maritimus* SCM1 (Martens-Habbena et al., 2009). Light limitation (L_{AO}^{PAR}) and effects of pH (L_{AO}^{pH}) are less well constrained, but nonetheless important. We set the half saturation term of photoinhibition (K_{AO}^{PAR}, Eqn. S4) to 0.75 W m^{-2}, which accounted for an 80% reduction in rates at photosynthetically active radiation levels of 3 W m^{-2} (Merbt et al., 2012). We set the reference pH (R_{pH}, Eqn. S5) below which negative effects on oxidation occur at 8.0, which reflects surface conditions of historical ocean and therefore the pH (i.e., NH_3 availability) that ammonia oxidizers are likely adapted to (Ward, 1987). With a pK_a of the NH_3-NH_4^+ equilibrium equal to 9.3 (Zeebe and Wolf-Gladrow, 2001), this treatment reduced oxidation rates by 27.5% for a decline in pH of 0.14 units, which is a more conservative change than the 36-38% declines in oxidation reported by Beman et al. (2011) for the same pH change.

For nitrite oxidation ($[NO_2^-]\rightarrow[NO_3^-]$),

$$[NO_2^-]\rightarrow[NO_3^-] = \mu_{NO}^{max} \cdot [NO_2^-] \cdot L_{NO}^{NO_2^-} \cdot L_{NO}^{PAR} \quad \text{S6}$$

$$L_{NO}^{NO_2^-} = \frac{NO_2^-}{NO_2^- + K_{NO}^{NO_2^-}} \quad \text{S7}$$

$$L_{NO}^{PAR} = 1 - \frac{PAR}{PAR + K_{AO}^{PAR}} \quad \text{S8}$$

The treatment of nitrite oxidation is like ammonia oxidation. However, there are two key differences. First, nitrite-oxidizing bacteria have lower growth yield per unit nitrogen oxidized compared to ammonia-oxidizing archaea (Bayer et al., 2022), which demands a slower growth rate in our model given that we are simulating this metabolism implicitly. Accordingly, we set the maximum growth rate of nitrite-oxidizing bacteria (μ_{NO}^{max}) to a constant 0.15 day^{-1}, informed by doubling times in excess of four days of marine cultures held at optimal conditions (Spieck and Lipski, 2011). Second, pH has no effect on NO_2^- concentrations. Otherwise, we maintain the same half-saturation coefficients for the substrate ($L_{NO}^{NO_2^-}$, Eqn. S7) and light limitation (L_{NO}^{PAR}, Eqn. S8) terms as for ammonia oxidizers, being 0.1 µM for $K_{NO}^{NO_2^-}$ and 0.75 W m^{-2} for K_{NO}^{PAR} (Table S3). All parameters for nitrification are presented in Table S3.

We did not include oxygen or iron limitation. Oxygen was ignored due to reports of high activity and biomass of nitrifiers in low oxygen zones, due perhaps to a combination of high cellular affinity for oxygen (Bristow et al., 2016) and potential anaerobic pathways of oxidation via alternative electron acceptors (Babbin et al., 2020; Kraft et al., 2022). We ignored iron limitation, despite its potential for limiting growth of ammonia oxidizers (Shafiee et al., 2019), because little is known regarding its effects on the growth of nitrite-oxidizing bacteria. In addition, changes to the availability of iron for biology in the future ocean are highly uncertain and models have little skill in this regard (Tagliabue et al., 2016). We acknowledge, however, that changes in both oxygen and iron availability may be important additional factors governing shifts in the NH_4^+ to DIN ratio in a future ocean.

Supplementary References

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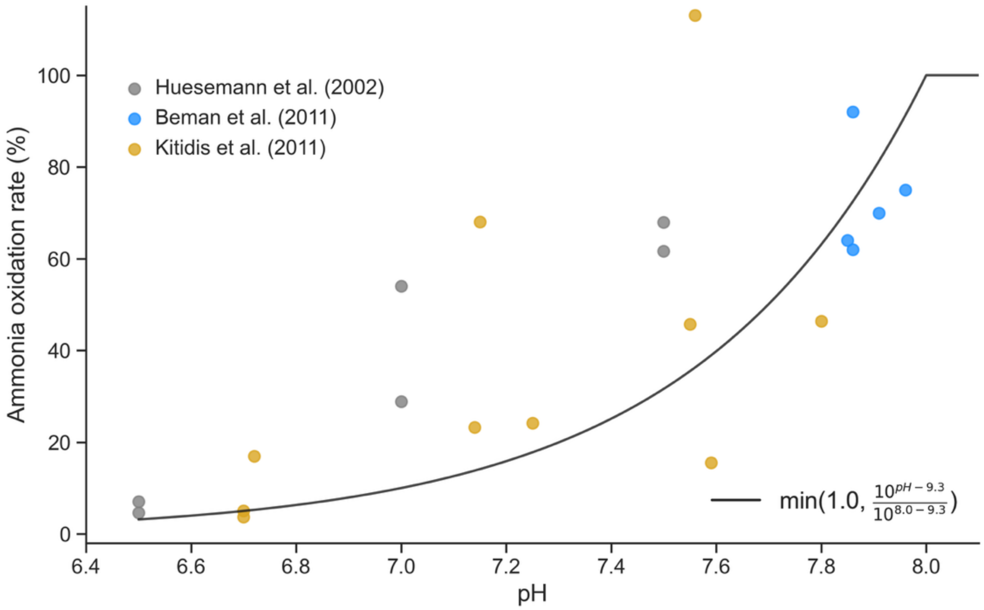

Fig. S1. Parameterisation of ocean acidification on ammonia oxidation. Measurements of rate change in ammonia oxidation due to forced declines in pH (markers) are compared with a parameterisation for the relationship between pH and ammonia oxidation rate (solid line). This parameterisation returns a Pearson's correlation of 0.68 ($R^2 = 0.46$).

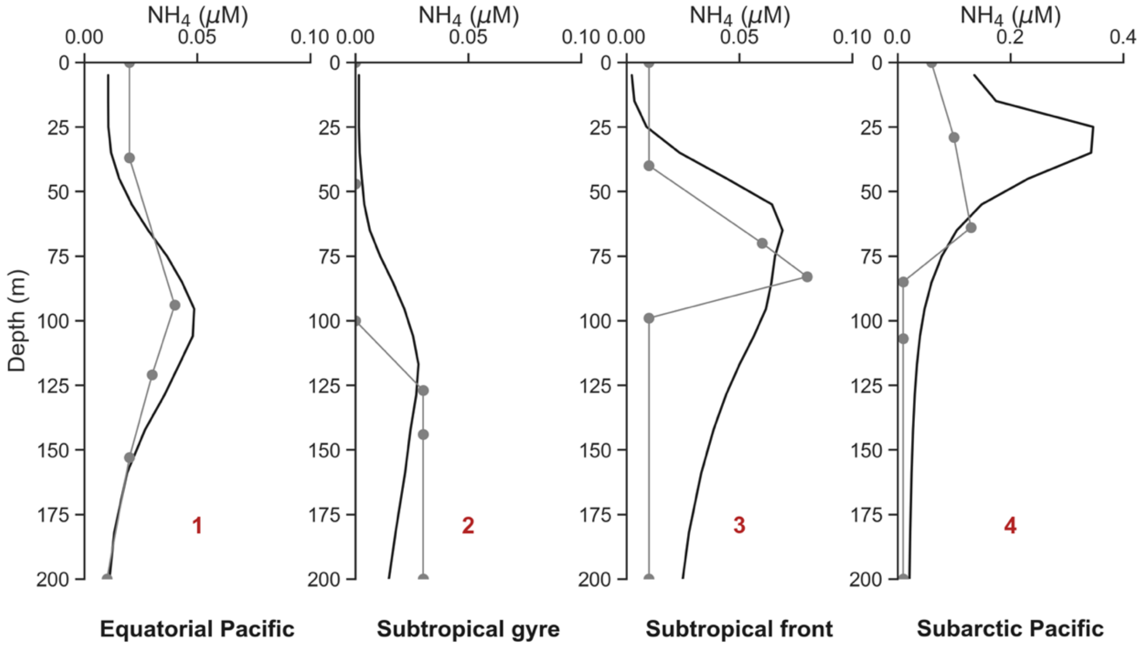

Fig. S2. Simulated and observed depth profiles of NH_4^+ at four locations in the North Pacific Ocean (Shiozaki et al., 2016).

