A host-derived viral transporter protein for nitrogen uptake in infected marine phytoplankton

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Phytoplankton community structure is shaped by both bottom-up factors such as nutrient availability, and top-down processes, such as predation. Here we show that marine viruses can blur these distinctions, being able to amend how host cells acquire nutrients from their environment while also predating and lysing their algal hosts. Viral genomes often encode genes derived from their host. These genes may allow the virus to manipulate host metabolism to improve viral fitness. Here we identify in the genome of a phytoplankton virus, which infects the small green alga *Ostreococcus tauri*, a host-derived functional ammonium transporter. This gene is transcribed during infection and when expressed in yeast mutants the viral protein is located to the plasma membrane and rescues growth when cultured with ammonium as the sole nitrogen source. We also show that viral infection alters the nature of nitrogen compound uptake of host cells, by both increasing substrate affinity and allowing the host to access diverse nitrogen sources. This is important because the availability of nitrogen often limits phytoplankton growth. Collectively, these data show that a virus can acquire genes encoding nutrient transporters from a host genome and that expression of the viral gene can alter the nutrient uptake behavior of host cells. These results have implications for understanding how viruses manipulate the physiology and ecology of phytoplankton, influence marine nutrient cycles and act as vectors for horizontal gene transfer.

Phycodnaviridae | NCLDV | Prasinophytes | Mamiellophyceae | Horizontal / Lateral Gene Transfer

Phytoplankton underpin the biogeochemistry of the surface oceans and drive the marine carbon and nitrogen cycles [1]. Nutrients fuel cyanobacteria and eukaryotic single-celled algae with the elements essential for organic matter biosynthesis, especially nitrogen (N) and phosphorus (P); hence nutrient availability exerts a bottom-up control on phytoplankton cell growth and oceanic productivity [2, 3]. In particular, N and P are found in low concentrations over much of the open ocean, limiting phytoplankton growth rates. Nutrient limitation, including co-limitation by several nutrients, results in competition among phytoplankton. In oligotrophic environments, and transiently nutrient depleted environments, phytoplankton species have evolved a range of strategies to optimize nutrient acquisition [4]. The genetic repertoire of N and P transporters show evidence of gene duplication, differential loss and horizontal gene transfer (HGT) in phytoplankton genomes as well as contrasting gene expression levels [5–9] suggesting that the evolution of these genes has been driven by adaptation to environmental limitation. Ammonium (NH_4^+) and nitrate (NO_3^-) are commonly available N source for marine phytoplankton [10, 11] and, as such, the gene repertoire of cyanobacterial and eukaryotic phytoplankton are configured towards utilization of these two forms of inorganic N [12].

In addition to bottom-up nutrient limitation, phytoplankton community structure are influenced by top-down controls [13]. For phytoplankton communities these include predation by grazers and viral infection (see e.g., [14]). Marine viruses are the most abundant biological entities in the oceans; they are estimated to induce 10^{28} infections daily [15] and are thought to control phytoplankton abundance, biomass and species composition through taxon-specific infections [16, 17]. There is a growing appreciation of the role of viruses in oceanic nutrient cycles, based on lytic infections leading to the release of dissolved and particulate organic matter, which is then recycled by other microorganisms [15, 18]. This virus-mediated process, referred to as the viral shunt, was suggested as a mechanism that maintains availability of organic matter in the euphotic zone by lysing cells before they sink [15, 18]. However, the influence of viruses on oceanic ecosystems extends beyond top-down host mortality. Genomic and metagenomic analyses show that marine viruses –either phages or eukaryotic viruses– harbor host-derived genes encoding a diverse range of putative functions [19–21], including whole biochemical pathways [22]. These 'auxiliary metabolic genes' (AMGs) may allow the virus to manipulate the host via metabolic reprogramming during infection, and have been experimentally shown to alter

Significance Statement

Viruses often carry genes acquired from their host. In the present work, we show that a virus of a marine alga carries a gene encoding a transporter protein that mediates nutrient uptake. We confirm that the viral transporter protein is expressed during infection and show that the protein functions to take up sources of nitrogen. This is important because acquisition of nutrients often determines the ecological success of phytoplankton populations. This work demonstrates how a virus can amend host-viral dynamics by modulating acquisition of nutrients from the environment.

A.M., D.S.M. and T.A.R. designed research; A.M., A.C., D.S.M., V.A. and E.D. performed research; A.M. analyzed data; H.M. and E.D. contributed reagents; A.M. and T.A.R. wrote the paper with contributions from all authors.

The authors declare no conflict of interest.

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the central carbon metabolism and pigment biosynthesis of cyanobacteria [23, 24], and to 'reprogram' lipid biosynthesis of eukaryotic algal cells [25–27]. AMGs are thought to modulate host function to improve fitness of the virus and, in some cases, temporarily the host. For example, it was hypothesized that virally-encoded putative phosphate transporters increase accumulation of P in host cells [28, 29], which may in turn increase virus fitness given that P-depleted phytoplankton cells limit virus proliferation (e.g., [30, 31]).

Given the evidence of HGT for genes involved in both N and P metabolisms [7, 9, 32], the presence of host-derived phosphate transporters in phytoplankton viral genomes [29], and the importance of nutrient availability for phytoplankton and viral replication [33], we hypothesize that functional N transporters would also be found in genomes of phytoplankton viruses. Indeed, a recent analysis of marine viral metagenomes extended the catalog of functions encoded by AMGs, and reported the presence of genes putatively encoding NH_4^+ transporters in metagenomic assemblies which harbored phage genes [21]. To confirm the existence of potential virus-mediated N uptake processes, we searched available viral genomes for the presence of N transporters. Here, we report the identification of a host-derived N transporter harbored by an algal virus, OtV6. This virus infects the green alga *Ostreococcus tauri* and we show that the viral transporter is transcribed during the infection cycle. Cloning and phenotype analysis in yeast demonstrate that the viral protein transports NH_4^+, methylammonium and potentially a range of alternative N sources and that the viral transporter mediates a higher rate of methylammonium uptake at low environmental concentrations compared to the *O. tauri* homolog. Algal culture experiments show viral infection alters host nutrient uptake dynamics during infection.

Results

OtV6 genome harbors a putative NH_4^+ transporter. To identify viral transporter proteins putatively involved in N uptake, all available viral amino acid sequences were screened using similarity searches based on hidden Markov models (HMM) encompassing the main N transporter protein families. These HMM searches discovered a single viral protein potentially involved in direct N uptake. This viral protein sequence (UniProtKB [34] identifier: H8ZJB2) generated a significant hit with the Amt/Mep/Rh superfamily HMM (Fig. S1A). Members of this superfamily are integral membrane proteins involved in the electrogenic transport of ammonium ions, either the direct transport of NH_4^+ or ammonia (NH_3)/H^+ co-transport [35]. Several proteins from this superfamily have been shown to mediate the uptake of methylammonium, which can be used as a radiolabeled tracer ($^{14}CH_3NH_3^+$) to infer NH_4^+ uptake rates [36]. The viral transporter identified is encoded in the genome of OtV6, a virus belonging to the Phycodnaviridae family of nucleocytoplasmic large dsDNA viruses (NCLDV [37]). We name this viral putative NH_4^+ transporter vAmt (viral ammonium transporter).

Phycodnaviridae infect a broad range of eukaryotic algae [38]. To date, 12 genome sequences of viruses infecting the prasinophyte alga *Ostreococcus* –a widely distributed marine Mamiellophyceae [39, 40] and the smallest known free-living eukaryotic cell– are available [41–46]. These include viruses that infect one of three species: *O. tauri*, *O. lucimarinus* and *O. mediterraneus*. OtV6 infects a distinct population of

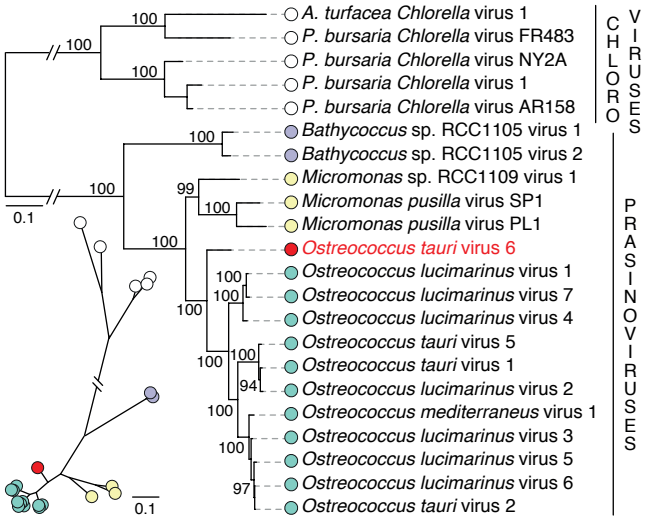

Fig. 1. OtV6 branches basal to all other available *Ostreococcus* spp. viral genomes. ML phylogenetic tree of green algal viruses inferred from a concatenated sequence alignment of 22 core proteins shared among these viruses (7668 sites) under the LG+G+F model. The unrooted version of this tree is presented below the midpoint-rooted tree. A red circle indicates OtV6 branch; other colored circles represent the taxonomy of the viral hosts: green (*Ostreococcus*), purple (*Bathycoccus*), yellow (*Micromonas*) and white (chloroviruses, viruses of *Chlorella*, as outgroup clade). Node support was calculated from 1000 non-parametric bootstrap replicates; only bootstrap values > 90% are shown. The scale bar represents the number of estimated substitutions per site. The branch connecting the prasinoviruses to the chloroviruses was truncated for display.

O. tauri (shown to be resistant to another virus, OtV5 [44]), an alga originally isolated from a coastal NW Mediterranean lagoon [47].

