



universität
wien

MASTERARBEIT | MASTER'S THESIS

Titel | Title

Phage-host dynamics across a coastal Vibrionaceae bloom

verfasst von | submitted by

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angestrebter akademischer Grad | in partial fulfilment of the requirements for the degree of

Master of Science (MSc)

Wien | Vienna, 2026

Studienkennzahl lt. Studienblatt |
Degree programme code as it appears on the
student record sheet:

UA 066 830

Studienrichtung lt. Studienblatt | Degree
programme as it appears on the student record
sheet:

Masterstudium Molecular Microbiology, Microbial
Ecology and Immunobiology

Betreut von | Supervisor:

Dr. Martin F. Polz

Acknowledgements

I would like to express my sincere gratitude to Professor Martin Polz for giving me the opportunity to conduct my Master thesis in the Polz lab, allowing me to learn from him and from the entire research group. I am especially thankful for his guidance and support throughout my laboratory work.

I also gratefully acknowledge the Department of Microbial Ecology and CeMESS for their support and for providing a welcoming and inspiring working environment.

I thank all members of the Polz group for their help, feedback, and the collaborative atmosphere that made this work possible. In particular, I am grateful to Jacob Bobonis for his valuable advice and extensive assistance with the transposon mutagenesis experiments and the growth assays using the Tecan plate reader. I also want to thank Michael Wolfram for the support in the lab, sharing his expertise and guidance during my practical work.

Above all, I would like to thank my laboratory supervisor, Nina Bartlau. Her tireless support, thoughtful mentorship, and practical guidance were highly valuable throughout the entire project.

Zusammenfassung

Bakteriophagen spielen eine zentrale Rolle bei der Regulierung bakterieller Populationen in nahezu allen Ökosystemen. Durch ihre Auswirkungen auf bakterielle Mortalität, den Nährstoffumsatz und den horizontalen Gentransfer beeinflussen sie maßgeblich die Struktur und Dynamik mikrobieller Gemeinschaften. Ein detailliertes Verständnis von Phagen-Wirt-Interaktionen ist daher entscheidend, insbesondere da diese Interaktionen stark von zufälligen Begegnungen abhängen, die wiederum durch die Populationsdichte der Wirtsbakterien beeinflusst werden. Ereignisse wie bakterielle Blüten, die häufig durch erhöhte Nährstoffverfügbarkeit ausgelöst werden, erhöhen die Begegnungsraten zwischen Phagen und Wirten und bieten somit ein geeignetes Modell, um Phagen-Wirt-Dynamiken unter natürlichen Bedingungen zu untersuchen.

Die Nahant-Zeitreihe stellt ein solches Modellsystem dar. Dabei handelt es sich um eine 93-tägige, hochauflösende Küstenzeitreihe, die im Jahr 2010 an der Küste von Nahant (Massachusetts, USA) täglich beprobt und wobei *Vibrio* Bakterien und ihre ko-auf tretenden Phagen isoliert wurden. Innerhalb dieser Zeitreihe wurde eine neun Tage andauernde Blüte der Familie der *Vibrionaceae* beobachtet, die vor allem durch *Vibrio cyclitrophicus* und *Vibrio splendidus* geprägt war. Während allerdings *V. splendidus* über den gesamten Beobachtungszeitraum hinweg in einer nahezu konstanten Abundanz vorkam, zeigte *V. cyclitrophicus* einen ausgeprägten, transienten Anstieg während der Blüte, gefolgt von einem raschen Rückgang. Wegen dieser spezifischen Dynamik wurde *V. cyclitrophicus* als Modell gewählt, um Phagen-Wirt-Interaktionen im Kontext des Blüteereignis zu untersuchen. Darüber hinaus eignen sich Vertreter der Gattung *Vibrio* aufgrund ihres schnellen Wachstums, ihrer möglichen genetischen Manipulation und ihrer guten Kultivierbarkeit im Labor besonders für experimentelle Analysen.

Im Rahmen dieser Arbeit wurden *Vibrio*-Isolate des Tag 244 der Nahant-Zeitreihe untersucht, einem Zeitpunkt am Ende der *Vibrionaceae* Blüte. Insgesamt 893 Vibrionen wurden isoliert und mittels ihrer *hsp60*-Marker-Gene taxonomisch eingeordnet. Zur Untersuchung der Phagen-Wirt-Interaktionen wurden alle 563 *Vibrio cyclitrophicus* in Agar-Overlay-Spot-Assays

mit 76 Phagen getestet, die an unterschiedlichen Zeitpunkten der Nahant-Zeitreihe isoliert wurden. Das daraus resultierende Interaktions-Netzwerk war spärlich und modular. Nur etwa 0,005% der getesteten Interaktionen führten zur Lyse, und nur rund 9% der Isolate unterstützten die Replikation von Phagen. Drei eng Verwandte Phagen (3.330.B, 5.330.B und 7.330.B) verursachten bei hoher, unverdünnter Titerkonzentration eine weitreichende Lyse in ca. 90% der Isolate, dieser Phänotyp verschwand allerdings nach Verdünnung des verwendeten Phagenkonzentrats. In Folgeexperimenten konnten wir einen extrazellulären Phagen induzierenden Faktor nachweisen, der aus Phagen-behandelten Agar-Overlay-Platten gewonnen werden konnte. Dieser Faktor löste eine mit dem Phagen 3.330.B assoziierte Aktivität, sowohl in Agar-Platten als auch in flüssigem Medium basierten Tests aus. Erste Charakterisierungen ordneten die Aktivität einem hitzeempfindlichen, polaren Molekül zu, dessen Größe zwischen 3 und 30kDa liegt. Der Versuch, den Rezeptor des Phagen 3.330.B zu identifizieren, blieb ohne eindeutiges Ergebnis, da der eingesetzte Assay, der auf einer Transposon-Mutagenese-Bibliothek basiert und primär für Phagen konzipiert ist, die ein strikt lytisches Infektionsverhalten zeigen. Im Verlauf der Experimente zeigt sich jedoch, dass 3.330.B dieses Verhalten nicht aufweist. In Kolonien, die die Phagenexposition überlebten, konnte 3.330.B-DNA mittels PCR nachgewiesen werden. Dennoch entwickelten diese Kolonien, in denen der Phage 3.330.B nachgewiesen werden konnte, keine längerfristige Resistenz. Vielmehr waren sie bei erneuter Exposition gegenüber dem Phagen 3.330.B infizierbar und zeigten weiterhin Lyse, was für eine nicht-klassische temperate Assoziation des Phagen und seinem Wirt spricht, wie etwa eine instabile Persistenz des Phagen-Materials oder eine carrier-state-ähnlich Interaktion.

Insgesamt deuten die Ergebnisse dieser Arbeit darauf hin, dass Phagen-Wirt-Beziehungen in marinen *Vibrio*-Populationen sehr stammspezifisch sind. Wobei insbesondere temperate Phagen eine signifikante Rolle spielen, deren Interaktionen mit ihren Wirten nicht ausschließlich klassischen lytischen Infektionsverläufen folgen, sondern nicht klassische Persistenzformen, sowie extrazelluläre Induktionsphänomene miteinschließen. Damit trägt diese Arbeit zum besseren Verständnis von Phagen-Wirt-Interaktionen in natürlichen

mikrobiellen Systemen bei und verdeutlicht den Wert hochauflösender Zeitreihenstudien, um ökologische Muster mit zugrunde liegenden biologischen Prozessen zu verknüpfen.

Abstract

Bacteriophages are widely recognized as major drivers of microbial mortality, nutrient turnover and horizontal gene transfer in the ocean, yet predicting their effects in nature remains difficult because phage-host interactions are highly specific and can change rapidly over short time scales. High-resolution, genome-resolved field systems, where bacteria and their co-occurring phages can be isolated alongside matched environmental context and are therefore essential for connecting ecological patterns to mechanisms. Building on prior work from the Nahant coastal time series that revealed rapid shift in *Vibrio* susceptibility and strong strain resolved, nested-modular interaction networks, this study focuses on the post-bloom phase to examine how phages, particularly temperate phages may contribute to phage-host dynamics in natural populations.

We mapped interactions between 76 phages and 563 newly-isolated *Vibrio cyclitrophicus* strains collected on Julian day 244 using systematic cross-infection assays. The resulting network was sparse and modular, wherein only around 0.005% of the tested phage-host combinations produced lysis and roughly 9% of the isolates supported phage replication. Three closely related phages (3.330.B, 5.330.B, and 7.330.B) produced widespread clearing (~90%) when applied at high titers, whereas this phenotype was strongly reduced upon dilution. During follow-up experiments, we detected a transferable extracellular inducing agent, which could be recovered from phage-challenged agar-overlays. This agent reproducibly triggered 3.330.B phage-associated activity in both agar- and liquid-based assays. Initial characterization localized this activity to a heat-sensitive, polar molecule, ranging in size between 3-30kDa, although its molecular identity and mechanism remained unresolved. Attempts to identify the receptor of phage 3.330.B did not yield a clear result, as the assay was based on a transposon mutagenesis library and was primarily designed for phages that display a strictly lytic infection mode. During the experiments, however, it became apparent that phage 3.330.B does not follow this pattern. In colonies that survived phage exposure, 3.330.B DNA could be detected by PCR. Nevertheless, these colonies did not develop stable resistance, since upon re-challenge with the phage 3.330.B, they remained susceptible, which is indicative of a non-classical temperate

association between phage 3.330.B and its host strain, such as unstable retention of phage material or a carrier-state-like interaction.

Collectively, these results indicate that temperate phage-host interactions in coastal *Vibrio* population can be highly strain-specific and may include non-classical lifestyles and extracellularly transferable induction compounds, with implications for predicting phage impacts during bloom-associated community shifts and motivating future work to define their molecular basis and ecological relevance.

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List of Abbreviations

abi	abortive infection
bp	base pairs
CFU	Colony forming units
Cm	Chloramphenicol
DAP	Diaminopimelic acid
DATC	Diaminopimelic Acid Thymine Complementary (or auxotrophic for DAP)
DNA	Deoxyribonucleic Acid
dNTPs	Deoxynucleoside Triphosphates
kb	kilobases
LE	Low Electroendosmosis (agarose)
LI	Lysis from within
LPS	Lipopolysaccharides
LO	Lysis from without
MB	Marine Broth
MOI	Multiplicity of Infection
mTCBS	marine Thiosulfate-Citrate-Bile-Sucrose Agar
NODF	Nestedness metric based on overlap and decreasing fill
PCR	Polymerase Chain Reaction
PFU	Plaque forming unit
RefSeq	Reference Sequences
rcf	Relative Centrifugal Force
RNA	Ribonucleic Acid

rpm	Rotations per minute
SOP	Standard Operating Procedure
SM	Saline-Magnesium (buffer)
TAE	Tris-Acetate-EDTA (buffer)
TSB	Tryptic Soy Broth
1G07	strain: 10N.239.311.G07

Introduction

Viruses are tiny infectious entities that invade living cells to replicate, injecting their genetic material into their host cells and hijacking their machinery for propagation. With an estimated 10^{31} virus particles in the biosphere, viruses represent the most abundant biological entities on earth (Rohwer et al. 2009). In aquatic ecosystems, viruses play a critical ecological role through the viral shunt, a process by which viral lysis redirects their hosts biomass into dissolved organic matter, thereby fueling the microbial loop and maintaining nutrient turnover (Suttle, 2007). Through lytic infections, phages accelerate the recycling of carbon (C) and nitrogen (N) by fragmenting bacterial biomass into dissolved and particulate organic matter, influencing biogeochemical fluxes and microbial communities, particularly in dynamic coastal environments (Wang et al. 2022; Bates and Mathis, 2009; Roux et al. 2016). Generally, phage-mediated lysis is estimated to account for 20 – 40% of the daily bacterial mortality in surface waters (Suttle, 1994), highlighting their crucial roles in shaping microbial community structure, function and evolutionary trajectories (Koskella & Brockhurst 2014).

Beyond their role in microbial biomass turnover, bacteriophages profoundly influence bacterial evolution by mediating horizontal gene transfer via transduction and by encoding auxiliary metabolic genes that can modulate the hosts metabolism during infection (Breitbart et al. 2018). Phage genomes are highly mosaic, reflecting extensive genetic exchange with bacterial hosts and other phages, and collectively constitute a vast reservoir of unexplored genetic diversity (Roux et al. 2015).

