

Abstract

Marine phytoplankton play a central role in global carbon cycling, and coccolithophores such as *Gephyrocapsa huxleyi* are important contributors to marine primary production. Species-specific giant viruses known as *Emiliana huxleyi* viruses (EhVs) strongly influence coccolithophore populations, yet the relationship between host evolutionary history and viral susceptibility remains poorly understood. This study investigated viral infectivity, host susceptibility, and infection outcomes among multiple *G. huxleyi* strains and EhV isolates. Plaque assays, burst size measurements, and infection dynamics experiments were conducted, while mitochondrial and plastid genomes were assembled from Illumina sequencing data and used for phylogenetic reconstruction. The results revealed substantial variation in viral infectivity and host susceptibility, producing resistant-like, fluctuating, and collapsed infection phenotypes among different host–virus combinations. Mitochondrial phylogenetic analyses resolved three major host lineages, whereas plastid phylogenies exhibited a more complex clustering pattern, indicating phylogenetic incongruence between organellar genomes. Despite this genetic diversity, infection phenotypes were distributed across multiple mitochondrial and plastid clades, and closely related strains frequently displayed contrasting responses to viral exposure. In addition, individual EhV isolates differed considerably in infectivity and replication characteristics, with certain isolates repeatedly producing distinct infection dynamics across multiple host strains. Comparative phylogenetic analyses therefore indicated that organellar evolutionary relationships did not consistently correspond with infection outcomes, suggesting that organellar phylogeny alone is insufficient to explain variation in susceptibility. Overall, these findings demonstrate that host–virus interactions in *G. huxleyi* are highly strain-specific and are influenced by factors beyond organellar evolutionary history.

Keywords: *Gephyrocapsa huxleyi*, coccolithophores, *Emiliana huxleyi* virus (EhV), host–virus interactions, phylogenomics