OtV6 is evolutionarily distinct from other *Ostreococcus* viruses. To determine the phylogenetic position of OtV6 among the Phycodnaviridae that infect green algae, we used the OtV6 genomic data [44] for a maximum-likelihood (ML) phylogenetic analysis. The ML tree reconstruction was based on a concatenated alignment of 22 conserved protein sequences [46] with a sampling of 7668 sites. In the resulting ML phylogeny OtV6 branched at the base of all other *Ostreococcus* viruses (Fig. 1); both the basal position of OtV6 and the clustering of all other *Ostreococcus* viruses in a single clade were strongly supported (100% bootstrap support). This intermediate phylogenetic position was also found in a ML phylogenetic tree of the viral DNA polymerase B (915 sites; Fig. S2) a gene commonly used as a marker for NCLDV phylogenetic and diversity analyses [48–50].

The phylogenies of both the viral core protein set and DNA polymerase B trees demonstrate that OtV6 is positioned almost equidistant between the sampled *Ostreococcus* virus and *Micromonas* virus clades. By comparing the amino acid conservation levels of the 250 open reading frame (ORF) sequences of OtV6 with those of the other 11 *Ostreococcus* viruses and 3 *Micromonas* viruses, we found that 20% of OtV6 ORFs were more similar to *Micromonas* virus homologs than to ones from *Ostreococcus* viruses (Fig. S3). In addition, 13 OtV6 ORFs had homologs in the genomes of *Micromonas* viruses, which were absent from all other *Ostreococcus* viruses. Given current sampling of Phycodnaviridae genomes, these results suggest that OtV6 represents an intermediate prasinovirus lineage.

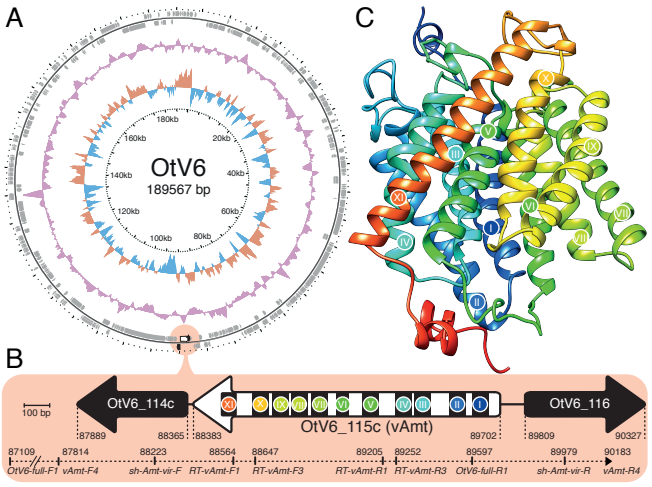

Fig. 2. vAmt genomic context and putative protein structure. (*A*) Circular depiction of the OtV6 genome. Oriented ORFs are mapped in grey on the outer ring. The light red circle indicates the vAmt locus along with neighboring ORFs. The colored plots drawn as intermediate rings display the biases in dinucleotide usages across the OtV6 genome: the red and blue plot shows the A+T skew, and the mauve plot shows the G+C content. (*B*) vAmt locus and neighboring ORFs. A white arrow represents the vAmt ORF (OtV6_115c), and black arrows represent the 5′ and 3′ vAmt flanking ORFs (OtV6_114c and OtV6_116, respectively; Fig. S4 displays the phylogenies of these flanking ORFs demonstrating viral provenance). The 11 predicted transmembrane domains along the vAmt ORF are indicated by black rectangles with colored circles, and numbered with Roman numerals. ORF lengths were scaled according to the 100 bp scale bar. Genomic coordinates indicate the 5′ and 3′ boundaries of each depicted ORF. The PCR amplified region is represented by a dashed line along with the corresponding amplicon genomic cooordinates. (*C*) vAmt protein structure prediction. The predicted protein structure is composed of 11 helices corresponding to the transmembrane domains indicated by colored circles and Roman numerals, as in panel B (see Fig. S6 for sequence and structural comparisons of both host and viral copies and Fig. S7 for TMHMM posterior probabilities).

vAmt is virally-encoded and expressed during infection. Sequence searches and ML phylogenetic tree reconstructions confirmed the viral provenance of both vAmt flanking genes (OtV6_114c and OtV6_116; Fig. S4). To rule out contamination and genome assembly artifact, we confirmed the presence of the vAmt encoding gene (OtV6_115c) on the OtV6 genome by targeted PCR amplification (Fig. 2A,B). Three sets of PCR primers were designed to amplify through the complete vAmt encoding gene and its 5′ and 3′ flanking genes (Fig. 2B; Table S1; GenBank identifier: KX254356). These results confirm that the transporter encoding gene is linked to viral genes OtV6_114c and OtV6_116 and therefore residing on the viral genome. In addition, no spliceosomal introns were identified in the vAmt encoding gene, while all *Ostreococcus* spp. homologs have one intron with the exception of *Ostreococcus* sp. RCC809, which has no introns (Fig. S1B).

Next, we sought to confirm that the vAmt encoding gene is expressed during infection. We isolated RNA from infected and uninfected *O. tauri* cultures in parallel. Two different sets of reverse transcription (RT) PCR primers directed against the vAmt encoding transcript (*RT-vAmt* primer sets; Fig 2B; Table S1) amplified products in the infected cultures; no amplicons were found in the uninfected cultures (Fig. S5). We sequenced both RT-PCR amplicons from the infected cultures and confirmed that they corresponded to the vAmt encoding gene and that this viral gene is expressed during infection.

vAmt is a NH_4^+ transporter. The vAmt ORF is located on the reverse strand of the OtV6 genome (Fig. 2A) and encodes a putative protein of 439 amino acids. Sequence similarity searches of UniProtKB demonstrate the Amt1.1 sequence from the OtV6 host *O. tauri* (UniProtKB identifier: A0A096PA30) has the highest similarity with 75.8% amino acid similarity and 62.3% nucleotide identity (Fig. S6A). In the curated SwissProt database [34], the best match to the viral protein was *Arabidopsis thaliana* Amt1.3 sequence (Q9SQH9; 65.9% amino acid similarity with vAmt), which was shown to mediate NH_4^+ uptake in N-replete and N-deplete conditions [51].

The vAmt predicted protein secondary structure has 11 transmembrane domains, a structural feature shared by other NH_4^+ transporter proteins including the *O. tauri* Amt1.1 (Fig. 2B, Fig. S6A and Fig. S7). These transmembrane domains corresponded to 11 alpha-helices, which have been shown for several NH_4^+ transporters to cross the membrane making up a conserved hydrophobic pore and to contribute to the overall channel stability of the transporter, as revealed by crystal structures [52–54]. In addition, the vAmt has a predicted extracellular N-terminal and cytosolic C-terminal topology, a topology also found for eukaryotic Amt proteins [35] (Fig. S7; see fig. S1C for comparison of Amt homolog C-termini). Furthermore, vAmt possess another hallmark of NH_4^+ transporters: two conserved histidine residues in the hydrophobic pore consistently found in helices V and X (Fig. S6A), and shown to be essential for transport activity [55]. In addition to the high level of sequence conservation between the vAmt and its *O. tauri* Amt1.1 homolog, protein structures inferred from viral (Fig. 2C) and host (Fig. S6B) homologs showed a high level of structural similarity (Fig. S6C).

To confirm the vAmt is a functional transporter, we cloned the vAmt encoding gene (pAG416 GPD vAmt) and transformed it into the yeast *S. cerevisiae* mutant 31019b [56], which has had the three known native yeast NH_4^+ Mep transporters deleted (*mep1*Δ*mep2*Δ*mep3*Δ). We compared growth of this mutant with parallel cultures of the same strain but containing only an empty vector (pAG416 GPD) and under culture conditions where 100 or 500 µM NH_4^+ were available as the sole N source. Complementation of the yeast mutant with vAmt increased growth rate and culture density consistent with vAmt encoding a functional NH_4^+ transporter (Fig. 3A and S8A). For comparison we showed that addition of pAG416 GPD vAmt did not facilitate growth of the YNVW1 *S. cerevisiae* mutant [57], which has had its urea transporter *dur3* gene deleted (*dur3*Δ), on medium containing 100 or 500 µM urea as sole N source (Fig. S8), indicating that vAmt does not transport urea in addition to NH_4^+. GFP tagging of either the vAmt C- or N-termini identifies a plasma membrane localization, with some additional patchy localization, in yeast (Fig. 3B). Similar patterns of localization have been reported for plant Amt transporters, when expressed and tagged in yeast [58].

Comparison of radiolabeled methylammonium uptake rates in yeast mutants (strain 31019b) complemented with either the vAmt encoding or the *O. tauri* Amt1.1 genes demonstrated that the viral variant encodes a protein mediating the uptake of methylammonium with a higher rate at lower concentrations, for example 50 - 100 µM, compared to its *O. tauri* homologous protein which showed an improved uptake rate at higher methylammonium concentrations (e.g., 500 µM;