Phage infection is initiated by a highly specific adsorption process that determines host recognition and infection success. The first step in phage infection, phage attachment, is mediated by highly specific interactions between the host surface receptors (such as LPS, polysaccharides, outer-membrane proteins, flagella, pili, in gram negative bacteria and cell wall teichoic acids, their bound sugar moieties and peptidoglycan in gram positive bacteria (Sørensen et al. 2011; Leprince and Mahillon, 2023) and the phage receptor binding proteins, mostly

located on the phage tail fibers or baseplates (Dowah & Clokie, 2018). This process takes place in three distinct kinetic phases: 1) diffusion-driven random encounter with the bacterial surface, 2) finding the appropriate primary receptor site, the phage can bind reversibly, and 3) when the correct secondary receptor is found, irreversible binding occurs, triggering structural rearrangements in the phage tail machinery and the activation of virion-associated enzymes such as tail lysozymes, which allows penetration of the cell wall/ membrane, leading to the injection of the genetic material of the phage into the host cytoplasm (Fernandes & Sao-Jose, 2018). Since receptor recognition governs host specificity, the adsorption step is crucial to define the phage-host range and important to understand phage ecology and the development of phage-based therapeutics (Bertozzi Silva et al. 2016).

Upon successful adsorption to its host cell, phages can follow two primary infection strategies: the lytic and the lysogenic cycles. Hijacking the hosts cellular machinery to replicate, the lytic cycle leads to fast killing of the bacterial host, releasing new virions (Abedon 2008). While in contrast, the lysogenic cycle pathway allows phages to remain within their hosts by integrating their genomic material into the host genome or by remaining as extrachromosomal plasmids (Waldor et al. 2005; Clokie et al. 2011). This association can remain stable across many bacterial generations. Through a process named lysogenic conversion, the phage may change the bacterium's phenotype by activating genes that are typically not expressed during a lytic infection (Kuzio et al. 2010). An important consequence of lysogeny is that prophage-harboring bacteria often gain resistance to subsequent infections by the same or closely related phages. This is known as superinfection exclusion, which is mediated by prophage encoded proteins that interfere with phage adsorption or the injection of the genetic material (Mahony et al. 2008).

Bacteria employ a diverse set of intracellular and surface-associated defense mechanisms to limit bacteriophage infection and replication (Hampton et al. 2020). In addition to mutations in the receptors, the restriction-modification (R-M) systems, which cleave invading phage genetic material, while safeguarding the hosts DNA through methylation, and CRISP-Cas adaptive immunity. Another important defense system is the abortive infection system, which triggers premature host cell death upon phage invasion, preventing phage replication and protecting the

bacterial population (Stern and Sorek, 2011). Abortive infection systems, which are often triggered by the hosts defense systems, can also be induced by phage infection itself, environmental stress, or exposure to certain antibiotics, which can act as phage-inducing compounds (Chopin et al. 2005; Labrie et al. 2010). Similar to the abortive infection system are toxin-antitoxin systems, which are serving as intracellular fail-safes – normally balanced by an unstable antitoxin, a toxin released under phage attack disrupts essential processes such as translation or DNA replication, stopping phage propagation at the cost of host viability (Hayes, 2003; Boss and Kedzierska, 2023).

In response, phages have evolved a broad repertoire of anti-defense strategies, to counteract bacterial immunity. Against restriction-modification (R-M) systems, many phages encode anti-restriction proteins, shielding their genomes from endonuclease cleavage, for instance proteins that mimic DNA to sequester restriction enzymes (Dryden, 2006). To bypass the abortive infection systems (Abi), phages have developed anti-Abi proteins, that inhibit the Abi pathways and restore productive infection (Emond et al. 1997). Furthermore, phages encode anti-CRISPR (Acr) proteins, which directly inhibit the components of the bacterial CRISPR-Cas systems. Acting through diverse mechanisms, such as blocking DNA binding by the Cas nucleases or preventing recruitment of cleavage factors (Allemailem et al. 2024). Arc proteins have been described across multiple phage families, highlighting their widespread role in phage-host dynamics. This ongoing arms-race between phages and bacteria underscores their coevolution and the importance of a deeper understanding of defense and counter-defense systems.

Marine *Vibrio* species, together with the genomes-resolved Nahant coastal time series, provide a profound system for dissecting phage-host interaction networks across ecological, genomic and experimental scales. Species within the genus *Vibrio* are widely seen as effective model organisms to explore phage-host dynamics in controlled laboratory settings due to their high biomass, ecological relevance, rapid growth rates and genetic trackability. Moreover, they exhibit a large genomic and phenotypic diversity and are often co-isolated with a diverse set of phages, permitting detailed investigation of host specificity and resistance mechanisms in an

environmental context (Kauffman et al. 2022). The Nahant collection represents one of the largest curated dataset of co-occurring, cultivated and genome-sequenced marine *Vibrionaceae* viruses and their hosts, including the corresponding metagenomes, isolated during a 93-day coastal time series from Canoe Cove Beach in Nahant, Massachusetts (Martin-Platero et al. 2018; Kauffmann et al. 2018; Lien et al. 2024). The Nahant time series was previously used for the analysis of phage-bacteria interaction networks (Kauffmann et al. 2022), including a cross-infection assay which mapped the host ranges of 248 phages against 279 *Vibrionaceae* strains. As well as the work of (Kreutter 2024) analyzing hundreds of *V.cyclitrophicus* strains from eight different time points within the Nahant time series, assessing their host-range with the same set of 76 phages also used and described in this thesis. By incorporating genome-sequenced isolates, the Nahant dataset enables nuanced analysis of how host and phage phylogenetic diversity influences phage-host interaction networks in marine systems.

Further contributing to a better understanding of phage-host dynamics in a marine environment, this study focuses on the *Vibrionaceae* isolated from Julian day 244, immediately following a distinct *Vibrio* bloom that occurred over a ten-day period, from Julian days 236 to 245 (Martin-Platero et al. 2018), during which parts of the corresponding phage populations were also sampled (partially described by Lopatina et al. 2024), the other phages used were isolated from the day 222 before the bloom and from the sampling days 261 and 286, after the bloom (Kauffmann et al. 2022). The *Vibrionaceae* community reaches a notable peak on Julian day 239. The metagenomic data derived from the unfractionated microbial community indicated an overall increase in *Vibrionaceae* abundance, revealing that *V. cyclitrophicus* in the free-living fraction drastically increased during the bloom and began to decline again after day 240, while for instance other highly abundant *Vibrio* species, like *Vibrio splendidus* maintained a steady presence over the whole time series. Based on that, *V.cyclitrophicus* strains were focused on to elucidate phage-host interactions during bloom conditions (Kreutter 2024).

A cross-infection assay was performed using a set of 76 genomically diverse phages and 563 *V. cyclitrophicus* isolates from day 244. In addition to the cross-infection assay described by (Kreutter 2024) was repeated. In both assays a group of three closely related phages (3.330.B,

5.330.B and 7.330.B) stood out due to their high number of lysed hosts. To identify the phages receptor, a transposon mutagenesis assay was conducted, but due to the potentially temperate lifestyle of these phages, their receptor could not be determined. A novel phage-inducing compound was extracted from agar overlay plates. The compound triggered either growth inhibition, or lysis patterns nearly identical to those observed after spotting the three related phages (3.330.B, 5.330.B and 7.330.B).

Prophage induction is classically associated with DNA-damaging agents such as mitomycin C, however previous studies have shown that additional endogenous or exogenous factors, including antimicrobial or phage-associated compounds, can influence prophage dynamics under certain conditions (Castillo et al. 2019; Schmelcher et al. 2012). Although the molecular nature of the inducing factor identified here remains unknown, its activity highlights the potential existence of previously uncharacterized mechanisms that modulate prophage behavior in natural microbial systems.

Together, this study integrates phage-host interaction networks with mechanistic investigation of phage induction, providing new insights into how temperate phages and inducible factors shape bacterial population dynamics during coastal bloom events.

Methods

2.1 *Vibrionaceae* isolation from day 244 of the Nahant time series

From the free-living size fraction (0.2 – 1 μm) of day 244 of the Nahant time series sampled from Canoe Cove Beach in Nahant, Massachusetts, *Vibrionaceae* were isolated. This was done by plating out from 3 community glycerol stocks (10N.244.34, 10N.244.35, 10N.244.36) on marine-thiosulfate-citrate-bile salts-sucrose agar (mTCBS; BD Difco TCBS Agar, 265020, complemented with 10 g NaCl per liter), as selective media. The plates were closed with parafilm and incubated overnight at room temperature. All single colonies were transferred first onto MB 2216 2% agar plates (Difco Marine Broth 2216, 279110, with 20 g Agar Millipore, per liter) next onto mTCBS agar plates and again onto MB 2216 2% agar plates for serial purification, incubating all plates overnight at room temperature between each streak, streaking out 3 isolates per plate. In total 893 isolates were obtained, and their morphology was noted from the second streak plate on mTCBS (Supplementary Table S 1.1). For long term storage, the isolates were inoculated in 800 μl of MB 2216 into 96-well deep well plates. The plates were sealed with breathable foil (Diversified Biotech/ Breath-easy) and incubated, shaking at 200rpm, at 25°C overnight. 171 μl of culture were transferred from the deep well (stock A) to a low-well plate (stock B (backup)). 78 μl of 80% glycerol (80% Glycerin Rotipuran 3783.1, supplemented with 20mM MgCl_2 to a final concentration of 25% w/v Glycerol) were added to the low-well plate, while 197 μl of the 80% glycerol are added to the deep-well culture plate. The plates were sealed with adhesive aluminum foil, frozen in liquid nitrogen and stored at -80°C. In total 10 sets of storage plates were created (10N.244.45 till 10N.244.54, for each 2 plates – one deep well plate and a low well plate).

2.2 Hsp60 colony PCR and Hsp60 sequencing

In order to allow for taxonomical assignment of the isolates, their hsp60 gene was amplified in a PCR, the product was purified and Sanger sequenced. On the same day as the glycerol stocks

were made, from each isolate, one colony was transferred in 40 µl PCR H₂O into 96-well PCR plates. The plates were sealed with foil. To disrupt the cell wall, three freeze and thaw cycles were performed, freezing the plates at -20°C for 40-60 minutes. Followed by incubation on room temperature, till the plate was completely thawed. The steps were repeated three times. Finally, the plate was heated up to 100°C for 10 minutes in a thermocycler. This DNA served as template in the PCR reaction. The total reaction volume of 25 µl was prepared the following: 3 µl template, 8.5 µl PCR H₂O, 12.5 µl Dream Taq (thermoscientific DreamTaq™ Green PCR Master Mix (2X)), 0.5 µl hsp60 forward primer (H279) 10 µM, 0.5 µl hsp60 reverse primer (H280) 10 µM. Wherein the primer sequence for H279 was: 5'-GAA TTC GAI III GCI GGI GAY GGI ACI ACI AC-3', and for H280: 5'-CGC GGG ATC CYK IYK ITC ICC RAA ICC IGG IGC YTT-3' 61 (Goh et al., 1996). The reaction setup for the thermocycler was the following: initial denaturation at 95°C for 2 min; 35 cycles of 95°C for 1 min, 37°C for 1 min, 72°C for 1 min; and the final elongation at 72°C for 5 min; infinite hold at 12°C. Reviewing the amplification, 4 µl of the PCR product were analyzed on a 2% LE agarose gel with Gel Red (1x / 1:10.000 dilution) for 35 minutes at 120 V with TAE buffer, and imaged on a ChemiDoc MP imaging system (BioRad). The PCR products were cleaned up using the ZR-96 DNA Clean-up kit (Zymo Research) according to the kits protocol, adding 100 µl of binding buffer to the 21 µl of sample. All centrifugation steps were performed at 2.000 rcf. Finally the reaction was eluted in 40 µl of PCR H₂O and the plates were stored at -20°C. The hsp60 eluate was prepared and sent to sequencing with the company Microsynth, as follows: 3 µl of eluate, 3 µl of 20 µM hsp60 reverse primer (H280).

