Scarcity of fixed carbon transfer in a model microbial phototroph-heterotroph interaction

Short Title: Scarcity of microbial carbon transfer

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ABSTRACT

While the green alga *Chlamydomonas reinhardtii* has long served as a reference organism, few studies have interrogated its role as a primary producer in microbial interactions. Here, we quantitatively investigated *C. reinhardtii's* capacity to support a heterotrophic microbe using the established coculture system with *Mesorhizobium japonicum*, a vitamin B_{12}-producing α-proteobacterium. Using stable isotope probing and nanoscale secondary ion mass spectrometry (nanoSIMS), we tracked the flow of photosynthetic fixed carbon and consequent bacterial biomass synthesis under continuous and diel light with single-cell resolution. We found that more ^{13}C fixed by the alga was taken up by bacterial cells under continuous light, invalidating the hypothesis that the alga's fermentative degradation of starch reserves during the night would boost *M. japonicum* heterotrophy. $^{15}NH_4$ assimilation rates and changes in cell size revealed that the carbon transferred was insufficient for balanced growth of *M. japonicum* cells, which instead underwent reductive division. However, despite this sign of starvation, *M. japonicum* still supported a B_{12}-dependent *C. reinhardtii* mutant. Finally, we showed that bacterial proliferation could be supported solely by the algal lysis that occurred in coculture, highlighting the role of necromass in carbon cycling. Collectively, these results reveal the scarcity of fixed carbon in this microbial trophic relationship, demonstrate B_{12} exchange even during bacterial starvation, and underscore the importance of quantitative approaches for assessing metabolic coupling in algal-bacterial interactions.

KEY WORDS

rhizobia; chlorophyte; photoautotroph; diurnal; cobalamin; co-cultivation; symbiosis; SIP

INTRODUCTION

Photosynthetic microbes are responsible for a large fraction of the primary productivity on our planet [1]. These organisms supply the microbial world with raw materials for life, thereby shaping communities and driving carbon cycling [2, 3]. Through exudation, lysis, and predation, photosynthetic microbes provide a variety of reduced carbon substrates with various diffusion rates and accessibility to heterotrophic bacteria. The primary consumers recycle carbon back to inorganic forms, closing the "microbial loop" that constitutes a major component of biogeochemical carbon cycling [2, 4, 5]. Heterotrophic bacteria can also influence algal productivity, for example, by changing the availability of critical micronutrients for algal growth and metabolism [6–8].

The green alga *Chlamydomonas reinhardtii* has served as a reference organism for discoveries in photosynthesis, cilia-based motility, and the eukaryotic cell cycle [9]. Extensive work on axenic (bacteria-free) cultures has provided detailed knowledge of the pathways and regulons for photosynthesis and primary metabolism. This chlorophyte has a flexible metabolic repertoire, with the capacity to grow by photoautotrophy alone or by acetate assimilation. Under diel cycles, *C. reinhardtii*'s metabolism is shaped by programmed waves of gene expression that accommodate rhythmic changes in light and oxygen availability that occur in natural environments [10, 11]. While extensive knowledge of its metabolism makes *C. reinhardtii* an attractive model organism to study microbial trophic interactions, relatively little is known about how *C. reinhardtii* contributes to its environment and influences its neighbors in the microbial world.

In its natural soil context, *C. reinhardtii* is surrounded by other microbes that exchange nutrients, compete for resources, and communicate with one another. *C. reinhardtii* can enrich for particular heterotrophic bacteria from bulk soil, demonstrating that the alga's growth can influence

the metabolisms and behaviors of various bacteria [12, 13]. Studies of *Chlamydomonas*-bacteria

interactions have primarily focused on impacts to the alga's behavior, in part due to technical

challenges in probing bacterial physiology in mixed cultures. Bacteria are known to supply

vitamins and fixed nitrogen, facilitate iron assimilation, and impart thermal tolerance to algal

cultures [6, 7, 14–20]. Coculture of *C. reinhardtii* with various heterotrophic bacteria (e.g.

Bradyrhizobium japonicum, *Pseudomonas* sp.) has been shown to stimulate algal H_2 production,

starch accumulation, and viability under sulfur deprivation by consuming O_2 and alleviating

accumulation of fermentation byproducts from the medium [21]. Bacterial secondary metabolites

can also influence *C. reinhardtii*'s cell cycle and aggregation [22, 23]. In addition, symbioses

between *C. reinhardtii* and vitamin B_{12}-producing rhizobia like *Mesorhizobium japonicum*

(previously referred to as *Mesorhizobium loti*), *Sinorhizobium meliloti*, and *Rhizobium*

leguminosarum have been used to study the evolution of vitamin dependency across the algal tree

of life [6, 15, 24–28]. *C. reinhardtii* does not require vitamin B_{12} for growth since it has retained

a functional cobalamin-independent isoform of methionine synthase, METE1. However, when

supplied vitamin B_{12}, transcription of *METE1* is repressed, and the vitamin is used as a cofactor

for the cobalamin-dependent isoform, METH1. When grown in the laboratory with a continuous

supply of the vitamin, *C. reinhardtii* acquired deleterious mutations in the repressed *METE1* gene

yielding B_{12}-requiring strains (*mete1*) in less than 500 generations of growth [25].

The interaction between the *C. reinhardtii mete1* mutant and *M. japonicum* has been

suggested to be facultatively mutualistic: the mutant alga receives the vitamin cofactor, and the

bacterium is believed to receive reduced carbon compounds that support heterotrophic growth.

The literature provides some clues of potential substrates that could be exchanged. *C. reinhardtii*

secretes small amounts of glycerol when grown in nitrogen deficient minimal medium in

continuous light, supporting some growth of cocultured *Methylobacterium* spp [29]. In dark and

anoxic conditions, *C. reinhardtii* produces formate, acetate, ethanol, and minor products lactate,

malate, and succinate, which could also be used by co-cultivated heterotrophs [30–35]. Rhizobia

are known to metabolize C4 dicarboxylic acids like succinate, malate, and fumarate, which are the

primary carbon sources in the root nodules of legumes where the bacterium persists in the bacteroid

form [36–39]. They can also utilize other organic acids present in plant root exudates [40], as well

as glycerol and sucrose. However, the mechanism and magnitude of the flux of carbon transfer

from *C. reinhardtii* to *M. japonicum* remains unclear.