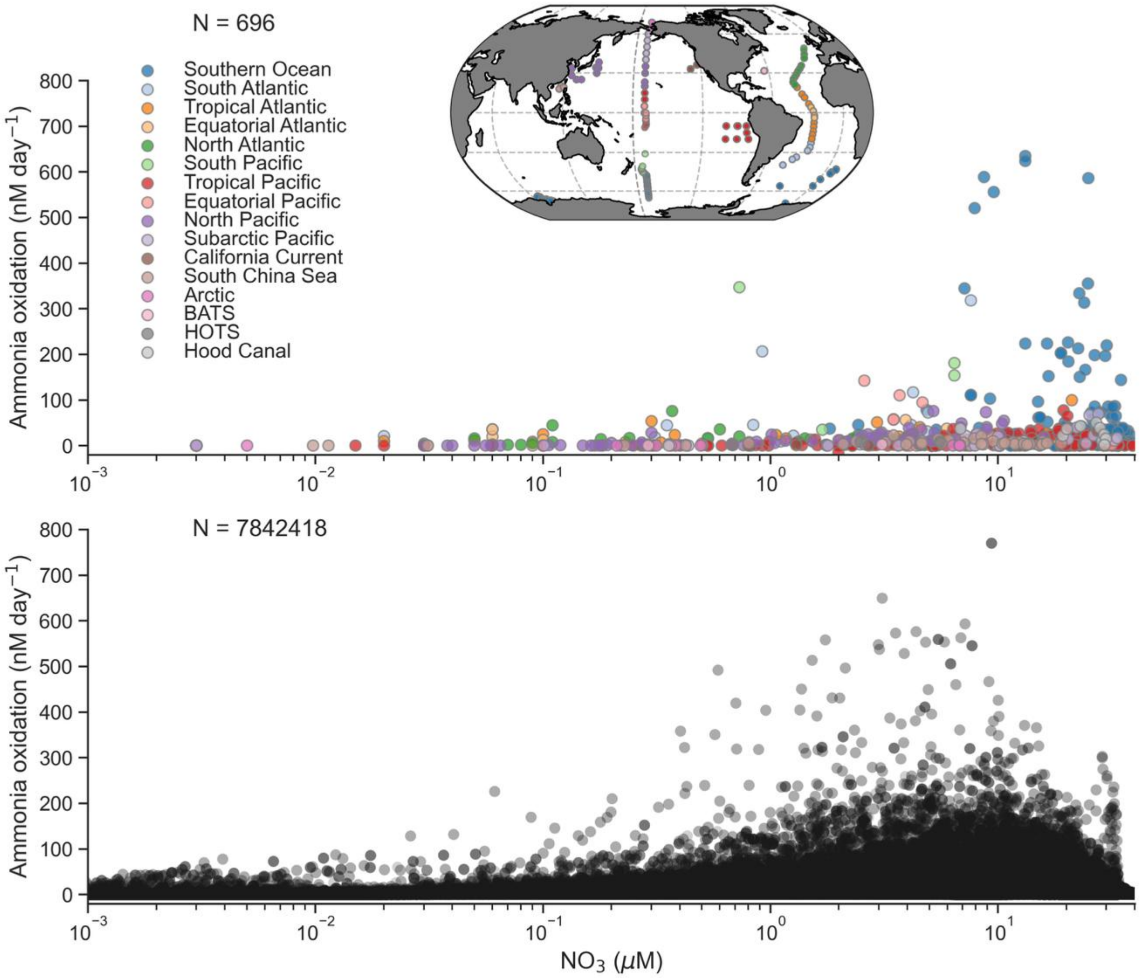

Fig. S3. Measured (top) and modelled (bottom) ammonia oxidation rates from the global ocean plotted against the $\log_{10}$ of nitrate (NO_3), which indicates a spectrum of oligotrophy-eutrophy from left to right along the x-axis.

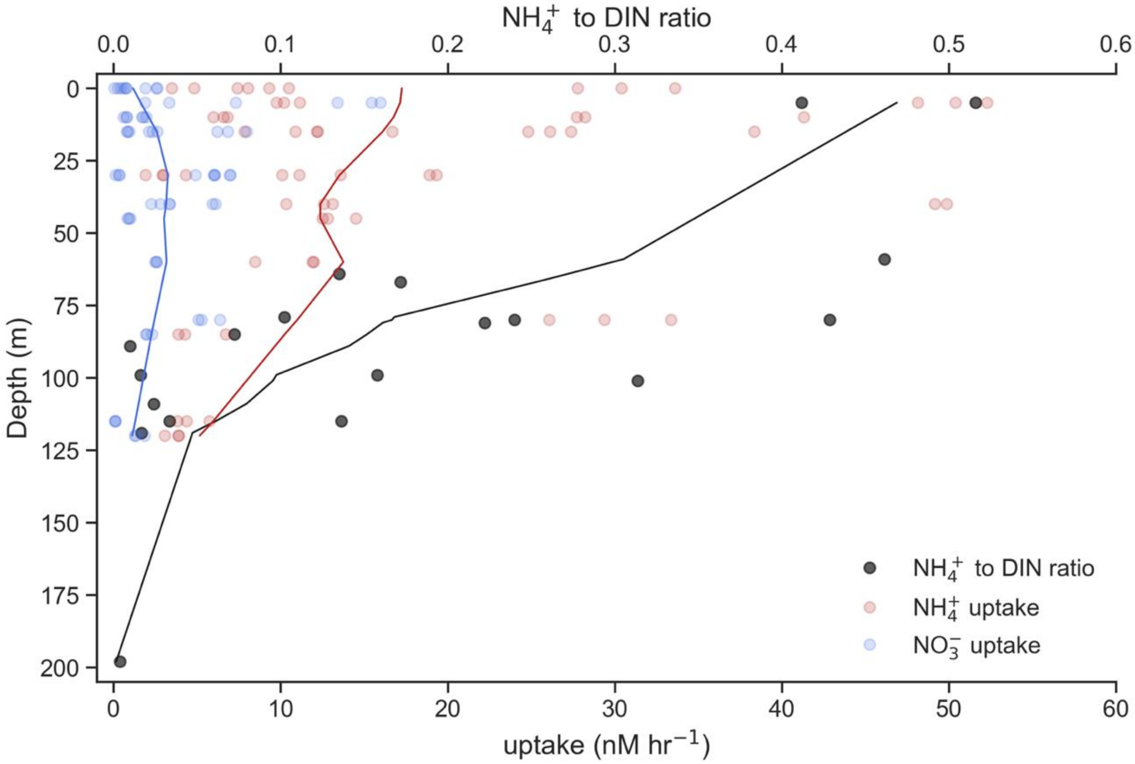

Fig. S4. Nutrient and community uptake rate data from the Gulf of Mexico (Yingling et al., 2021). Linear interpolations in depth are constructed and the interpolated values are used in Figure S5.

