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Title: Impact of ocean phytoplankton diversity on phosphate uptake

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Abstract

We have a limited understanding of the consequences of variations in microbial biodiversity on ocean ecosystem functioning and global biogeochemical cycles. A core process is macronutrient uptake by microorganisms, as the uptake of nutrients controls ocean CO$_2$ fixation rates in many regions. Here, we ask if variations in ocean phytoplankton biodiversity lead to novel functional relationships between environmental variability and phosphate ($P_i$) uptake. We analyzed $P_i$ uptake capabilities and cellular allocations among phytoplankton groups and the whole community throughout the extremely $P_i$-depleted Western North Atlantic Ocean. $P_i$ uptake capabilities of individual populations were well described by a classic uptake function but displayed adaptive differences in uptake capabilities that depend on cell size and nutrient availability. Using an eco-evolutionary model as well as observations of in situ uptake across the region, we confirmed that differences among populations lead to previously uncharacterized relationships between ambient $P_i$ concentrations and uptake. Supported by novel theory, this work provides a fundamentally new empirical basis for describing and understanding assimilation of limiting nutrients in the oceans. Thus, it demonstrates that microbial biodiversity, beyond cell size, is important for understanding the global cycling of nutrients.
**Significance statement**

Nutrient uptake is a central property of ocean biogeochemistry; but our understanding of this process is based on lab cultures or bulk environmental studies. Thus, mathematical descriptions of nutrient uptake, at the heart of most biogeochemical models (including ones used by the Intergovernmental Panel on Climate Change), must rely on this limited information. Hence we have little knowledge of how natural phytoplankton populations vary in their abilities to take up key nutrients. Using new analytical techniques, this study provides the first comprehensive *in situ* quantification of nutrient uptake capabilities among dominant phytoplankton groups. Supported by a model that considers plastic ecological responses in an evolutionary context, this work further provides a fundamentally new framework for the integration of microbial diversity to describe and understand the controls of ocean nutrient assimilation.
Introduction

The composition of microbial communities varies among different ocean regions and along environmental gradients (e.g., 1, 2). This variation includes phylogenetic, genomic, and functional diversity among and between hetero- or autotrophic groups. Presently, we have a limited understanding of the consequences of these different levels of microbial biodiversity on specific processes and more broadly on global ocean biogeochemical cycles (3). An important process is macronutrient uptake by microorganisms, as the uptake of nitrate and/or inorganic phosphate \((P_i)\) controls ocean CO\(_2\) fixation rates in many regions (4). Indeed, mathematical descriptions of nutrient uptake are at the heart of most marine ecosystem models (5). The ability of microorganisms to assimilate nutrients as a function of concentration is commonly described by a hyperbolic uptake kinetics curve (6, 7). Analogous to the classical Michaelis-Menten curves for enzyme kinetics (8), the parameters quantifying this relationship are the maximum uptake rate \((V_{\text{max}})\), the half saturation concentration \((K_s)\), and the ratio of the two parameters named the nutrient affinity \((\epsilon)\). Despite the importance of accurate descriptions of nutrient uptake capabilities for the understanding of competition and ocean biogeochemistry (7), our knowledge of these properties is mostly limited to lab studies of cultured strains (9). However, culture-based kinetics estimates would suggest plankton are proliferating at <25% of the growth rates observed in the oligotrophic subtropical gyres. Thus, we need to quantify this key process in naturally competing populations (10–12) and explain the discrepancies. Furthermore, we have a limited quantitative knowledge of \textit{in situ} uptake capabilities under conditions where the focal nutrient is extremely depleted. The latter is
important as marine microorganisms like Prochlorococcus often have unique genomic adaptations to maximize nutrient assimilation under such conditions (13, 14).

To address this lack of knowledge for a globally relevant ecosystem process, we here aimed at identifying the influence of different levels of microbial biodiversity on \textit{in situ} $P_i$ uptake in the Western Subtropical North Atlantic Ocean. Phosphate plays a central role in regulating the functioning of microbial communities in this region as the surface waters likely have the lowest $P_i$ concentration observed anywhere in the ocean (15). We used a combination of shipboard cell-sorting and isotopically labeled $P_i$ to quantify nutrient uptake capabilities for the whole field community and four phytoplankton groups of different sizes – Prochlorococcus, Synechococcus, small eukaryotes (<20 $\mu$m), and the nitrogen fixer Trichodesmium. We asked: (i) Do the \textit{in situ} $P_i$ uptake capabilities differ among abundant phytoplankton groups, (ii) what is the variation in uptake capabilities within each group between environments, and (iii) what is the integrative effect of marine microbial diversity and environmental variability on nutrient uptake across the region? The answers to these questions will provide both a theoretical and empirical basis for describing how microbial diversity affects a core ocean ecosystem process.