Here, we quantified the transfer of fixed carbon from wild-type *C. reinhardtii* to *M.*

japonicum using stable isotope probing and nanoscale secondary ion mass spectrometry

(nanoSIMS). We found that a small but significant amount of photosynthetically fixed carbon was

taken up by the bacterial population, but that *M. japonicum* growth was severely limited, resulting

in reductive bacterial division. Thus, *C. reinhardtii* primary productivity yields a low carrying

capacity for this bacterium. Nonetheless, *M. japonicum* provided adequate B_{12} to enable growth of

the *C. reinhardtii mete1* strain even when the bacterium itself exhibited signs of starvation. These

results highlight that in natural contexts, bacterial populations may not proliferate to the cell

densities possible in the gourmand rich media often used in the laboratory, but they can still greatly

influence the metabolism and evolution of their neighbors in the microbial world.

MATERIALS AND METHODS

Strains and culture conditions

Three strains of *C. reinhardtii* were used in this study. The *mete1* strain generated through

experimental evolution on 1000 ng/l vitamin B_{12} [25] and its parental wild-type strain were

provided by Alison G. Smith (University of Cambridge, UK). For experiments testing the impact

of diel light, we used the cell-wall reduced strain CC-5390 [10]. This strain is amenable to

synchronization under diel cycles, providing a system with exceptional signal-to-noise for

resolving diel patterns. While CC-5390 exhibits a reduced cell wall, we found no significant

difference in the amount of nonpurgeable organic carbon (NPOC) released into the spent medium

between this strain and the other wild-type strain used (SI Fig. 1). *M. japonicum* strain

MAFF303099 was also provided by Alison G. Smith.

All experiments were performed in amended HSM minimal medium [41] with a modified

trace element solution [42], 2 mM $MgSO_4.7H_2O$, 10 µg/l biotin, and 10 µM $CoCl_2$ unless otherwise

specified. Cultures were grown in either 250 ml Erlenmeyer flasks containing 100 ml medium and

bubbled with filter-sterilized air (provided by an aquarium pump), 6-well plates with 3 ml medium,

or 250 ml beakers with 50 ml medium. Algal cultures and cocultures were incubated at 28°C,

agitated at 110–130 rpm, and illuminated with 200 µmol photons/m^2/s cool white light (Sylvania

Dulux L55WFT55DL/841) continuously or under diel 12-h-light/12-h-dark cycles.

C. reinhardtii cells were precultivated in photoautotrophic conditions for at least 3 passages

prior to experiments. The *met1* strain was precultivated with 200–250 ng/l vitamin B_{12}

(cyanocobalamin), collected by centrifugation at 1000 xg, then gently resuspended in fresh

medium without B_{12} before use as inoculum. For experiments comparing coculture in continuous

light versus diel light, *C. reinhardtii* CC-5390 cells were precultivated in flat-panel

photobioreactors (Photon System Instruments, Drásov, Czechia) as previously described under the

respective light regime to achieve adequate synchrony of the diel populations [10].

Bacterial cells were precultivated in 14 ml polystyrene round bottom tubes with 3 ml

amended HSM containing 0.2% sucrose, agitated at 200 rpm, and incubated at 28°C. When larger

volumes were required for inoculation, cells were precultivated instead in 250 ml Erlenmeyer

flasks containing 100 ml medium, continuously bubbled with air, and agitated at 110–130 rpm.

Bacterial cells were collected by centrifugation at 8000 xg and washed three times in 0.85% NaCl

to remove sucrose before use as inoculum. Optical density (OD) at 600 nm was used to estimate

the cell density of washed cell suspensions used for inoculation.

Cell number, size, and cytotoxicity measurements

C. reinhardtii cell density and size were determined using a hemocytometer and ImageJ or

a Beckman Coulter Multisizer 3 with a 50 µm orifice (Beckman Coulter, CA, USA). Bacterial cell

density was determined by counting colony forming units (CFU) in 10 µl spots of serial dilutions

on Typtone Yeast (TY) agar medium after 4 d of incubation at 30°C in the dark.

Algal cellular integrity was estimated using CellTox Green Cytotoxicity Assay (Promega,

WI, USA). *C. reinhardtii* sample densities were adjusted to $1x10^5$–$1x10^6$ cells/ml. Triplicate killed

control samples were prepared by heating cells at 90°C for 10 min. Fluorescence was measured in

a black-walled 96-well plate using a SpectraMax iD3 plate reader (Molecular Devices, CA, USA).

Background fluorescence of a medium blank was subtracted from all values, and results were

reported relative to killed control samples.

Samples for fluorescence microscopy were fixed overnight in 4% paraformaldehyde at 4°C

in the dark. Fixed samples were then collected by centrifugation at 10,000 xg, washed in phosphate

buffered saline (PBS) (pH 7), and stored in 1:1 ethanol:PBS at -20°C. For imaging, samples were

spotted on 0.22 µm GTTP type isopore polycarbonate filters and washed with sterile water to

remove residual salts. Prepared filters were mounted on slides with 5 µg/ml DAPI in Citifluor

antifade mounting medium buffered with PBS and imaged using a Zeiss Axioimager M2

microscope with a DAPI filter set (Ex 350/50, Em 460/50) at the UC Berkeley Biological Imaging

Facility. Bacterial cell lengths were measured using ImageJ.

Total organic carbon measurements

Total nonpurgeable organic carbon content (NPOC) of cells was determined using a TOC-L Shimadzu Total Organic Carbon Analyzer (Shimadzu, Kyoto, Japan). 10–40 ml culture was collected by centrifugation at 8000 xg for 2 min, and the supernatant was collected and then stored at -20°C until analysis. Spent media were diluted 2-fold and HCl was added to 27 mM. All samples were sparged to remove inorganic carbon. Some organic carbon may be purged from the sample by this method, so we report "nonpurgeable" organic carbon.

Stable isotope labelling and nanoSIMS

$^{15}NH_4Cl$ (99% ^{15}N, Cambridge Isotope Laboratories, MA, USA) was provided directly in the culture medium, replacing 50% of the NH_4Cl in HSM. 13 h after inoculation, $^{13}CO_2$ was provided to cultures by bubbling air through a solution of $NaH^{13}CO_3$ (99% ^{13}C, Cambridge Isotope Laboratories) and then into the cultures as previously described [43]. Killed controls were generated by treating cells with 4% paraformaldehyde for 20 min in the dark. Coculture experiments were otherwise conducted as described above.