2.3 Taxonomic Analysis

The obtained Sanger sequences were checked, and the wobbly bases were corrected manually if possible. Too short sequences were sorted out, and the sequences were trimmed at the ends manually, trimming off around 20-30 bp at each end, depending on the quality of the read. Since the reverse primer (H280) was used, the sequences were reversed. Sequence analysis was performed using Geneious Prime software version 24.0.5. As reference sequences the extracted

hsp60 sequences from the RefSeq genomes of the family *Vibrionaceae* (218, NCBI, Nov. 2023) was used and *Shewanella* spp. (GCF_000013765) was used as outgroup. All sequences and reference sequences were aligned with Clustal Omega (v.1.2.4) using standard parameter (Sievers F, Barton GJ, Higgins DG, 2020). The alignment file was trimmed to 430 bp and was used to calculate a phylogenetic tree using FastTree (v2.1.11), with standard parameters (Price, M.N., Dehal, P.S., Arkin, A.P., 2009). For visualization of the tree, ITOL (v7) <https://itol.embl.de/> was used.

2.4 Cross-infection assay

To assess the host range, an infection assay was conducted in which 563 *Vibrio cyclitrophicus* strains from day 244, were exposed to a panel of 76 phages (including duplicates of phages 2.332.B, 4.332.O, 8.332.A, as internal control - Phages isolated on different days (e.g., 8.332.B 10N.V238.NB39 and 8.332.B 10N.V238.NB93; 2.332.B 10N.V239 and 2.332.B 10N.V237; 4.332.O 10N.V240 and 4.332.O 10N.V237; 8.332.A 10N.V282 and 8.332.A 10N.V238) (Supplementary Table S 1.3). For each strain one colony was inoculated in 5 ml 2216 MB and incubated at 25°C, shaking at 200 rpm overnight. Agar overlays were made using 250 µl host overnight culture and mixed with 10 ml pre-warmed (42°C) top agar (0.4% agar, 2216 MB), which was transferred onto squared bottom (company Greiner) agar plates (40 ml, 1% agar, 2216 MB). The plates were incubated at room temperature for 30 min to 1 h. A set of 79 phages was prepared in a 96-well PCR plate (used for a maximum of 3 days), aliquoting from high-titer phage stocks (Phage stock preparation according to SOP). As negative control a position was filled with SM buffer only, the same buffer which was used for the phage stocks. In all host range assays the same phage-set layout was used (Supplementary Table S 1.3). The host range was determined by spotting 2 µl of each phage stock on the bottom agar plate with the bacterial host lawn. The plates were then incubated at room temperature overnight and the viral lysis formation was monitored and noted for each phage on each of the host strains (Supplementary Table S 1.4), all plates were scanned for documentation and further analysis. One week later the plates were observed again, to check for late lysis. Every combination where a phage was able

to lyse, the host was then further characterized by repeating the agar overlay of the respective strain and spotting 2 µl of the corresponding phage stock in a dilution series from 10^0 to 10^{-11} on the bacterial lawn. The plates were also incubated overnight at room temperature and the strength of the interaction was noted to classify the host sensitivity and described the lytic interaction – distinguishing between lysis from without (LO) and lysis from within (LI). Wherein lysis from within refers to the classical phage infection cycle, in which a phage attaches to the susceptible bacterial cell, injects its genome and undergoes replication, assembly and the release of phage progeny. The host cell is lysed ultimately as part of this process, freeing new infectious virions that sustain the infection cycle. On agar overlay plates, LI typically appears as discrete, well-defined plaques, which reflect localized rounds of phage replication and bacterial cell destruction (Abedon, 2011; Young, 1992). In contrast, lysis from without arises under conditions of very high multiplicity of infection (MOI), where high number of phage particles are adsorbed simultaneously to the bacterial surface. This overload compromises the structural integrity of the membrane and cell wall, which can result in bacterial death without the production of phage progeny. Alternatively, such a stress can trigger the abortive infection (abi) system, in which an infected cell undergoes programmed cell death to halt the phage replication and prevent further spread within the population. In the overlays, LO is distinguished by diffuse or incomplete clearing of the bacterial lawn, without the formation of any discrete plaques. In this study, interactions were classified as LI when distinct plaque-forming units (PFUs) could be identified, whereas weak or hazy clearing zones without clear plaque morphology were registered as LO.

2.4.1 Cross infection assay of *V. cyclitrophicus* strains from the Nahant time series

Due to different phage stock concentrations used in the cross-infection assay performed and described by (Kreutter, 2024), the characterized *V. cyclitrophicus* strains were tested again. The strains were streaked out from glycerol stocks on MB 2216 agar plates and incubated overnight at 25°C. The set of phages used in the assay was expanded, including the inducing agent (position A12) that was extracted from 10N.239.311.G07 (short 1G07) challenged with phage

3.330.B, described in section 2.10. In addition, dilution series of the phages 3.330.B, 5.330.B and 7.330.B (10^0 to 10^{-11}) were prepared and 2 μ l of each dilution were spotted on the agar overlay plates, in addition to the phage set. The agar overlays were performed as described above in section 2.4. The plates were incubated overnight at room temperature, scanned and monitored again after one week, noting the lysis patterns (Supplementary Table S 1.5).

2.4.2 Characterization of Phage-Host Interaction Dynamics

A heatmap plot was constructed, using excel, to illustrate the structure of the cross-infection matrix, incorporating all 164 bacterial strains that showed at least one confirmed infection event with one of the tested phages; host strains without detectable susceptibility were excluded, with the exception of the LO isolate. The structural characteristics of the resulting phage-bacteria interaction network were analyzed in MATLAB using built-in functionality from the Bioinformatics Toolbox, the Statistics and Machine Learning Toolbox, Graph and Network Algorithms, and Core MATLAB components (MathWorks Inc., 2022). Network modularity was evaluated using the leading eigenvector algorithm as described by Flores et al. (2013). Prior to analysis, the matrix was binarized to represent the presence (1) or absence (0) of interactions and was subsequently converted into a binary adjacency matrix. This matrix was used to derive key network parameters, including node count (n), edge count (m), and degree distribution (k). Eigenvalues and corresponding eigenvectors of the modularity matrix were computed, and community assignments were determined using the leading eigenvector with a threshold set to zero. The resulting modularity score (Q) was tested for statistical significance against 1,000 null model simulations generated by randomizing the original matrix structure. Nestedness was assessed via the NODF metric (Nestedness metric based on Overlap and Decreasing Fill), adapted from the method outlined by Kauffman et al. (2022), and expressed as a percentage. To determine the significance of the observed nestedness, NODF values from the empirical data were compared against 1,000 randomized matrices, and associated z-scores and p-values were calculated.

2.5 Transposon mutant library of strain 10N.239.311.G07

The Nahant collection isolate 10N.239.311.G07 (1G07) was isolated from bloom day 239 and is the host of isolation of the three closely related phages 3.330.B; 5.330.B; 7.330.B making it a suitable candidate to study the host receptor for those three phages. To identify the phage receptor, the host strain 1G07 was genetically modified with the help of a suicide conjugation plasmid (pSC189) (Supplementary Figure S 2.1), resulting in the creation of a mutant library of strain 1G07 with different transposon insertions at random positions in the genome, leading to random gene disruption. As a donor strain, the highly conjugative *Escherichia coli* DATC + pSC189-cm was used (Bobonis, Yang, Voogdt, & Typas, 2024). The transformation of the plasmid pSC189-cm into *E.coli* DATC was previously performed (Kreutter, 2024). The Chloramphenicol tolerance of 1G07 was tested, by streaking out the strain onto TSB (Tryptic Soy broth – from Sigma-Aldrich) 2 (15 g/l NaCl) agar plates with different Chloramphenicol concentrations (5 µg/ml, 10 µg/ml, 12.5 µg/ml). A streak out of 1G07 on a TSB-2 plate without Chloramphenicol was used as negative control. The plates were incubated at 25°C overnight. To determine the optimal mating conditions between *E.coli* DATC and 1G07, donor:recipient ratios (3:1, 1:1, 1:3), different temperatures (25°C and 30°C) and different recipient growth media TSB-1 (5 g/l NaCl) and TSB-2 (15 g/l NaCl) were tested, according to SOP (Transposon mutagenesis). The conjugation efficiency of the drop spot mating was determined for the optimized condition of a donor:recipient 3:1 ratio at an incubation temperature of 25°C. The drop spot was collected in 500 µl SM buffer and a dilution series (10^0 to 10^{-5}) was prepared. From each dilution 100 µl were plated out on TSB-1 Cm (5 µg/ml) agar plates. The plates were incubated at 25°C for 48 h and the colonies were counted.

2.5.1 10N.239.311.G07 transposon mutant library preparation

To prepare the mutant library overnight cultures of the donor *E.coli* DATC pSC189-cm and the recipient 1G07 were prepared, each from a single colony into 10 ml media. *E.coli* DATC pSC189-cm was inoculated into 10 ml LB supplemented with DAP (0.3 mM) and Cm (5 µg/ml), incubated at 37°C shaking at 200 rpm. The recipient strain 1G07 was inoculated into

10 ml TSB-1, incubated at 25°C at 200 rpm shaking. Aliquots from the overnight cultures were prepared in 1.5 ml Eppendorf tubes using 900 µl from the donor and 300 µl from the recipient. The aliquots were pelleted separately centrifuging at 8000 rpm for 2 min. The supernatant was discarded, and the cells were washed in 1 ml prewarmed (37°C) mating media (TSB-1 supplemented with 10 mM Mg₂SO₄ and 0.3 mM DAP). The washing step was repeated with 500 µl prewarmed mating media. The *E.coli* DATC pSC189-cm cell pellet was resuspended in 500 µl mating media and this volume was then transferred to the 1G07 cell pellet to dissolve the second cell pellet by pipetting up and down. This mixed culture was centrifuged again at 8000 rpm for 2 min, the supernatant was fully discarded, and the pellet was resuspended in 20 µl of prewarmed mating media. The complete volume of 20-30 µl from the mating was then dropped on TSB-1 DAP (0.3 mM) agar plates. The plates were dried open in the laminar flow for 30 min and afterwards incubated overnight at 25°C. Two mating spots were collected with a 10 µl sterile inoculation loop and resuspended each in 1 ml SM buffer. Both resuspended mating spots were transferred into a 50 ml falcon tube with 18 ml SM buffer, and the solution was mixed by pipetting up and down. 190 selective plates TSB-1 Cm (5 µg/ml) were prepared by plating 100 µl of the suspension on each plate. The plates were incubated at 25°C for 48 h. To check if the transposon was inserted into our mutant strains 22 colonies were picked and transferred into 50 µl of PCR H₂O, as negative control a 1G07 wildtype colony was included and as positive control a colony of *E.coli* DATC pSC189-cm was picked. The colonies were broken up in 3 freeze and thaw cycles, followed by a heating step at 100°C for 10 min. A colony PCR was performed wherein this DNA served as template in the PCR reaction. The total reaction volume of 25 µl was prepared the following: 3ul template, 8.5 µl PCR H₂O, 12.5 µl Dream Taq (thermoscientific DreamTaqTM Green PCR Master Mix (2X)), 0.5 µl cat2 forward primer 10 µM (primer sequence: 5'-TTACGCCCCGCCCTGCCACT-3'), 0.5 µl cat2 reverse primer 10 µM (primer sequence: 5'-TGATCGGCACGTAAGAGGTTCCAAC-3'). The reaction setup for the thermocycler was the following: initial denaturation at 95°C for 2 min; 30 cycles of 95°C for 1 min, 59°C for 45 sec, 72°C for 1 min; and the final elongation at 72°C for 5 min; infinite hold at 12°C. To confirm the presence of the desired transposon in the colonies, 5 µl of the PCR products were analyzed on a 2% LE agarose gel with GelRed (1x /

1:10.000 dilution). The gel was run for 40 min at 120 V, as marker GeneRuler 1 kb (Thermo Fisher) was used. As this test was successful, all the colonies from the selective plates were wiped off using a sterile 10 µl inoculation loop, collecting all colonies in 10 ml SM buffer in a 50 ml falcon tube. The suspension was carefully mixed by pipetting up and down with a 5 ml serological pipette. Glycerol stocks were created by pipetting 1 ml of mutant library suspension into tubes and adding 313 µl of 80% Glycerol (supplemented with 20 mM MgCl₂), inverted several times to mix and then the tubes were frozen in liquid nitrogen and stored at -80°C. Prior to collecting, the colonies from 15 plates were counted to assess the saturation of the mutant library. With an average of 427 CFU per plate, the saturation of the library was 23 CFU per gene ((427 CFU per plate x 190 plates) / ~ 3500 genes = 23.18 CFU per gene).