\textbf{Results}

We first examined the uptake capabilities for the whole community and four phytoplankton groups – Prochlorococcus, Synechococcus, small eukaryotes (<20 $\mu$m), and the nitrogen fixer Trichodesmium (Figure 1 and S1) across a range of environments (Figure S2). When we experimentally added increasing concentrations of $P_i$, the nutrient uptake response closely resembled a hyperbolic shape for all discrete populations as well
as the whole community ($R^2 > 0.9$, Figure 1 and S1). We then estimated the parameters $K_s$, $V_{max}$ and affinity ($\alpha$) (Table S1) and found significant (1-way ANOVA, $p < 0.05$) differences in $K_s$ among phytoplankton groups (Figure S3 and Table S1). *Prochlorococcus* had the lowest average $K_s$ followed by *Synechococcus*, small eukaryotic phytoplankton, and *Trichodesmium*, respectively. In comparison, the whole microbial community was characterized by $K_s$ values between those of *Prochlorococcus* and *Synechococcus*, the most abundant autotrophs. There was also significant variation in $V_{max}$ among phytoplankton lineages (1-way ANOVA, $p < 0.05$), and the order was analogous to $K_s$.

We then examined if differences in uptake abilities were related to cell size and found a significant positive relationship for both $K_s$ and $V_{max}$ (Figure 2, $p_{\text{spearman}} < 0.05$), but not affinity. The latter would suggest that small cells do not have a distinct competitive advantage at very low substrate concentrations. However, we also measured the $P_i$ cell quota ($Q_p$) for all groups (Table S1) and observed that affinity normalized to $Q_p$ ranked *Prochlorococcus* > *Synechococcus* > eukaryotic phytoplankton > *Trichodesmium*. An identical pattern was observed for $V_{max}$ normalized to $Q_p$. Thus, *Prochlorococcus* had the highest potential for uptake in relation to demand at low concentrations, despite having a low absolute $V_{max}$.

In addition to size-dependent variations across phytoplankton groups, we also observed differences in nutrient uptake capabilities within each group. For example, samples 2 and 10 at BATS during the highly stratified late summer/early fall period consistently had a higher $V_{max}$ but not $K_s$ for the whole community and three discrete phytoplankton lineages in comparison to samples from the less stratified springtime (#4
and 5) (Figure 1 and Table S1). Similarly, we observed a higher $V_{max}$ for a surface (#5) vs. 80 m sample (#6) (Figure S4). We hypothesized that these differences were related to $P_i$ availability. To investigate this result further, we compared uptake capabilities to ambient $P_i$ concentration at the time of sampling and found $V_{max}$, and especially affinity, were negatively correlated to $P_i$ (Figure 3, $p_{ANCOVA} < 0.05$). In further support, $V_{max}$ was lower in Prochlorococcus field populations from samples with higher $P_i$ from the North Pacific Ocean (10). Thus, populations growing in low $P_i$ environments showed significantly enhanced uptake capabilities.

We finally asked whether the presence of the observed physiologically (and possibly genetically) diverse populations would influence the link between nutrient availability and in situ uptake ($V_{Pi}$) across environments. To address this, we built an eco-evolutionary model in which, according to our observations, each lineage was influenced by a size-dependent scaling of $K_s$ and $V_{max}$ (resulting from adaptation) as well as a regulation of the concentration of transport proteins (and associated $V_{max}$) in response to ambient nutrient availability (i.e., acclimation) (Figure S5). This theoretical model predicted a relationship between ambient $P_i$ and $V_{Pi}$ that was very different from a traditional Michaelis-Menten type curve. Moreover, in contrast to a classic hyperbolic model, the emergent uptake curves accurately replicated our measurements of $V_{Pi}$ of four phytoplankton groups in samples collected across the whole Western North Atlantic region (Figure 4 and S2). However, our model required specific allometries for each phytoplankton group, which suggested that size alone could not describe differences in $P_i$ uptake between the lineages. Overall, these biodiversity effects also manifested themselves on the whole community $V_{Pi}$, where a linear fit replicated our observations.
better than a hyperbolic one (Figure S6). These results highlight how the interaction of size and lineage diversity with physiological plasticity of phytoplankton had a direct impact on in situ nutrient uptake patterns in this region.

Discussion

Theoretical studies and culture data have both suggested that differences in microbial biodiversity can have an impact on nutrient uptake capabilities (5, 9, 16). Our results support culture studies showing an allometric scaling of $K_s$ and $V_{max}$ (9) including the lowest values in the small Prochlorococcus and Synechococcus. A recent compilation of available marine culture data does not report data for organisms as small as Prochlorococcus and Synechococcus (9), but based on their size, the values for Prochlorococcus and Synechococcus cells fall well below the predicted allometric line. Indeed, the best possible match between our eco-evolutionary model output and observations could only be achieved by using lineage-specific allometries for the traits involved. As a result, uptake capabilities of a given lineage cannot solely be described by specific cell-size-dependent $K_s$ and $V_{max}$ values.

Biodiversity may also influence nutrient uptake by a taxonomic group via differences in genomic content (14, 17, 18) and associated physiological capabilities of the cells (19, 20). We see strong support for a variation in uptake capabilities within populations that is likely linked to acclimation through the regulation of nutrient transporters in response to changes in the nutrient environment. To illustrate this further, we examined the ratio of $V_{max}$ to $Q_p$, which can be interpreted as a proxy for the maximum growth rate (if we assume no leakage). However, we find values up to 27 d$^{-1}$ for Prochlorococcus and 7.7 d$^{-1}$ for Synechococcus, which are much higher than
previously described maximum growth rates for these groups (21, 22). This suggests that
at least *Prochlorococcus* and *Synechococcus* have highly induced active *P*<sub>i</sub> transporters at
very low substrate levels. A maintenance of high *V*<sub>max</sub> under strongly nutrient-limited
conditions has been observed in marine diatom cultures (20), but this is the first
demonstration of such *V*<sub>max</sub> response mechanism in natural phytoplankton populations
from the open ocean.

