Impact of ocean phytoplankton diversity on phosphate uptake

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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 whether variations in ocean phytoplankton biodiversity lead to novel functional relationships between environmental variability and phosphate (Pi) uptake. We analyzed Pi uptake capabilities and cellular allocations among phytoplankton groups and the whole community throughout the extremely Pi-depleted western North Atlantic Ocean. Pi 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 Pi concentrations and uptake. Supported by novel theory, this work provides a robust empirical basis for describing and understanding assimilation of limiting nutrients in the ocean. Thus, it demonstrates that microbial biodiversity, beyond cell size, is important for understanding the global cycling of nutrients.

phosphate kinetics | cyanobacteria | adaptive dynamics | eco-evolutionary dynamics

The composition of microbial communities varies among different ocean regions and along environmental gradients (e.g., refs. 1 and 2). This variation includes phylogenetic, genomic, and functional diversity among and between heterotrophic 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 (Pi) 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 halfsaturation concentration ($K_s$), and the ratio of the two parameters named the nutrient affinity ($\alpha$). 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 laboratory 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 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 in situ Pi 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 Pi concentration observed anywhere in the ocean (15). We used a combination of shipboard cell sorting and isotopically labeled Pi to quantify nutrient uptake capabilities for the whole field community and four phytoplankton groups of different sizes—Prochlorococcus, Synechococcus, small eukaryotes (<20 μm), and the nitrogen fixer Trichodesmium. We asked the following: (i) do the in situ Pi 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.

Results

We first examined the uptake capabilities for the whole community and four phytoplankton groups—Prochlorococcus, Synechococcus, small eukaryotes (<20 μm), and the nitrogen fixer Trichodesmium (Fig. 1 and Fig. S1) across a range of environments (Fig. S2). When we experimentally added increasing concentrations of Pi, the

Significance

Nutrient uptake is a central property of ocean biogeochemistry, but our understanding of this process is based on laboratory cultures or bulk environmental studies. Thus, mathematical descriptions of nutrient uptake, at the heart of most biogeochemical models, 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 advanced 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.

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nutrient uptake response closely resembled a hyperbolic shape for all discrete populations as well as the whole community ($R^2 > 0.9$, Fig. 1 and Fig. S1). We then estimated the parameters $K_s$, $V_{max}$, and affinity ($\alpha$) (Table S1) and found significant (one-way ANOVA, $P < 0.05$) differences in $K_s$ among phytoplankton groups (Fig. 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 (one-way ANOVA, $P < 0.05$), and the order was analogous to $K_s$.

We then examined whether differences in uptake abilities were related to cell size and found a significant positive relationship for both $K_s$ and $V_{max}$ (Fig. 2A and B, $P_{\text{Spearman}} < 0.05$), 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 Pi 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 the Bermuda Atlantic Time-series 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 (Fig. 1 and Table S1). Similarly, we observed a higher $V_{max}$ for a surface (number 5) vs. 80 m sample (number 6) (Fig. S4). We hypothesized that these differences were related to Pi availability. To investigate this result further,

![Image](https://example.com/fig1.png)
we compared uptake capabilities to ambient P\textsubscript{i} concentration at the time of sampling and found V\textsubscript{max} and especially affinity, were negatively correlated to P\textsubscript{i} (Fig. 3, P\textsubscript{ANCOVA} < 0.05). In further support, V\textsubscript{max} was lower in Prochlorococcus field populations from samples with higher P\textsubscript{i} from the North Pacific Ocean (10). Thus, populations growing in low P\textsubscript{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\textsubscript{Pi}) across environments. To address this, we developed an eco-evolutionary model in which, according to our observations, each lineage was influenced by a size-dependent scaling of K\textsubscript{s} and V\textsubscript{max} (resulting from adaptation) as well as a regulation of the concentration of transport proteins (and associated V\textsubscript{max}) in response to ambient nutrient availability (i.e., acclimation) (Fig. S5). This theoretical model predicted a relationship between ambient P\textsubscript{i} and V\textsubscript{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\textsubscript{Pi} of four phytoplankton groups in samples collected across the whole Western North Atlantic region (Fig. 4 and Fig. S2). However, our model required specific allometries for each phytoplankton group, which suggested that size alone could not describe differences in P\textsubscript{i} uptake between the lineages. Overall, these biodiversity effects also manifested themselves on the whole-community V\textsubscript{Pi}, where a linear fit replicated our observations better than a hyperbolic one (Fig. 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.