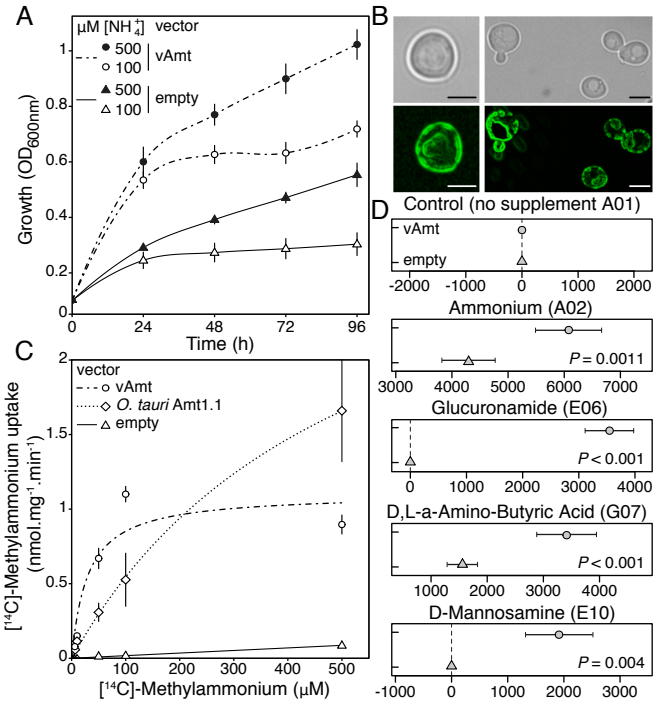

Fig. 3. vAmt is a functional NH_4^+ transporter that takes up alternative substrates, is localized to the cell membrane and mediates an uptake at higher rate for low substrate concentrations than *Ostreococcus* Amt1.1 homolog when expressed in yeast. (*A*) Culture optical density (OD_{600nm}) of an NH_4^+ uptake defective yeast mutant (strain 31019b) transformed either with an empty vector or a vAmt-containing vector in two NH_4^+ concentrations (100 and 500 μM). Error bars represent standard errors based on culture triplicates. The lines represent local polynomial regression fits (see Fig. S8 for the equivalent results of an additional experiment with *O. tauri* Amt1.1). Growth of empty vector transformed mutant is facilitated by passive diffusion of NH_4^+ across yeast membrane and/or scavenging of intracellular N stocks. (*B*) vAmt GFP fusion proteins expressed in yeast, cloned in-frame in N-terminus (left panel) or in C-terminus (right panel); scale bars display 3 μm distances. (*C*) [^{14}C]-methylammonium uptake rates in mutant strain 31019b complemented with vAmt or the *O. tauri* Amt1.1 homolog. Lines show Michaelis-Menten curves; error bars represent standard errors based on culture triplicates. (*D*) Omnilog® comparison of mean point estimates and their 95% confidence intervals for N sources showing significant increase in respiration (area under the curve) of vAmt-transformed 31019b yeast cultures compared to non-vAmt transformed 31019b cultures; data was normalized by subtracting negative control. See Fig. S8 for complementation experiments confirming culture growth phenotypes in all of these results apart from D,L-a-amino butyric acid where complementation is not confirmed; see Fig. S9 for OmniLog® Phenotype Microarray respiration curves.

Fig. 3C). Strikingly, these analyses demonstrate that both transporter proteins have distinct substrate affinities and kinetics, specifically *O. tauri* Amt1.1 transporter has a K_m of 520 μM (± 250 s.e.; V_{max} = 3.38 ± 0.91 nmol.mg^{-1}.min^{-1}) and the vAmt has a K_m of 30 μM (± 10; V_{max} = 1.1 ± 0.1 nmol.mg^{-1}.min^{-1}). These distinct properties of host and viral transporters indicate that production of the vAmt protein during infection has the potential to alter the N uptake dynamics of infected cells.

Using the OmniLog® system [59], we investigated the range of N substrates that showed an increased respiration rate phenotype in yeast. Comparisons of the NH_4^+-uptake deficient 31019b strain carrying pAG416 GPD vAmt with 31019b carrying only an empty vector (pAG416 GPD) were used to identify potential alternative substrates of the vAmt transporter that resulted in increased respiratory rates. In addition to NH_4^+, this phenotype assay identified a significant increase in respiratory rate on three alternative N sources: D,L-a-amino-butyric acid, glucuronamide and D-mannosamine (Fig. 3D and Fig. S9). Two of these three alternative vAmt substrates were further confirmed by functional complementation experiments in yeast cultures (Fig. S8). We note that this method likely underestimates the range of substrates transported by vAmt because alternative substrates may have no 'metabolic' effect in yeast but could be utilized in other cellular background such as *O. tauri*.

Viral infection alters the uptake rate of methylammonium by *Ostreococcus* cells. Next we carried out infection experiments of *O. tauri* cultures with OtV6, in order to determine if infection and expression of the vAmt encoding gene altered the NH_4^+ uptake rates of the host alga (relative to non-infected, control cultures; $n = 3$). To this aim, we conducted an infection timecourse experiment. For 16 hours post infection (hpi), we monitored *O. tauri* and virus-like particle (VLP) abundances (enumerated by flow cytometry; FCM) and methylammonium uptake rates (Fig. 4, Tables S2 and S3).

Based on FCM estimates of cell and VLP abundances, the ratio OtV6 particle to *O. tauri* cell (as a proxy for multiplicity of infection [60]) at the start of the experiment was of 0.42 ± 0.06 s.e.; algal growth was not significantly affected by viral infection for the first 12 hpi (Fig. 4A). At 12 hpi, temporal change in cell abundance significantly differed between control and infected algal cultures (two-sample t-test, $t_4 = 7.03$, $P = 0.002$; Table S2), with a sharp decrease of 11.8% on average in abundance for the infected cultures (corresponding to a loss of 0.59×10^7.cells.ml^{-1} ± 0.12 s.e.); in contrast, the control *O. tauri* cultures were steadily growing, with an average gain of 33% between 8 and 12 hpi (a gain of 1.44×10^7.cells.ml^{-1} ± 0.53). This drop in *O. tauri* cell number in infected cultures indicate occurrences of cell burst and lysis caused by viral shedding. The OtV6 latent period is thus between 8 and 12 hpi, a time frame comparable to other prasinovirus of *Ostreococcus* and *Micromonas* spp. [31, 41]. FCM enumeration of VLPs confirmed the reduction in VLPs prior to 12 hpi, consistent with virus adsorption followed by increase in VLPs after 12 hpi, which is in turn consistent with OtV6 particle release (Fig. 4A; Table S3).

During the infection experiment, we used two methods to track NH_4^+ flux in *O. tauri* cells. First, we determined [^{14}C]-methylammonium uptake rates of standardized subsamples of *O. tauri* cells throughout the timecourse experiments. This analysis demonstrated significant increases in methylammonium uptake rates for infected cells, consistent with viral infection altering the NH_4^+ uptake phenotype of the phytoplankton host (Fig. 4C). We also monitored by fluorometry NH_4^+ concentration in the cell-free culture media, which showed depletion at 8 hpi in NH_4^+ concentration compared to 0 hpi in the infected cultures, although not significant (Fig. S10).

In addition, we used quantitative PCR (qPCR) to quantify the transcript levels of several *O. tauri* and OtV6 genes (Table S4) during the latent period of infected cultures (i.e., 0 - 12 hpi). The qPCR shows that transcription of the vAmt encoding gene is maintained relatively constant during infection, and at a similar level to that of the viral DNA polymerase B gene, while transcription of the gene encoding the major capsid protein increases until 4 hpi and is then expressed at relatively high level throughout 4 to 12 hpi (Fig. 5). Taken together, VLP and host cell dynamics, along with gene transcription, all

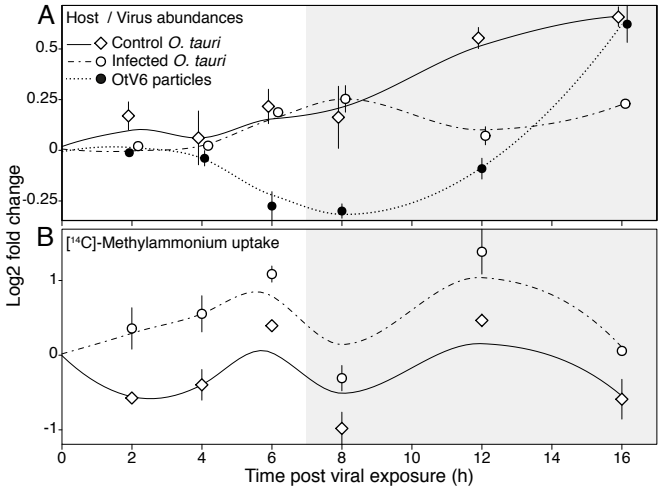

Fig. 4. Nitrogen source uptake during viral infection. (*A*) Temporal dynamics of host cell and viral particle abundances, and (*B*) [^{14}C]-methylammonium uptake rates in OtV6-infected and non-infected *O. tauri* cultures. Three *O. tauri* cultures were exposed to OtV6 (timepoint 0 hpi) and three other non-infected cultures were used as controls. For each panel, (log2) fold changes are based on timepoint 0 hpi (i.e., time of viral inoculation for infected *O. tauri* cultures); plots summarize the fold change distribution of three cultures for a given timepoint during the experiment, and trend lines were estimated by local polynomial regressions (loess). Shaded overlays indicate incubator dark period ('night'). *O. tauri* cells and virus-like particles were enumerated using flow cytometry; uptake rates were estimated by tracing the isotope labeled [^{14}C]-methylammonium uptake in cultures taken as subsamples throughout the timecourse experiment. See Tables S2 and S3 for two-sample t-test results.

indicate a substantial viral infections of *O. tauri* cells resulting in an altered methylammonium uptake phenotype.

OtV6 acquired vAmt from an *Ostreococcus* host. We sought to explore the ancestry of the vAmt encoding gene by conducting phylogenetic tree reconstruction using a comprehensive sampling of protein sequences of the Amt/Mep/Rh superfamily (Fig. 6A). Proteins of this superfamily are found across all three domains of life and are involved in the transport (uptake and excretion) of ammonium ions through cell membranes [35]. This superfamily of membrane proteins has a complex evolutionary history marked by gene duplications, losses and HGT events, probably driven by environmental selection linked to N availability [7, 32]. In a phylogenetic study, McDonald and colleagues updated the Amt/Mep/Rh superfamily phylogeny [32], showing a partitioning into distinct clades: the monophyletic groups 'Amt-Euk' (originally named Amt1) and 'Mep', as well as two distantly related clades, 'Rh' (Rhesus) and a cluster of archaeal and bacterial homologs grouped into 'Mep-grade'. The Amt-Euk clade is composed of eukaryotic sequences, with a large representation of phytoplankton and plant species. For the host of OtV6, *O. tauri*, four Amt/Mep/Rh transporters were identified in its genome [7], two Amt-Euk (eukaryotic origin; Amt1.1 and 1.2) and two Mep$_\alpha$ (probably acquired via HGT; Amt2.1 and 2.2).