Identifying the linkages between marine biodiversity, environmental variation,
and nutrient uptake rates has significant biogeochemical implications. A *Prochlorococcus*
*K*<sub>s</sub> of 0.8 nM reported here is the lowest value detected for any group yet, and we
generally see high uptake rates for the whole community at low *P*<sub>i</sub>. Thus, our data suggest
that abundant phytoplankton groups can readily satisfy their P requirements, whether
directly from *P*<sub>i</sub> or from lyzed dissolved organic phosphorus, at less than 10 nM and thus
lower the threshold for when *P*<sub>i</sub> becomes limiting for growth. Our nutrient kinetics values
are consistent with past studies of *Trichodesmium* (11) as well as the whole community
(23) but add important quantitative information for specific unicellular lineages. Another
biogeochemical consequence of our work concerns the parameterization of nutrient
uptake in ocean models and associated skills in predicting future ocean chemical
conditions, competition for limiting nutrients, and estimates of primary production.
Several ocean biochemical models use *K*<sub>s</sub> for *P*<sub>i</sub> above 0.5 µM (24, 25), which results in
gross model over-predictions of dissolved *P*<sub>i</sub> concentrations in many oligotrophic regions.
As a corollary, this results in under-estimation of primary production, which is important
given the interest in predicting future rates of biological productivity in ocean gyres.
Furthermore, given the hypothesis that open ocean gyres will continue to expand into the
future due to increasing stratification (26), these data suggest that *a priori* assumptions about reductions in ocean productivity need to be reevaluated.

We find strong support for a hyperbolic link between $P_i$ and uptake for individual populations but the summed outcomes for $P_i$ uptake by specific microbial lineages across environment gradients in $P_i$ have a unique functional form. These results likely apply to a large fraction (~30%) of the global ocean surface area where $P_i$ is similarly low. Thus, static $K_s$ and $V_{max}$ parameters for individual populations do not adequately describe the uptake rates across the region. Therefore, we recommend including these quantitative responses (e.g., much lower $K_s$ values, feedback from plastic or adaptive responses, etc.) in ocean models if the aim is to accurately identify ecosystem processes in oligotrophic regions. This may be particularly pertinent if the goal is to predict future ocean biogeochemistry where increased warming may lead to decreases in $P_i$ concentration (26) but not necessarily in phytoplankton abundances (27).

Methods

**Sample collection.** The data presented in this study were collected on 7 cruises throughout the Western North Atlantic Ocean (cruise X0606, X0705, X0804, BVAL 39, BVAL 46, AE1206, and AE1319). All samples for $P_i$ uptake rates and kinetics experiments were collected in acid-cleaned Niskin bottles attached to a CTD rosette and kept in subdued lighting until experiments were initiated (< 1 h). Samples for whole community ambient uptake rates were collected from ~4 depths in the upper 60 m, while samples for taxon-specific ambient uptake rates were collected from 5 m, 40 m, and the deep chlorophyll maximum (DCM; ranging from 80 to 120 m) (28). *Trichodesmium*
colonies were collected from the near surface (roughly within the top 20 m) by vertically hauling a handheld 100 µm net. Single colonies were transferred a second time into fresh 0.2 µm-filtered water to reduce contamination of closely associated organisms, and subsequently separated by morphotype (either ‘puff’ with radial trichomes or ‘raft’ with parallel trichomes); only data for ‘rafts’ are presented here.

**33Phosphate incubations.** The approach for ambient whole community and population-specific uptake rate measurements were previously published (28). Briefly, duplicate aliquots of 10 ml seawater were amended with 0.15 µCi (~80 pmol L⁻¹) additions of H₃²³PO₄ (3000 Ci mol⁻¹; PerkinElmer, USA), and incubated for 30 - 60 min in subdued lighting (~100 µmol photons m⁻² s⁻¹) at ~23°C. This temperature was within ~3°C of the coolest/warmest in situ temperature from which the samples were collected. The duration of each incubation varied depending on turnover time of the added isotope, such that efforts were made to keep uptake to <25% of the tracer added. Duplicate killed control incubations were conducted for each station. Killed controls were amended with paraformaldehyde (0.5% final concentration) for 30 min prior to the addition of isotopic tracer and incubation. Whole community incubations were terminated by filtration onto 0.2 µm polycarbonate filters that were subsequently placed in glass scintillation vials. Population-specific ambient uptake incubations were terminated by the addition of paraformaldehyde (0.5% final concentration), and stored at 4°C until sorting (<12 h) as described in the next section.

Whole community and population-specific kinetics experiments were conducted by adding 0.15 µCi (~80 pM) of H₃²³PO₄ to ~10 replicate 10 ml seawater samples that were further amended by increasing additions of ‘cold’ KH₂PO₄ up to 100 nM. Samples
were incubated as above, but the incubations were terminated by the addition of KH$_2$PO$_4$ to a final concentration of 100 µM (29). Whole community samples were filtered onto 0.2 µm polycarbonate filters, and rinsed with an oxalate wash (30). Surface bound phosphate in population-specific samples was accounted for by subtracting $^{33}$P counts for sorted populations to which 100 µM phosphate had been added prior to addition of the isotopic tracer. It is assumed that addition of such a high level of phosphate would result in negligible uptake of radioactive phosphate and thus any signal was attributed to surface absorption; this correction was always <2-3%. Population-specific kinetics experiments for samples collected in the deep chlorophyll maximum were first gravity concentrated and resuspended in phosphate-free Sargasso Sea surface water prior to incubation as described. Population-specific samples were stored at 4°C in the dark until sorting (<3 h) as described in the next section. Kinetics experiments for *Trichodesmium* spp. were conducted in the same manner as above for whole community samples but with picked and rinsed colonies and increasing additions of ‘cold’ KH$_2$PO$_4$ up to 1000 nM.