Fig. 2. Relationship between K\textsubscript{s}, V\textsubscript{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).

Fig. 3. Relationships between the ambient P\textsubscript{i} concentration and uptake capabilities (i.e., K\textsubscript{s}, V\textsubscript{max}, and \(\alpha\)) for the whole community and Prochlorococcus, Synechococcus, and eukaryotic phytoplankton populations.
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 $V_{\text{max}}$ 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 $V_{\text{max}}$ to $Q_{\text{m}}$, 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 Pi transporters at very low substrate levels. A maintenance of high $V_{\text{max}}$ under strongly nutrient-limited conditions has been observed in marine diatom cultures (20), but this is the first demonstration (to our knowledge) of such $V_{\text{max}}$ 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 $K_s$ 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 Pi. Thus, our data suggest that abundant phytoplankton groups can readily satisfy their P requirements, whether directly from Pi or from hydrolysed dissolved organic phosphorus, at less than 10 nM, and thus lower the threshold for when Pi 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 $K_s$ for Pi above 0.5 μM (24, 25), which results in gross model overpredictions of dissolved Pi concentrations in many oligotrophic regions. As a corollary, this results in underestimation 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 Pi and uptake for individual populations, but the summed outcomes for Pi uptake by specific microbial lineages across environmental gradients in Pi have a unique functional form. These results likely apply to a large fraction (∼30%) of the global ocean surface area where Pi is similarly low. Thus, static $K_s$ and $V_{\text{max}}$ 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 Pi concentration (26) but not necessarily in phytoplankton abundances (27).
mium colonies were collected from the near surface (roughly within the deep chlorophyll maximum (ranging from 80 to 120 m) (28). Specific ambient uptake rates were collected from 5 m, 40 m, and the approximately four depths in the upper 60 m, whereas samples for taxon-parallel trichomes); only data for rafts are presented here.

Methods

Sample Collection. The data presented in this study were collected on seven cruises throughout the western North Atlantic Ocean (cruise X0606, X0705, X0804, BVAL 39, BVAL 46, AE1206, and AE1319). All samples for Pi uptake rates and kinetic experiments were collected in acid-cleaned Niskin bottles and kept in subdued lighting until experiments were initiated (~1 h). Samples for whole-community ambient uptake rates were collected from approximately four depths in the upper 60 m, whereas samples for taxon-specific ambient uptake rates were collected from 5 m, 40 m, and the deep chlorophyll maximum (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.

32PPhosphate Incubations. The approach for ambient whole community and population-specific uptake rate measurements were previously published (28). Briefly, duplicate aliquots of 10 mL of seawater were amended with 0.15 μCi (~80 pmol) additions of H32PO4 (3,000 Ci/mol; PerkinElmer), 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 due to the variable turnover time of the added disodium phosphate 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 before 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 H32PO4 to ~10 replicate 10-ml seawater samples that were further amended by increasing additions of “cold” KH2PO4 up to 100 mM. Samples were incubated as above, but the incubations were terminated by the addition of KH2PO4 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 32P counts for sorted populations to which 100 μM phosphate had been added before addition of the isotopic tracer. It is assumed that addition of such a high level of phosphate would result in negligible uptake of radioinactive 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 before 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 KH2PO4 up to 1,000 nM.