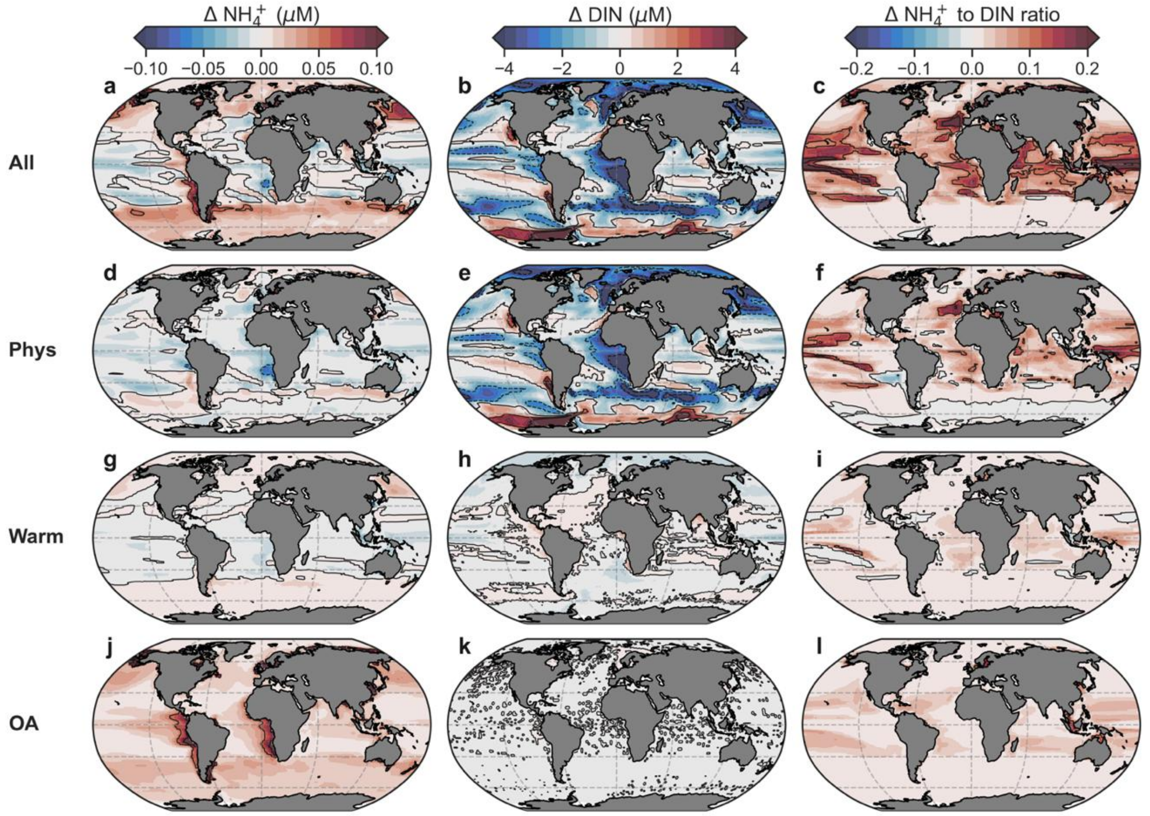

Fig. S5. Anthropogenic impacts on concentrations of NH_4^+, DIN and NH_4^+:DIN ratios. a-c, The difference in concentrations and the NH_4^+ to DIN ratio averaged over the euphotic zone at the end of the 21st century (2081-2100) with all anthropogenic impacts (All). d-f, same as a-c but for physical changes (circulation + light) only (Phys). g-i, same as a-c but for warming effects on metabolism only (Warm). j-l, same as a-c but for ocean acidification only (OA).

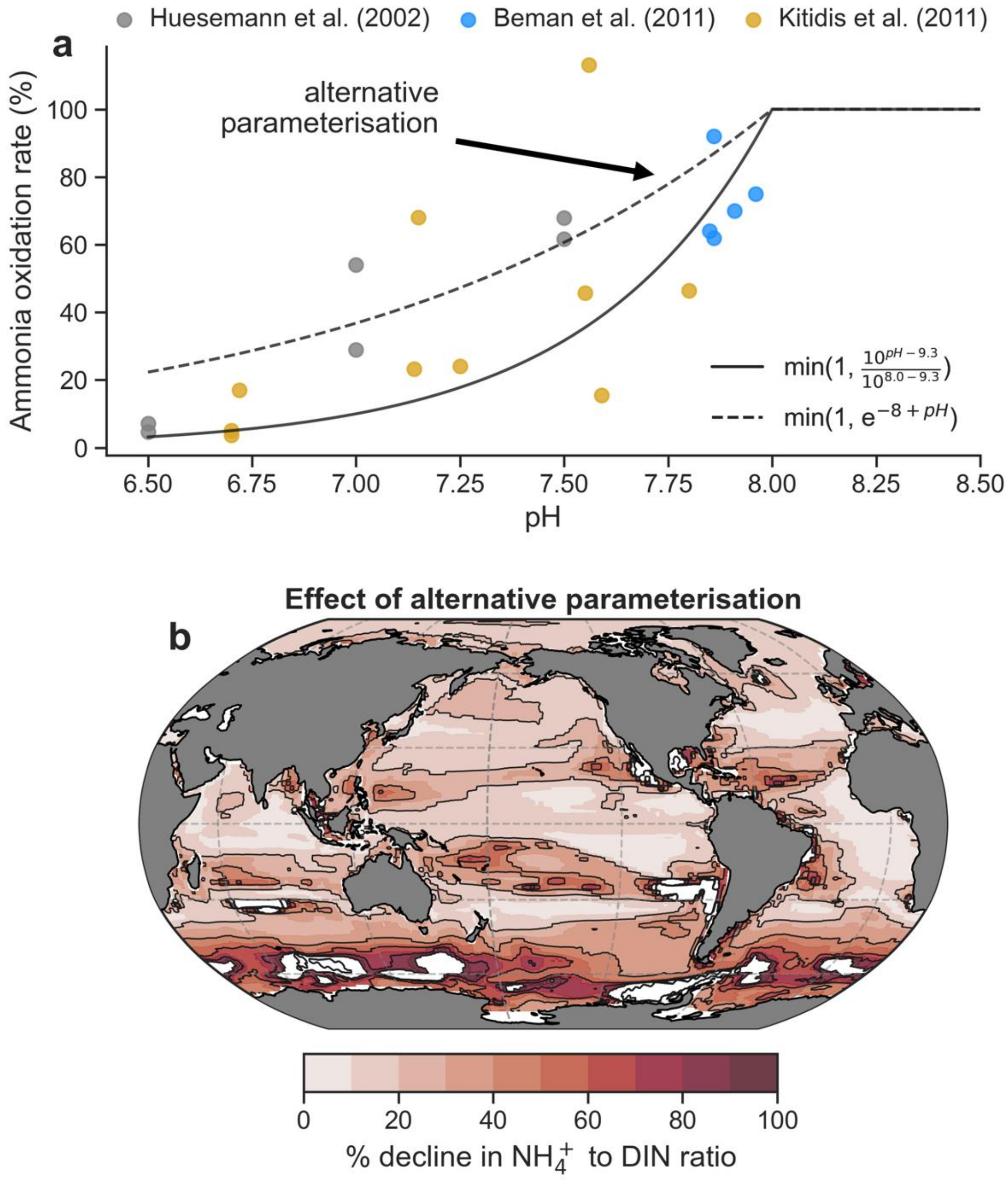

Fig. S6. Alternative parameterisation of pH effect on ammonia oxidation. a, The alternative parameterisation (dashed line), which includes a weaker effect of pH decline on ammonia oxidation. b, How the weaker relationship between pH and ammonia oxidation ameliorates the increases in NH_4^+:DIN. As NH_4^+:DIN increases almost everywhere in these experiments, we only show how this alternative parameterisation works to reduce the increase.