2.5.2 10N.239.311.G07 mutant library phage 3.330.B._10N.239.311.G07 resistance selection

The mutant library was challenged by phage 3.330.B in an agar overlay assay. The phage stock 3.330.B PPA.02370 was used in this assay, having a titer of 2×10^{10} plaque forming units per ml. Two streak plates MB 2216 agar, from the 1G07 wildtype were prepared and incubated overnight at 25°C. Serving as a positive control in the experiment, the colonies of all four plates were collected using a sterile 10 µl inoculation loop and washed in 1 ml of MB 2216. Four tubes of the 1G07 mutant library were defrosted and centrifuged at 5000 rpm for 5 min. The supernatant was discarded, and the pellets were washed with 1 ml MB 2216 Cm (5 µg/ml). Next, the tubes from the library as well as the wildtype tube were pelleted centrifuging at 5000 rpm for 5 min. The wildtype pellet was dissolved in 1 ml of MB 2216, and the volume was then transferred into an Erlenmeyer flask with 9 ml of MB 2216. The pellets of the mutant library were dissolved in 1 ml MB 2216 Cm (5 µg/ml), the volume was transferred into an Erlenmeyer flask with 9 ml MB 2216 Cm (5 µg/ml). Both cultures were incubated for 1 h, at 25°C, shaking at 200 rpm. After the incubation dilution series of both cultures, wildtype and mutant library were prepared (wildtype 10^0 to 10^{-3} ; mutant library 10^0 to 10^{-8}). 250 µl of each dilution were transferred into 1.5 ml tubes containing 25 µl of 3.330.B concentrated phage stock. For each

dilution a control without phage addition was included in the assay. The tubes were mixed gently by pipetting up and down and the tubes were incubated for 15 min at room temperature. The total volume of 275 μ l of the host-phage mix was transferred into prewarmed (42°C) 7 ml top agar (0.4% agar + 5 μ g/ml Chloramphenicol) and the mixture was poured on large, squared petri dishes with bottom agar (40 ml, 1% agar + 5 μ g/ml Chloramphenicol). In addition, a dilution series from a mutant library tube in 2216 media was made to determine the CFU per tube. The dilution (10^{-5} to 10^{-7}) were plated out using 100 μ l per MB 2216 Cm (5 μ g/ml) agar plate. All plates were incubated at 25°C overnight. On average one mutant library tube contains around 3.7×10^7 CFU per ml (calculated based on the colony counts from agar plates, using different dilutions (10^{-5} to 10^{-8}) of the defrozen mutant library directly). The controls without phage addition and the ones challenged with the phage showed the same amount of bacterial growth. 15 colonies were picked and transferred into 40 μ l of PCR H₂O. The colonies were broken up in three freeze and thaw cycles, followed by a heating step at 100°C for 10min. As preliminary test, the arbitrary PCR was performed with those 15 colonies (TML_A1 to TML_B3, Supplementary Table S 1.8) serving as template, the reaction mix and PCR program used was the same as described below (section 2.5.3). The PCR product of the second PCR was cleaned up using the innuPREP PCRpure kit according to the kits manual and sent to Sanger sequencing to the firm Microsynth. Submitting 12 μ l of eluate with 3 μ l of primer Mar4_int2 (20 μ M) (primer sequence: 5'-GTCATCGTCATAATCG-3').

The agar overlay assay was repeated as described above, only using one tube of the mutant library instead of four tubes. After the phage addition to the diluted cell culture the tubes were mixed gently by pipetting up and down and the tubes were incubated for 20 min at room temperature, shaking in the rotating incubator. The agar overlay plates were poured as previously described and incubated at 25°C overnight. In addition, 50 μ l of the mutant library culture were transferred into 5ml MB 2216 Cm (5 μ g/ml) and incubated overnight at 25°C, 200 rpm shaking, to investigate the growth in more detail (section 2.6.1).

The agar overlay plates showed a difference in growth between the no-phage control plates and the ones that were challenged with phage 3.330.B. In total 189 colonies were randomly picked

and streaked on MB 2216 Cm (5 µg/ml) agar plates. The plates were incubated at room temperature overnight and then re-streaked for purification on MB 2216 Cm (5 µg/ml) three times, while incubating at room temperature overnight between each streak. For the creation of glycerol working stocks, the colonies were inoculated into two 1.2 ml deep well plates, each well containing 800 µl of MB 2216 Cm (5 µg/ml). The plates were sealed with breathable foil and incubated at 25°C, shaking at 200 rpm overnight. From each deep-well plate 172 µl of culture are transferred into a low-well plate, containing 78 µl of 80% Glycerol (supplemented with 20 mM MgCl₂ to a final concentration of 25% w/v Glycerol). To each well of the deep-well plates 197 µl of 80% Glycerol (supplemented with 20 mM MgCl₂ to a final concentration of 25% w/v Glycerol) is added. All plates were mixed well by pipetting up and down, sealed with aluminum foil, frozen in liquid nitrogen and stored at -80°C. In addition, from each mutant strain a colony was transferred into 40 µl of PCR H₂O into a 96-well PCR plate. The PCR plates were stored at -20°C, for further usage in the arbitrary PCR.

All mutant strains were challenged with the same set of 79 phages that were used for the host-range assay. The strains are inoculated in 5 ml of MB 2216 Cm (5 µg/ml) and incubated overnight at room temperature, shaking in a rotating incubator. For the agar overlay, 250 µl of each culture were transferred to 10 ml prewarmed (42°C) top agar (0.4% agar, 5 µg/ml Chloramphenicol) and poured on large, squared bottom agar (1% agar, 5 µg/ml Chloramphenicol) plates. The plates were dried for 30 min at room temperature. Spots of 2 µl from each concentrated phage stock were pipetted on the plates, using the same phage-set layout (Supplementary Table S 1.3). The plates were incubated at room temperature overnight. Next day the plates were checked and the lysis patterns were noted.

2.5.3 Arbitrary PCR and Sanger Sequencing

To determine the location of the transposon insertion in each mutant strain an arbitrary PCR was performed, the PCR product was cleaned up and sequenced to map the transposon insertion sites back to the host wildtype genome. As a template in the PCR reaction, the PCR plate with the mutant strain colonies was used. First, the DNA was made accessible in three

freeze and thaw cycles, followed by a heating step at 100°C for 10 min. The arbitrary PCR consists of two PCR reactions. In the first reaction the total volume of 25 µl was as follows: 2 µl template, 5 µl Green Flexi Buffer (Promega M891A), 2 µl 25 mM MgCl₂, 0.5 µl 10 mM dNTPs, 0.5 µl 25 µM SS9arb2 (primer sequence: 5'-GACCACGAGANACTAG-3'), 0.5 µl 10 µM Mar4 (primer sequence: 5'-TAGGGTTGAGCCAGTT-3'), 0.125 µl GoTaq G2 Hotstart DNA Polymerase (Promega M740B), 14.4 µl PCR H₂O. The PCR program was as follows: initial denaturation at 95°C for 5 min; 6 cycles of 95°C for 30 sec, 30°C for 30 sec, 72°C for 1.5 min; 32 cycles of 95°C for 30 sec, 55°C for 30 sec, 72°C for 1.5 min; final elongation at 72°C for 5 min; infinite hold 12°C. The PCR product of the first reaction was used as template in the second reaction. The second PCR reaction consisted of per reaction: 2.5 µl template, 5 µl Green Flexi Buffer, 2 µl 25 mM MgCl₂, 0.5 µl 10 mM dNTPs, 0.5 µl 10 µM Arb3 (primer sequence: 5'-GACCACGAGACACACT-3'), 0.5 µl 10 µM Mar4_int1 (primer sequence: 5'-GACTCACTATTAGAGC-3'), 0.125 µl GoTaq G2 Hotstart DNA Polymerase, 13.9 µl PCR H₂O, with a total reaction volume of 25 µl. The setup of the thermocycler for the second PCR reaction was: initial denaturation at 95°C for 5 min; 30 cycles of 95°C for 30 sec, 58°C for 30 sec, 72°C for 1.5 min; final elongation at 72°C for 5 min; infinite hold at 12°C. The PCR products of the second PCR were analyzed on a 2% LE-agarose gel with GelRed (1x / 1:10.000 dilution) in 1xTAE buffer, for 30 min at 120V and imaged on a ChemiDoc MP imaging system (BioRad). The PCR products were cleaned up using the Zymo Research ZR-96 DNA Clean-up kit, according to the kits protocol. 12 µl of each sample and 3 µl of primer Mar4_int1 (20 µM) (primer sequence: 5'-GACTCACTATTAGAGC-3') were submitted for Sanger sequencing to the firm Microsynth. In addition, a hsp60 colony PCR of the 1G07 plate, that was used to create the mutant library, was performed right before the creation of the transposon mutant library, as described above (section 2.2). Confirming that the used strain had the same hsp60 sequences as the wildtype 1G07. The genes of the host genome were annotated with RAST. The sequences were mapped to the 1G07 host genome using the Geneious Prime software version 24.0.5. (Supplementary Table S 1.7).

2.6 Growth of the 10N.239.311.G07 and its mutant library challenged with phage 3.330.B

During the resistance selection of the 1G07 mutant library (section 2.5.2) 50 µl mutant library culture were inoculated in 5 ml MB 2216 Cm (5 µg/ml). In addition, an overnight culture of 1G07 was prepared, transferring a single colony into 5 ml of MB 2216. Both incubated overnight at 25°C, 200 rpm shaking. Next day, both overnight cultures were diluted 1:100, 50 µl were transferred into 5 ml of MB 2216 for each culture. Incubating the cultures for 1 h at 25°C, shaking at 200 rpm. The mutant library culture reached an OD₆₀₀=0.22. A dilution series of the culture was made (10^0 to 10^{-8}). A 96 well plate was prepared filling the outer wells (row A and H, as well as columns 1 and 12) of the plate with 160 µl of MB 2216, whereas in the inner wells 40 µl of concentrated phage stock 3.330.B (PPA. 02370) were aliquoted. 150 µl of each dilution were transferred to the inner wells of the low well plate, having 5 replicates for each tested condition including the negative (no phage) control, mixing the culture and the phages in each well by pipetting up and down. The plate was sealed with breathable foil and incubated at 25°C, in a Tecan Spark plate reader at the lowest amplitude of orbital shaking. Growth was monitored by measuring OD₆₀₀ every 30 min overnight (figure 1.8). At the timepoint 3 h and 16 h after phage addition samples were taken, centrifuging them to pellet the cells at 8000 rpm for 5 min, washing the pellet with fresh media twice to wash of possible phages still present outside the cells and repeating the centrifugation. The cells were plated out on MB2216 agar plates and incubated overnight at room temperature. Single colonies were transferred into 5 ml MB 2216 and incubated overnight at 25°C, 200 rpm shaking and the next day agar overlays were performed wherein phage 3.330.B was again spotted onto the plate to test for the strains resistance to the phage.

As potential alternative host strain, an isolate from day 244 of the Nahant time series, strain 10N.244.47.E12 in which the phage 3.330.B was shown to be able to replicate in the cross-infection assay (section 2.4), was also tested. Their growth was monitored over 12 – 13 h when challenged with a high MOI of phage 3.330.B (PPA.02370 / MOI of 100), as described above

using the Tecan Spark plate reader to automate the incubation and OD600 measurement (figure 1.8).

2.6.1 Transposon mutant library 3.330.B resistance selection in liquid culture

One tube of 1G07 mutant library was defrosted and pelleted at 8000 rpm for 5 min. After the supernatant was discarded, the pellet was washed with MB 2216 Cm (5 µg/ml). The washing step was repeated, the pellet was resuspended in 1 ml of MB 2216 Cm (5 µg/ml), and the volume was transferred into 9 ml of MB 2216 Cm (5 µg/ml). The culture was incubated at 25°C, 200 rpm shaking for one hour for the culture to grow out of lag phase. A low well plate was prepared for growth monitoring in the Tecan Spark plate reader as previously described. 160 µl of the culture were used and 40 µl of concentrated phage stock 3.330.B (PPA. 02370) were used to challenge the bacteria. The plate was sealed, and the growth was observed using the Tecan Spark plate reader for incubation. Incubating the plate at 25°C, lowest amplitude of orbital shaking, while the OD600 was measured every 15 min for close monitoring of growth. After 45 min the plate was sampled, the culture was collected and centrifuged at 4000 rpm for 5 min. The supernatant was discarded, and the pellet was washed with MB 2216 Cm (5 µg/ml) to wash out the remaining phages. 100 µl of resuspension and its ten-fold dilution were plated out on MB 2216 Cm (5 µg/ml) agar plates, which were incubated overnight at 25°C. To test for the presence of phage DNA, colonies were picked and transferred into 50 µl of PCR H₂O. Making their genetic material available, the cells were broken up in three freeze and thaw cycles, followed by heating up to 100°C for 10 min. A colony PCR was performed using primers that target three different sites within the phage 3.330.B genome (section 2.8).