Flow Cytometry Analysis and Cell Sorting. Samples were sorted on an Influx cell sorter (BD) at an average flow rate of ~40 μL/min. Samples were sorted for Prochlorococcus, Synechococcus, and an operationally defined eukaryotic algae size fraction (eukaryocytes >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), phycocyanin (SBS/30 nm), and granularity (side scatter). Sheath fluid was made fresh daily from distilled deionized water (Millipore) and molecular-grade NaCl (Mallinckrodt Baker), prefiltered through a 0.2-μm capsule filter ( Pall), and a STERIVEX sterile 0.22-μm inline filter (Millipore). Mean coincident abort rates were <1% and mean recovery from secondary sorts (n = 25) was 97.5 ± 1.1% (data not shown). Spigot (BD) and FCS Express V3 (DeNovo Software) were used for data acquisition and postacquisition 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; version 10), and the ANCOVA analysis was done with R. All other statistical analyses were done in Matlab (MathWorks).

Biodiversity Uptake Model with Adaptation and Acclimation. To develop a theoretical model capable of predicting phosphate uptake and kinetic parameters Vmax and K of 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 Pi 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 SI Text for further details and Table S2 and Fig. S7 for model results). We did not include Trichodesmium in this comparison, as we did not measure ambient uptake rates for this lineage.

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Supporting Information

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SI Text

P Uptake Rate Calculations
Whole-community and taxon-specific assimilation rates were calculated using the same equation as follows:

\[ V_p = \left[ \frac{\beta_{\text{sample}}}{n} \right] \left[ \frac{\lambda}{B_{TA}} \right] \left[ \frac{1}{P} \right], \]

where \( V_p \) is the cell-specific utilization rate (in attomoles of \( ^{33}\text{P}_i \) per cell per hour); \( \beta_{\text{sample}} \) and \( B_{TA} \) are the beta emission activities (in counts per minute) for the sorted sample and the total activity added, respectively; \( n \) is the number of cells sorted; \( \lambda \) is the decay constant of \( ^{33}\text{P} \) (half life = 25.4 d); \( P \) is the ambient concentration of the P source (in nanomolar). The method detection limit following this protocol is \( \sim \)0.5 nM with a precision of \( \pm 5\% \) at 5 nM.

Phosphate Cell Quotas
Samples for taxon-specific cellular P quota (\( Q_p \)) were collected as previously described with all samples except station 2 representing newly available data (1). Briefly, whole water samples were collected and gently concentrated on a 0.4-μm polycarbonate filter. Cells were gently resuspended, and either sorted by flow cytometry immediately or fixed with paraformaldehyde [0.5% (vol/vol) final concentration] and stored at \( -80° \text{C} \) 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 phosphate samples using the ash-hydroslysis 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% (vol/vol) HCl] and precombusted 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 min. After cooling to room temperature, soluble reactive phosphate mixed reagent was added (4), sample was clarified by centrifugation, and absorbance was 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; Phosphate Nutrient Standard Solution).

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 (in moles per cell), the growth rate \( \mu \) (per day) follows the equation:

\[ \mu(Q) = \frac{\mu_{\text{max}} (1 - Q_{\text{min}}/Q)}{(1 - Q_{\text{min}}/Q_{\text{max}})}, \]

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:

\[ \frac{dQ}{dt} = V_p - \mu(Q)Q, \]

where \( V_p \) represents uptake rate (in attomoles per cell per hour). On the other hand, \( P \), uptake rate satisfies a Michaelis–Menten functional dependence as follows:

\[ V_p = \frac{V_{\text{max}}P}{P + K_{\text{eff}}}, \]

through which \( V_p \) depends on phosphate concentration, \( P \), 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):

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

where \( r_{\text{cell}} \) is cell radius (in decimeters) and \( D_p \) (in square decimeters per second) 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 (per day).

Next, we consider phytoplankton acclimation abilities by using an equation that links the change in time of the maximum uptake rate, \( V_{\text{max}} \), to the nutritional state of the cell (i.e., its quota) (7). Through this equation, the dynamics of \( V_{\text{max}} \) (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 following equation (7, 8):

\[ \frac{dV_{\text{max}}(t)}{dt} = k_1 \phi H(1 - A_{\text{cell}}(t))T \left( \frac{Q_{\text{max}} - Q(t)}{Q_{\text{max}} - Q_{\text{min}}} \right) - mV_{\text{max}}(t), \]
where \( V_{\text{max}} = B V_{\text{max}} \). \( H \) 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 \( A_{\text{cell}} \) 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): 

\[
k_2 = 4\pi D_p r_{\text{site}},
\]