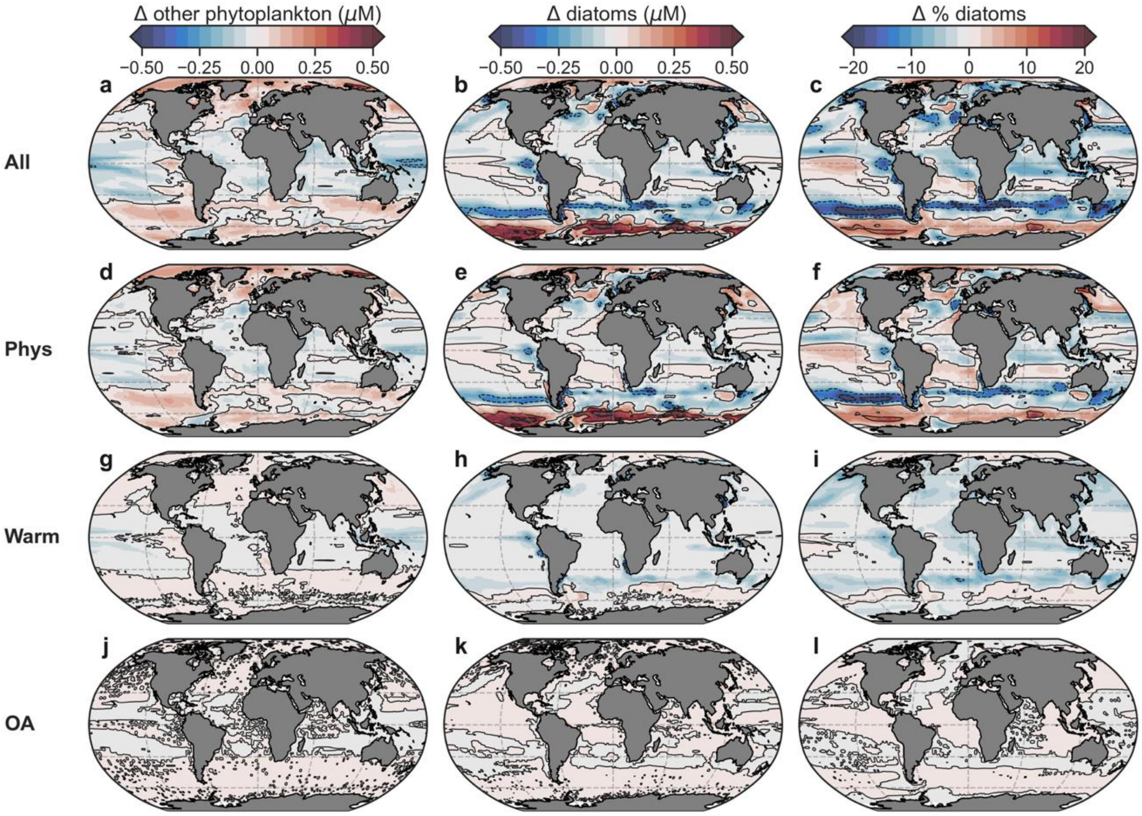

Fig. S7. Anthropogenic impacts on concentrations of other phytoplankton, diatoms and the relative abundance of diatoms. a-c, Concentrations and the relative abundance of diatoms are averaged over the depths at which total phytoplankton concentrations are greater than 0.1 μM of carbon at the end of the 21st century (2081-2100) with all anthropogenic impacts (All). d-f, same as a-c but for physical changes (circulation + light) only (Circ). g-i, same as a-c but for warming effects on metabolism only (Warm). j-l, same as a-c but for ocean acidification only (OA).

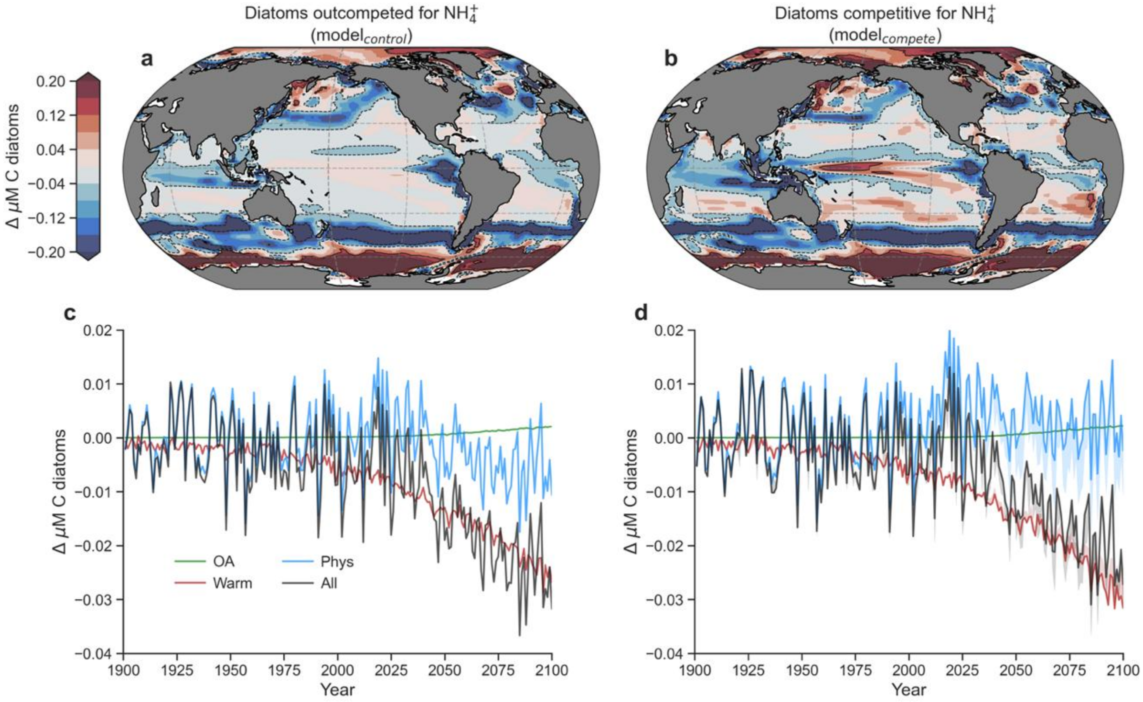

Fig. S8. Impact of NH_4^+ enrichment within DIN on diatom abundance. (a), Mean change (Δ) in the abundance of diatoms (μM C) by the end of the 21st century (2081-2100) as predicted by the control run of the ocean-biogeochemical model (model$_{\text{control}}$) under the RCP8.5 scenario and averaged over the euphotic zone. (b), Same as in (a), but for the model with equal affinities of diatoms and other phytoplankton for NH_4^+ (model$_{\text{compete}}$). (c), Global mean change in diatom abundance due to physical (circulation + light) changes (blue), warming effects on metabolic rates (red), ocean acidification effect on ammonia oxidation (green) and all stressors (black) for model$_{\text{control}}$. (d), The same as in (c), but for model$_{\text{compete}}$. Shading shows the change between (c) and (d).