To determine which clade the vAmt groups within, a large-scale, approximate ML phylogenetic tree reconstruction was conducted based on an alignment of all available, non-redundant Amt/Mep/Rh protein sequences, including those from the marine microbial eukaryotic transcriptome project (MMETSP [61]; which includes several *Ostreococcus* transcriptomes such as *O. mediterraneus*). The resulting Amt/Mep/Rh superfamily phylogeny (based on an alignment of 374 sites;

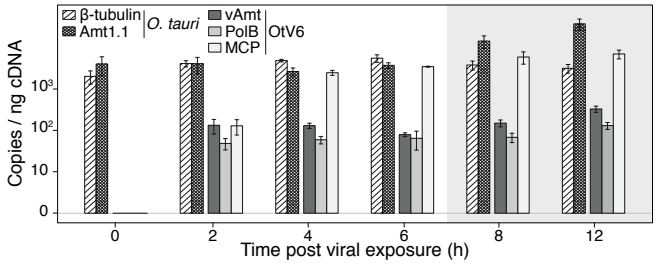

Fig. 5. OtV6-infected *O. tauri* gene expression. Transcript levels were RT-qPCR monitored in infected *O. tauri* cultures (n = 3; same infected cultures as presented in Fig. 4), and expressed as copies per ng of cDNA library (displayed on a log10 scale, Y-axis). Hatched bars show transcript copy numbers of two *O. tauri* genes (β-tubulin and the NH_4^+ transporter Amt1.1); solid color bars show copy numbers for three OtV6 genes (dark grey: viral NH_4^+ transporter, vAmt; light grey: DNA polymerase B; white: major capsid protein). Error bars represent standard errors. Shaded overlays indicate incubator dark period ('night').

Fig. 6A and Fig. S10) demonstrates that the vAmt branched within the Amt-Euk clade. To determine the branching position of the vAmt sequence more accurately, a ML phylogenetic tree was reconstructed using a subset of Amt-Euk homologs (364 sequences, alignment comprised of 429 sites; Fig. 6B and Fig. S11). This phylogeny shows the vAmt branching with the *Ostreococcus* Amt1.1 family radiation, demonstrating that the OtV6 vAmt encoding gene is derived from its host lineage, most likely via host-to-virus HGT. In addition to the recent identification of putative Amt transporters on phage contigs assembled from marine metagenomes [21], our phylogenetic analyses also demonstrated that two metagenomic sequences retrieved from the viral fraction of aquatic samples (Pacific solar salterns, San Diego, USA [62]) branch with the OtV6 vAmt (Fig. 6B and Fig. S11), suggesting a wider geographical distribution of viral NH_4^+ transporters.

Discussion

Here, we demonstrate that a virus of the marine phytoplankton *O. tauri*, representing a distinct lineage of *Ostreococcus* virus (Fig. 1), harbors a gene encoding a transporter protein that is expressed during infection (Fig. 5 and S5) and functions to take up NH_4^+ (Fig. 3A and S8A) and a range of alternative fixed N sources (Fig. 3D, S8 and S9). Phylogenetic analyses show that the viral transporter is the result of a HGT event and was acquired from the host *Ostreococcus* lineage (Fig. 6B).

Viral HGT and functional compatibility. Many host-derived AMGs, including the vAmt encoding gene reported here, are highly similar at the sequence level to their host homologs. This has two implications: first, it complicates the analysis of viral metagenomes, as the process of host-to-virus HGT is likely to 'contaminate' viral metagenomes with sequences that appear as though they should belong to larger sample filtration fractions (i.e., the fraction containing host genomes). This can be ameliorated by the use of metagenome assembly methods that control for host-derived genes harbored by viral genomes [21]. Second, it confirms that viruses are acquiring genes from their host lineage and therefore acting as vectors for HGT. HGT and viral integration of genes that function in how host cells interact with their environment demonstrates a selective scenario that can drive transfer of genes encoding functional traits. Indeed, bacterial genomic islands often

contain transporter encoding genes and have been shown to undergo gene gain at high relative rates (for instance in the pico-cyanobacterium *Prochlorococcus* [63]). Genes that encode transporter proteins are relevant because they encode the proteins responsible for nutrient uptake and are *functionally compatible*. We define a *functionally compatible* gene as a single gene that encodes a complete trait and also requires little protein-protein interaction network complexity to result in a function [64, 65]. As such, these gene classes are easily lost, duplicated or (re-)acquired during the diversification of a lineage, leading to these genes having complex evolutionary histories often involving HGT events [7, 29, 32, 66], as similarly observed for photosynthesis genes harbored by genomes of marine cyanophages [67–69].

The role of vAmt during infection. Both *O. tauri* and *O. lucimarinus* are able to grow with NH_4^+ as the sole N source [70]. Here we demonstrate that the vAmt encoding gene harbored by OtV6 is transcribed during viral infection (Fig. 5 and Fig. S5), and NH_4^+ (methylammonium) uptake in infected *Ostreococcus* cells is enhanced compared to uninfected cells (Fig. 4C). Interestingly, expression in a yeast mutant demonstrates that the viral vAmt transporter has a higher affinity (defined here as [^{14}C]-methylammonium uptake rate) at low environmental substrate concentrations compared to the algal transporter homolog, which has a higher relative NH_4^+ uptake rate at higher environmental concentrations. Competition for NH_4^+ is fierce in many marine systems, given that it is often the preferred source of inorganic N for phytoplankton cells [10]. Expression of the vAmt encoding gene during *O. tauri* infection may increase host NH_4^+ uptake rate and therefore may provide an advantage to infected host cells over non-infected algae in terms of N uptake, allowing an infected population to temporarily out-compete other phytoplankton species including uninfected sister cells. As such, production of vAmt transporter proteins is likely to act to fulfill the extended N requirements of viral replication within the infected host cell to sustain the physiological burden of viral replication through the uptake of various organic N sources.

Using comparative culture screening, we show that the vAmt protein potentially mediates the uptake of alternative organic N sources in addition to NH_4^+. Amt transporter proteins are known to mediate the uptake of at least one alternative to NH_4^+, methylammonium [71]. Most knowledge regarding substrate affinities of protein transporters derives from annotation resulting from sequence homology searches, and few experimental studies; it is thus important to take into account, when assessing the significance of transporter proteins in an ecological context, that these proteins may display affinities to additional substrates not described via bioinformatic annotation [72].

Viral manipulation of host elemental composition. Harboring genes coding for functional nutrient transporters implies that phytoplankton viruses directly manipulate the elemental composition of their host cells. This viral stoichiometric alteration would confer a strong advantage to viruses able to interfere with the hosts' nutrient uptake capabilities by encoding their own transporter repertoires. Availability of nutrients to phytoplankton hosts has been shown to be of critical importance for phytoplankton virus proliferation (see [33]). Infection experiments on phytoplankton cultures depleted in P and N