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

\[
F \left( \frac{Q_{\text{max}} - Q}{Q_{\text{max}} - Q_{\text{min}}} \right) = \frac{2}{1 + e^{-k_F \left( \frac{Q_{\text{max}} - Q}{Q_{\text{max}} - Q_{\text{min}}} \right)}} - 1.
\]

\( k_F \) 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, \( w \) (per day), to represent different locations. Thus, the dynamics for the resource concentration, \( P_i \) (in nanomoles per liter) are given by the following:

\[
dp{i}{t} = w(P_{i0} - P_i) - V_B_i,
\]

where \( P_{i0} \) 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 cubic micrometers), we can express the allometric relationship for \( Q_{\text{min}}, Q_{\text{max}} \) or \( \nu \) generically as \( X = a_K s^{b_K} \) and used the across-taxon allometries proposed for phosphorus (9, 10). In addition, we devised an allometry for the parameter \( \nu \) that ensured that the qualitative behavior expected for \( V_{\text{max}} \) against \( P \), relative to that of \( V_B \) [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. To also reach a quantitative agreement, we needed to make use of the wide ranges provided in (9) for \( a_K, b_K, a_\nu, \) and \( b_\nu \). 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, \( a_K = 2.00 \) nM, \( b_K = 0.56 \)), different from that of Cyanobacteria (\( a_K = 3.98 \) 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 \( b_\nu = -0.2 \) for eukaryotes and \( b_\nu = -0.3 \) for prokaryotes.

Finally, we assumed that lineages were represented by different \( a_\nu \). Thus, we tuned the latter parameter to identify the emergent trait values for each lineage (Table S2).

**Model Evaluation.** To replicate the observed \( P \) uptake kinetics curves (Fig. 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 \( a_\nu \), varying the dilution rate (that is, resource concentration) to replicate different locations.

Furthermore, 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 \( 10^{-3} \) to \( 10^{-2} \) \( \mu \text{m} \) 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 (Fig. 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 (Fig. 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 extinction allow the population to explore the trait space in a continuous way until the most competitive trait value is present.

**Model with No Regulation of Transport Proteins (i.e., Only Adaptation).** 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 \( \nu \) 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\(^{-1}\)-h\(^{-1}\), 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 the following:

\[
\lambda = 1 + \frac{dB}{dt} = \mu - m.
\]

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

\[
Q' = \frac{V_{\text{max}} (Q_{\text{max}} - Q_{\text{min}})P_i + \mu_{v_{\text{max}}} Q_{\min} Q_{\text{max}} (P_i + K_S)}{\mu_{v_{\text{max}}} Q_{\text{max}} (P_i + K_S)}
\]

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

\[ \lambda = \frac{\mu_{\text{max}} V_{\text{max}} Q_{\text{max}}}{V_{\text{max}}(Q_{\text{max}} - Q_{\text{min}}) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}} + \frac{P^*}{P^*_i + \frac{\mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}{S}} - m \]

\[ = \mu_{\text{max}} \frac{V_{\text{max}} Q_{\text{max}}}{P^*_i + \frac{\mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}{S}} - m. \]

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

\[ \mu_{\text{max}} = \frac{\mu_{\text{max}} V_{\text{max}} Q_{\text{max}}}{V_{\text{max}}(Q_{\text{max}} - Q_{\text{min}}) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}, \]

\[ \kappa = \frac{\mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}{V_{\text{max}}(Q_{\text{max}} - Q_{\text{min}}) + \mu_{\text{max}} Q_{\text{max}} Q_{\text{min}}}. \]

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 the following:

\[ \frac{\partial \lambda}{\partial Q_{\text{res}}} = 0, \]

\[ \frac{\partial^2 \lambda}{\partial Q_{\text{res}}^2} < 0. \]

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 \( \alpha_s \), 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 \( \alpha_s \) 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 of the observed phenomenology.