2.7 3.330.B PCR and primer design

Allowing for fast and easy detection through PCR and gel electrophoresis, primers were designed targeting three different sites within the genome of phage 3.330.B. Design tool Primer3Plus ([Primer3Plus - Pick Primers](#)) in its default setting was used for primer design,

offering the sequenced and known genome of phage 3.330.B as template. All primers were checked using the idt DNA Oligo analyzer ([OligoAnalyzer Tool - Primer analysis and Tm Calculator | IDT](#)) to exclude the formation of secondary structures and self- and heterodimerization. Three primer pairs were used, primer set 1 (forward primer sequence: 5'-GGAAACTGAAGAAATTAGGG-3'; reverse primer sequence: 5'-TGTGATACCGAAGATAGCC-3') targeting the end of the DNA polymerase and the start of the polynucleotide kinase within the phage genome, creating a PCR product of 385 bp in length. Primer set 2 targeting a non-coding region within the phage genome, its product being 360 bp long (forward primer sequence: 5'-CGCAAACCTATATAACTACGG-3'; reverse primer sequence: 5'-AACTGGTAGGAAACTAGCC-3'). The end of major capsid protein is targeted by primer set 3, with which a fragment of 380 bp length can be amplified (forward primer sequence: 5'-GTAACCCTGACTTCTACCC-3'; reverse primer sequence: 5'-ACCTTTAATCGTGTACGG-3'). The annealing temperature for all 3 primer pairs ranges around 56°C, enabling common analysis.

The PCR reaction had a total volume of 25 µl, having the following composition: 3 µl template, 8.5 µl PCR H₂O, 12.5 µl Dream Taq (thermoscientific DreamTaqTM Green PCR Master Mix (2X)), 0.5 µl forward primer 10 µM, 0.5 µl reverse primer 10 µM. Wherein any of the three primer pairs could be used. The reaction setup for the thermocycler was the following: initial denaturation at 95°C for 2 min; 34 cycles of 95°C for 1 min, 56°C for 45 sec, 72°C for 1.5 min; and the final elongation at 72°C for 5 min; infinite hold at 12°C. The optimum annealing temperature for all primer pairs was determined in a temperature gradient PCR (55°C to 65°C).

2.8 Plasmid extraction of 10N.239.311.G07 and its mutant strain TML_B3

To address the question, whether phage 3.330.B might be present in the bacterial cells as a plasmid, the plasmids of 1G07 and its mutant strain TML_B3 (transposon mutant library strain B3 test strain) were extracted from liquid cultures. The Monarch Spin Plasmid Miniprep Kit was used according to the kits manual, to extract the plasmids from 5 ml overnight culture of both strains grown in MB 2216. Since the achieved concentrations were too low, the Zymo

PURE 2 plasmid Midiprep Kit was used, following the kits protocol for low copy plasmids. Single colonies from both strains were inoculated into 100 ml of MB 2216 and incubated overnight, shaking at 200 rpm at room temperature. The centrifugation protocol was used, pre-heating the elution buffer to 50°C and eluting with 80 µl of RNase free H₂O three times. 20 µl of the eluate, supplemented with 2 µl of loading dye were analyzed on a 0.5% LE agarose gel with GelRed (1x / 1:10.000 dilution), run in 1xTAE for 160 min at 80 V, and imaged on a ChemiDoc MP imaging system (BioRad). As marker GeneRuler 1kb (Thermo Fisher) was used.

An enzymatic digest from the midiprep extracts was made using the following enzymes: Thermo Scientific™: DNase I, RNase-free (1 U/µL), S1 Nuclease (100 U/µL), Exonuclease I (20 U/µL); New England Biolabs Exonuclease III (100 U/ µL). In addition, the following restriction enzymes were included: BamHI, PvuII, NheI, SalI, NcoI, MluI, XhoI. 20 µl of the plasmid midiprep from 1G07 and TML_B3 were used, the amount of enzyme used was according to the company protocols, using twice as much enzyme and buffer and prolonging the reaction time to 1 h. The complete volume of each digest supplemented with 2 µl of loading dye was loaded on a 0.5% LE agarose gel with GelRed (1x / 1:10.000 dilution), run in 1xTAE for 160 min at 80 volt. As marker GeneRuler 1kb was used. To exclude host contamination of the plasmid preps, an hsp60 PCR was performed. The same PCR reaction mix and thermocycler setup which was described in section 2.2 was used. The PCR products were analyzed on a 2% LE agarose gel with GelRed, running the gel for 40 min at 100 V. 5 µl of the PCR products were loaded and as marker the GeneRuler 50bp (Thermo Fisher) was used.

2.9 Inducing agent

During the resistance selection process of the 1G07 mutant library (section 2.5.2), the induction of a temperate phage could be observed in some of the plates. A plaque was picked to identify the induced phage (section 2.10.1). To investigate the conditions leading to the induction, different incubation temperatures (20°C, 23°C, 25°C and 27°C) were tested. As in the previous growth experiments described above, the Tecan Spark plate reader was used to monitor and

observe the influence of different incubation temperatures on 1G07. Starting from overnight cultures of 1G07 and its mutant strain TML_B3, which were diluted 1:100 and incubated at 25°C, shaking at 200 rpm, for 1.5 to 2 hours, till an OD_{600nm} of around 0.2 was reached. At this point the cultures were distributed to the different wells of the low-well plate, each strain filling one half of the plate, with 200 µl of culture in each well. The plate was sealed with breathable foil and put in the plate reader, where it was incubated at 20°C, lowest amplitude of orbital shaking, measuring OD₆₀₀ every 30 min. Growth was monitored overnight and the experiment was repeated with different incubation temperatures, comparing growth at 20°C, 23°C, 25°C and 27°C (Supplementary Figure S 2.8).

To address a possible effect of the incubation temperature, overnight culture of the same strains, wildtype 1G07 and mutant strains that showed the induction pattern (T9, T46, T53) were incubated, at room temperature (22°C) and at 25°C, shaking at 200 rpm. Agar overlays from those overnight cultures were made as described above. The pH of the used media and buffer were determined, the MB 2216 had a pH 7.43, the MB 2216 Cm (5 µg/ml) used for the mutant strains had a pH of 7.48. The SM buffer that was used had a pH of 7.51. The different incubation temperatures did not make a difference, as the plates still showed the same induction patterns. Different salt concentrations were spotted on the strains in agar overlays, creating a different dilutions from a 5 M NaCl solution (pH 7.9), and spotting 2 µl of 5 M, 3 M, 1 M, 0.8 M, 0.6 M, 0.3 M, 0.2 M, 0.1 M, 0.05 M, 0.03 M, 0.02 M and 0.01 M NaCl, as well as milliQ water, only SM-buffer and MB 2216 media as controls. None of the spotted salt concentrations lead to induction, excluding osmolarity as factor.

In order to extract any excreted peptides or molecules that the bacterial strains might have released into the top agar, the agar overlay plate from the mutant strain T1 (challenged with the set of 79 phages) was covered with 15 ml of SM buffer and incubated for 4 hours at room temperature. The supernatant was retrieved carefully and transferred into a centrifugal filter unit with a 30 kDa filter (Amicon® ultra centrifuge filter, 30 kDa MWCO). The units were centrifuged at 3800 rcf for 90 min. The filtrate was pipetted into a sterile glass eprouvette and stored at 4°C. The filtrate was spotted (in duplicates) on an agar overlay plate of 1G07,

incubating the plate overnight at room temperature, revealing plaques the next day. A range of controls were prepared filtering the supernatant of agar overlay plates of strain T1 were only MB 2216 was spotted on, or only SM buffer or 1 M PBS. As positive control an agar overlay plate was included where 1G07 was challenged with the complete phage set. In addition, 5 ml of the phage stock 3.330.B (PPA.02370) and 5 ml of the phage stock 8.332.B. (PPA.02387) were filtered through the same filter units. All the filtrates were spotted on an agar overlay plate of 1G07. The plate was incubated overnight at room temperature (Supplementary Figure S 2.9).

2.9.1 Characteristics of the inducing agent

To characterize the composition of the inducing agent in the filtrate, the filtrate obtained from 1G07 challenged by the complete phage set, was enzymatically digested. 50 µl of the filtrate were used for each digest, using DNaseI (Thermo Scientific™ (1 U/µL)), RNase A (Thermo Scientific™ DNase and protease-free (10 mg/mL)), as well as Proteinase K (from the Invitrogen PureViral DNA/RNA Kit). According to the company's recommendations, all digests were performed at 37°C for 1 h. The Proteinase K digest was heat inactivated for 1 min at 100°C after the digest. In addition, 50 µl of the filtrate were heated at 100°C for 1 min. The different digests were then spotted on a 1G07 agar overlay plate, which was incubated overnight at room temperature.

Investigating whether the agent is polar or non-polar, 1 ml of the filtrate was mixed with 500 µl of Chloroform, till the two phase mingled and a white layer between the phases formed. The mixture was centrifuged for 4 min at 8000 rpm. Both phases were separated carefully and transferred into sterile glass epruvettes let in the fume hood for 72 h for the Chloroform to evaporate. 200 µl of methanol were added to the former Chloroform phase to dissolve the possible containing agent. An agar overlay plate was prepared of 1G07 and from both phases 2 µl were spotted (in triplicates) on the overlay plate (Supplementary Figure S 2.7 a). The necessity of salts in the buffer used to extract the agent from the agar overlays was tested, covering one agar overlay plate of strain 1G07 were the phage 3.330.B, 5.330.B and 7.330.B were spotted the previous day with 15 ml of nuclease free water and a second agar overlay plate with 15 ml

SM buffer. Both plates were incubated at room temperature for 4 h, afterwards the supernatants were collected and each passed through a <30 kDa centrifugal filter unit. Both filtrates were spotted on an agar overlay plate of strain 1G07 (in triplicates) which was incubated overnight at room temperature (Supplementary Figure S 2.7 b).

To narrow down the size range of the agent, an agar overlay plate of 1G07 was prepared as described (section 2.10.3), the plate was covered with 15 ml of SM buffer and incubated for 4 h at room temperature. One half of the supernatant was transferred into a centrifugal filter unit with a 30 kDa filter, while the other half was pipetted on a filter unit with a 3 kDa filter. Both were centrifuged for 90 min at 3800 rcf. To confirm the presence of the agent, both filtrates were spotted (2 µl drops) on an agar overlay plate of 1G07. The plate was incubated overnight at room temperature.

In addition, the inducing filtrate itself was tested in a 3.330.B PCR reaction, the filtrate and the phage stock 3.330.B (PPA.02370) were heated up for 10 min at 100°C, before serving as template in the reaction.

2.9.2 Identification of induced phage

During the resistant selection process of the 1G07 mutant library, prophage(s) were induced in a part of the agar overlay plates. From those induced plaques, two random plaques (T9-A; T9-B) were picked and transferred into 500 µl of SM buffer. The plaque was incubated in the buffer for 1 h at room temperature, afterwards a dilution series (10^0 to 10^{-6}) was made. Each dilution was used in an agar overlay, where 100 µl of the dilution were transferred on a bottom agar (1% agar) plate. 100 µl of a 1G07 overnight culture were pipetted into 3 ml of prewarmed (42°C) top agar (0.4% agar) and poured on the bottom agar plate. The plates were shaken carefully to spread the top agar over the whole plate and mix everything well. All plates were incubated at room temperature overnight. The next day, the dilution- overlay plate was checked and the plate with confluent lysis identified. This plate was used to create the phage stock, by pipetting 10 ml of SM buffer on the plate and resting the plate for 2 h at room temperature. The supernatant from the plate was sterile filtered through a 0.22 µm filter into a sterile glass epprouvette. The

volume of the filtrates (~8 ml each) was transferred into ultracentrifuge tubes (OpenTop 12.5 ml), the tubes were balanced and spun down in an ultracentrifuge for 2 h, at 4°C, 35000 rpm. The supernatant was discarded and 200 µl of SM buffer were transferred into the tubes. The Invitrogen Kit PureViral DNA/RNA Kit was used to extract the viral genetic material, whereby the kit protocol was followed. The extract was used as a template in a PCR reaction using the primers designed for phage 3.330.B (PCR reaction and settings as described in section 2.8).