For nanoSIMS analyses, samples were fixed and deposited on filters as described above for fluorescence microscopy. Dry filter pieces were then mounted on 1 inch round stubs using carbon tabs (Ted Pella, Inc., CA, USA) and gold coated. Data were collected on a NanoSIMS 50 (CAMECA, Gennevilliers, France) using a 1.5 pA Cs^+ primary ion beam at the Lawrence Livermore National Laboratory. The secondary ion masses of $^{12}C_2^-$, $^{12}C^{13}C^-$, $^{12}C^{14}N^-$, $^{12}C^{15}N^-$, and $^{32}S^-$ were collected. Raw nanoSIMS images were processed using L'image (L. Nittler, Carnegie Institution of Washington, D.C., USA). Individual cell regions of interest (ROIs) were manually circled using size and high $^{12}C^{14}N$ signal to identify bacterial cells and high $^{12}C^{13}C$ signal along with the secondary electron image to identify algal cells. Isotope enrichment in atom percent

enrichment (APE) for $^{12}C^{13}C^-/^{12}C_2^-$ and $^{12}C^{15}N^-/^{12}C^{14}N^-$ were calculated using standard ratios of

0.02247 and 0.00367, respectively. Enrichment data are also presented as net assimilation (N_{net}

and C_{net}), the fraction of newly synthesized biomass relative to total biomass, as defined by Dekas

et al. 2019, calculated against an unlabeled biomass standard [44]. For ^{15}N, net assimilation was

calculated using the known isotopic composition of the initial source substrate added to the

medium. For ^{13}C, net bacterial assimilation was calculated using the average algal biomass

composition in each experiment as a rough estimation of the source substrate.

Spent medium and cell lysate experiment

Wild-type *C. reinhardtii* was grown for 48 h in continuous light until density reached 1–

4×10^6 cells/ml. Cells were collected by centrifugation in 500 ml polypropylene bottles for 4 min

at 11,900 x*g* and 4°C. The supernatant was passed through a 0.22 µM filter to generate sterile spent

medium. Cell pellets were resuspended in fresh medium and then sonicated using a Fisherbrand

Model 505 Sonic Dismembrator (Fisher Scientific, PA, USA) on ice for 45 min with alternating

10 s at 30% intensity, 15 s "off" steps. The supernatant of the resulting cell lysate was then passed

through a 0.22 µM filter to generate sterile soluble cell lysate. Spent medium, soluble cell lysate,

and parallel live *C. reinhardtii* cultures were then inoculated with *M. japonicum* as described

above, and growth was monitored over another 48 h.

RESULTS

***M. japonicum* growth is severely limited in coculture with *C. reinhardtii*, especially under diel**

light

Previous work suggested that *C. reinhardtii* supports heterotrophic growth of the rhizobial

bacterium *M. japonicum* when cocultured in minimal medium given light and atmospheric CO_2

[25–27, 45]. As a first step in characterizing the transfer of fixed carbon in this relationship, we

compared the growth of *M. japonicum* when incubated alone or together with *C. reinhardtii* in

minimal medium with either no exogenous carbon source or with 150 µg/ml sucrose. While *M.*

japonicum grew considerably with sucrose and only marginally without it, we saw that coculture

with *C. reinhardtii* did not significantly increase the maximum bacterial density in either condition

(Fig. 1C, $p > 0.05$). Although the maximum density of *M. japonicum* in coculture without sucrose

(~$3x10^7$–$5x10^8$ CFU/ml) was similar to what has been observed previously [27], we found that the

bacterium was able to achieve a comparable density without the alga.

As the growth of *M. japonicum* was not significantly stimulated by *C. reinhardtii*, it seemed

that the alga did not supply adequate substrates for the bacterium's heterotrophic metabolism under

these conditions. This could be because *C. reinhardtii* released fixed carbon compounds in

insufficient quantities, or because *M. japonicum* is unable to metabolize the specific compounds

generated by *C. reinhardtii*. To address these possibilities, we monitored coculture growth and

organic carbon exchange under different light regimes, as diel light greatly alters *C. reinhardtii's*

metabolism [10]. During the day, the alga fixes carbon to build biomass and stores photosynthate

as starch. After sufficient growth during the light phase, cells initiate DNA synthesis and mitosis

in the dark, followed by a G0 phase during which starch reserves are degraded by glycolysis

followed by fermentation. We hypothesized that the alga's nighttime metabolism could stimulate

additional growth of *M. japonicum*.

To resolve diel patterns in growth and the reduced carbon content of the spent medium, we

used the readily synchronized *C. reinhardtii* strain CC-5390 and compared cocultures and

monocultures under continuous and diel light over several days with high temporal resolution.

Since *C. reinhardtii*'s doubling time is slower under diel light (cells only divide once per day), the

experiment was designed to achieve the same final amount of algal biomass under the two light

regimes. *C. reinhardtii* growth was unaffected by the bacterium, and algal cell density reached

roughly 4×10^6 cells/ml under all conditions (Fig. 2A, 2C). On the other hand, we found that *M.*

japonicum density increased significantly in the presence of CC-5390 under both light regimes

(Fig. 2B, 2D). We could not discern a clear temporal pattern in bacterial proliferation over the diel

cycles, and contrary to our hypothesis, we found that continuous light supported 3-fold more

bacterial cells than did diel light (Fig. 2E). Spent medium from continuous light-grown *C.*

reinhardtii had significantly more nonpurgeable organic carbon (NPOC) than spent medium from

diel light-grown *C. reinhardtii* of the same culture density, suggesting that more dissolved organic

carbon was available to the bacterium under continuous light (Fig. 2F). However, the presence of

M. japonicum did not significantly reduce the concentration of NPOC in the spent medium. This

could mean that either *M. japonicum* did not take up significant amounts of organic carbon from

the medium or that it could not fully oxidize it to CO_2, and instead released reduced carbon waste

products back into the extracellular milieu.

Stable isotope probing reveals mismatch between bacterial biomass synthesis and division in

coculture

To determine the amount of carbon fixed by *C. reinhardtii* that is taken up by *M.*

japonicum, we conducted stable isotope probing experiments using $^{13}CO_2$. Cocultures of CC-5390

and *M. japonicum* grown under continuous and diel light as in Fig. 2 were bubbled with air

containing $^{13}CO_2$, and $^{15}NH_4Cl$ was added to the medium as an independent tracer of biomass

synthesis, complementing measurements of cell density. Then, we assayed label uptake by single

cells using nanoSIMS.

We found substantial ^{13}C enrichment of the algal cells at a steady concentration throughout

the timepoints examined (Fig. 3A, SI Fig. 2, SI Fig. 3). In addition, we observed ^{13}C enrichment

of bacterial cells, which increased with time in cocultures under both light regimes (Fig. 3A, SI

Fig. 2, SI Fig. 3). Killed controls and a monoculture of *M. japonicum* grown with sucrose

demonstrated that this enrichment was not a result of nonspecific background or direct CO_2

incorporation during heterotrophic growth (i.e. anapleurotic carboxylation reactions) (SI Fig. 3).