Other Model Options. We also tried more phenomenological implementations of acclimation, such as replacing \( V_{\text{max}} \) by the following (15, 16):

\[ V_{\text{max}} = V_{\text{hi}}^{\text{max}} \left( \frac{Q_{\text{max}} - Q}{Q_{\text{max}} - Q_{\text{min}}} \right), \]

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

\[ V_{\text{max}} = V_{\text{hi}}^{\text{max}} - \left( \frac{Q - Q_{\text{min}}}{Q_{\text{max}} - Q_{\text{min}}} \right) \left( V_{\text{hi}}^{\text{max}} - V_{\text{lo}}^{\text{max}} \right), \]

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.

Fig. S1. Phosphate uptake kinetics for the N$_2$ fixer *Trichodesmium* across the western North Atlantic Ocean.

Fig. 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 were previously published in Casey et al. (1).

Fig. 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 represents the 25th and 75th percentiles, and the whiskers cover ~99.3% of the data. $K_s$ values are significantly different between groups (one-way ANOVA, $P < 0.05$).

Fig. S4. Comparison of the $P_i$ uptake kinetics for the whole community (A) as well as Prochlorococcus (B), Synechococcus (C), and eukaryotic phytoplankton (D) populations between surface and deep chlorophyll maximum (DCM).
Fig. S5. Eco-evolutionary model prediction for $V_{\text{max}}$. The predictions are for Prochlorococcus and eukaryotic phytoplankton as a function of ambient $P_i$ concentrations.

Fig. 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.

Fig. 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 $S_{\text{RES}}$ and invader $S_{\text{inv}}$ 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 of the different replicates of the numerical simulation, the reached ESS coincides with that obtained with the PIP.
Table S1. Whole-community and population-specific phosphate uptake kinetics and cell quota values from samples in the western North Atlantic Ocean

<table>
<thead>
<tr>
<th>Sample</th>
<th>Station</th>
<th>Latitude</th>
<th>Depth, m</th>
<th>Date</th>
<th>$P_s$, nM</th>
<th>$V_{max}^*$, nM/h, amol·cell$^{-1}$·h$^{-1}$, pmol·h$^{-1}$</th>
<th>$K_s$, nM</th>
<th>$R^2$</th>
<th>$\alpha$, $V_{max}/K_s$</th>
<th>$Q_p^\dagger$, nM, amol·cell$^{-1}$</th>
<th>$Q_p^\dagger$, pmol·colony$^{-1}$</th>
<th>$V_{max}/Q_p$ d$^{-1}$</th>
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<tbody>
<tr>
<td>1</td>
<td>BV46 20</td>
<td>39.7°N</td>
<td>5</td>
<td>10/2/11</td>
<td>0.5</td>
<td>2.1, 6.3, 0.92, 0.33, 8, 6.6</td>
<td>10.2</td>
<td>3</td>
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Average values

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<th>$V_{max}$, nM/h, pmol·h$^{-1}$</th>
<th>$K_s$, nM</th>
<th>$R^2$</th>
<th>$\alpha$, $V_{max}/K_s$</th>
<th>$Q_p$, nM, pmol·colony$^{-1}$</th>
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<td>0.3 ± 0.2</td>
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<tr>
<td>Synechococcus</td>
<td>47 ± 34</td>
<td>17 ± 13</td>
<td>3.9 ± 3.4</td>
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<tr>
<td>Eukaryotes</td>
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<td>79 ± 67</td>
<td>2.0 ± 1.9</td>
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</table>

*The unit for $V_{max}$ is nanomolar per hour for the whole community, attomoles per cell per hour for specific unicellular populations, and picomoles per colony per hour for *Trichodesmium*.

†The unit for $Q_p$ is nanomolar for the whole community, attomoles per cell for specific unicellular populations, and picomoles per colony for *Trichodesmium*. 
Table S2. Allometries used in the eco-evolutionary model and compilation of observed and model-emergent size and growth properties

<table>
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<th>Model parameters</th>
<th>Observed and emergent behavior</th>
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<td>Picoeukaryotes</td>
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<td>Nanoeukaryotes</td>
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