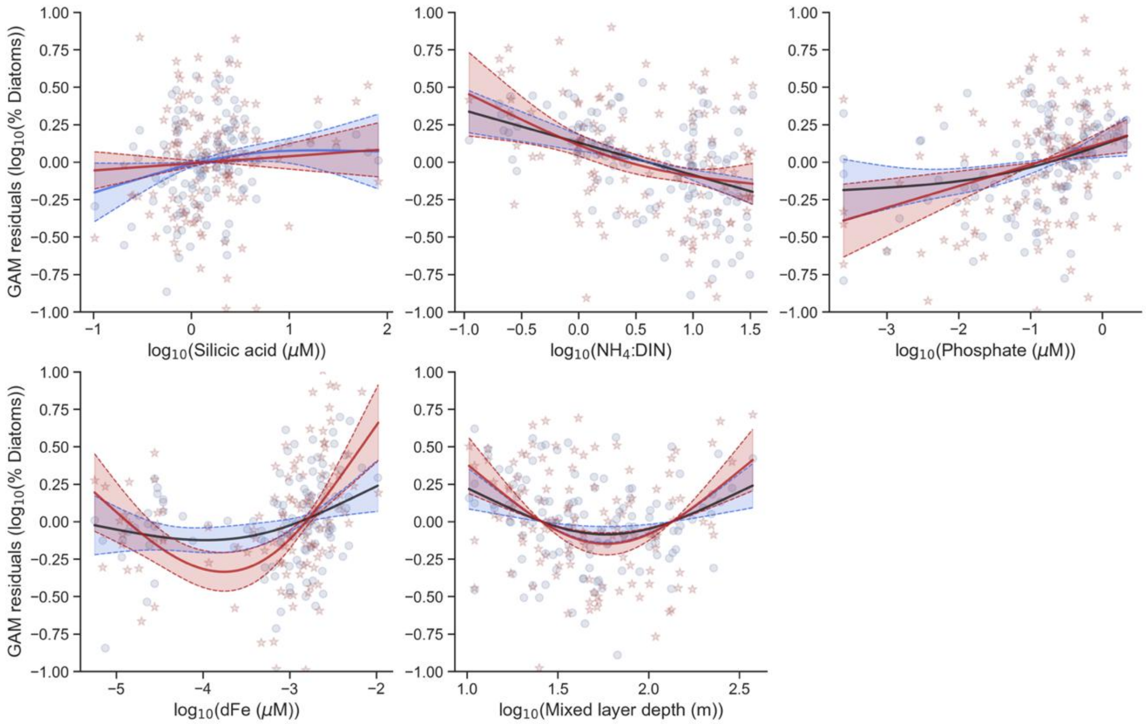

Fig. S9. Key predictors of diatom relative abundance as a proportion of eukaryotic phytoplankton (blue) and all phytoplankton (red) generated by a GAM. The predictors are the $\log_{10}$ transformed silicic acid concentration (*in situ*), ratio of NH_4^+:DIN (model-derived), phosphate concentration (*in situ*), dissolved iron concentration (model-derived) and mixed layer depth (*in situ*). Dots are the partial residuals of the fitted GAM. The deviance explained and significance of each predictor are reported in Table S1.

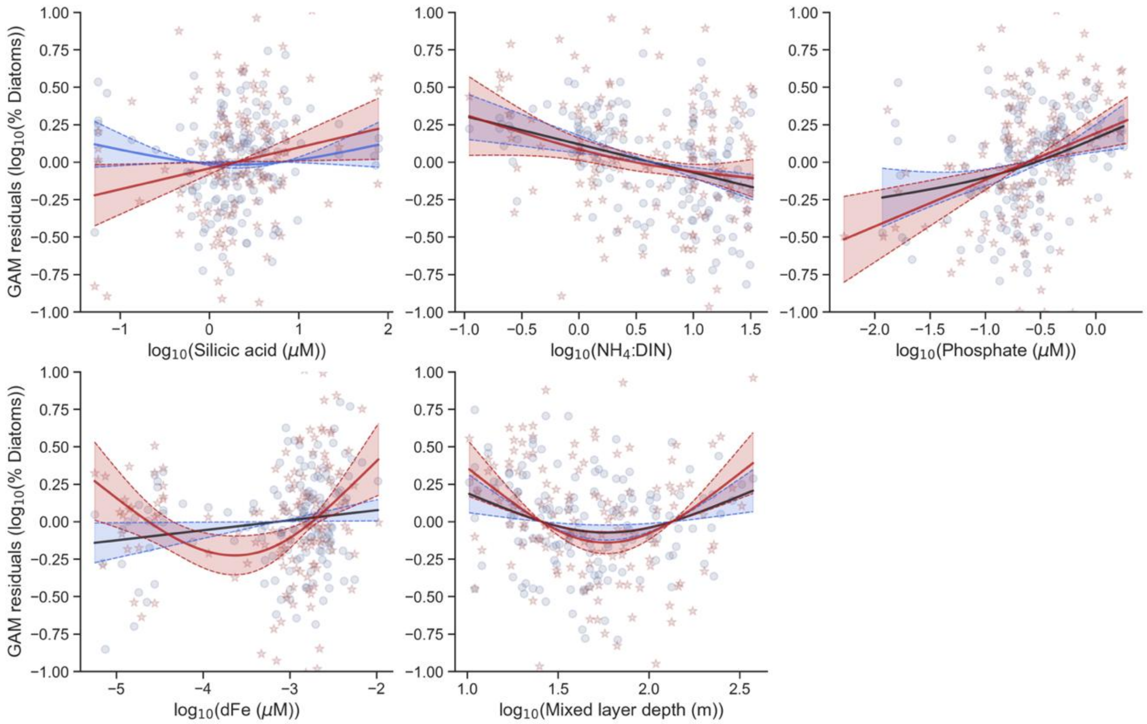

Fig. S10. Key predictors of diatom relative abundance as a proportion of eukaryotic phytoplankton (blue) and all phytoplankton (red) generated by a GAM. The predictors are the $\log_{10}$ transformed silicic acid concentration (WOA18 (Garcia et al., 2019)), ratio of NH_4^+:DIN (model-derived), phosphate concentration (WOA18 (Garcia et al., 2019)), dissolved iron concentration (model-derived) and mixed layer depth (*in situ*). Dots are the partial residuals of the fitted GAM. The deviance explained and significance of each predictor are reported in Table S1.

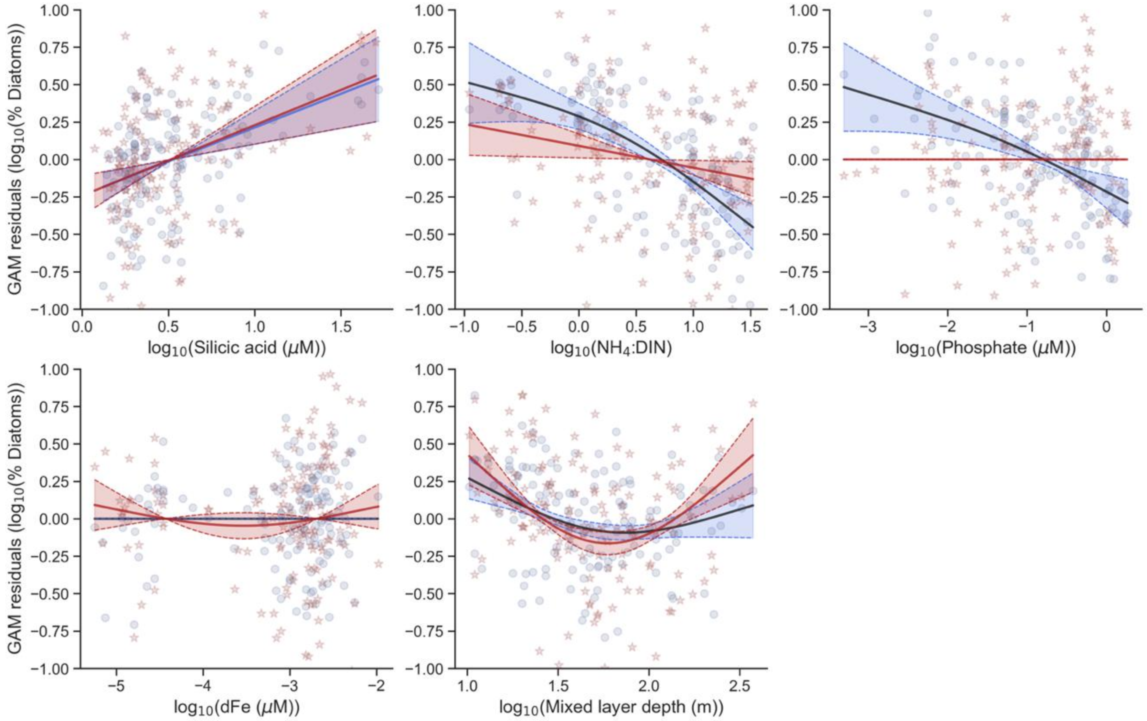

Fig. S11. Key predictors of diatom relative abundance as a proportion of eukaryotic phytoplankton (blue) and all phytoplankton (red) generated by a GAM. The predictors are the $\log_{10}$ transformed silicic acid concentration (model-derived), ratio of NH_4^+:DIN (model-derived), phosphate concentration (model-derived), dissolved iron concentration (model-derived) and mixed layer depth (*in situ*). Dots are the partial residuals of the fitted GAM. The deviance explained and significance of each predictor are reported in Table S1.