Thus, a meaningful amount of carbon derived from algal photoautotrophy was in fact incorporated

into *M. japonicum* biomass in these cocultures. We compared the extent of carbon transfer under

continuous and diel light by calculating the fraction of bacterial biomass derived from algal carbon

(C_{net}), using the average algal biomass ^{13}C content over the course of the experiment as a rough

measure of the source carbon isotopic composition. We found that significantly more algal ^{13}C

was transferred to bacterial cells under continuous light over 48 h (0.17 median C_{net} in continuous

light, 0.09 median C_{net} in diel light) (Fig. 3B), consistent with our observation that spent medium

NPOC and *M. japonicum* cell density were greater in cocultures exposed to continuous light than

to diel light (Fig. 2, SI Fig. 4).

Both the ^{13}C and ^{15}N enrichment in *M. japonicum* cells were lower than we had expected

from the increase in bacterial CFUs observed in the experiment (>3-fold increase in CFUs during

the first 24 h of coculture under continuous light), suggesting a mismatch between the change in

cell density and the bacterial biomass synthesized (Fig. 3C, SI Fig. 4). We quantified the magnitude

of this mismatch using the ^{15}N label, for which the source isotopic composition was better

constrained, as opposed to that of the ^{13}C label which was delivered in the gas phase in an open

system. Using the source ^{15}N composition and the measured isotopic composition of bacterial

ROIs at each timepoint, we calculated the fraction of newly synthesized biomass generated from

the source substrate over the course of the experiment (N_{net}) [44]. We compared this to the expected

N_{net} that would be observed if each doubling in CFUs in the culture occurred upon a doubling in

bacterial biomass (0.99 N_{net} for cells grown on sucrose after 8–13 doublings, 0.63–0.97 N_{net} for

cells co-cultivated with *C. reinhardtii* after 1–5 doublings) (SI Fig. 4). Indeed, the measured N_{net}

of *M. japonicum* cells in the cocultures was much lower than the expected values at all measured

timepoints (0.18–0.34 N_{net}), whereas the measured values matched the expected values during

logarithmic-phase growth on sucrose (Fig. 4A). This suggested that in coculture with *C.*

reinhardtii, *M. japonicum* cells had ceased biomass synthesis by 24 h and yet continued to divide,

a hallmark of bacterial starvation known as reductive division [46, 47].

If this deviation of the observed N_{net} from the expected N_{net} reflected reductive division of

M. japonicum, we predicted that bacterial cells in the coculture would be smaller than cells in the

logarithmic phase of growth on sucrose, which are typically 2 µm in length. As predicted, *M.*

japonicum exhibited a mean cell length of 1.4–1.5 µm after 24 h in the cocultures, relative to the

mean cell length of 2.3 µm after 24 h of growth on sucrose (Fig. 4B, 4C). When sucrose was

depleted from the medium over the subsequent day in the monoculture, mean cell length decreased

to a similar extent, demonstrating that reductive division occurs upon carbon limitation in *M.*

japonicum.

Taken together, these data show that photosynthetically fixed carbon was indeed

transferred from *C. reinhardtii* to *M. japonicum* under both continuous and diel light, and that

while this amount was not sufficient for balanced logarithmic-phase growth of the bacterium, it

allowed for a small amount of bacterial proliferation.

Reductively dividing bacteria still deliver sufficient vitamin B$_{12}$ to support growth of the B$_{12}$-

requiring *mete1* strain

As reductive division had not previously been reported in the *C. reinhardtii-M. japonicum*

interaction, we wondered whether the phenomenon also occurs during coculture with the B$_{12}$-

requiring *mete1* strain of *C. reinhardtii*, and if so, whether the bacterium still synthesizes adequate

B_{12} to support the mutant's growth. We compared the change in bacterial cell size after growth on

150 μg/ml sucrose to changes during coculture with either wild-type *C. reinhardtii* or *mete1*. In all

conditions, we observed a 50–60% reduction in *M. japonicum* cell length over 54 h of cultivation

(Fig. 5A, 5B). This suggested that bacterial carbon limitation occurs to a similar extent during

coculture with the *mete1* strain as with the wild type. In addition, there was no significant

difference in *M. japonicum* density between the two cocultures (Fig. 5C).

To test whether reductively dividing *M. japonicum* still delivers vitamin B_{12} to *C.*

reinhardtii, we compared the growth of the *C. reinhardtii mete1* strain in coculture and

monoculture without exogenous B_{12}. Despite reductive division, *M. japonicum* supported

significant growth of the B_{12}-requiring *mete1* strain (Fig. 5D), demonstrating that bacterial B_{12}

synthesis and sharing still occur even under starvation.

While there was no difference in *M. japonicum* density after coculture with either the *C.*

reinhardtii wild type or *mete1*, there were many more *C. reinhardtii* cells present in the wild-type

coculture than the mutant coculture, which was B_{12}-limited (Fig. 5D). This demonstrated that

greater algal density does not translate into greater *M. japonicum* growth, as noted previously [27].

We observed this phenomenon in cocultures inoculated at several starting relative abundances (SI

Fig. 5). This suggests that carbon transfer from the alga to the bacterium could be indirect.

***C. reinhardtii* lysis can explain observed *M. japonicum* proliferation in coculture**

To distinguish the source of the fixed carbon that supports *M. japonicum* proliferation in

coculture, we compared *M. japonicum* growth in coculture with live *C. reinhardtii* to growth in *C.*

reinhardtii spent medium and in the soluble fraction of *C. reinhardtii* cell lysate. Spent medium

supported the same number of *M. japonicum* cells as did coculture, demonstrating that the

observed increase does not require a direct interaction with the alga (Fig. 6A). Cell lysate from *C.*

reinhardtii supported almost an order of magnitude more *M. japonicum* proliferation. Therefore,

we hypothesized that the fixed carbon transferred in our cocultures could be sourced from a few

lysed *C. reinhardtii* cells rather than from photosynthate exuded by live algal cells.

Having determined the increase in viable *M. japonicum* cells supported by lysate from a

known density of *C. reinhardtii* cells (1.7×10^8 CFU/ml on average after 48 h in lysate from 1.6×10^6

C. reinhardtii cells/ml culture), we estimated the theoretical increase in *M. japonicum* CFUs

supported by a single lysed *C. reinhardtii* cell to be 101.5±42.8 CFU in 48 h. From that, we

estimated how many *C. reinhardtii* cells would have to lyse in the coculture to enable the *M.*

japonicum proliferation observed: roughly 1.1×10^5 *C. reinhardtii* cells/ml, which corresponds to

1.8% of the *C. reinhardtii* populations in those cocultures. To test the actual degree of algal lysis

in our cultures, we measured algal cellular integrity using the CellTox Green Cytotoxicity Assay.

This assay uses a membrane-impermeable DNA dye, resulting in fluorescence from cells whose

plasma membrane has been compromised or from extracellular DNA [48]. We compared live

culture fluorescence to killed control samples and found that 1–3% of the wild-type *C. reinhardtii*

population had compromised cellular integrity (Fig. 6B). Thus, the fraction of dead or dying *C.*

reinhardtii cells measured by this assay is comparable to that needed to explain the observed *M.*

japonicum proliferation. These data are consistent with the interpretation that *M. japonicum*

growth in coculture is enabled by substrates that are released through *C. reinhardtii* cell lysis,

rather than by substrates exuded by live *C. reinhardtii* cells.

