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Molecular Mechanisms of Auxiliary Metabolic Genes in Marine Viruses

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Abstract

Marine viruses possess auxiliary metabolic genes (AMGs) acquired through horizontal gene transfer from their hosts, enabling them to reprogram host metabolic pathways during infection. These genes significantly influence processes such as photosynthesis, nitrogen, sulfur, and carbon metabolism, lipid biosynthesis, and transport systems, thereby impacting host physiology and global biogeochemical cycles. Recent large-scale metagenomic surveys, like the Tara Oceans project, have identified thousands of AMGs across various metabolic pathways. Functional studies are beginning to reveal how AMGs modulate enzyme activity, host energy flux, and nutrient cycling in illuminated and dark oceans, sediments, oxygen minimum zones (OMZs), and under nutrient-limited conditions. However, key gaps remain in linking AMG expression to protein function and ecological impact. Future research integrating single-cell and single-virion omics, structural biology, synthetic biology, and ecological modeling is likely to illuminate both the molecular mechanisms involved and their broader ecological consequences. This understanding is crucial for comprehending the role of marine viruses in ecosystem dynamics and global nutrient cycles.

Marine viruses, Auxiliary metabolic genes, Biogeochemical cycles, Nitrogen metabolism, Sulfur metabolism, Metagenomics, Host-virus interactions

Key words:

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Introduction

Marine viruses are the most abundant biological entities in the oceans, with an estimated 10^31 particles globally (Suttle, 2007). They play fundamental roles in regulating microbial populations, influencing nutrient cycles, and shaping the evolution of marine ecosystems (Middelboe & Brussaard, 2017). Beyond their classical role in host cell lysis and horizontal gene transfer, viruses have emerged as key modulators of host metabolism during infection (Zimmerman et al., 2020). Among their molecular arsenals are auxiliary metabolic genes (AMGs), which encode host-derived metabolic functions that are not strictly required for viral replication but provide a selective advantage by reprogramming host metabolism to enhance viral fitness (Hurwitz & U'Ren, 2016). Initially discovered in cyanophages carrying photosystem genes (psbA and psbD), AMGs are now known to span diverse metabolic pathways including carbon fixation, nitrogen and sulfur cycling, phosphate acquisition, lipid biosynthesis, and stress response (Wang et al., 2023). These viral genes enable viruses to redirect the flow of energy and nutrients within infected cells, thereby modifying microbial community function and global biogeochemical processes (Zimmerman et al., 2020). Recent advances in high-throughput metagenomics, metatranscriptomics, and single-cell technologies have dramatically expanded our understanding of AMGs, revealing their widespread distribution and functional diversity across marine environments from surface waters to the deep sea (Aplakidou et al., 2024).

Molecular Mechanisms of AMGs

AMGs function by supplementing or modifying host metabolic pathways to favor viral replication. Mechanistically, they can operate through several strategies (Luo et al., 2022): Host Metabolic Reprogramming: Viral AMGs encode enzymes that directly participate in key metabolic reactions. For example, cyanophage psbA and psbD maintain photosystem II activity during infection, ensuring continued ATP and NADPH production (Puxty et al., 2015). Nutrient Acquisition: Viruses infecting phytoplankton encode ammonium transporters (vAmt) and phosphate-binding proteins to enhance host nutrient uptake in oligotrophic environments (Monier et al., 2012). Redox Balancing: AMGs such as ferredoxin and flavodoxin redirect electron flow within the photosynthetic electron transport chain, maintaining redox homeostasis (Riaz et al., 2022). Epigenetic Regulation: Some viral proteins modulate host chromatin or DNA methylation to prioritize viral gene expression while suppressing competing host pathways (Rajeev et al., 2021). Protein-Protein Interactions: Viral enzymes integrate into host metabolic complexes, such as Rubisco activases or sulfur oxidation machinery, redirecting flux toward viral needs (Kosmopoulos & Anantharaman, 2025). Table 1 summarizes key AMGs identified in marine viruses, highlighting their host-virus context, molecular mechanism, and ecological significance. These examples illustrate the diverse strategies viruses use to manipulate host metabolism and influence global nutrient cycles (Kieft et al., 2021).

Current Gaps and Challenges

Despite the rapidly growing catalog of AMGs, several critical knowledge gaps remain. Functional validation of AMG proteins is limited, as most discoveries are based on metagenomic predictions (Ufarté et al., 2015). Regulation of AMG expression under varying environmental conditions is poorly understood (Zhu et al., 2024). Quantitative assessments of AMG contributions to ecosystem-level biogeochemical fluxes remain challenging due to complex virus-host interactions and environmental heterogeneity (Liang et al., 2025). Additionally, host range and specificity of many AMGs are uncertain, complicating efforts to trace their ecological impact (Gios et al., 2024).

Table 1. Representative Auxiliary Metabolic Genes (AMGs) in Marine Viruses

AMG / Function	Host / Virus Context	Molecular Mechanism	Ecological Implication
psbA/psbD (Photosystem II)	Cyanophages infecting Prochlorococcus and Synechococcus	Maintain photosynthetic electron transport to sustain ATP and NADPH production during infection.	Supports carbon fixation and viral replication in oligotrophic oceans.
amoC (Ammonia monooxygenase)	Thaumarchaeota-infecting viruses	Encodes nitrification enzyme to oxidize ammonia, supplementing host nitrification capacity.	Modulates nitrogen cycling in marine nitrifying communities.
dsr/sox genes (Sulfur oxidation)	Phages infecting sulfur-oxidizing bacteria	Enable oxidation of reduced sulfur compounds to gain energy for viral production.	Influence sulfur turnover in oxygen minimum zones and hydrothermal vents.
vAmt (Ammonium transporter)	Prasinoviruses infecting Ostreococcus tauri	Facilitates ammonium uptake under nitrogen limitation.	Enhances viral yield in nutrient-poor environments.
SPT (Serine palmitoyltransferase)	Coccolithovirus infecting Emiliania huxleyi	Redirects host lipid metabolism to produce viral glycosphingolipids.	Affects bloom dynamics and carbon export.

Future Perspectives

Future research should integrate single-cell omics, cryo-electron microscopy, and synthetic biology to experimentally validate AMG functions and structural mechanisms. Incorporating AMG activity into Earth system models will enable predictions of how virus-driven metabolic reprogramming influences global carbon sequestration, nitrogen cycling, and climate feedback loops under changing ocean conditions.

Conclusion

Auxiliary metabolic genes represent a powerful strategy by which marine viruses manipulate host physiology and shape biogeochemical processes. By encoding host-like metabolic functions, viruses extend their influence beyond infected cells to entire microbial communities and global nutrient cycles. Continued advances in omics technologies, experimental validation, and modeling will transform our understanding of AMGs from descriptive catalogs to mechanistic frameworks, ultimately revealing their role in Earth's climate system.

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