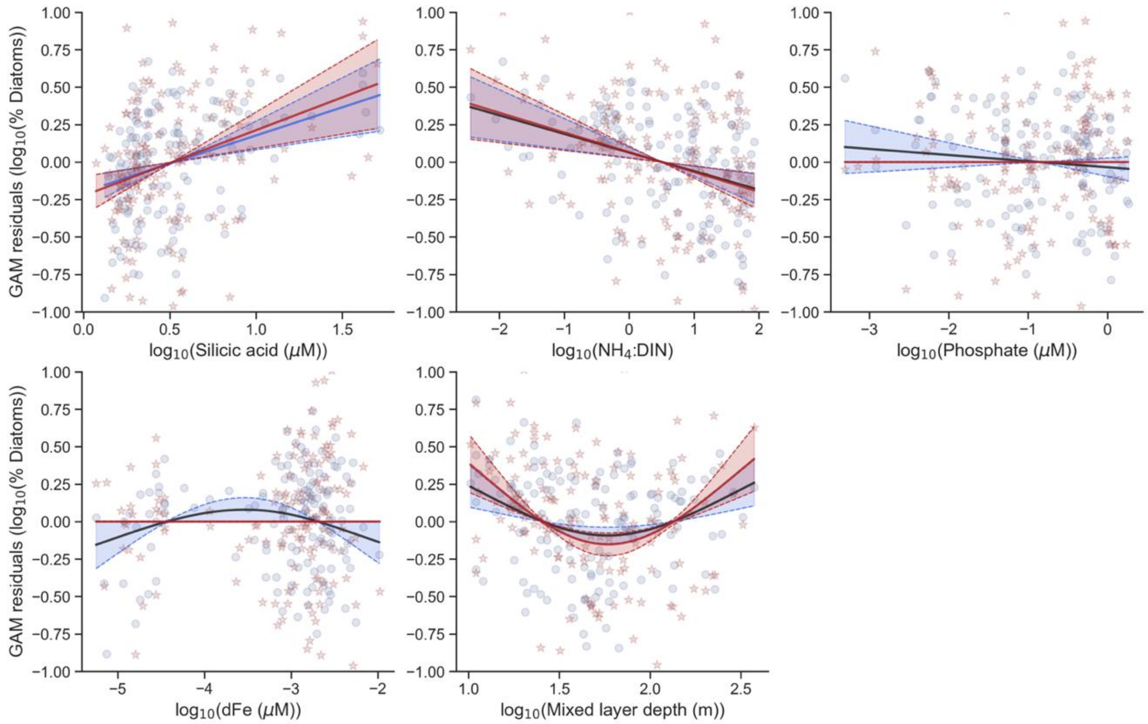

Fig. S12. Key predictors of diatom relative abundance as a proportion of eukaryotic phytoplankton (blue) and all phytoplankton (red) generated by a GAM. The predictors are the $\log_{10}$ transformed silicic acid concentration (model-derived), ratio of NH_4^+:DIN (Darwin model), phosphate concentration (model-derived), dissolved iron concentration (model-derived) and mixed layer depth (*in situ*). Dots are the partial residuals of the fitted GAM. The deviance explained and significance of each predictor are reported in Table S1.

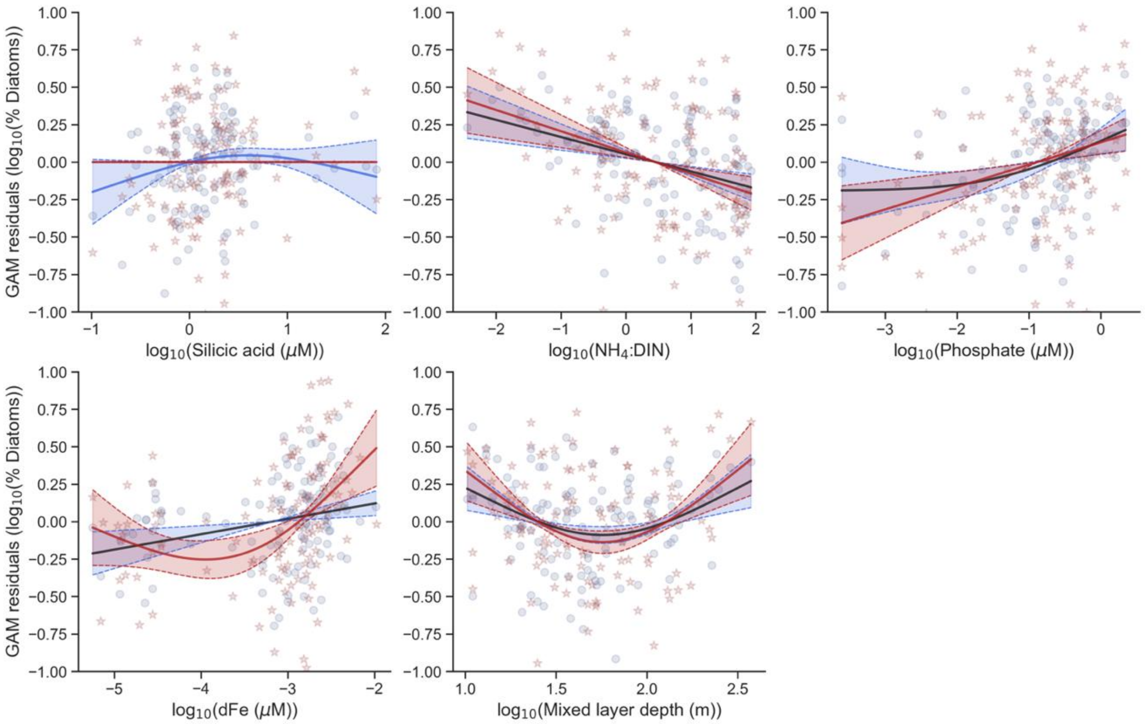

Fig. S13. Key predictors of diatom relative abundance as a proportion of eukaryotic phytoplankton (blue) and all phytoplankton (red) generated by a GAM. The predictors are the $\log_{10}$ transformed silicic acid concentration (*in situ*), ratio of NH_4^+:DIN (Darwin model), phosphate concentration (*in situ*), dissolved iron concentration (model-derived) and mixed layer depth (*in situ*). Dots are the partial residuals of the fitted GAM. The deviance explained and significance of each predictor are reported in Table S1.