DISCUSSION

Most studies of symbioses between *C. reinhardtii* and heterotrophic bacteria to date have

focused on impacts on the alga, leaving open the question of how this model phototroph might

influence bacterial growth and physiology. Here, we have investigated *C. reinhardtii's* role as a

primary producer in the established coculture system with *M. japonicum*. Under continuous light,

we found that the alga increased the number of viable bacterial cells, albeit marginally so. We

tested whether nighttime metabolism might increase the alga's propensity for carbon sharing but

found that diel illumination actually decreased the productivity of the partnership. Using single-

cell analysis of ^{13}C enrichment by nanoSIMS, we quantitatively demonstrated transfer of carbon

fixed by the model alga to the bacterium. Roughly 17% of the carbon in *M. japonicum* cells was

derived from *C. reinhardtii* over 36 h under continuous light, whereas only ~9% of the *M.*

japonicum carbon came from *C. reinhardtii* over the same amount of time under diel light. Bulk

measurements showed that algal cultures of similar densities had more organic carbon in their

spent medium after continuous illumination than after diel illumination. Together, these results

suggest that the increased metabolic rate realized under continuous light may be more beneficial

for *M. japonicum* (and potentially other bacteria) than algal nighttime catabolism of starch.

With *C. reinhardtii* as the sole source of fixed carbon, *M. japonicum* exhibited signs of

starvation, even under continuous light, highlighting the meagerness of the microbial trophic

relationship. The quantitative stable isotope probing experiments revealed that during coculture

with *C. reinhardtii*, *M. japonicum* synthesized significantly less biomass than expected, given the

increase in viable bacterial cells. By direct measurement, we showed that *M. japonicum* undergoes

reductive division in coculture, dividing into small daughter cells within 24 h of carbon limitation.

Studies on freshwater and marine bacteria have similarly documented up to 90% reduction in cell

volume during carbon limitation [49–52]. Reductive division is a common strategy for surviving

starvation and has been studied in many Gram-negative bacteria including *Escherichia*, *Klebsiella*,

Vibrio, *Pseudomonas*, and *Rhizobium* species [46, 47]. By increasing cell number and reducing

cell volume, these bacteria increase the probability that a member of the population will encounter

sufficient nutrients again and increase their surface area-to-volume ratio to improve nutrient

uptake. Reductively dividing cells also exhibit changes in macromolecule synthesis and stress

resistance. Importantly though, we found that despite its apparent starvation, *M. japonicum*

provided enough vitamin B_{12} to support a B_{12}-dependent *C. reinhardtii* mutant. Vitamin supply

enables growth of auxotrophs, influences gene expression and metabolism, and can even give rise

to vitamin dependency in algae [25, 53]. Thus, our results suggest that even under austere

conditions with meager supply of growth substrates, bacteria can still influence algal physiology

and evolution.

375   We also found that a direct interaction with *C. reinhardtii* was not required to achieve the

M. japonicum proliferation observed in coculture: growth in algal spent medium yielded the same

maximum density of viable *M. japonicum* cells as did coculture. Furthermore, mechanically lysed

C. reinhardtii cells yielded considerably higher *M. japonicum* densities. This observation led us to

hypothesize that perhaps this bacterium does not metabolize the exudates of live *C. reinhardtii*

cells at all. Instead, perhaps the small amount of bacterial growth observed in coculture and in

spent medium is due to the death of a small fraction of algal cells. It has long been appreciated that

even during rapid exponential growth, microbial cultures experience a small death rate [54].

Furthermore, cell lysis is an important mechanism of nutrient transfer in natural environments, and

microbial necromass is a major component of the soil organic carbon pool [55, 56]. For the

experimental conditions examined here, we showed that ~2% of the *C. reinhardtii* population in

our cultures are present as necromass. Based on the *M. japonicum* growth yields achieved in

mechanically lysed *C. reinhardtii* cells, we calculated that this is almost exactly the amount of

algal necromass required to explain the degree of *M. japonicum* proliferation that occurred in

coculture. Therefore, we propose that lysis is the primary mechanism of trophic transfer in this

coculture system, rather than exudation or direct exchange.

Given that very little growth of *M. japonicum* was observed from an interaction with *C.*

reinhardtii – even under conditions optimized for algal productivity – our results may suggest that

this model alga exhibits a low carrying capacity for heterotrophic bacteria in the environment.

Similar bacterial densities have been reported for other *C. reinhardtii* cocultures in minimal media,

including those with *Methylobacterium aquaticum* [29, 57]. On the other hand, it is possible that

other bacteria, such as those that may have co-evolved with *C. reinhardtii* in its native

environment, may possess greater capacity to metabolize compounds that *C. reinhardtii* releases

during growth or may achieve greater access to growth substrates through chemotaxis, interspecies

signaling and direct exchange, or algicidal activity [3, 58–61]. In addition, the mode of cell lysis

(i.e. mechanical vs. viral) can greatly impact the nutrients released [62]. Yet, the system studied

here has revealed important aspects of algal-bacterial interactions, and our quantitative approach

can serve as a roadmap for the future work necessary to understand *C. reinhardtii*'s full potential

as a primary producer in the microbial world.

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COMPETING INTERESTS

416 The authors declare no competing financial interests.

DATA AVAILABILITY

418 All data underlying this article are available in Supplementary Data File S1.

REFERENCES

1. Field CB, Behrenfeld MJ, Randerson JT, Falkowski P. Primary Production of the

Biosphere: Integrating Terrestrial and Oceanic Components. *Science* 1998; **281**: 237–240.

2. Azam F, Fenchel T, Field J, Gray J, Meyer-Reil L, Thingstad F. The Ecological Role of

Water-Column Microbes in the Sea. *Mar Ecol Prog Ser* 1983; **10**: 257–263.

3. Seymour JR, Amin SA, Raina J-B, Stocker R. Zooming in on the phycosphere: the

ecological interface for phytoplankton–bacteria relationships. *Nat Microbiol* 2017; **2**:

17065.

4. Pomeroy LR. The Ocean's Food Web, A Changing Paradigm. *Bioscience* 1974; **24**: 499–

504.

5. Azam F, Malfatti F. Microbial structuring of marine ecosystems. *Nat Rev Microbiol* 2007;

5: 782–791.

6. Croft MT, Lawrence AD, Raux-Deery E, Warren MJ, Smith AG. Algae acquire vitamin

B_{12} through a symbiotic relationship with bacteria. *Nature* 2005; **438**: 90–93.