**Flow cytometry analysis and cell sorting.** Samples were sorted on an InFlux cell sorter (BD, Seattle, WA) at an average flow rate of ~40 µL min$^{-1}$. Samples were sorted for *Prochlorococcus*, *Synechococcus*, and an operationally defined eukaryotic algae size fraction (eukaryotes >2 µm). A 100 mW blue (488 nm) excitation laser was used. After exclusion of laser noise gated on pulse width and forward scatter, autotrophic cells were discriminated by chlorophyll fluorescence (>650 nm), PE (585/30 nm), and granularity (side scatter). Sheath fluid was made fresh daily from distilled deionized water (Millipore, Billerica, MA) and molecular grade NaCl (Mallinckrodt Baker, Phillipsburg, NJ), pre-filtered through a 0.2 µm capsule filter (Pall, East Hills, NY), and a STERIVEX
sterile 0.22 μm inline filter (Millipore, Billerica, MA). Mean coincident abort rates were < 1% and mean recovery from secondary sorts (n = 25) was 97.5 ± 1.1% (data not shown). Spigot™ (BD Seattle, WA) and FCS Express V3™ (DeNovo Software, Seattle, WA) were used for data acquisition and post acquisition analysis, respectively. Sorted cells from each sample were gently filtered onto 0.2 μm Nucleopore polycarbonate filters, rinsed with copious amounts of 0.2 μm filtered seawater, an oxalate wash(30), and placed in a 7 ml scintillation vial for liquid scintillation counting.

**Data analysis.** Parameters for the hyperbolic nutrient uptake curves from all samples were estimated in SigmaPlot (Systat Software, San Jose, CA, Version 10) and the ANCOVA analysis was done with R. All other statistical analyses were done in Matlab (Mathworks, Natick, MA).

**Biodiversity uptake model with adaptation and acclimation.** In order to develop a theoretical model capable of predicting phosphate uptake and kinetic parameters \( V_{\text{max}} \) and \( K_s \) observed in the field across diverse populations, we used standard expressions for growth (Droop) and uptake (Michaelis-Menten). To these expressions, we added the possibility for phytoplankton to regulate kinetic parameters in reaction to environmental changes. We explicitly did not include the option of shifting expression between high and low affinity transporters as at least *Prochlorococcus* and *Synechococcus* only contain one type of \( P_i \) transporter system (14, 18). We then considered this ecological description within an evolutionary framework, which allowed us to calculate the most competitive within-taxon strain for each environmental setup. For each taxon, the compilation of winning strains in different locations provided the data we then contrasted with our observations (See supplementary information for further details). We did not include
*Trichodesmium* in this comparison, as we did not measure ambient uptake rates for this lineage.

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**Author contributions**

MWL and ACM designed the research, MWL made the analytical measurements, ACM conducted the data analysis, JAB, ACM, and SAL developed the eco-evolutionary model and ACM wrote the paper with input from all authors.

**References**


Legends

Figure 1. *In situ* phosphate uptake curves for the whole community and most abundant phytoplankton groups. The lines represent the best fit of a hyperbolic curve. Each row represents the whole community or specific population and each column represents a discrete station as listed in Table S1 and noted at the top of the panels. In panels B, F, I, and M, data from both October and March are shown as denoted in the legend in panel F. Panels C, G, J, and N show samples from 39N taken approximately one year apart. Triangle symbols and associated error bars represent the mean +/- stdev of duplicate experiments at this station.

Figure 2. Relationship between $K_s$, $V_{max}$, and cell mass across phytoplankton groups. Due to difficulties of accurately estimating cell volume, we used cellular carbon biomass as a proxy for cell size (31).

Figure 3. Relationships between the ambient $P_i$ concentration and uptake capabilities (i.e., $K_s$, $V_{max}$, and $\alpha$) for the whole community and *Prochlorococcus*, *Synechococcus*, and eukaryotic phytoplankton populations.

Figure 4. Relationship between *in situ* phosphate uptake rates ($V_{pi}$, black dots) and the ambient $P_i$ concentration. The dashed lines are predictions from our eco-evolutionary model and the solid lines are traditional Michaelis-Menten functions applied to each
phytoplankton group. The Michaelis-Menten curves are based on the mean values for $K_s$ and $V_{max}$ (Table S1).
Supplementary Information:

**P uptake Rate Calculations.** Whole community and taxon-specific assimilation rates were calculated using the same equation as follows

\[ V_{pi} = \left( \frac{\beta_{sample}}{n} \right) \left( \frac{\Delta T - \ln 2}{\lambda T_o} \right) \left( \frac{1}{P} \right) \]

where \( V_{pi} \) is the cell-specific utilization rate (amol \(^{33}\)P cell\(^{-1}\) hr\(^{-1}\)); \( \beta_{sample} \) and \( \beta_{T_o} \) are the \( \beta \)-emission activities (counts min\(^{-1}\)) for the sorted sample and the total activity added, respectively; \( n \) is the number of cells sorted; \( \Delta T \) is the elapsed time from \(^{33}\)P isotopic tracer addition to counting; \( T_o \) is the incubation duration; \( \lambda \) is the decay constant of \(^{33}\)P (half life = 25.4 d); \( P \) is the ambient concentration of the P source (nmol L\(^{-1}\)). The method detection limit following this protocol is ~0.5 nM with a precision of ± 5% at 5 nM.