2.9.3 Growth of 1G07 in addition of the inducing agent in liquid culture

An overnight culture of 1G07 was 1:100 diluted and incubated at 25°C, 200 rpm shaking for 1.5 h. To monitor the plate in the Tecan Spark plate reader, a low well plate was prepared aliquoting 50 µl of the inducing agent filtrate into all wells, but the three negative control wells. 200 µl of culture were added to all the wells and the plate was sealed with breathable foil. The plate was incubated in the plate reader overnight at 25°C, orbital shaking at the lowest amplitude, while the OD600 was measured every 15 min. The wells where the agent was added were sampled in two falcon tubes, which were then spun for 15 min at 5000 rpm. The supernatant was split in half, one half was sterile filtered through a 0.22 µm filter into sterile glass eprouvette, while the other half was not filtered, just transferred into a sterile glass eprouvette. Both stocks were prepared for the ultracentrifuge and spun for 2 h at 4°C at 35000 rpm. The potential viral DNA/RNA was then extracted with the Invitrogen PureViral DNA/RNA Kit, according to the kits manual. The extracts were then tested in a 3.330.B PCR (section 2.8) and the PCR products were analyzed on a 2% LE agarose gel run in 1x TAE for 45 min at 100 V, as marker GeneRuler 50bp (Thermo Fisher) was used, and imaged on a ChemiDoc MP imaging system (BioRad).

2.9.4 Inducing agent extraction

To find the best conditions for the creation of highly concentrated stock of the inducing agent, different incubation temperatures, room temperature and 25°C of the agar overlay plates were

tested. Different agar concentration in the bottom (0.8% and 1%) and top agar (0.3% and 0.4%), as well as two prewarming temperatures of the top agar, 40°C and 42°C were tested.

The highest inductive activity was obtained from the following procedure: on an agar overlay plate of 1G07 was prepared, pipetting 250 µl of 1G07 overnight culture into 10 ml top agar (0.4% agar, preheated to 42°C) and pouring it on a bottom agar plate (1% agar), the plate was dried for 30 min. The three related phages 3.330.B, 5.330.B, 7.330.B were spotted on the top agar layer, each phage was spotted 18 to 20 times, each spot containing 2 µl of concentrated phage stock. The plate was incubated overnight on 25°C. On the next day, the plate was covered with 15 ml SM-buffer and incubated for 4 h on room temperature. The supernatant was transferred into a centrifugal filter unit with a 30 kDa filter (Amicon® ultra centrifuge filter, 30 kDa MWCO) and centrifuged at 3.800 rcf for 90 min. An additional filtration step was included, passing the filtrate through a sterile 0.22 µm filter, into a sterile glass eprouvette. To test the inducing activity of the filtrate, a dilution series was made (10^0 to 10^{-11}), which was spotted on an agar overlay plate of 1G07. The plate was incubated overnight at room temperature.

To further concentrate the obtained inducing agent, the filtrate was added to a 3 kDa filter and centrifuged for 10 min at 3.800 rcf. The centrifugation step was repeated till, only about 2 ml remained above the filter. The liquid above the filter was retrieved with a pipette and transferred into a steril glas eprouvette. Again, the inducing activity of the filtrate was tested, and dilution series were made (10^0 to 10^{-11}), which were spotted on an agar overlay plate of 1G07. The plate was incubated overnight at room temperature. An up to 4 times higher concentration (10x from 10^{-4} to 10^{-8}) was observed after this step.

Results

3.1 Isolation of marine *Vibrionaceae*

From day 244 of the Nahant time series, 893 *Vibrionaceae* isolates were obtained. Those isolates were classified via their hsp60 gene sequence (Figure 1.2). The most abundant *Vibrionaceae* species from this isolation day are displayed (Table 1.1).

Table 1.1: Distribution of the *Vibrionaceae* strains isolated from day 244. Classification based on their hsp60 genes (colors correspond to the phylogenetic tree (Figure 1.2)).

<i>Vibrio species</i>	Number of isolates
<i>Vibrio cyclitrophicus</i>	563
<i>Vibrio owensii</i>	74
<i>Vibrio atlanticus</i>	58
<i>Vibrio lentus</i>	44
<i>Vibrio chagasii</i>	31
<i>Virbio splendidus</i>	25
<i>Vibrio pomeroyi</i>	5
<i>Vibrio atypicus</i>	4
<i>Vibrio rotiferianus</i>	1

Tree scale: 0.1

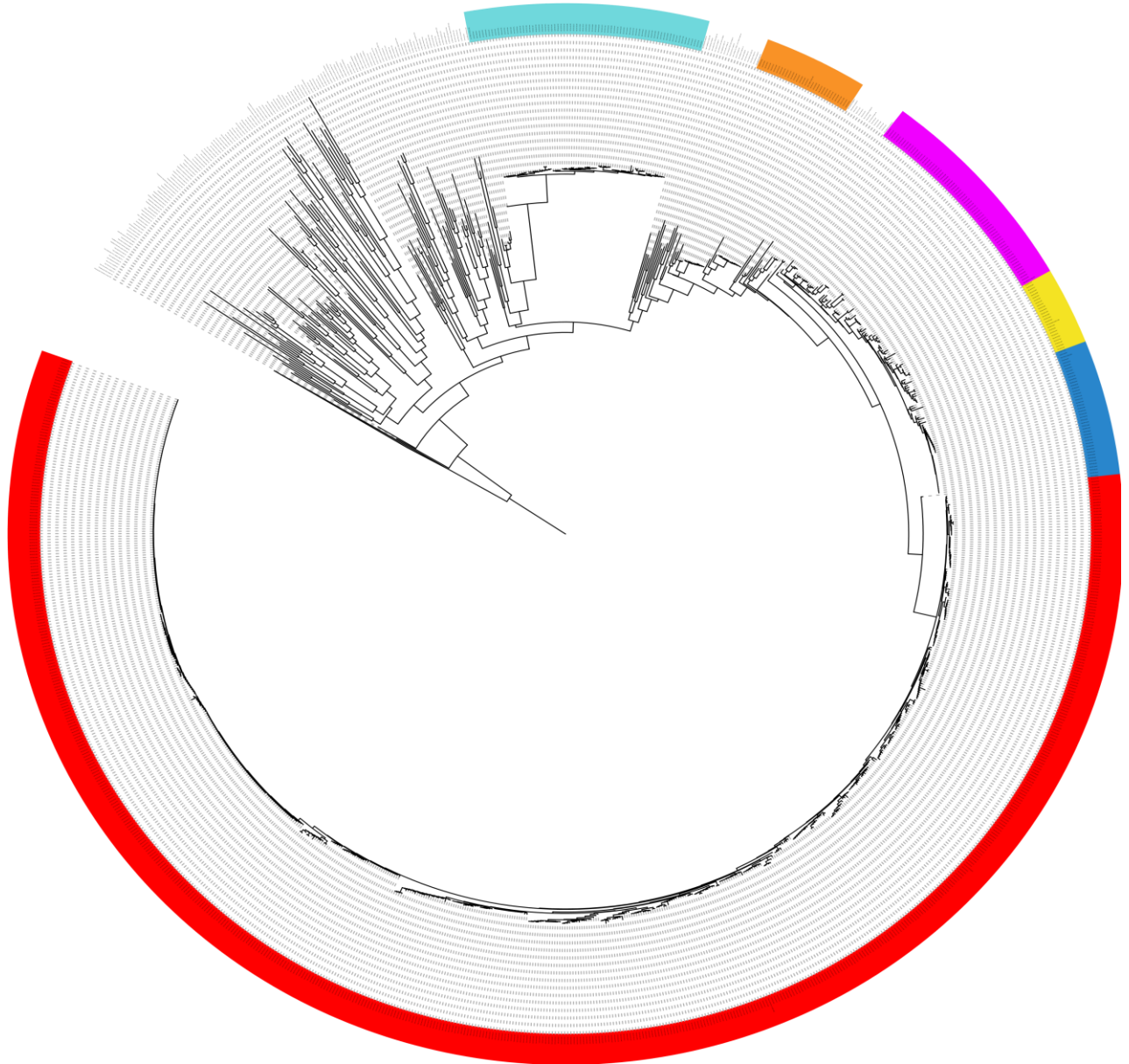


Figure 1.2: Phylogenetic tree based on the *hsp60* gene sequences of the 893 *Vibrionaceae* isolates of day 244. As reference sequences, 182 sequences from the RefSeq genomes of the *Vibrionaceae* were included. Sequences of the genus *Shewanella* (black) were included to build the outgroup (clade collapsed). The 6 most abundant species were colored (see Table 1.1).

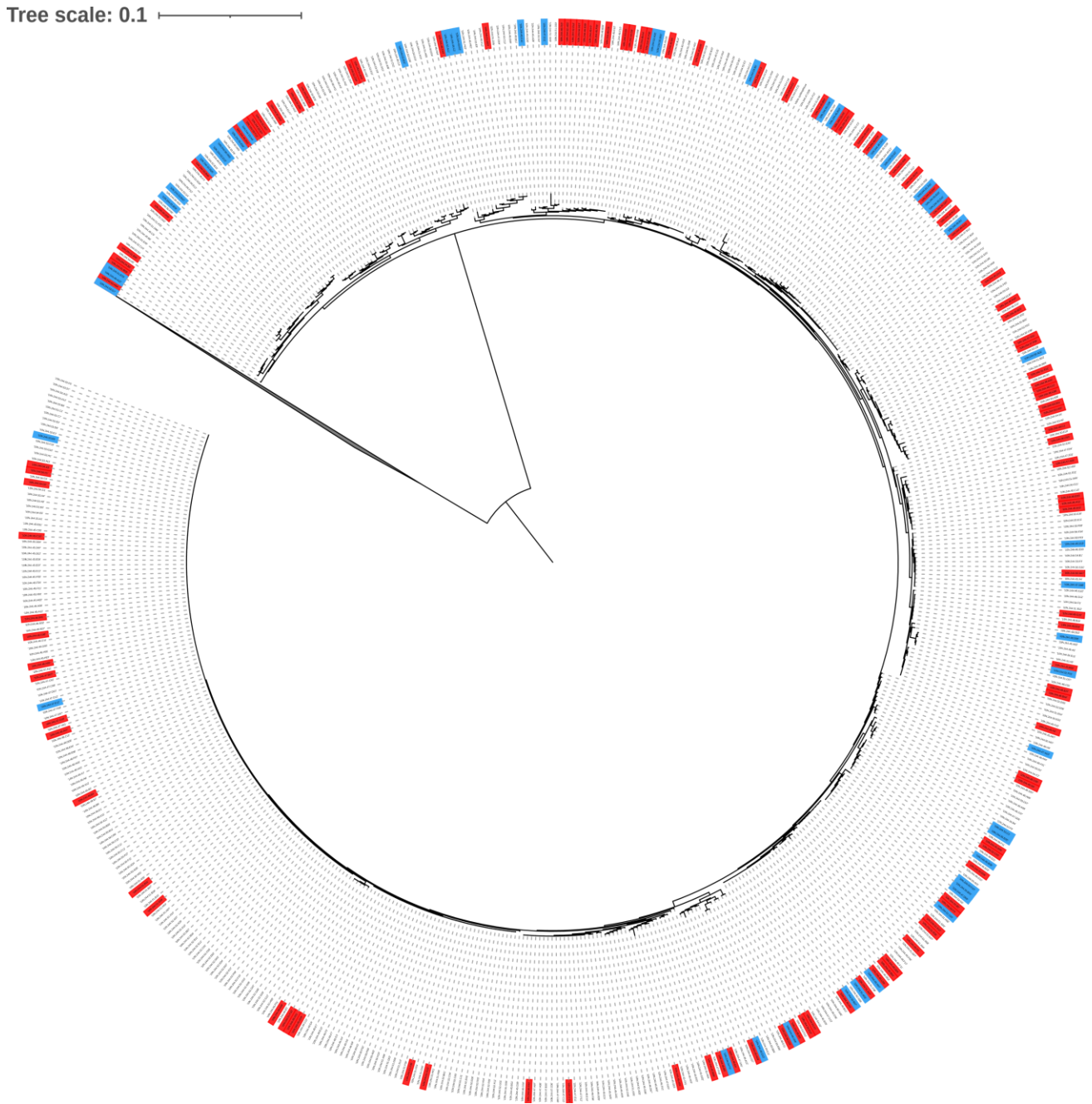


Figure 1.3: Phylogenetic tree based on the hsp60 gene sequences of the 563 *V. cyclitrophicus* isolates of day 244. Sequences of the genus *Shewanella* (black) were used as outgroup and as further reference, the RefSeq strain for *V. cyclitrophicus* was included. Strains that could be lysed by at least one phage are colored: the strain in which at least one phage could replicate in (blue); the strains that could only be lysed from without (red) (excluding interactions with the undiluted phage stocks of the phages 3.330.B, 5.330.B and 7.330.B).