7.   Amin SA, Green DH, Hart MC, Küpper FC, Sunda WG, Carrano CJ. Photolysis of iron–

siderophore chelates promotes bacterial–algal mutualism. *Proc Natl Acad Sci* 2009; **106**:

17071–17076.

8.   Hom EFY, Aiyar P, Schaeme D, Mittag M, Sasso S. A Chemical Perspective on

Microalgal-Microbial Interactions. *Trends Plant Sci* 2015; **20**: 689–693.

9.   Salomé PA, Merchant SS. A Series of Fortunate Events: Introducing Chlamydomonas as a

Reference Organism. *Plant Cell* 2019; **31**: 1682–1707.

10.   Strenkert D, Schmollinger S, Gallaher SD, Salomé PA, Purvine SO, Nicora CD, *et al.*

Multiomics resolution of molecular events during a day in the life of Chlamydomonas.

Proc Natl Acad Sci 2019; **116**: 2374–2383.

11.   Zones JM, Blaby IK, Merchant SS, Umen JG. High-resolution profiling of a synchronized

diurnal transcriptome from *Chlamydomonas reinhardtii* reveals continuous cell and

metabolic differentiation. *Plant Cell* 2015; **27**: 2743–2769.

12.   Durán P, Flores-Uribe J, Wippel K, Zhang P, Guan R, Melkonian B, *et al.* Shared features

and reciprocal complementation of the Chlamydomonas and Arabidopsis microbiota. *Nat*

Commun 2022; **13**: 406.

13.   Kim B-H, Ramanan R, Cho D-H, Oh H-M, Kim H-S. Role of Rhizobium, a plant growth

promoting bacterium, in enhancing algal biomass through mutualistic interaction. *Biomass*

Bioenergy 2014; **69**: 95–105.

14.   Lőrincz Z, Preininger É, Kósa A, Pónyi T, Nyitrai P, Sarkadi L, *et al.* Artificial tripartite

symbiosis involving a green alga (Chlamydomonas), a bacterium (Azotobacter) and a

fungus (Alternaria): Morphological and physiological characterization. *Folia Microbiol*

(Praha) 2010; **55**: 393–400.

15. Xie B, Bishop S, Stessman D, Wright D, Spalding MH, Halverson LJ. *Chlamydomonas*

reinhardtii thermal tolerance enhancement mediated by a mutualistic interaction with

vitamin B_{12}-producing bacteria. *ISME J* 2013; **7**: 1544–1555.

16. Amin SA, Parker MS, Armbrust EV. Interactions between Diatoms and Bacteria.

Microbiol Mol Biol Rev 2012; **76**: 667–684.

17. Gobler C, Norman C, Panzeca C, Taylor G, Sañudo-Wilhelmy S. Effect of B-vitamins

(B_1, B_{12}) and inorganic nutrients on algal bloom dynamics in a coastal ecosystem. *Aquatic*

Microbial Ecol 2007; **49**: 181–194.

18. Sañudo-Wilhelmy SA, Gobler CJ, Okbamichael M, Taylor GT. Regulation of

phytoplankton dynamics by vitamin B_{12}. *Geophys Res Lett* 2006; **33**: L04604.

19. Helliwell KE. The roles of B vitamins in phytoplankton nutrition: new perspectives and

prospects. *New Phytol* 2017; **216**: 62–68.

20. Keshtacher-Liebso E, Hadar Y, Chen Y. Oligotrophic Bacteria Enhance Algal Growth

under Iron-Deficient Conditions. *Appl Environ Microbiol* 1995; **61**: 2439–41.

21. Fakhimi N, Gonzalez-Ballester D, Fernández E, Galván A, Dubini A. Algae-Bacteria

Consortia as a Strategy to Enhance H_2 Production. *Cells* 2020; **9**: 1353.

22. Krespach MKC, Stroe MC, Flak M, Komor AJ, Nietzsche S, Sasso S, *et al.* Bacterial

marginolactones trigger formation of algal gloeocapsoids, protective aggregates on the

verge of multicellularity. *Proc Natl Acad Sci* 2021; **118**.

23. Windler M, Stuart R, Deutzmann JS, Mayali X, Navid A, D'haeseleer P, *et al.* Bacterial

exometabolites influence *Chlamydomonas* cell cycle and double algal productivity. *FEMS*

Microbiol Ecol 2022; **98**.

24.   Kazamia E, Czesnick H, Nguyen TT Van, Croft MT, Sherwood E, Sasso S, *et al.*

479   Mutualistic interactions between vitamin B$_{12}$-dependent algae and heterotrophic bacteria

480   exhibit regulation. *Environ Microbiol* 2012; **14**: 1466–1476.

481   25.   Helliwell KE, Collins S, Kazamia E, Purton S, Wheeler GL, Smith AG. Fundamental shift

482   in vitamin B$_{12}$ eco-physiology of a model alga demonstrated by experimental evolution.

483   *ISME J* 2015; **9**: 1446–1455.

484   26.   Bunbury F, Helliwell KE, Mehrshahi P, Davey MP, Salmon DL, Holzer A, *et al.*

485   Responses of a Newly Evolved Auxotroph of Chlamydomonas to B$_{12}$ Deprivation. *Plant*

486   *Physiol* 2020; **183**: 167–178.

487   27.   Bunbury F, Deery E, Sayer AP, Bhardwaj V, Harrison EL, Warren MJ, *et al.* Exploring

488   the onset of B$_{12}$-based mutualisms using a recently evolved Chlamydomonas auxotroph

489   and B$_{12}$-producing bacteria. *Environ Microbiol* 2022; **24**: 3134–3147.

490   28.   Helliwell KE, Scaife MA, Sasso S, Araujo APU, Purton S, Smith AG. Unraveling

491   Vitamin B$_{12}$-Responsive Gene Regulation in Algae. *Plant Physiol* 2014; **165**: 388–397.

492   29.   Calatrava V, Hom EFY, Llamas Á, Fernández E, Galván A. OK, thanks! A new

493   mutualism between Chlamydomonas and methylobacteria facilitates growth on amino

494   acids and peptides. *FEMS Microbiol Lett* 2018; **365**.

495   30.   Dubini A, Mus F, Seibert M, Grossman AR, Posewitz MC. Flexibility in Anaerobic

496   Metabolism as Revealed in a Mutant of *Chlamydomonas reinhardtii* Lacking

497   Hydrogenase Activity. *J Biol Chem* 2009; **284**: 7201–7213.

498   31.   Gfeller RP, Gibbs M. Fermentative Metabolism of *Chlamydomonas reinhardtii*. *Plant*

499   *Physiol* 1984; **75**: 212–218.