**Phosphate cell quotas.** Samples for taxon-specific cellular P quota \((Q_p)\) were collected as previously described with all samples except Sta. 2 representing newly available data (1). Briefly, whole water samples were collected and gently concentrated on a 0.4 \( \mu \)m polycarbonate filter. Cells were gently resuspended, and either sorted by flow cytometry immediately or fixed with paraformaldehyde (0.5% v/v final concentration) and stored at -80°C until they could be sorted. Once sorted, samples were filtered on 13 mm silver filters (Prochlorococcus and Synechococcus) or GF/F filters (eukaryotes) and analyzed as particulate phosphorus samples using the ash-hydrolysis method (2, 3). All samples were corrected for filter blanks. Paired comparison of unfixed and fixed cells from the same station/depth found that fixation had no effect on estimates of cellular P content (data not
shown). No efforts were made to separate particulate inorganic from organic phosphorus so data are simply referred to as particulate phosphorus. For analysis, sample filters were placed in acid-cleaned (10% HCl) and pre-combusted glass scintillation vials along with 2 ml of 17 mM MgSO$_4$, dried down at 80-90°C and then combusted at 500°C for 2 h. After cooling to room temperature, 5 ml of 0.2 M HCl was added to each vial and hydrolyzed at 80°C for 30 minutes. After cooling to room temperature, SRP mixed reagent was added (4), sample was clarified by centrifugation, and absorbance read at 885 nm. Samples were calculated against a potassium monobasic phosphate standard. Oxidation efficiency and standard recovery was tested with each sample run using an ATP standard solution and a certified phosphate standard (Ocean Scientific International Ltd. Phosphate Nutrient Standard Solution). In our laboratory, the precision of this method is ~9% at 2.5 nmol of P in the sample, and ~1% at 15 nmol of P in the sample. The method detection limit, defined herein as three times the standard deviation of the lowest standard (2.5 nM) is ~0.1 nmol L$^{-1}$.

**Biodiversity uptake model with adaptation and acclimation**

**Model design:** The Droop model links cell growth rates to the internal content of the most limiting nutrient (5). If $Q$ represents the cell quota for such limiting nutrient (mol/cell), the growth rate $\mu$ (d$^{-1}$) follows the equation:

$$\mu(Q) = \mu_{\text{max}} \left( \frac{1 - \frac{Q_{\text{min}}}{Q}}{1 - \frac{Q_{\text{min}}}{Q_{\text{max}}}} \right)$$

where $Q_{\text{max}}$ represents the maximum value for the quota (related to the maximum storage capacity of the cell), and $Q_{\text{min}}$ is the minimum nutrient content required for growth. Note
that we chose a normalized version of the model (6), with which we ensured that the parameter \( \mu_{\text{max}} \) expresses the (measurable) maximum value of the growth rate when \( Q \) reaches its maximum possible value. The cell quota, in turn, changes with time following a simple balance equation:

\[
\frac{dQ}{dt} = V_{pi} - \mu(Q)Q
\]

where \( V_{pi} \) represents uptake rate (in amol/cell/h). On the other hand, \( P_i \) uptake rate satisfies a Michaelis-Menten functional dependence:

\[
V_{pi} = \frac{V_{\text{max}}P_i}{P_i + K_{\text{eff}}}
\]

through which \( V_{pi} \) depends on phosphate concentration, \( P_i \), following a hyperbolic function modulated by the kinetic parameters, \( V_{\text{max}} \) and \( K_{\text{eff}} \). The latter represents a diffusion-limitation correction that takes into account that the cell may develop a boundary layer due to the very low phosphate concentrations typical for the Western North Atlantic Ocean (7):

\[
K_{\text{eff}} = K_S + \frac{V_{\text{max}}}{4\pi D_{pi}r_{\text{cell}}}
\]

where \( r_{\text{cell}} \) is cell radius (in \( \text{dm} \)) and \( D_{pi} \) (in \( \text{dm}^2/s \)) is the diffusivity constant for the focal resource (7). The dynamics of the population are represented by the simple equation:

\[
\frac{dB}{dt} = (\mu(Q) - m)B
\]

where \( B \) is the number of cells in the population, and \( m \) encodes any source of mortality for phytoplankton (in \( d^{-1} \)).
Next, we consider phytoplankton acclimation abilities by using an equation that links the change in time of the maximum uptake rate, $V_{max}$, to the nutritional state of the cell (i.e., its quota) (7). Through this equation, the dynamics of $V_{max}$ (i.e. changes in the number of uptake proteins) depend on the internal content of the nutrient and, by extension, on the nutritional history of the cell. Thus, cells regulate the number of proteins in response to quota changes: when $Q$ is low, the cell up-regulates the synthesis of such proteins to increase the absorbing area of the cell, thereby increasing the uptake rate; on the other hand, quotas close to the maximum storage limit allow the cell to down-regulate protein production and save associated synthesis and maintenance energy (7). All this phenomenology can be modeled, at the population level, using the equation (7, 8):