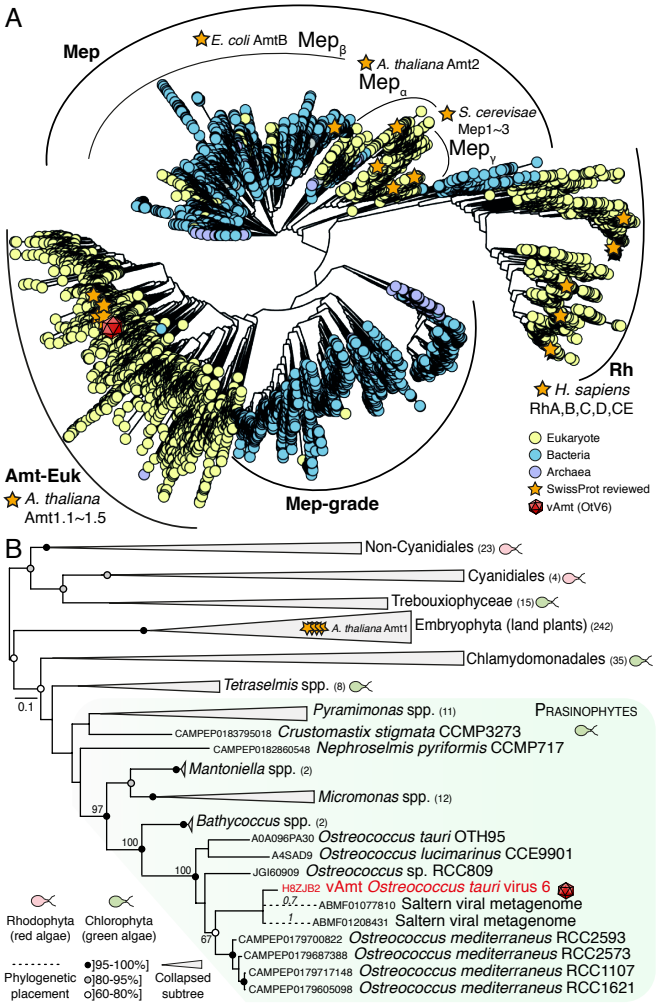

Fig. 6. vAmt phylogenetic ancestry shows it is derived by HGT from the host lineage. (*A*) Amt/Mep/Rh superfamily phylogenetic tree. This large-scale approximate ML tree was inferred under WAG+G model. Homologs were recruited based on a similarity search using the Pfam HMM corresponding to the Amt/Mep/Rh superfamily (PF00909) against UniRef100 (i.e., non-redundant version of UniProtKB), MMETSP protist transcriptomes and predicted proteomes from various protist genome projects; the final curated alignment was composed of ∼20k protein sequences encompassing 374 sites. Curved black lines indicate the phylogenetic positions of the main clades (Amt-Euk, Mep, Mep-grade and Rh) as well as Mep subclades (α, β and γ). The red capsid graphics shows the phylogenetic position of the vAmt within the superfamily tree, positioned within the Amt-Euk clade. For contextual reference, orange stars represent SwissProt reviewed protein entries; yellow, blue and purple circles represent eukaryotic, bacterial and archaeal proteins, respectively. See Fig. S10 for additional information, including local support values, MMETSP sequence positions and scale bar. (*B*) vAmt evolutionary relationships with Amt-Euk (Amt1) homologs. This ML phylogenetic tree was inferred under LG+I+G+F model, based on a multiple alignment of 364 proteins totaling 429 sites. These vAmt homologs were recruited and selected based on the Amt/Rh/Mep superfamily phylogenetic tree reconstruction. Green and red cell schematics represent green and red algal lineages. vAmt is highlighted in red with a capsid graphics, and branched within the prasinophyte green algae, delimited by a green frame. Code numbers in front of species names represent sequence identifiers from either the MMETSP transcriptomes (*O. mediterraneus*, *N. pyriformis* and *C. stigmata*), UniProtKB (*O. lucimarinus* and *O. tauri*) and the *Ostreococcus* sp. RCC809 genome project available at the DoE-Joint Genome Institute. Numbers in parentheses besides clade names are the number of sequences present in collapsed nodes. Branch node supports were computed from 1000 non-parametric bootstrap replicates. Grey and black circles correspond to bootstrap values of]80 – 95%] and]95% - 100%], respectively. The dashed branches represent the phylogenetic placement of two short environmental sequences, with placement posterior probabilities indicated on their corresponding branches; both sequences originate from a saltern viral metagenome (NCBI BioProject: PRJNA28353), and their GenBank sequence identifiers are provided. See Fig. S11 for additional data and uncollapsed branch information.

have shown that low concentrations of these nutrients can significantly hamper viral cycle dynamics in terms of latent period and burst size (i.e., the number of viral progeny per lysed cell) as well as decreasing the infectivity of viral progenies; such constraints on viral replication has been shown for various clades of Phycodnaviridae (e.g., [30, 73]), including for a *Micromonas* virus, a close relative of OtV6 (Fig. 1).

Although most studies have focused on the effect of low P availability on phytoplankton virus replication, recent studies have shown the importance of N availability for the quality of viral replication [31, 73]. In particular, the burst size of PBCV1, a virus of the green alga *Chlorella*, was shown to decrease with higher C:N ratio of the algal host cell [73]. Furthermore, the effect of N depletion was shown to be more detrimental to viral proliferation than low P availability for a Phycodnaviridae-phytoplankton system [31]. These results are somewhat anticipated because of the stoichiometric requirements of phytoplankton virus replication, which is exacerbated by the strong discrepancy in C:N:P ratios between viral particle and the host phytoplankton cell [74]. Viruses exhibit much lower C:P and C:N ratios than their hosts, as shown for PBCV1's 17C:5N:1P composition [75], compared to the Redfield ratio of 106C:16N:1P, the elemental composition of an average phytoplankton [74].

In the case of the Phycodnaviridae EhV, a virus of the coccolithophore *Emiliania*, it was noted that viral genomes were being overproduced during the infection cycle, relative to the number of capsids being produced by the infected phytoplankton [76]. Such discrepancy between genome and capsid productions may be linked to a shortage in amino acids and/or lipids, constituent of EhV lipid membrane, limiting viral production [76, 77]. This is predictable for Phycodnaviridae given the N requirements of PBCV1 capsid, which is composed of ∼5050 major capsid proteins (MCP; [78]). Based on the MCP protein sequence of PBCV1, the elemental composition of the complete PBCV1 capsid would be $C_{2161}H_{3301}N_{577}O_{657}S_9$, that is, a C:N ratio of 4:1. Hence, the ability of OtV6 to express its gene encoding vAmt and enhance or maintain NH_4^+ uptake would allow the host to fulfill the requirements in N imposed by the viral replication, in turn providing a strong fitness advantage to OtV6 relative to marine viruses without a N transporter gene repertoire. Further work will be required to understand the role of virally-encoded nutrient transporters in the dynamics of viral replication, especially in contrasting nutrient concentrations.

Blurring top-down and bottom-up controls. Consistent with the idea that viral proteins act to amend host N metabolic function, a putative glutamine synthetase gene has also been identified in the genomes of NCLDVs such as Mimivirus and Mamavirus [79]. These data suggest that viral reprogramming of host N metabolism may be a wider phenomenon [21, 80], as has been shown for photosynthetic function [81], sulfur oxidation [82], lipid [25–27] and phosphate metabolism [83]. Evidence that a viral lineage can acquire host genes to amend host nutrient uptake has implications for our understanding of phytoplankton ecology. Specifically, this phenomenon blurs the lines between bottom-up and top-down regulation of phytoplankton communities, because here a top-down viral agent has acquired the host genes which allow it to amend phytoplankton nutrient acquisition from the environment, which is normally considered a bottom-up process.

Materials and Methods

vAmt identification, sequence and structure analyses. To identify a viral transporter sequence putatively involved in NH_4^+ uptake, all protein sequences available in UniProtKB [34] and the NCBI non-redundant Reference Sequence database [84] were searched using 'hmmsearch', part of the HMMer v3 software suite [85], with the Pfam [86] HMM corresponding to the NH_4^+ transporter superfamily (Pfam release 3.0 identifier: PF00909). Hits were filtered using E-value ($1e^{-10}$) and gathering cutoffs. This large-scale search identified only a single viral encoded putative transporter protein, OtV6 vAmt (HMMer search statistics with PF00909 model: score: 418.4, E-value: $1e^{-129}$). To avoid missing additional putative viral NH_4^+ transporters –potentially due to inaccurate viral gene modeling– a HMM based search was repeated on 6-frame translations of all viral genomes available at the NCBI genomic sequence repository (ORF minimal size: 60 amino acid residues). In addition to the Pfam-based HMM searches, further searches using the TIGRfam [87] NH_4^+ transporter HMM (TIGR00836; release 15) were conducted using the aforementioned protein sequence datasets. These additional searches did not recover any other viral sequences matching the NH_4^+ transporter HMMs.

Transmembrane domains of the vAmt and *O. tauri* Amt1.1 protein sequences were identified using TMHMM v2 [88]. Protein structures were predicted using I-TASSER v4.2 [89]; the C-scores of the vAmt and *O. tauri* Amt1.1 3D structure models were 1.36 and 0.72, respectively. *O. tauri* Amt1.1 and vAmt predicted structures were aligned using MatchMaker (UCSF Chimera [90]).

Phylogenetic tree reconstructions. The Amt/Mep/Rh superfamily phylogeny was reconstructed using an approximate ML method as implemented in FastTree v2.1 ([91]; compiled using the double precision flag) and based on an alignment of 19,493 protein sequences sampled from UniProt100 (clustered at 100% sequence identity; [34] in order to reduce redundancy). HMM searches were also conducted against predicted protein sequences from the MMESTP transcriptomic data [61] and from protist genome projects available at the DoE-Joint Genome Institute. All identified putative Amt/Mep/Rh sequences were then aligned using 'hmmalign' [85] and sequences shorter than 50 amino acid residues were discarded. Alignment sites composed of more than 50% of gaps were discarded. Mis-aligned and/or false positive sequences were detected using preliminary phylogenetic reconstructions with FastTree (default parameters). Sequences that resulted in very long branches were then removed allowing a final tree calculation using the 'accurate' mode (-slownni) with the WAG+G substitution matrix.

For the ML phylogeny, different strategies were applied for putative homolog sampling. For the viral DNA polymerase B and the vAmt flanking ORFs, homologous protein sequences were identified with BLASTP [92] similarity searches against UniProtKB. The homologous sequences were then aligned using the iterative refinement method E-INS-i as implemented in MAFFT v7.2 [93], edited with trimAl v1.4 'strict' algorithm [94] and manually inspected and corrected. For the phylogeny based on the 22 core proteins shared among green algal viruses [46], the OtV6 predicted proteome was parsed using BLASTP and homologous sequences from other *Ostreococcus* spp. viruses were used as search queries. The resulting 22 OtV6 core proteins were then concatenated, aligned and added to the original viral core protein alignment using MAFFT.

For the vAmt/Amt-Euk ML phylogenetic subtree, vAmt homologs were identified using the previous large-scale, superfamily phylogenetic reconstruction described above. Sequences branching with vAmt were identified; corresponding full-length sequences were retrieved and aligned with MAFFT E-INS-i, and manually inspected. After homolog sequence selection and alignment, the same methodology was applied for all ML phylogenetic tree reconstructions. The most likely tree was identified from 100 ML reconstructions, using RAxML v8.2 [95], and under the substitution model best fitting the data, as identified by ProtTest v3 [96] using the Akaike information criterion; branch support values were based on 1000 non-parametric bootstrap replicates.

Metagenome screening and phylogenetic mapping. To investigate the wider distribution of vAmt-like homologs, we screened metagenomes for similar sequences in GOS, *Tara Oceans* giant virus dataset [50] as well as all aquatic metagenomes available at iMicrobe [97]. Putative vAmt homologs were aligned to alignment corresponding to the vAmt subtree (Fig. 6B and Fig. S10) using MAFFT (without altering the original alignment) and then phylogenetically mapped onto the ML tree using pplacer v1.1 [98]. Within this tree, two Amt-Euk sequences mapped to the vAmt branch.

vAmt genomic amplification. To confirm the vAmt encoding gene was harbored by OtV6, we designed specific primer pairs (listed in Table S1) and the vAmt gene along with its 5′ and 3′ flanking regions were amplified, represented by a ∼2500 bp sequence. For each PCR reaction, a negative control (distilled H_2O) was included. PCR reactions (25 µL total volume) were conducted using GoTaq® Green Master Mix (Promega, Madison, WI, USA) with 1 µL of virus OtV6. Cycling reactions were as follows: 5 m at 95 °C, followed by 30 cycles of 30 s at 95 °C, 30 s at 54 °C, 120 s at 72 °C and with an additional 10 m extension at 72 °C. The PCR reactions were checked on 1% agarose gel stained with GelRed™ (Biotium, Hayward, CA, USA). The positive PCR reactions were then directly cloned using the StrataClone™ PCR cloning kit (Agilent Technologies, Santa Clara, CA, US) according to the manufacturer's instructions. One clone per library was selected and double strand sequenced using universal *M13* primers. All amplicon sequencing was performed externally by Eurofins Genomics (Ebersberg, Germany).