32.   Mus F, Dubini A, Seibert M, Posewitz MC, Grossman AR. Anaerobic Acclimation in

Chlamydomonas reinhardtii. *J Biol Chem* 2007; **282**: 25475–25486.

33.   Yang W, Catalanotti C, Wittkopp TM, Posewitz MC, Grossman AR. Algae after dark:

mechanisms to cope with anoxic/hypoxic conditions. *Plant J* 2015; **82**: 481–503.

34.   Ghirardi ML, Subramanian V, Wecker MSA, Smolinski S, Antonio RV, Xiong W, *et al.*

Survey of the anaerobic metabolism of various laboratory wild-type *Chlamydomonas*

reinhardtii strains. *Algal Res* 2018; **35**: 355–361.

35.   Nishio K, Hashimoto K, Watanabe K. Light/electricity conversion by defined cocultures

of Chlamydomonas and Geobacter. *J Biosci Bioeng* 2013; **115**: 412–417.

36.   Lodwig E, Poole P. Metabolism of *Rhizobium* Bacteroids. *CRC Crit Rev Plant Sci* 2003;

22: 37–78.

37.   Ronson CW, Lyttleton P, Robertson JG. C_4-dicarboxylate transport mutants of *Rhizobium*

trifolii form ineffective nodules on *Trifolium repens*. *Proc Natl Acad Sci* 1981; **78**: 4284–

4288.

38.   Finan TM, Oresnik I, Bottacin A. Mutants of *Rhizobium meliloti* defective in succinate

metabolism. *J Bacteriol* 1988; **170**: 3396–3403.

39.   Geddes BA, Oresnik IJ. Physiology, genetics, and biochemistry of carbon metabolism in

the alpha-proteobacterium *Sinorhizobium meliloti*. *Can J Microbiol* 2014; **60**: 491–507.

40.   Zhalnina K, Louie KB, Hao Z, Mansoori N, da Rocha UN, Shi S, *et al.* Dynamic root

exudate chemistry and microbial substrate preferences drive patterns in rhizosphere

microbial community assembly. *Nat Microbiol* 2018; **3**: 470–480.

41.   Sueoka N. MITOTIC REPLICATION OF DEOXYRIBONUCLEIC ACID IN

CHLAMYDOMONAS REINHARDI. *Proc Natl Acad Sci* 1960; **46**: 83–91.

42.   Kropat J, Hong-Hermesdorf A, Casero D, Ent P, Castruita M, Pellegrini M, *et al.* A

revised mineral nutrient supplement increases biomass and growth rate in

Chlamydomonas reinhardtii. *Plant J* 2011; **66**: 770–780.

43.   Lingappa UF, Dupuis S, Mayali X, Merchant SS. Isotopically labelled inorganic carbon

delivered to algal cultures via bubbler bottle. *protocols.io* 2023.

44.   Dekas AE, Parada AE, Mayali X, Fuhrman JA, Wollard J, Weber PK, *et al.*

Characterizing Chemoautotrophy and Heterotrophy in Marine Archaea and Bacteria With

Single-Cell Multi-isotope NanoSIP. *Front Microbiol* 2019; **10**.

45.   Laeverenz Schlogelhofer H, Peaudecerf FJ, Bunbury F, Whitehouse MJ, Foster RA, Smith

AG, *et al.* Combining SIMS and mechanistic modelling to reveal nutrient kinetics in an

algal-bacterial mutualism. *PLoS One* 2021; **16**: e0251643.

46.   Thorne SH, Williams HD. Adaptation to nutrient starvation in *Rhizobium leguminosarum*

bv. phaseoli: analysis of survival, stress resistance, and changes in macromolecular

synthesis during entry to and exit from stationary phase. *J Bacteriol* 1997; **179**: 6894–

6901.

47.   Shimaya T, Okura R, Wakamoto Y, Takeuchi KA. Scale invariance of cell size

fluctuations in starving bacteria. *Commun Phys* 2021; **4**: 238.

48.   Haire TC, Bell C, Cutshaw K, Swiger B, Winkelmann K, Palmer AG. Robust Microplate-

Based Methods for Culturing and in Vivo Phenotypic Screening of *Chlamydomonas*

reinhardtii. *Front Plant Sci* 2018; **9**.

49.   Vrede K, Heldal M, Norland S, Bratbak G. Elemental composition (C, N, P) and cell

volume of exponentially growing and nutrient-limited bacterioplankton. *Appl Environ*

Microbiol 2002; **68**: 2965–71.

50.   Troussellier M, Bouvy M, Courties C, Dupuy C. Variation of carbon content among bacterial species under starvation condition. *Aquatic Microbial Ecol* 1997; **13**: 113–119.

51.   Holmquist L, Kjelleberg S. Changes in viability, respiratory activity and morphology of the marine Vibrio sp. strain S14 during starvation of individual nutrients and subsequent recovery. *FEMS Microbiol Ecol* 1993; **12**: 215–223.

52.   Mårdén P, Tunlid A, Malmcrona-Friberg K, Odham G, Kjelleberg S. Physiological and morphological changes during short term starvation of marine bacterial isolates. *Arch Microbiol* 1985; **142**: 326–332.

53.   Sokolovskaya OM, Shelton AN, Taga ME. Sharing vitamins: Cobamides unveil microbial interactions. *Science* 2020; **369**.

54.   Kelly CD, Rahn O. The Growth Rate of Individual Bacterial Cells. *J Bacteriol* 1932; **23**: 147–153.

55.   Gude S, Pherribo GJ, Taga ME. Emergence of Metabolite Provisioning as a By-Product of Evolved Biological Functions. *mSystems* 2020; **5**.

56.   Sokol NW, Slessarev E, Marschmann GL, Nicolas A, Blazewicz SJ, Brodie EL, *et al.* Life and death in the soil microbiome: how ecological processes influence biogeochemistry. *Nat Rev Microbiol* 2022; **20**: 415–430.

57.   Ban S, Lin W, Wu F, Luo J. Algal-bacterial cooperation improves algal photolysis-mediated hydrogen production. *Bioresour Technol* 2018; **251**: 350–357.

58.   Samo TJ, Kimbrel JA, Nilson DJ, Pett-Ridge J, Weber PK, Mayali X. Attachment between heterotrophic bacteria and microalgae influences symbiotic microscale interactions. *Environ Microbiol* 2018; **20**: 4385–4400.

59.   Jackrel SL, Yang JW, Schmidt KC, Denef VJ. Host specificity of microbiome assembly

and its fitness effects in phytoplankton. *ISME J* 2021; **15**: 774–788.

60.   Aiyar P, Schaeme D, García-Altares M, Carrasco Flores D, Dathe H, Hertweck C, *et al.*

Antagonistic bacteria disrupt calcium homeostasis and immobilize algal cells. *Nat*

Commun 2017; **8**: 1756.

