

Chapter 1

Introduction

1.1 Background

Marine phytoplankton are responsible for approximately half of the global primary production of carbon and play a central role in oceanic carbon cycling (Wang et al., 2023). Among them, coccolithophores are a major group of calcifying phytoplankton that fix organic carbon and make calcium carbonate (CaCO_3) by making coccoliths (Brownlee et al., 2021; Li et al., 2024). *Gephyrocapsa huxleyi* is one of the most abundant and widely distributed coccolithophore species, forming large-scale blooms across diverse marine environments. Due to its ecological importance and tractability in laboratory cultures, *G. huxleyi* has become a key model organism for studying phytoplankton physiology, biogeochemistry, and host–virus interactions (Wheeler et al., 2023).

Viruses are major drivers of phytoplankton mortality and exert strong top-down control on bloom dynamics. In the case of *G. huxleyi*, infections by species-specific giant double-stranded DNA viruses, collectively referred to as *Emiliana huxleyi* viruses (EhVs), can rapidly terminate blooms and substantially influence carbon export to the deep ocean (Redondo et al., 2024; Sun et al., 2020). EhV infections typically lead to host cell lysis, releasing organic matter and viral particles into the surrounding environment. However, experimental studies have demonstrated that infection outcomes can vary widely among *G. huxleyi* strains, ranging from rapid population collapse to delayed mortality or partial recovery of host populations following viral exposure (Buchholz et al., 2025; Dikstein et al., 2024).

Previous work on *G. huxleyi*–EhV interactions has provided important insights into viral infection kinetics, viral gene expression, host lipid remodeling, and the molecular underpinnings of lytic infection (Homola et al., 2024; Malitsky et al., 2016; Ruiz et al., 2017; Schleyer et al., 2023). Despite this progress, most experimental investigations have focused on a limited number of host strains,

often without placing them in a broader genomic or evolutionary context. Consequently, it is uncertain whether the observed variations in viral susceptibility and recovery are indicative of conserved host genetic backgrounds, recent genetic divergence, or ephemeral physiological responses.

An additional unresolved aspect of coccolithophore–virus interactions concerns host recovery following viral infection. While EhV infections are typically considered lytic, several studies have reported the survival and regrowth of host populations after viral exposure, suggesting the presence of resistance or tolerance mechanisms (Joffe et al., 2024; Shaler et al., 2025). The mechanisms underlying resistant-like and recovery phenotypes remain poorly understood, particularly the extent to which host genetic background contributes to variation in infection outcome. Distinguishing between true host resistance, phenotypic plasticity, and viral adaptation is critical for understanding the long-term ecological and evolutionary consequences of host–virus interactions in marine systems.

1.2 Objective

This study examines the interactions between *G. huxleyi* and its specific giant viruses (EhVs), focusing on viral infectivity, host susceptibility, infection dynamics, and the relationship between host evolutionary history and infection outcome. Understanding these processes will help clarify how host genetic diversity influences responses to viral infection in coccolithophores.

First, the infectivity and replication characteristics of different EhV isolates were evaluated through plaque assays and burst size measurements. Second, host susceptibility was assessed by analyzing infection dynamics and population responses following exposure to multiple EhV isolates, allowing host–virus interactions to be classified into resistant-like, fluctuating, or collapsed phenotypes. Finally, mitochondrial and plastid genome phylogenies were compared with observed infection outcomes to determine whether organellar evolutionary relationships are associated with variation in susceptibility among *G. huxleyi* strains.

1.3 Hypothesis

Null Hypothesis (H_0):

G. huxleyi strains do not exhibit significant differences in susceptibility, infection dynamics, or recovery following exposure to EhVs, and and organellar phylogenetic diversity is not associated with observed infection phenotypes.

Alternative Hypothesis (H_1):

G. huxleyi strains exhibit significant differences in susceptibility, infection dynamics, and recovery following exposure to EhVs, and variation in susceptibility and infection outcome is associated with genetic differences among *G. huxleyi* strains.