$$\frac{dV_{max}}{dt} = k_2 \left[ \nu H(1 - A_{rel}(t)) F\left(\frac{Q_{max} - Q(t)}{Q_{max} - Q_{min}}\right) \right] - m V_{max}$$

where $V_{maxB} = B \cdot V_{max}$. $H$ is a Heaviside function that introduces a limit to the maximum number of uptake proteins for the cell, set by the cell’s surface area, with $A_{rel}$ the ratio of absorbing to total cell area (which, therefore, depends on the number of proteins). $k_2$ is the assimilation rate (inverse of the handling or assimilation time):

$$k_2 = 4\pi D_p r_{site}$$

$r_{site}$ is the absorbing radius of an uptake protein, and $\nu$ is the maximum number of sites produced per unit time. $F(x)\in[0, 1]$, is a sigmoid function, defined here as:

$$F\left(\frac{Q_{max} - Q}{Q_{max} - Q_{min}}\right) = \frac{2}{1 + e^{-k_y \left(\frac{Q_{max} - Q}{Q_{max} - Q_{min}}\right)}} - 1$$
k_F is a shape factor. The choice of F is justified because protein synthesis is the result of gene expression, typically represented by sigmoid functions (e.g., Hill function); however, other functional forms with similar Q-dependence do not alter the qualitative behavior of the ecological model (7).

Finally, we set chemostat conditions in which we altered the dilution rate, \( w \) (d^{-1}), in order to represent different locations. Thus, the dynamics for the resource concentration, \( R \) (in mmol/l) are given by:

\[
\frac{dP_i}{dt} = w(P_{10} - P_i) - V B
\]

where \( P_{10} \) is a (fixed) input of nutrient that can be tuned in chemostats.

**Size-based parameterization.** We considered size as the master trait representing phytoplankton strains. Thus, we chose a size-based parameterization; if \( s \) is cell size (or volume, in \( \mu m^3 \)), we can express the allometric relationship for \( Q_{min}, Q_{max}, \) or \( v \) generically as \( X = a_X s^{b_X} \) and used the across-taxon allometries proposed for phosphorus (9, 10). In addition, we devised an allometry for the parameter \( v \) that ensured that the qualitative behavior expected for \( V_{max} \) against \( P_i \), relative to that of \( V_{P_i} \) [e.g. both should converge for high \( P_i \) (8, 11)], was observed regardless of cell size.

These allometries sufficed to find a qualitative agreement with our observations. In order to also reach a quantitative agreement, we needed to make use of the wide ranges provided in (9) for \( a_K, b_K, a_P, \) and \( b_P \). This approach was justified by the fact that each taxon should be really represented by its own specific allometry for each trait. In this way, we assumed that eukaryotes shared an allometry for \( K_s \) (specifically, \( a_K=2.00 \text{ nM, } b_K=0.56 \)), different from that of Cyanobacteria (\( a_K=3.98 \text{ nM, } b_K=0.3 \)). Note that this
choice stretched the value of the coefficients $a_K$ considerably beyond the limits obtained previously (9). Still, our selected coefficients and exponent ensured that smaller cells (Cyanobacteria) showed smaller $K_s$ than bigger cells (eukaryotes). Similarly, we used $b_\mu = -0.2$ for eukaryotes and $b_\mu = -0.3$ for prokaryotes. Finally, we assumed that lineages were represented by different $a_\mu$. Thus, we tuned the latter parameter to identify the emergent trait values for each lineage (Table S2).

Model evaluation. To replicate the observed $P_i$ uptake kinetics curves (Figure 1), we focused on each taxon separately. Our assumption was that the biggest contribution to the measured taxon-specific curves arose from the dominant within-taxon strain in each location. Thus, we used the model described above to calculate the most competitive strain for a fixed value of $a_\mu$, varying the dilution rate (that is, resource concentration) to replicate different locations. Further, we used three different methods to calculate the most competitive strain for each of those locations.

For the first method, we initialized our system by randomly assigning sizes ranging from $10^{-3} \, \mu m^3$ to $10^8 \, \mu m^3$ to 300-500 ecotypes, aiming at representing any possible within-taxon variability. Then, we let them compete for the single available resource. According to expectations, only one winner was observed per location. We used several replicates to obtain the characteristic winner of each location, due to the stochastic nature of the initial condition. The second method was devised to obtain the pairwise invasibility plot (PIP) for each location (Figure S7A). PIPs allow one to identify whether the strain is a local or a global winner in the trait space (12). Thus, we confronted a resident strain of size $s$ with an immigrant strain of size $s'$, and let them
compete until one single winner was observed. The process was then repeated sweeping all possible combinations of $s$ and $s'$ within specific ranges. Thus, we confirmed the results of the previous analyses, obtaining in all cases (global) winner’s sizes in agreement with the previous simulations (Figure S7A). The third method considered evolution explicitly by using an eco-evolutionary framework (13). Starting from a random strain, new mutant strains are introduced according to the dynamics of the population and a fixed mutation rate. Competition for resources makes strains disappear; mutation and extinction allow the population to explore the trait space in a continuous way until the most competitive trait value is present. Due to its competitive advantage, this strain grows and resists invasion by any other strain. Thus, the average trait value for the population remains stable around the most competitive strain's trait value – i.e., the Evolutionarily Stable Strategy (ESS). Using this framework, the resulting ESS matched the sizes obtained with the other two methods above (Figure S7B). As an important additional result, the emergent $V_{\text{max}}$ dependence on the size of the winning ecotypes shared, for all four lineages explored through simulations, a similar exponent $b_{V_{\text{max}}} \approx 1$.