***Ostreococcus* culture infection and vAmt RT-PCR.** *O. tauri* cells from the RPN2 population (OtV5 resistant; see [44]) were grown in L1 medium exponentially under 12:12 light (32.3 photons µmol m^{-2} s; 1700 lux). Infection experiments proceeded as followed: 5 mL of *O. tauri* at exponential growth were infected using 250 µL of purified OtV6; as a negative control, 5 mL of *O. tauri* culture were incubated with 250 µL of L1 medium. To test for the expression of the vAmt encoding gene during the infection cycle, the *O. tauri* cultures were sampled 12 h after OtV6 inoculation; 1 mL of the infected and uninfected cultures were sampled and centrifuged at 8000 rpm during 10 m. After removal of the supernatant, the pellets were flash frozen and stored at -80 °C. RNA was extracted using the RNeasy® Plus Universal Kits (Qiagen, Valencia, CA, USA). An extra step to remove all genomic DNA was added after the RNA extraction protocol using the RTS DNase™ kit (MO BIO Laboratories, Qiagen).

Using three sets of primers that amplify an overlapping region of the vAmt encoding gene (*OtV6-full-F1/R1*, *vAmtF4/R4* and *sh-Amt-vir-F/R*; Fig. 2B and Table S1), we first checked for the presence of DNA contamination in the RNA samples using PCR amplification. For every PCR reactions, we included a negative control (distilled H_2O) and a positive control (1 L of purified OtV6). PCR reactions were performed in 25 µL total volume using GoTaq® Green Master Mix with 1 µL of RNA sample. Cycling reactions were as follows: 5 m at 95 °C, followed by 35 cycles of 30 s at 95 °C, 30 s at 50 °C, 45 s at 72 °C and with an additional 10 m extension at 72 °C. The PCR reactions were checked on 1% agarose gel stained with GelRed™. The RT-PCR reactions were conducted using OneTaq® One-Step RT-PCR (Qiagen). 1 µL of RNA was mixed in 50 µL with 10 µL of Buffer 5×, 2 µL of 10 mM dNTP, 1 µL of each primer (0.2 mM final concentration), 2 µL enzyme mix and finally 0.25 µL of RNaseOUT™ (10 u/µL; Invitrogen, Life Technologies, Carlsbad, CA, USA). Negative controls were made with 1 µL of water instead of the RNA samples. Each PCR amplification was checked on 1% agarose gel stained with GelRed™. Positive RT-PCRs were cloned using Strataclone™ PCR cloning kit; one clone per library was selected and double strand sequenced using *M13* primers.

Cloning and functional analysis of vAmt in yeast. The vAmt ORF was synthesized *de novo* by Genscript (Piscataway, NJ, USA), codon optimized for expression in *S. cerevisiae*, and fused to a C-terminal GFP tag in vector p426 GPD. For complementation assays, the vAmt ORF was amplified with primers *vAmt-attF/R* (Table S1) using Phusion® polymerase (New England Biolabs, Ipswich, MA, USA) to remove the GFP coding region; cloned into pDONR221 using Gateway® recombination (Life Technologies) and mobilized into pAG416 GPD (low copy constitutive expression vector). For fluorescence microscopy, the ORF was mobilized into pAG426 GPD EGFP (N-terminal EGFP vector) or the original p426 GPD EGFP (C-terminal) construct was used.

For yeast transformations, competent cells were prepared as described in Thomson et al. [99], mixed with ∼500 ng of plasmid DNA, and pulsed at 1.5 kV in an Eppendorf electroporator. *S. cerevisiae* strain 31019b was transformed with pAG416 GPD vAmt or pAG416 GPD empty vector, as described above. Transformed yeast 31019b cultures were grown to stationary phase at 30 °C and centrifuged at 3200× *g* for 2 m, washed twice in water and diluted to OD_{600nm} 0.1 in 10 mL YNB liquid medium (0.19% Yeast Nitrogen Base without amino acids and without $(NH_4)_2SO_4$; Formedium, Norfolk, UK) containing a final concentration of 0.1 or 0.5 mM $(NH_4)_2SO_4$, D-mannosamine, D-glucuronamide or D,L-a-amino-butyric Acid. Cells were then incubated at 30 °C and OD_{600nm} measurements were taken at 24 h intervals. This method was also used to assess growth of *S. cerevisiae* YNVW1 (Δ*dur3*) and Σ23346c (wild type) on urea, with YNB supplemented with urea (0.1 – 2 mM) instead of $(NH_4)_2SO_4$. R v3 and *ggplot2* [100] were used for statistical analyses and plots.

Spinning disc confocal microscopy. GFP constructs were transformed into *S. cerevisiae* strain BY4742, as described above, grown to mid-log phase and suspended in PBS. Spinning disc confocal microscopy of EGFP-labelled cells was performed using an Olympus IX81 inverted microscope and CSU-X1 Spinning Disc unit (Yokogawa, Tokyo, Japan). A ×60/1.35 oil or ×100/1.40 oil objective was used with a 488 nm solid-state laser to excite the EGFP fluorophore. A Photometrics® CoolSNAP™ HQ2 camera (Roper Scientific, Martinsried, Germany) was used for imaging with the VisiView® software (Visitron Systems, Puchheim, Germany).

Transporter protein phenotyping. To prepare cells for OmniLog® Phenotype Microarray (PM) plates (Biolog, Hayward, CA, USA), each yeast strain (*S. cerevisiae* 31019b transformed with either pAG416 GPD or pAG416 GPD vAmt) was grown on YNB+KNO3-ura at 30 °C for 48 - 72 h. Colonies were suspended in Yeast Nutrient Supplement solution (Biolog) and adjusted to 62% turbidity. 250 µL of cell suspension was made up to a final volume of 12 mL of inoculating fluid, containing 1× IFY-0, 1× Dye Mix D, 50 mM D-glucose, 1 mM disodium pyrophosphate and 2 mM sodium sulfate and 100 µL was inoculated into each well of a PM3 MicroPlate™ (N sources). Assays were run in triplicate using independently obtained transformants. OmniLog® Phenotype Microarray outputs were analyzed by normalizing each individual plate against well A01 (negative control) to control for any background growth as a result of the inoculation solution, then analyzed using the R package *opm* [101]. Data were aggregated using the 'opm-fast' method, analyzed using the area under curve (AUC) parameter and tested by t-test to detect significant increase in respiration rates in the pAG416 GPD vAmt strain.

Yeast methylammonium uptake assays. *S. cerevisiae* strains were grown in 25 mL minimal proline medium [102] for 16 h at 30 °C shaking. Cells were then diluted and grown until early log-phase and harvested by centrifugation at 1000 × *g* for 3 m. Cells were washed once and suspended in 2 mL medium lacking proline. The dry weight of each sample was noted, before 90 µL aliquots of cells were exposed to 5 concentrations (5 – 500 µM) of methylamine [^{14}C] hydrochloride for 1 m at 24 °C. Reactions were stopped by the addition of 1 mL 120 mM methylamine hydrochloride. Background adsorption was also calculated by exposing cells to 1 mL of 120 mM unlabeled methylamine hydrochloride prior to the addition of the radiolabeled substrate. Cells were collected by centrifugation at 14000 × *g* for 3 m, washed and suspended in 500 µL deionized water, then radioactivity was determined by liquid scintillation counting in a liquid scintillation analyzer (LS 6500; Beckman Coulter, Brea, CA, USA) after addition of 2.5 mL Emulsifier-Safe™ scintillation cocktail solution (Perkin Elmer, Waltham, MA, USA). The R package *drc* [103] was used to calculate Michaelis-Menten kinetics and curves.

Infection timecourse experiments. Two 15 mL cultures of *O. tauri* were inoculated with OtV6 viruses and the infection was allowed to proceed until culture bleaching after 5 days. Cell debris were removed by centrifugation at 3200 × *g* for 20 m followed by filtering

through a 0.2 µm syringe filter. Viruses were concentrated 10-fold using a 50 kDa Amicon® Ultra-15 Centrifugal Filter (Merck Millipore, Darmstadt, Germany) followed by a centrifugation at 3200 × *g* for 2.5 m. 18 mL *O. tauri* cultures were cultured using 10 mL preculture and 8 mL media, 2 days prior to the experiment. To begin the infection timecourse experiments, 750 µL OtV6 were added and at each timepoint, 1 mL sample was pelleted and frozen in liquid nitrogen for RNA preservation and the supernatant was stored at -80 °C for fluorometric NH_4^+ detection. Two 200 µL samples were also taken for flow cytometry: i) 2 µL 25% glutaraldehyde were added and the sample incubated for 15 m before freezing in liquid nitrogen for *O. tauri* counts; ii) 8 µL 25% glutaraldehyde were added and the sample incubated for 30 m at 4 °C before freezing for viral counts. *O. tauri* and VLP abundances were monitored by a FACSCanto™ flow cytometer (BD Biosciences, San Jose, CA, USA) according to their right-angle scatter and the fluorescence emission due either to the chlorophyll *a* pigment for *O. tauri* [104] or to SYBR® Green I (Roche Diagnostics, Penzberg, Germany) staining for VLPs [105]. A 900 µL sample was also removed for assessing methylammonium uptake at each timepoint. Cells were harvested by centrifugation at 5000 × *g* for 3 m and suspended in 450 µL media. For each sample, uptake rate for methylamine [^{14}C] hydrochloride was determined as aforementioned. The orthophtaldialdehyde (OPA) method [106] was used for fluorometric NH_4^+ detection in cell-free medium (supernatant, see above). 20 µL of the working reagent (OPA, borate buffer and sodium sulfite) was added to 80 µL of the culture sample (or NH_4^+ standard); samples and standards were processed on a 96-well plate, which was incubated in the dark at 25 °C with shaking for 2 - 3 h. Fluorescence was then read at 355 nm excitation and 420 nm emission on an Infinite® M200 plate reader (Tecan, Männedorf, Switzerland).