3.2 Cross infection assay of isolation day 244

The 563 *V. cyclitrophicus* isolates from day 244 were tested in a drop spot assay for susceptibility to a set of 76 genomically diverse phages (Supplementary Table 1.3). Two different phages were included as biological replicates and served as controls (8.332.A_10N.239.312.A01.SH1_10N.V.238 – spot positions C3 and E4 / 8.332.B_10N.239.312.A01.SH1_10N.V.238 – spot positions B3 and F4). Across the assay, both replicates showed consistent results, with only minor variations in interaction strength, that were most likely due to differences in phage concentrations. While around 71% (401 isolates) of all the isolates from day 244, a day towards the end of the *Vibrionaceae* bloom, could not be lysed by any of the tested phages, the other isolates were susceptible to at least one phage. In 117 strains only lysis from without could be observed. Overall, 9% of the tested *V. cyclitrophicus* isolates from day 244 permitted replication of at least one phage. However, across the full phage panel of the 76 tested phages, only ten phages were able to replicate and lyse hosts from within (1.178.O, 3.330.B, 5.330.B, 7.330.B, 1.286.O, 1.199.A, 1.199.B, 1.248.O, 1.293.O, 1.215.A). The vast majority of bacterial strains exhibited resistance to most phages, with only 232 lytic interactions observed out of a total of 44.477 possible combinations.

Regarding the other previously described isolation days (Kreutter, 2024), phage 1.215.A stood out as one of the most effective, exhibiting lytic activity against 81 *V. cyclitrophicus* isolates from day 244 and successful replication in 43 of them. Most phages that were isolated during the bloom could not infect any of the tested hosts. Three phages (3.330.B, 5.330.B, and 7.330.B) appeared to lyse over 90% of all isolates from day 244, and 70% of the isolates from the other isolation days tested, but only when the undiluted titer (10^0) was applied. This broad lytic activity was not observed at higher dilutions, suggesting that the effect is unlikely resulting from true phage infection, which is why those interactions were removed from the matrix shown (Figure 1.4 a) and from any statistical tests.

The structure of the phage-host interaction matrix was analyzed using nestedness and modularity metrics to identify underlying ecological patterns such as host range overlap and specialization. The cross-infection matrix exhibited high modularity, with a standard modularity

score of $Q_b = 0.7316$ and an intra-module interaction ratio of $Q_r = 0.8376$. These values indicate a division of the matrix into sixteen discrete modules, each likely corresponding to a subgroup of phages and their preferred host range. While these modularity values were lower than the average values obtained from the equiprobable null model (z-scores: $Q_b = -13.40$, $Q_r = -4.28$). In contrast, the nestedness measured using the NODF (Nestedness metric based on Overlap and Decreasing Fill) was exceptionally low (NODF = 0.0107). The matrix visualization (Supplementary Figure S 2.2) confirms the absence of strong nested structure: interactions are not concentrated in the upper-left triangle or organized along a clear generalist-to-specialist gradient. Instead, blocks of interactions appear distinctly separated, visually supporting the modular structure inferred from quantitative metrics. But one has to keep in mind that this analysis is based on a single time point (day 244) within a 93-day time series, which may not fully capture the temporal variability of phage-host interactions. As such, the observed modularity and low nestedness might reflect transient ecological patterns, rather than stable community structures.

The cross-infection assay revealed temporal changes in the proportion of the lysed host strains (Figure 1.6), observed both with and without inclusion of the LO isolate. As expected, relative infectivity was higher when LO was included, beginning at 40% on pre-bloom day 232. Infectivity rose during the early bloom phase, reaching 55% on day 236. Following this peak, both infection and observed lysis rates declined sharply, with infection dropping below 10% and lysis to around 2% by day 241, before partially recovering towards the end of the bloom (infection 25%, lysis 10% on day 246). In parallel, the *V. cyclitrophicus* abundance peaked around day 236-237, corresponding with the highest infection levels, and subsequently declined as the lysis events increased.

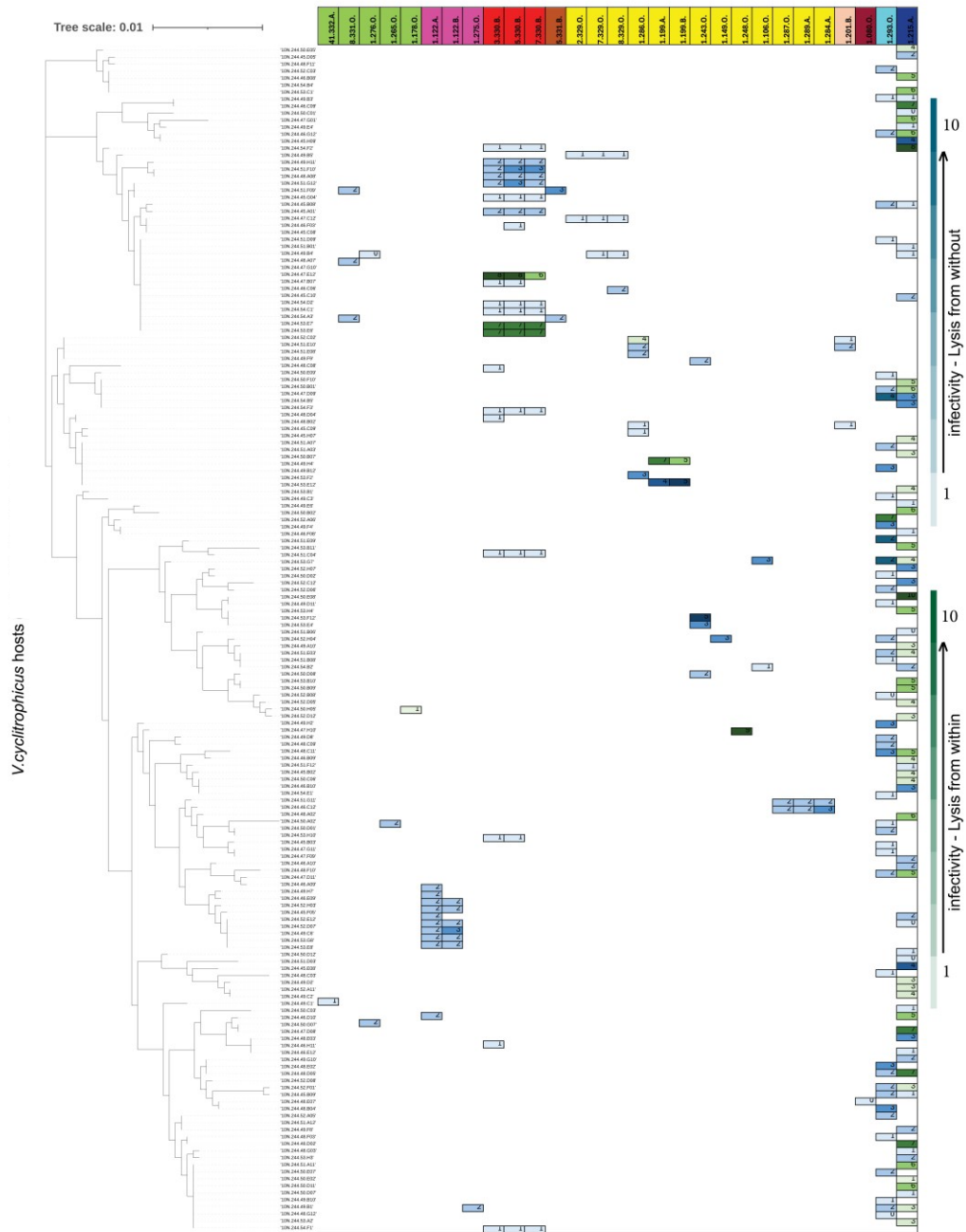


Figure 1.4 a): Phage-host interaction matrix of all *V. cyclitrophicus* isolates of day 244, on the y-axis (ordered according to their hsp60 phylogeny) that were lysed by at least one phage (excluding lysis from undiluted titer (10^0) of all phages). The x-axis contains all phages, that were able to lyse. Phage infectivity displayed as heatmaps (infection strength is represented using color gradient scales, with numerical values indicating the lowest phage dilution (on a log. scale) at which plaque formation was still detectable on bacterial lawn. The green color gradient corresponding to interactions of lysis from within (phage replication), whereas the blue gradient represents lysis from without.

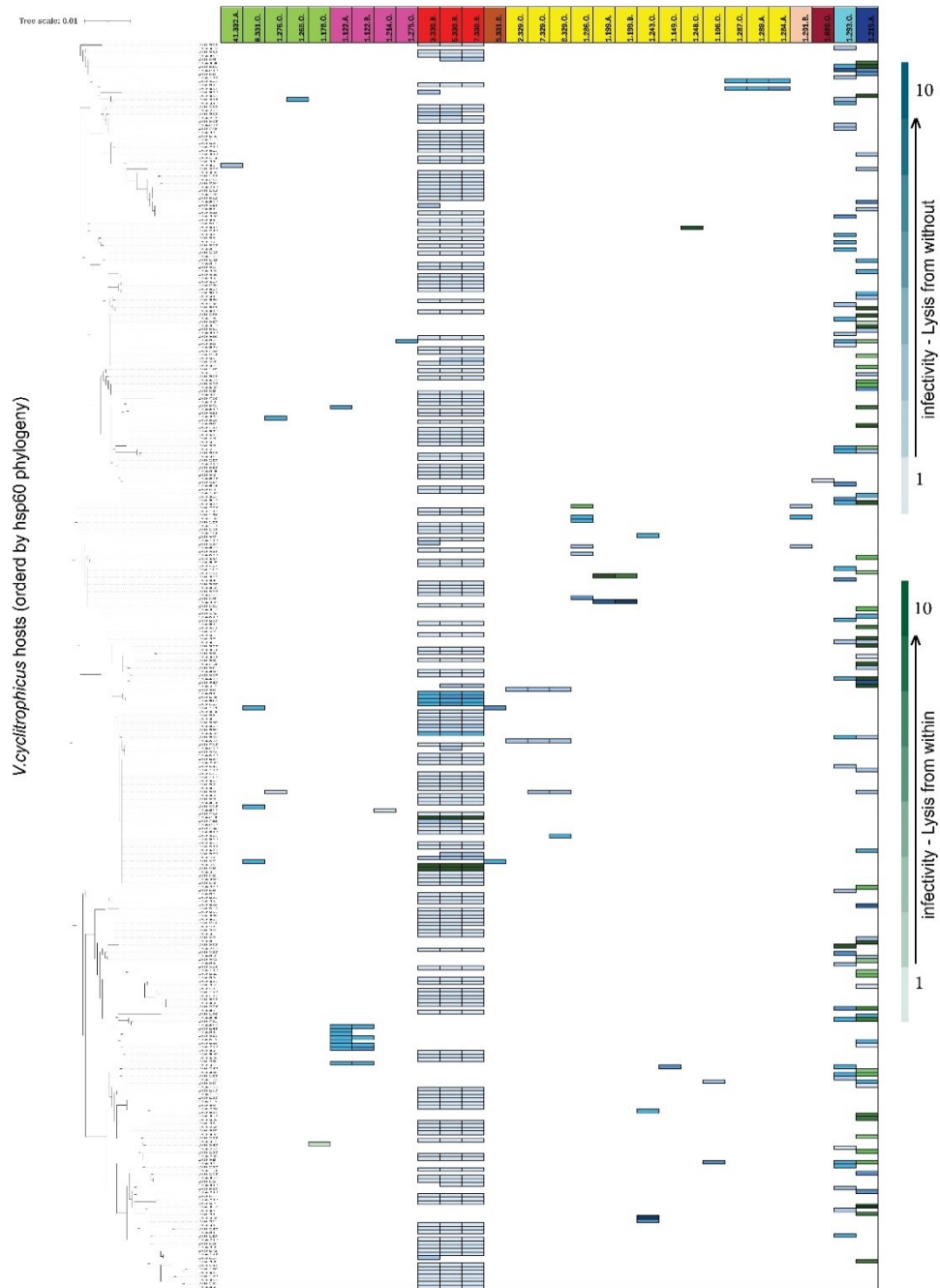


Figure 1.4 b): Phage-host interaction matrix of all *V.cyclitrophicus* isolates of day 244, on the y-axis (ordered according to their hsp60 phylogeny) that were lysed by at least one phage (including lysis from undiluted titer (10^0) of all phages). The x-axis contains all phages, that were able to lyse. Phage infectivity displayed as heatmaps (infection strength is represented using color gradient scales, with numerical values indicating the lowest phage dilution (on a log. scale) at which plaque formation was still detectable on bacterial lawn). The green color gradient corresponding to interactions of lysis from within (phage replication), whereas the blue gradient represents lysis from without.