Finally, to replicate the variation in $V_{\text{max}}$ observed under conditions of different phosphate availability (Figure 3), we used the same model and allometries described above but setting a fixed characteristic size representing each lineage. More specifically, we used $s=0.1 \, \mu m^3$ for Prochlorococcus and $s=20 \, \mu m^3$ for Eukaryotes. Then, we quantified the kinetic parameters $V_{\text{max}}$, $K_s$, and their ratio, $\alpha$, resulting from the different stationary states (i.e. different nutrient conditions) obtained with chemostat environments varying the dilution rate, $w$ (Figure S5).
Model with no regulation of transport proteins (i.e. only adaptation). In order to discern to what extent the combination of adaptation (evolutionary changes in cell size and, therefore, in size-related traits) and acclimation (regulation of transporters) was responsible for the observed patterns, we used a more simplistic approach in which we suppressed acclimation in the model above by keeping $V_{\text{max}}$ constant. This approach was, thus, not able to replicate the kinetic curves.

Assuming that $dV_{\text{max}}/dt = 0$, we could use an allometry to initialize a constant $V_{\text{max}}$. We assumed $a_{v_{\text{max}}}=33.08$ amol/cell/h, and $b_{v_{\text{max}}} = 1$ (9). This simplification allowed us to obtain an explicit expression for the population growth rate and the ESS for size. By definition, the per-capita growth rate is given by:

$$\lambda = \frac{1}{B} \frac{dB}{dt} = \mu - m$$

By solving for stationary state, the quota dynamic equation, we obtain:

$$Q^* = \frac{V_{\text{max}} \left(Q_{\text{max}} - Q_{\text{min}}\right) P_i^* + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}} \left(P_i^* + K_S\right)}{\mu_{\text{max}} Q_{\text{max}} \left(P_i^* + K_S\right)}$$

And, replacing the expression above into the population growth rate:

$$\lambda = \frac{\mu_{\text{max}} V_{\text{max}} Q_{\text{max}}}{V_{\text{max}} \left(Q_{\text{max}} - Q_{\text{min}}\right) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}} + \frac{P_i^*}{P_i^* + K_S} - m$$

$$= \frac{\mu_{\text{max}} \mu}{P_i^* + \kappa} - m$$

Thus, the population growth rate can be expressed as a Monod-like growth rate (14), with parameters given by:

$$\mu_{\text{max}} \mu = \frac{\mu_{\text{max}} V_{\text{max}} Q_{\text{max}}}{V_{\text{max}} \left(Q_{\text{max}} - Q_{\text{min}}\right) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}$$
\[ \kappa = \frac{\mu_{\text{max}} Q_{\text{max}} Q_{\text{min}} K_S}{V_{\text{max}} (Q_{\text{max}} - Q_{\text{min}}) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}} \]

The population growth rate can subsequently be used as invasion fitness. Therefore, the ESS is the point where the lines for \( \lambda = 0 \) cross in a PIP (i.e. considering a resident and an invading phenotype, see above). The ESS is also a point where the resident's fitness reached a maximum (12) and fulfills:

\[ \frac{\partial \lambda}{\partial s} \bigg|_{\mu = \mu', r'_{\text{res}}} = 0 \]

\[ \frac{\partial^2 \lambda}{\partial s^2} \bigg|_{\mu = \mu', r'_{\text{res}}} < 0 \]

As a consequence, we can use the expression above to numerically estimate the size of the most competitive sizes within a taxon (i.e. fixed \( a_{\mu} \)), for a variety of environments (i.e., for several \( w \)). Note that this simple model could not replicate quantitatively the observed patterns even although the allometry used for \( V_{\text{max}} \) is similar to that emerging from the complete model. Parameterizing this simpler model to replicate observations quantitatively involved fine-tuning most of the available allometric coefficients. In contrast, observed values emerged from the complete model by acknowledging essential functional differences between eukaryotes and Cyanobacteria (affecting here the allometry for \( K_s \)), and using \( a_{\mu} \) as a taxon-specific parameter. In addition, the complete model allowed us to replicate the observed behavior for the kinetic parameters, also within realistic ranges. This discrepancy highlights the important role of acclimation in creating those patterns.
In summary, although this simple model and calculations showed that adaptation could be responsible for the qualitative shape of the uptake curves, only a combination of adaptation and acclimation was able to fully explain all the observed phenomenology.