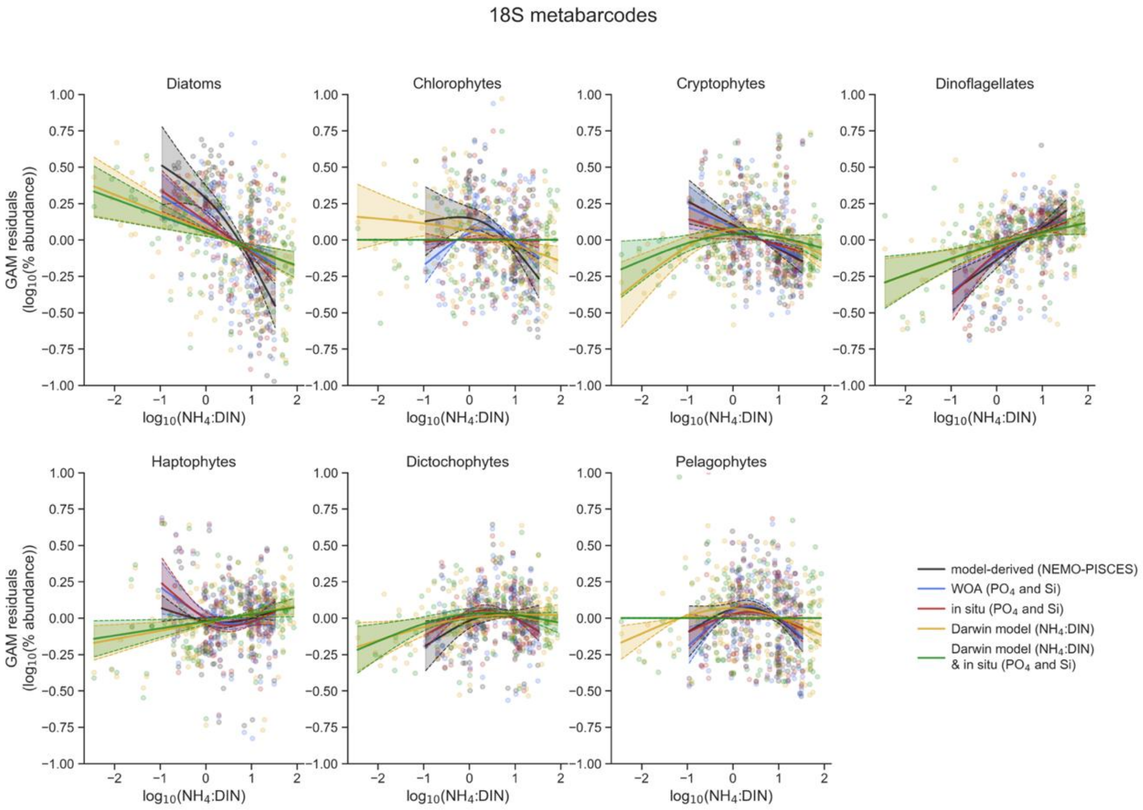

Fig. S14. GAM relationships between NH_4^+ to DIN ratios and the relative abundance of each major phytoplankton taxa from the 18S metabarcoding estimates. Dots are the partial residuals of the fitted GAM. Each colour indicates a different combination of predictor variables.

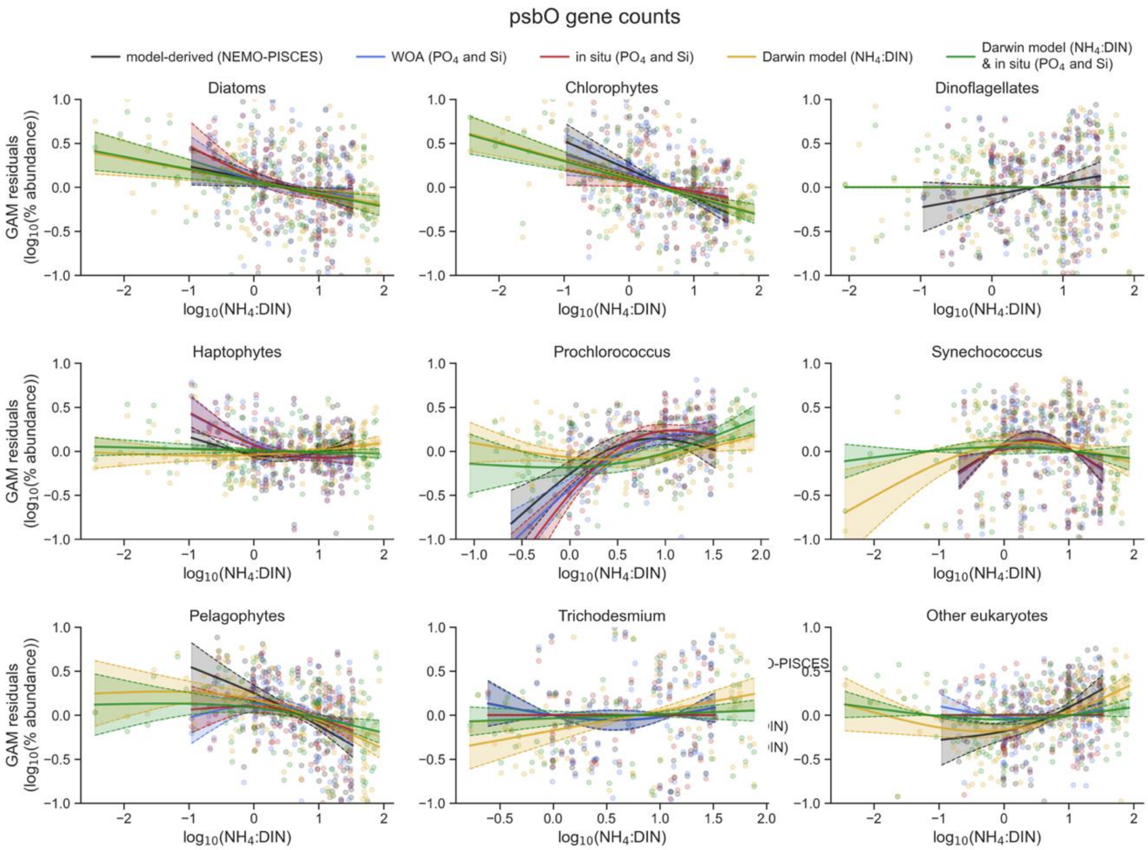

Fig. S15. GAM relationships between NH$_4^+$ to DIN ratios and the relative abundance of each major phytoplankton taxa from the *psbO* gene count estimates. Dots are the partial residuals of the fitted GAM. Each colour indicates a different combination of predictor variables.