61.   Raina J-B, Giardina M, Brumley DR, Clode PL, Pernice M, Guagliardo P, *et al.*

Chemotaxis increases metabolic exchanges between marine picophytoplankton and

heterotrophic bacteria. *Nat Microbiol* 2023; **8**: 510–521.

62.   Pherribo GJ, Taga ME. Bacteriophage-mediated lysis supports robust growth of amino

acid auxotrophs. *ISME J* 2023; **17**: 1785–1788.

FIGURES

Figure 1: ***C. reinhardtii* does not significantly improve growth of *M. japonicum*.** Triplicate cultures (*n* = 3) were inoculated with or without sucrose and maintained under continuous light, bubbled with air, and shaken at 110 rpm. (A) Representative image of cultures 72 h after inoculation. (B) Wild-type *C. reinhardtii* cell density in cultures over time after inoculation. (C) *M. japonicum* cell density in cultures over time after inoculation.

Figure 2: Coculture light regime impacts organic carbon release and *M. japonicum* growth. Quadruplicate (*n* = 4) monocultures (colors) and cocultures (black and white) were bubbled with air, and shaken at 125 rpm. (A, C) Growth of cell wall reduced strain CC-5390 in continuous light or diel (12-h-light/12-h-dark) light, respectively, with and without *M. japonicum*. The grey backgrounds indicate sample timepoints that occurred during the dark phase. Under diel light, CC-5390 exhibits synchronous growth, doubling roughly once per day upon nightfall. Cultures were inoculated to reach the same final algal cell density at the end of the experiment. (B, D) *M. japonicum* growth under the continuous and diel light regimes, respectively, with and without CC-5390. (E) Maximum bacterial density achieved under the various trophic conditions tested. Asterisks indicate significant differences by Student's *t*-test ($p < 0.05$). (F) NPOC in spent medium from CC-5390 and cocultures sampled at the indicated times from the continuous and diel light regimes in (A) and (C), respectively. Lower-case letters indicate significantly different groups by paired Student's *t*-test ($p < 0.05$). Error bars represent the standard deviation from the mean.

Figure 3: Stable isotope probing demonstrates carbon flux in continuous and diel light. Duplicate cocultures ($n = 2$) of CC-5390 and *M. japonicum* were grown as described in Fig. 2 but with 50% of their NH_4^+ provided as ^{15}N and with $^{13}CO_2$ added to the air used to bubble the cultures starting 13 h after inoculation. Isotope enrichment was measured using nanoSIMS at the indicated times after inoculation. The grey backgrounds indicate sample timepoints that occurred during the dark phase. (A) ^{13}C atom percent enrichment (APE) data of $n \geq 5$ individual cells grown under continuous light or diel light. The dashed lines represent the maximum ^{13}C APE that occurred in *M. japonicum* monoculture controls provided sucrose as a result of nonspecific background or direct CO_2 incorporation during heterotrophic growth; see SI Fig. 3 for more details. (B) C_{net} of *M. japonicum* cells ($n \geq 10$), calculated relative the algal biomass as the source. Median values are indicated, and asterisks indicate significant differences by Student's *t*-test ($p < 0.05$). (C) ^{15}N APE data of $n \geq 5$ individual cells grown under continuous light or diel light.

Figure 4: ***M. japonicum* undergoes reductive division upon depletion of sucrose and during algal coculture.** Duplicate cultures ($n = 2$) (monoculture with 150 µg/ml sucrose (pink) or coculture under continuous light (white) or diel light (grey)) were grown as described in Fig. 2 but with 50% of their NH_4^+ provided as ^{15}N and with $^{13}CO_2$ added to the air used to bubble the cultures starting 13 h after inoculation. Isotope enrichment was measured using nanoSIMS and cells were imaged by fluorescence microscopy at the indicated times after inoculation. The grey backgrounds indicate sample timepoints that occurred during the dark phase. (A) N_{net} *M. japonicum* cells ($n \geq$ 10) (circles) relative to the calculated expected N_{net} (blue bars) if each doubling in CFU/ml (SI Fig. 4) represented a doubling in biomass; black lines represent mean values. (B) Representative fluorescence microscopy images of cells stained with DAPI. (C) Cell length of $n \geq 50$ *M. japonicum* cells per culture type measured using ImageJ. Mean cell length is indicated, and asterisks indicate significant differences by Student's *t*-test ($p < 0.05$).

Figure 5: *M. japonicum* **delivers vitamin B$_{12}$ to** *C. reinhardtii* **despite reductive division.**
Triplicate cultures (n = 3) were maintained under continuous light and shaken at 130 rpm for 54 h after inoculation. (A) Representative fluorescence microscopy images of *M. japonicum* monoculture with 150 µg/ml sucrose, coculture of *C. reinhardtii* wild type and *M. japonicum*, and coculture of *C. reinhardtii mete1* and *M. japonicum* stained with DAPI. *C. reinhardtii* cells are indicated with white arrowheads. (B) Cell length of *M. japonicum* cells (n = 50) per culture type was measured using ImageJ. Mean cell length is indicated. (C) *M. japonicum* density in monoculture with 150 µg/ml sucrose (pink bars) or in coculture (black bars) with wild-type (circles) and *mete1 C. reinhardtii* (triangles), estimated as CFU. (D) Cell density of *C. reinhardtii* wild type (circles) or *mete1* (triangles) in coculture (black bars) and of *mete1* alone without vitamin B$_{12}$ (green bars). Error bars represent the standard deviation from the mean, and asterisks indicate significant difference ($p < 0.05$).

Figure 6: A small degree of algal lysis can explain the *M. japonicum* growth that occurs in coculture. Triplicate cultures ($n = 3$) of wild-type *C. reinhardtii* were grown under continuous light and shaken at 125 rpm for 24 h, reaching $1–4\times10^6$ cells/ml. These cultures were then split and used to generate parallel live algal cultures, algal spent media, and algal cell lysate, each then inoculated with *M. japonicum* in triplicate ($n = 3$). (A) *M. japonicum* density 45 h after inoculation in monoculture with no reduced carbon source, coculture with live *C. reinhardtii cells*, *C. reinhardtii* spent medium, or *C. reinhardtii* cell lysate. Asterisks indicate significant differences by Student's *t*-test ($p < 0.05$). (B) The approximate degree of *C. reinhardtii* cell lysis required to explain *M. japonicum* growth in coculture based on *M. japonicum* growth yield in *C. reinhardtii* cell lysate (blue bar), and the degree of *C. reinhardtii* cell lysis measured in the cultures used for the experiment in panel (A) by CellTox Green, reported relative to a 100% killed control. The expected value and the mean value are indicated. Error bars represent the standard deviation from the mean.