Quantitative PCR. RNA was extracted using the RNeasy® Plus Universal Mini kit (Qiagen) following the manufacturer's instructions and incorporating a 5 m elution step using 30 µL RNase-free water. Residual DNA was removed using the Turbo DNA-free™ kit (Ambion, Life Technologies) and 6 µL RNA reverse-transcribed using the Superscript® III First Strand Synthesis SuperMix (Invitrogen) and oligo(dT)$_{20}$ primers, following the manufacturer's instructions. cDNA was quantified using a Qubit™ ssDNA Assay Kit (Life Technologies) and stored at -20 °C prior to performing qPCR. Plasmids for each gene of interest were generated by Phusion® polymerase (New England Biolabs) PCR using cDNA templates, followed by A-tailing using Taq polymerase and cloning using a Strataclone™ PCR cloning kit (Agilent Technologies). Each plasmid was confirmed by sequencing (Eurofins Genomics) and serial dilutions (10^8 – 10 copies) were used to generate standard curves for each primer pair and probe. Efficiencies ranged from 96 - 102% (Table S4). qPCR reactions were performed in a StepOnePlus™ Real-Time PCR system (Thermo Fisher Scientific, Waltham, MA, USA). Each 25 µL reaction contained 12.5 µL TaqMan™ Gene Expression Master Mix (Thermo Fisher Scientific), 900 nM each primer, 250 nM hydrolysis probe and 1 µL cDNA/plasmid DNA and was performed in duplicate alongside no-template and minus-RT controls. Cycling conditions were as follows: UDG activation for 2 m at 50 °C and DNA polymerase activation for 10 m at 95 °C, followed by 40 cycles of 15 s at 95 °C and 1 m at 60 °C. ROX was used as an internal reference dye for analysis of CT values, which were determined using StepOne™ Software v2.3 (Thermo Fisher Scientific), and standard curves were used for quantification of each gene.

Data access. Phylogenetic and experimental data are available at Zenodo: zenodo.org/record/61901. PCR-amplified sequence assembly of the vAmt locus was deposited in GenBank (KX254356).

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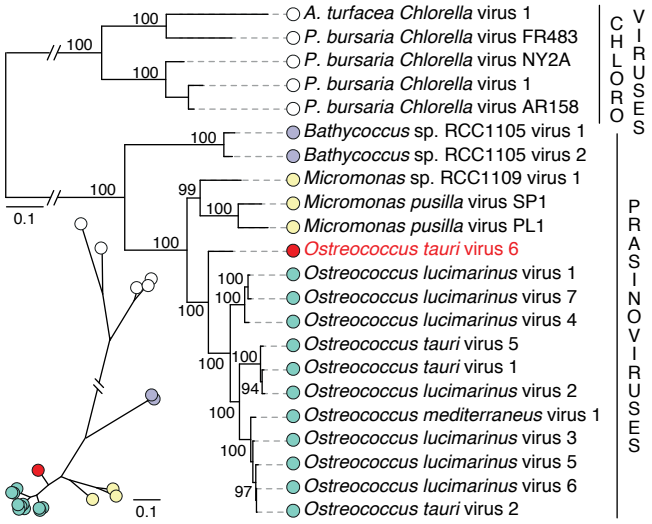
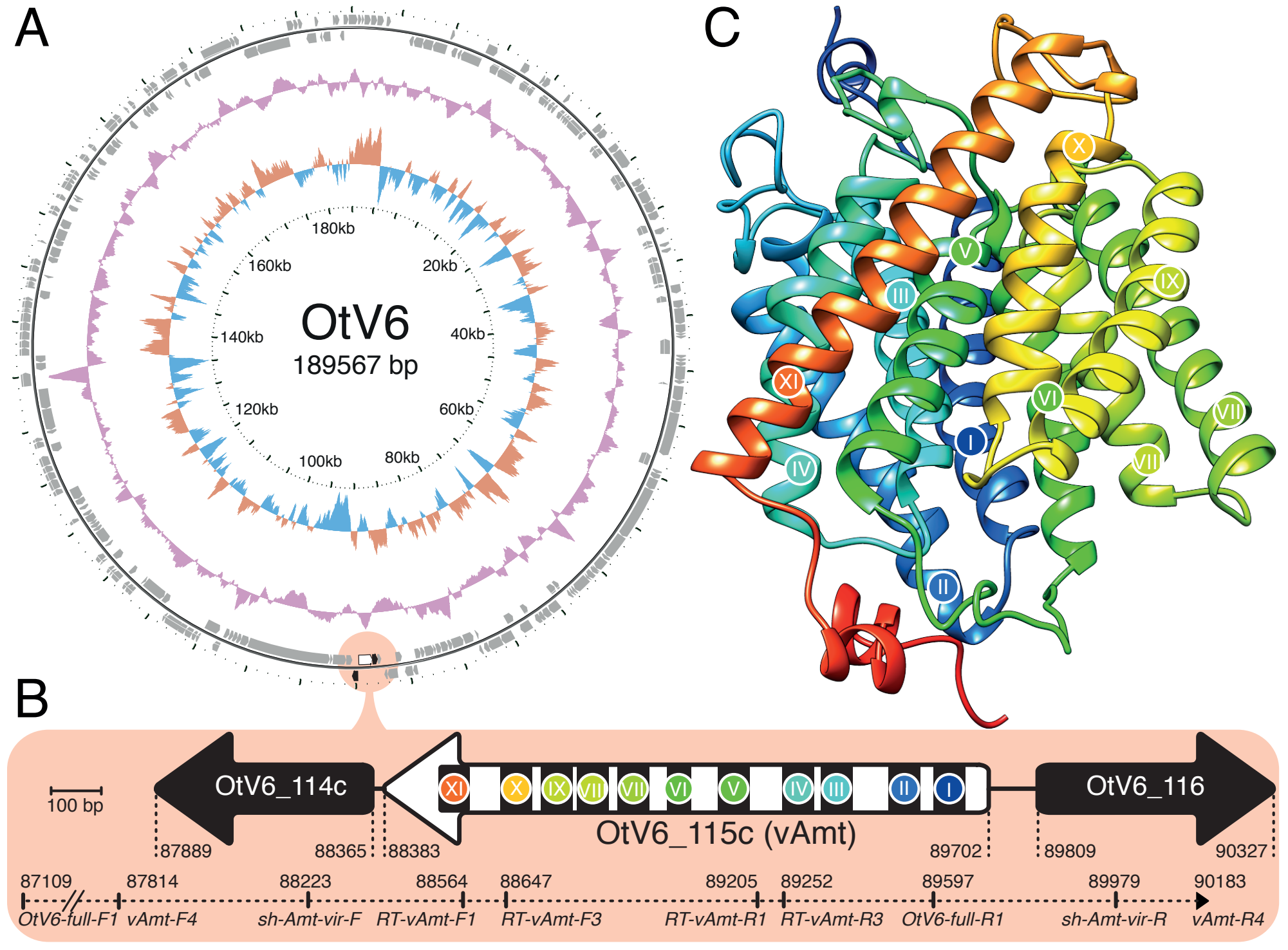
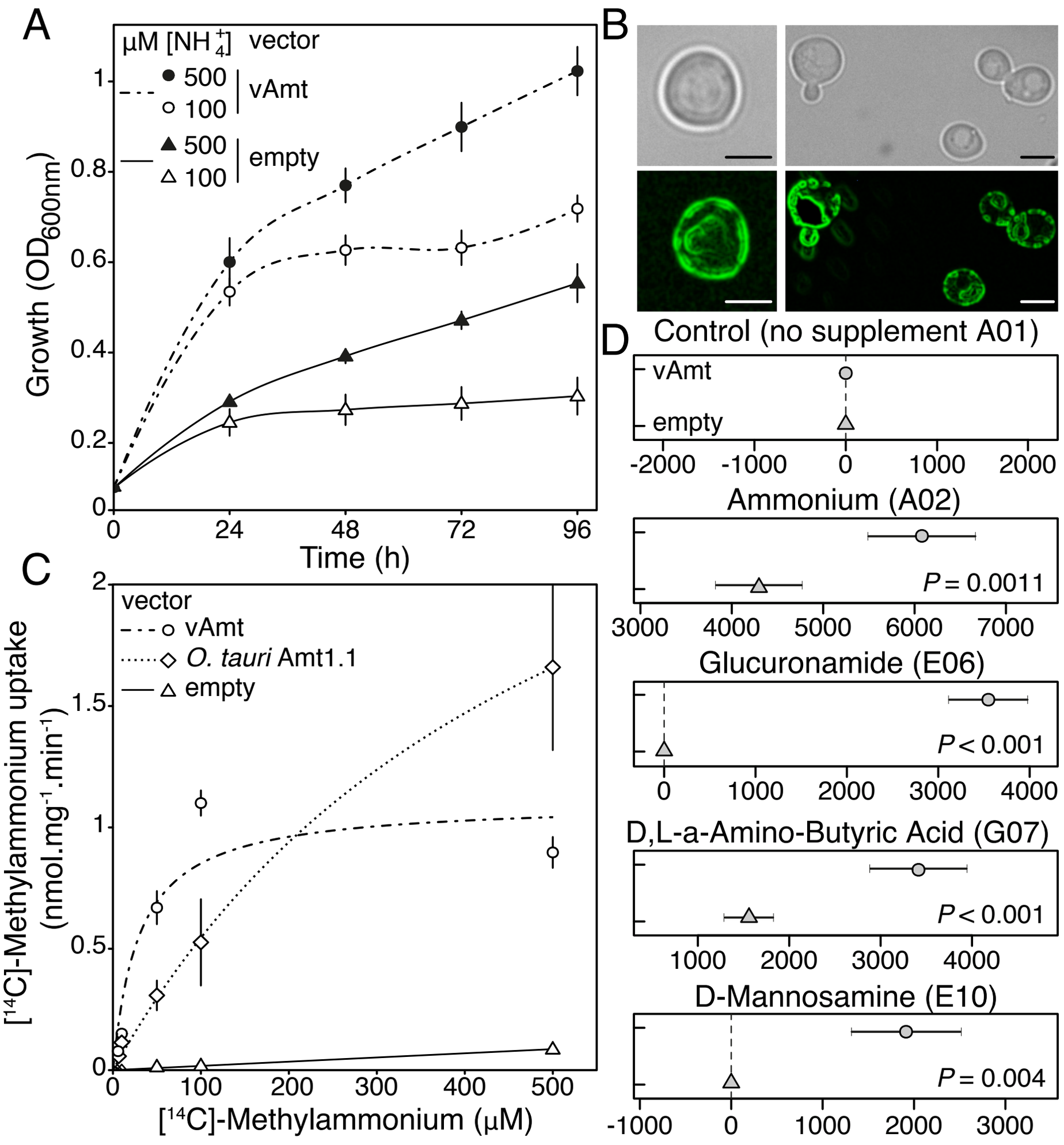
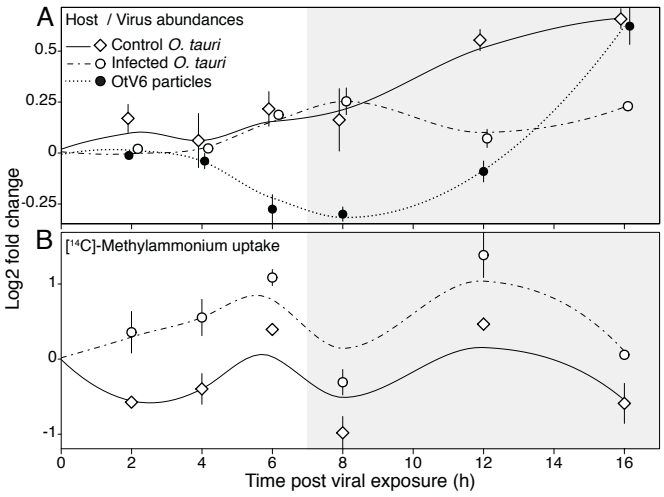
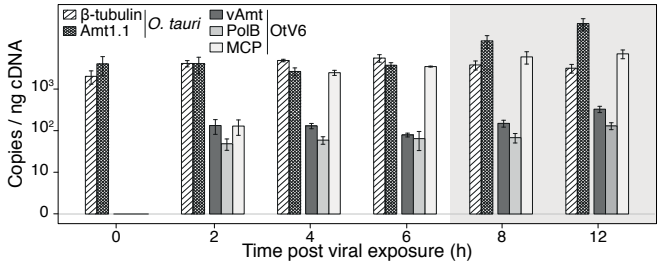
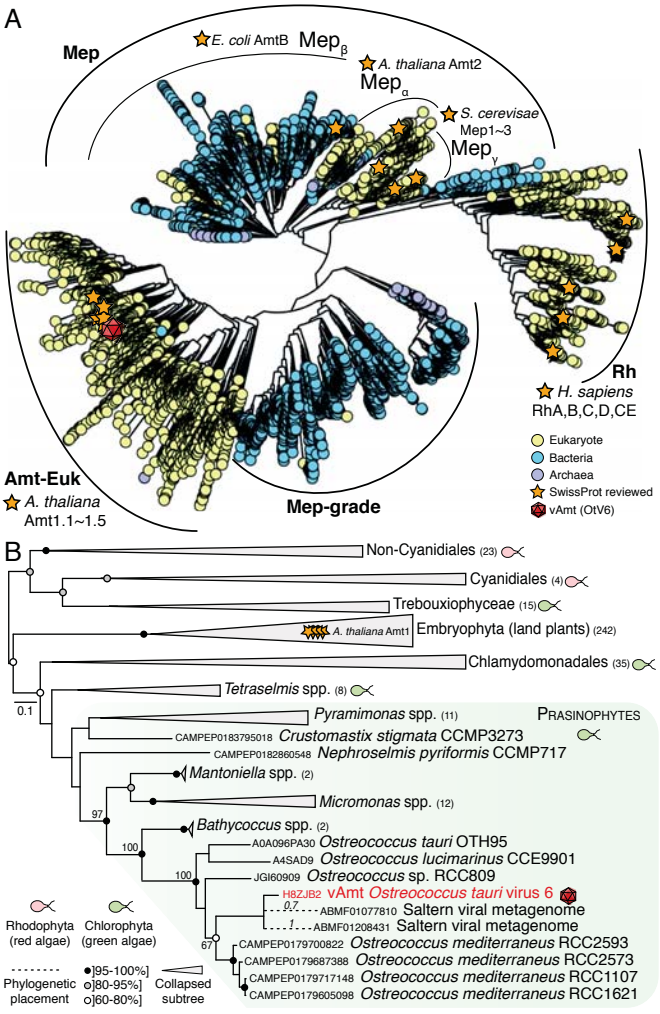