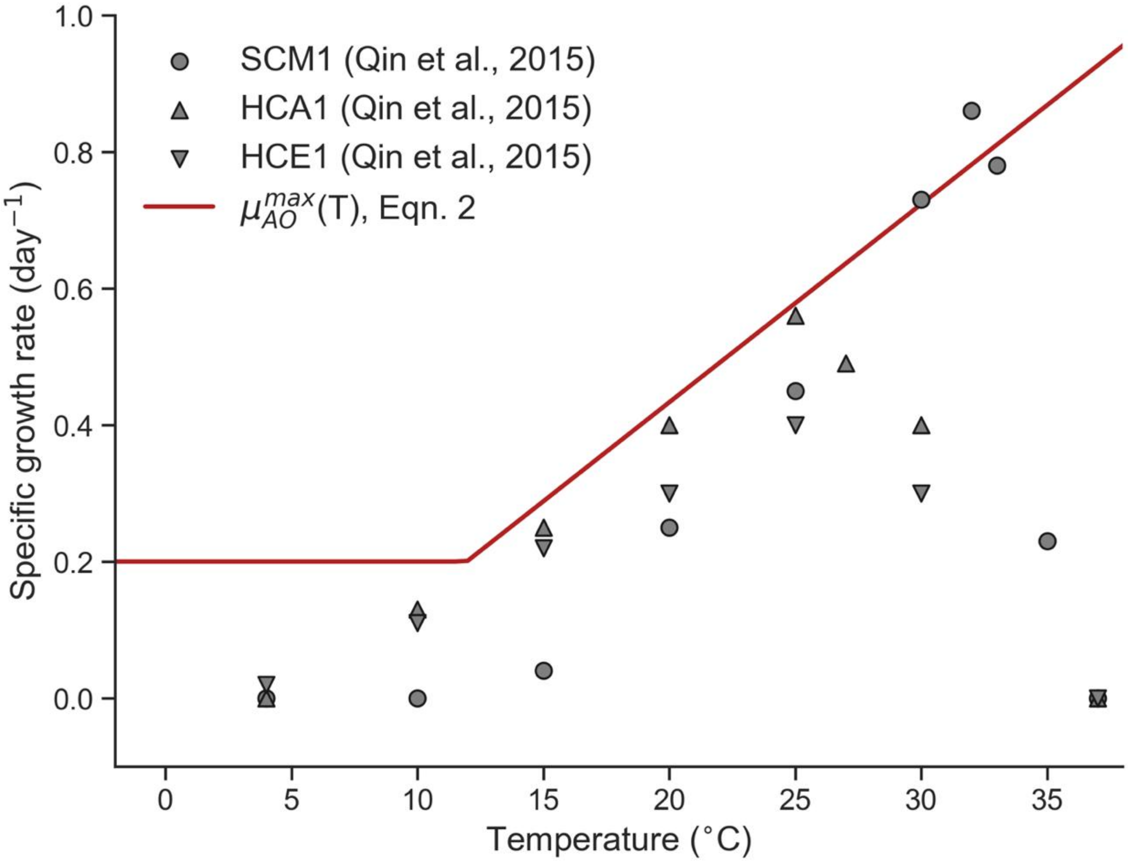

Fig. S16. Temperature dependence of the maximum growth rate (μ) of ammonia oxidising archaea ecotypes (Qin et al., 2015).

significance	**18S metabarcodes**				
Predictor	**Model-derived**	**WOA**	***in situ***	**Darwin NH_4^+:DIN**	**Darwin + *in situ***
Si	***	ns	*	**	ns
NH_4^+:DIN	***	***	***	***	***
PO_4^{2-}	***	*	*	ns	**
dFe	ns	ns	*	ns	**
MLD	***	*	**	**	**

significance	***psbO* gene counts**				
Predictor	**Model-derived**	**WOA**	***in situ***	**Darwin NH_4^+:DIN**	**Darwin + *in situ***
Si	**	ns	ns	**	ns
NH_4^+:DIN	**	*	**	***	***
PO_4^{2-}	ns	**	**	ns	**
dFe	ns	**	***	ns	***
MLD	***	**	***	***	**

% Deviance explained	**18S metabarcodes**				
Predictor	**Model-derived**	**WOA**	***in situ***	**Darwin NH_4^+:DIN**	**Darwin + *in situ***
Si	24 (5)	21 (1)	17 (2)	24 (4)	17 (2)
NH_4^+:DIN	30 (16)	30 (4)	29 (7)	22 (6)	24 (2)
PO_4^{2-}	11 (8)	32 (3)	24 (3)	11 (1)	24 (4)
dFe	4 (0)	4 (1)	5 (5)	4 (2)	5 (4)
MLD	17 (6)	17 (3)	19 (5)	18 (5)	19 (5)

% Deviance explained	***psbO* gene counts**				
Predictor	**Model-derived**	**WOA**	***in situ***	**Darwin NH_4^+:DIN**	**Darwin + *in situ***
Si	25 (1)	17 (1)	13 (0)	25 (2)	13 (0)
NH_4^+:DIN	18 (2)	18 (2)	18 (3)	24 (4)	30 (3)
PO_4^{2-}	15 (0)	27 (4)	15 (4)	15 (0)	15 (3)
dFe	7 (1)	7 (6)	13 (13)	7 (0)	13 (8)
MLD	19 (9)	19 (5)	21 (7)	19 (6)	21 (6)

Table S1. Generalized Additive Model (GAM) results for predictions of the relative abundance of diatoms. Data provided by *Tara* Oceans 18S rRNA gene metabarcoding and *psbO* gene counts. Rows are the different predictor variables. Si = Silicate, PO_4^{2-} = Phosphate, dFe = dissolved iron, MLD = mixed layer depth. Significance is assessed by applying a smoothing penalty to the predictor in question. Deviance explained is calculated by fitting a GAM with only the predictor in question, and by removing the predictor from the full model and comparing the difference in deviance explained with the full model (this result is provided in the parantheses). The most significant or most explanatory are highlighted. (*) p-value < 0.05. (**) p-value < 0.01. (***) p-value < 0.001.

18S metabarcodes

Taxa	Model-derived	Darwin model
Diatoms	29.9% (***)	21.6% (***)
Cryptophytes	2.4%	4.3% (*)
Chlorophytes	2.6%	1.6%
Dinoflagellates	36.8% (***)	30.6% (***)
Haptophytes	4.3% (*)	5.9% (**)
Dictyochophytes	9.1% (**)	11.4% (***)
Pelagophytes	0.0%	6.8% (**)

***psbO* gene counts**

Taxa	Model-derived	Darwin model
Diatoms	17.6 (***)	24.3% (***)
Prochlorococcus	23.4% (***)	16.0% (***)
Synechococcus	5.9% (**)	7.7% (**)
Chlorophytes	13.2% (***)	21.2% (***)
Dinoflagellates	1%	0.0%
Haptophytes	13.6% (***)	1.2%
Pelagophytes	11.2% (***)	12.5% (***)
Trichodesmium	4%	9.3% (**)
Other eukaryotes	0.1%	8.5% (**)

Table S2. Deviance explained from the Generalized Additive Models using NH_4^+:DIN as the sole predictor of the relative abundance of different eukaryotic phytoplankton taxa. Data provided by *Tara* Oceans 18S rRNA gene metabarcoding and *psbO* gene counts. Significance of NH_4^+:DIN as a predictor of diatom relative abundance is denoted by the number of *. No * means p-value > 0.05. (*) p-value < 0.05. (**) p-value < 0.01. (***) p-value < 0.001. NH_4^+:DIN may be model-derived from PISCES-v2 or from the Darwin model (Follows et al., 2007).

Parameter	Description	Value	Units
μ_{AO}^{max}	Maximum rate of ammonia oxidation	Eqn. S2	day^{-1}
$K_{AO}^{NH_4^+}$	Ammonia oxidation half-saturation constant for ammonium	0.1	mmol m^{-3}
K_{AO}^{PAR}	Ammonia oxidation half-saturation constant for photosynthetically active radiation	0.75	W m^{-2}
R_{AO}^{pH}	Reference pH below which ammonia oxidation is limited	8.0	pH units
pK_a	pH at which all NH_x is NH_3	9.3	pH units
μ_{NO}^{max}	Maximum rate of nitrite oxidation	0.15	day^{-1}
$K_{NO}^{NO_2^-}$	Nitrite oxidation half-saturation constant for nitrite	0.1	µmol m^{-3}
K_{NO}^{PAR}	Nitrite oxidation half-saturation constant for photosynthetically active radiation	0.75	W m^{-2}

Table S3. Parameters and their values used to simulate ammonia and nitrite oxidation in the PISCES-v2 ocean biogeochemical model, detailed in equations S1-S8. Values are informed by field and laboratory studies cited in the methods.

Data Set S1. Nutrient concentration data.

Data Set S2. Ammonia oxidation rate data.

Data Set S3. Coincident nutrient and regenerated to new primary production rate data.

Data Set S4. Variations in ammonia oxidation rates for pH changes. Rates normalized to a pH of 8.