Other model options. We also tried more phenomenological implementations of acclimation, such as replacing $V_{\text{max}}$ by (15, 16):

$$V_{\text{max}} = V_{\text{max}}^{hi} \left( \frac{Q_{\text{max}}}{{Q_{\text{max}}} - {Q_{\text{min}}}} \right)$$

or a generalization of the above (8, 11):

$$V_{\text{max}} = V_{\text{max}}^{hi} - \left( \frac{Q_{\text{max}}}{{Q_{\text{max}}} - {Q_{\text{min}}}} \right) \left( V_{\text{max}}^{hi} - V_{\text{max}}^{lo} \right)$$

where the superscript $hi$ and $lo$ refer to the value of the maximum uptake rate for low and high $P_i$, respectively. The two expressions above showed an ultimate dependence of $V_{\text{max}}$ on resource concentration qualitatively similar to that emerging from the mechanistic model used in the main text and observed in the data (i.e., $V_{\text{max}}$ decreasing with $P_i$).

Unfortunately, although these expressions allowed for analytical solutions in the spirit of that presented in the previous section, none of them were able to replicate both qualitatively and quantitatively the behavior for uptake and kinetic parameters described in the main text. Thus, only a mechanistic implementation of such acclimation could reproduce the mentioned observations.

References


**Figure legends**

Figure S1. Phosphate uptake kinetics for the N$_2$-fixer *Trichodesmium* across the Western North Atlantic Ocean.

Figure S2. Map of samples used in this study, collected over multiple cruises led by Lomas in the western subtropical North Atlantic Ocean. This includes samples for P$_i$ uptake kinetics, *in situ* uptake rates for the whole community as well as specific population, and other factors (particulate phosphate, dissolved inorganic phosphate, and P cell quota for specific populations). The taxon-specific P$_i$ uptake data from two of the six cruises was previously published in Casey et al. 2009.

Figure S3. Phosphate uptake half-saturation concentrations ($K_s$) for the whole community and specific phytoplankton groups. The line in the box represents the median, the box the 25 and 75 percentile, and the whiskers cover approximately 99.3% of the data. $K_s$ values are significantly different between groups (1-way ANOVA, p < 0.05).

Figure S4. Comparison of the P$_i$ uptake kinetics for the whole community as well as specific phytoplankton populations between surface and DCM.
Figure S5. Eco-evolutionary model prediction for $V_{max}$. The predictions are for *Prochlorococcus* and eukaryotic phytoplankton as a function of ambient $P_i$ concentrations.

Figure S6. *In situ* $P_i$ uptake rates for the whole community. The samples are taken across the Western North Atlantic Ocean region ($n = 250$) at depths less than 50 m. The solid line represents a simple linear regression with an intercept $= 0$.

Figure S7. Biodiversity model evaluations. A. Pairwise invasibility plot (PIP) obtained with the evolutionary model that includes acclimation, with a *Synechococcus* parameterization and $w=0.5$; yellow regions indicate values of resident and invader sizes for which the resident is outcompeted, whereas the resident resists invasion in the black regions. B. Evolutionarily stable strategy (ESS) obtained with the eco-evolutionary framework with a *Synechococcus* parameterization and $w=0.5$; for all the different replicates of the numerical simulation, the reached ESS coincides with that obtained with the pairwise invasibility plot.
Table S1: Whole community and population-specific phosphate uptake kinetics and cell quota values from samples in the Western North Atlantic Ocean.

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<td>0.3</td>
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<td>BV46 8</td>
<td>25.7°N &lt;25m 10/10/11 0.6</td>
<td>Trichodesmium</td>
<td>55</td>
<td>246</td>
<td>0.8</td>
<td>0.22</td>
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<td>0.92</td>
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<td>1.6</td>
<td>0.3</td>
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</table>

Whole com. | 1.5±0.6 | 12±10 | 0.3±0.2 |
Prochlorococcus | 8.4±6.4 | 3.8±3.8 | 2.4±1.7 |
Synechococcus | 47±34 | 17±13 | 3.9±3.4 |
Eukaryotes | 115±137 | 79±67 | 2.0±1.9 |
Trichodesmium | 33±16 | 342±247 | 0.1±0.1 |

\(^1\)The unit for \(V_{\text{max}}\) is nM/h for the whole community, amol/cell/h for specific unicellular populations, and pmol/colony/h for \textit{Trichodesmium}.

\(^2\)The unit for \(Q_p\) is nM for the whole community, amol/cell for specific unicellular populations, and pmol/colony for \textit{Trichodesmium}.
Table S2. Taxon-specific and group-specific allometries used in the eco-evolutionary model and compilation of observed and model-emergent biovolume and maximum growth rates for the different taxa considered in this work.

<table>
<thead>
<tr>
<th>Model parameters</th>
<th>Observed and emergent behavior</th>
<th>Prochlorococcus</th>
<th>Synechococcus</th>
<th>Picoeukaryotes</th>
<th>Nanoeukaryotes</th>
</tr>
</thead>
<tbody>
<tr>
<td>$a_n$ (nM)</td>
<td>$b_n$ ($d^{-1}$)</td>
<td>$a_o$</td>
<td>$b_o$</td>
<td>$a_n$ (µm$^3$)</td>
<td>$b_m$ ($d^{-1}$)</td>
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<td>0.75</td>
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<td>0.70</td>
<td>0.07</td>
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<td>3.00</td>
<td>-0.3</td>
<td>0.50</td>
<td>1.00</td>
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<td>1.50</td>
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<td>0.6-1.2</td>
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<tr>
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<td>8.00</td>
<td>-0.2</td>
<td>180</td>
<td>0.6-1.8</td>
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