A. turfacea Chlorella virus 1
P. bursaria Chlorella virus FR483
P. bursaria Chlorella virus NY2A
P. bursaria Chlorella virus 1
P. bursaria Chlorella virus AR158
Bathycoccus sp. RCC1105 virus 1
Bathycoccus sp. RCC1105 virus 2
Micromonas sp. RCC1109 virus 1
Micromonas pusilla virus SP1
Micromonas pusilla virus PL1
Ostreococcus tauri virus 6
Ostreococcus lucimarinus virus 1
Ostreococcus lucimarinus virus 7
Ostreococcus lucimarinus virus 4
Ostreococcus tauri virus 5
Ostreococcus tauri virus 1
Ostreococcus lucimarinus virus 2
Ostreococcus mediterraneus virus 1
Ostreococcus lucimarinus virus 3
Ostreococcus lucimarinus virus 5
Ostreococcus lucimarinus virus 6
Ostreococcus tauri virus 2
CHLORO VIRUSES
PRASINOVIRUSES
100
100
100
100
99
100
100
100
100
100
100
100
100
94
100
100
97
0.1
0.1


A
OtV6
189567 bp
180kb
20kb
40kb
60kb
80kb
100kb
120kb
140kb
160kb
C
X
V
IX
III
XI
VI
VII
I
VII
IV
II
B
100 bp
OtV6_114c
OtV6_115c (vAmt)
OtV6_116
XI
X
IX
VII
VII
VI
V
IV
III
II
I
87889
88365
88383
89702
89809
90327
87109
87814
88223
88564
88647
89205
89252
89597
89979
90183
OtV6-full-F1
vAmt-F4
sh-Amt-vir-F
RT-vAmt-F1
RT-vAmt-F3
RT-vAmt-R1
RT-vAmt-R3
OtV6-full-R1
sh-Amt-vir-R
vAmt-R4


A
μM [NH4+]
vector
500
100
vAmt
500
100
empty
Growth (OD600nm)
Time (h)
B
C
vector
vAmt
O. tauri Amt1.1
empty
[14C]-Methylammonium uptake (nmol.mg-1.min-1)
[14C]-Methylammonium (μM)
D
Control (no supplement A01)
vAmt
empty
Ammonium (A02)
P = 0.0011
Glucuronamide (E06)
P < 0.001
D,L-a-Amino-Butyric Acid (G07)
P < 0.001
D-Mannosamine (E10)
P = 0.004


A
Host / Virus abundances
Control O. tauri
Infected O. tauri
OtV6 particles
0.5
0.25
0
-0.25
B
[14C]-Methylammonium uptake
1
0
-1
Log2 fold change
0
2
4
6
8
10
12
14
16
Time post viral exposure (h)


β-tubulin
Amt1.1
O. tauri
vAmt
PolB
MCP
OtV6
Copies / ng cDNA
10³
10²
10
0
0
2
4
6
8
12
Time post viral exposure (h)


A
Mep
E. coli AmtB Mepβ
A. thaliana Amt2
Mepα
S. cerevisae
Mep1~3
Mepγ
Rh
H. sapiens
RhA,B,C,D,CE
Eukaryote
Bacteria
Archaea
SwissProt reviewed
vAmt (OtV6)
Amt-Euk
A. thaliana
Amt1.1~1.5
Mep-grade
B
Non-Cyanidiales (23)
Cyanidiales (4)
Trebouxiophyceae (15)
A. thaliana Amt1
Embryophyta (land plants) (242)
Chlamydomonadales (35)
Tetraselmis spp. (8)
0.1
Pyramimonas spp. (11)
PRASINOPHYTES
CAMPEP0183795018 Crustomastix stigmata CCMP3273
CAMPEP0182860548 Nephroselmis pyriformis CCMP717
Mantoniella spp. (2)
Micromonas spp. (12)
97
Bathycoccus spp. (2)
100
A0A096PA30 Ostreococcus tauri OTH95
A4SAD9 Ostreococcus lucimarinus CCE9901
100
JGI60909 Ostreococcus sp. RCC809
H8ZJB2 vAmt Ostreococcus tauri virus 6
0.7
ABMF01077810 Saltern viral metagenome
1
ABMF01208431 Saltern viral metagenome
67
CAMPEP0179700822 Ostreococcus mediterraneus RCC2593
CAMPEP0179687388 Ostreococcus mediterraneus RCC2573
CAMPEP0179717148 Ostreococcus mediterraneus RCC1107
CAMPEP0179605098 Ostreococcus mediterraneus RCC1621
Rhodophyta (red algae)
Chlorophyta (green algae)
Phylogenetic placement
●]95-100%]
o]80-95%]
o]60-80%]
Collapsed subtree