3.3 Cross infection assay of *V. cyclitrophicus* strains from the Nahant time series

Due to differences in phage stock concentrations between the previously used stocks in the cross-infection assay previously performed and described by Kreutter, 2024, the *V. cyclitrophicus* strains from that study were tested again, with mostly higher concentrated phage titers, to compare the results, especially regarding the three closely related phages 3.330.B, 5.330.B and 7.330.B. Overall, no major discrepancies could be observed between the original and new cross-infection matrices, suggesting that host range is stable (Figure 1.5) (List of the tested isolates Supplementary Tables S 1.5). However, the higher phage-stock concentration of the genetically closely related phages 3.330.B, 5.330.B and 7.330.B, when spotting the phage stock undiluted (10^0) exhibited a noticeably broader host range in the updated cross-infection assay. In any higher dilutions of the phage stocks, their newly monitored activity was lost.

Additionally, an unidentified phage-inducing agent was included in the cross-infection assay. This agent was extracted from agar plates on which the three aforementioned phages had been spotted onto their host of isolation (10N.239.31.JE.1G07). Interestingly, the lysis pattern of this inducing agent overlapped strongly with the lysis profiles of the three related phages, when the concentrated phage titer (10^0 undiluted) was spotted. This indicates that the observed lysis following application of the undiluted phage stock is not caused by the phage itself, but rather by the phage-inducing agent. Hence caution is to be exercised when interpreting cross-infection data, particularly in cases where lysis only occurred when the undiluted phage stock (10^0) was applied. We therefore excluded such interactions from the further statistical analyses of the cross-infection assay described here from isolation day 244.

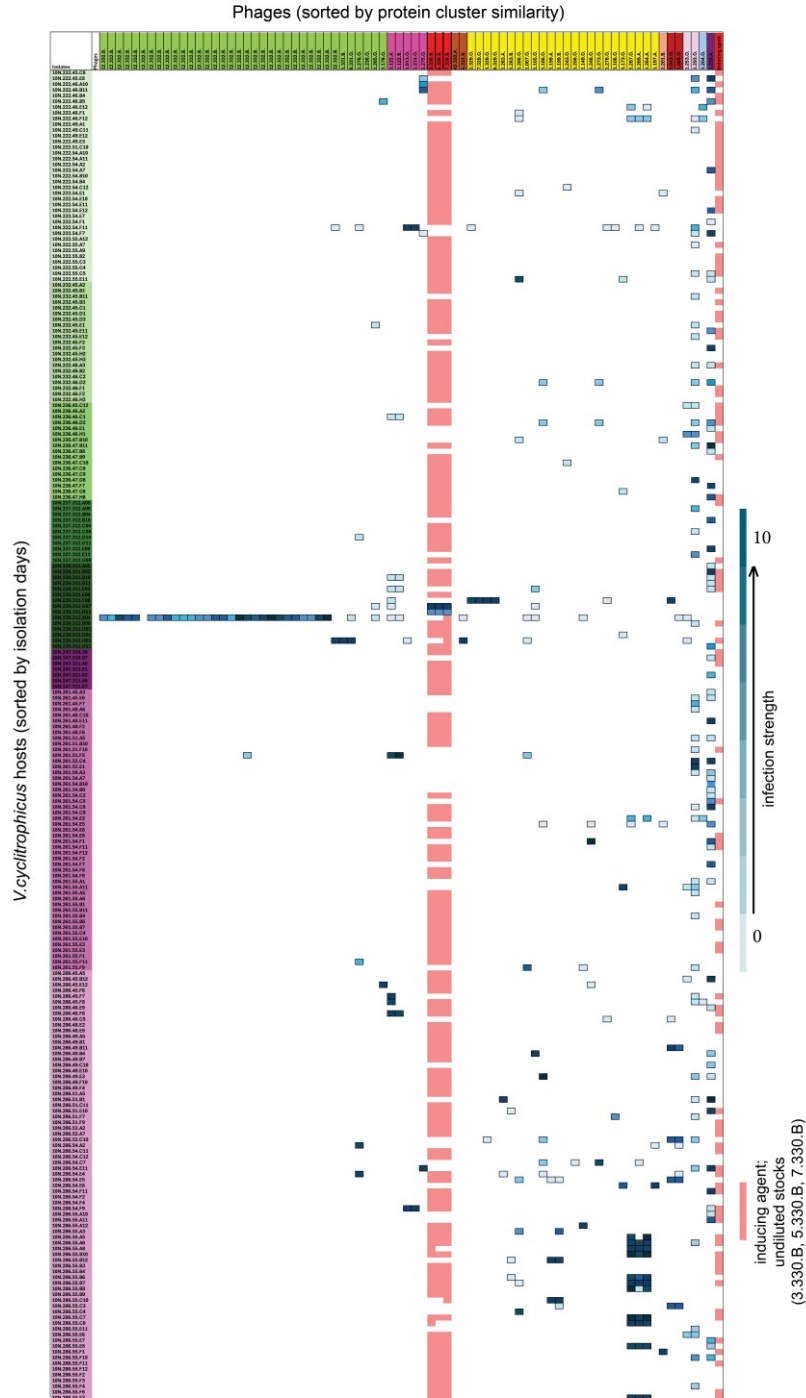


Figure 1.5: Phage-host interaction matrix of *V. cyclitrophicus* isolates from the Nahant time series – repetition and validation of the matrix from Kreutter, 2024. The isolates (y-axis) are organized by the different isolation days, while the phages (x-axis) are sorted via their protein cluster similarities. Phage infectivity displayed as a heatmap (infection strength is represented using a color gradient scale, with numerical values indicating the lowest phage dilution (on a log. scale) at which plaque formation was still detectable on a bacterial lawn. The matrix includes the lysis pattern observed after spotting the inducing agent. Displayed in rose are the interactions resulting from the undiluted phage stocks of the phages 3.330.B, 5.330.B, 7.330.B and the inducing agent.

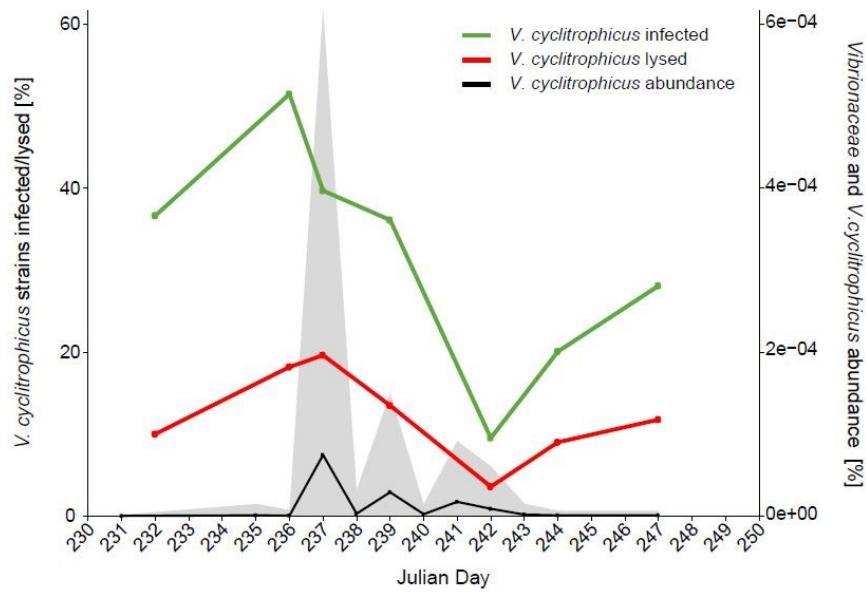


Figure 1.6: Temporal dynamics of *V. cyclitrophicus* infection, lysis and abundance around a natural bloom event. The percentages of *V. cyclitrophicus* strain infected (green) and lysed (red) by phages (left y-axis), was monitored over a time span of 20 days (x-axis), alongside with the relative abundance of *V. cyclitrophicus* within the *Vibrionaceae* community (black line; right y-axis). The shaded area represents the total *Vibrionaceae* abundance (right y-axis).

3.4 Transposon mutagenesis assay of strain 10N.239.311.G07

To enable phage receptor identification, a genome-wide mutant library of strain 1G07 was generated using the suicide plasmid pSC189, producing around 80.000 clones each carrying a random transposon insertion that disrupts a different host gene (expected insertions per gene: ~25 -30; statistical gene coverage: ~100% of all non-essential genes). Following resistance selection in an agar-overlay assay against phage 3.330.B, 189 putatively resistant colonies were isolated, of which 93 were sequenced to identify the corresponding genes, disrupted by the transposon (Supplementary Data Table 2.3). The susceptibility of the mutant strains was tested again, plating out the strains in agar overlays, spotting the same set of 76 phages on the bacterial lawn. The lysis pattern of the plate was checked (Supplementary Table S 1.5), showing that 24% still showed susceptibility to 3.330.B. In 38 of the 189 strains (20% of the strains), at least one temperate phage was induced in the agar overlays. From those plates a phage inducing agent was extracted (see Methods 2.10). Whereas 65% (124 of 189 tested strains) of the mutant strains

appeared resistant to phage 3.330.B in the spotting assay. However, the sequencing data revealed that the transposon positions, within the bacterial genome were widely dispersed, not pointing towards any phage receptor or common pathway. Yet some of the mutant strains seem to have acquired resistances, which the wildtype strain lacks. It is important to note that in this assay only the concentrated phage titer (10^0) was used, testing higher dilutions would be necessary to obtain more comprehensive data and to rule out possible effects of antimicrobial activity, or lysis from without.

Intriguingly, 10% of the mutant strains were susceptible to the phages 1.043.O. and 1.080.O., while the wildtype strain wasn't. Indicating that for instance a defense system might be influenced by the insertion. But also in those cases, the insertion locations revealed by the sequencing results, were distributed all over the genome, rather than pointing towards a common pathway. Further investigation needs to be undertaken to determine the cause of this putative lack of resistance.

In addition, the resistance selection was assessed in liquid culture, to observe the general growth behavior of the mutant library and to assess the impact of a much higher MOI of phage 3.330.B. At an MOI of 100, a slight growth of 10N.239.311.G07 was observed at first, but 1 h after phage addition a sharp drop in the optical density (OD_{600 nm}) of the culture was observed, likely due to phage-mediated lysis. For the wildtype strain the growth stabilizes after approximately 2 h and starts rising slowly after 5 to 7 h, until it almost reaches the control levels (0.65 – 0.7 OD_{600nm}), though with a delay (Figure 1.7). A strain isolated from day 244, 10N.244.47.E12 was tested as alternative to strain 1G07 in the experiment, but both showed very similar growth behavior when challenged with phage 3.330.B. While the growth pattern, that could be observed for the mutant library in the same experiment shows slight differences. Although the non-challenged control group behaves similarly to the wildtype control, indicating no significant fitness cost for most transposon insertions, the mutant library challenged with MOI 100 of phage 3.330.B showed a very slow and limited growth, different from the challenged wildtype. With no major drop in optical density in the early hours and the culture plateauing at an OD_{600nm} of around 0.4, not catching up to the control.

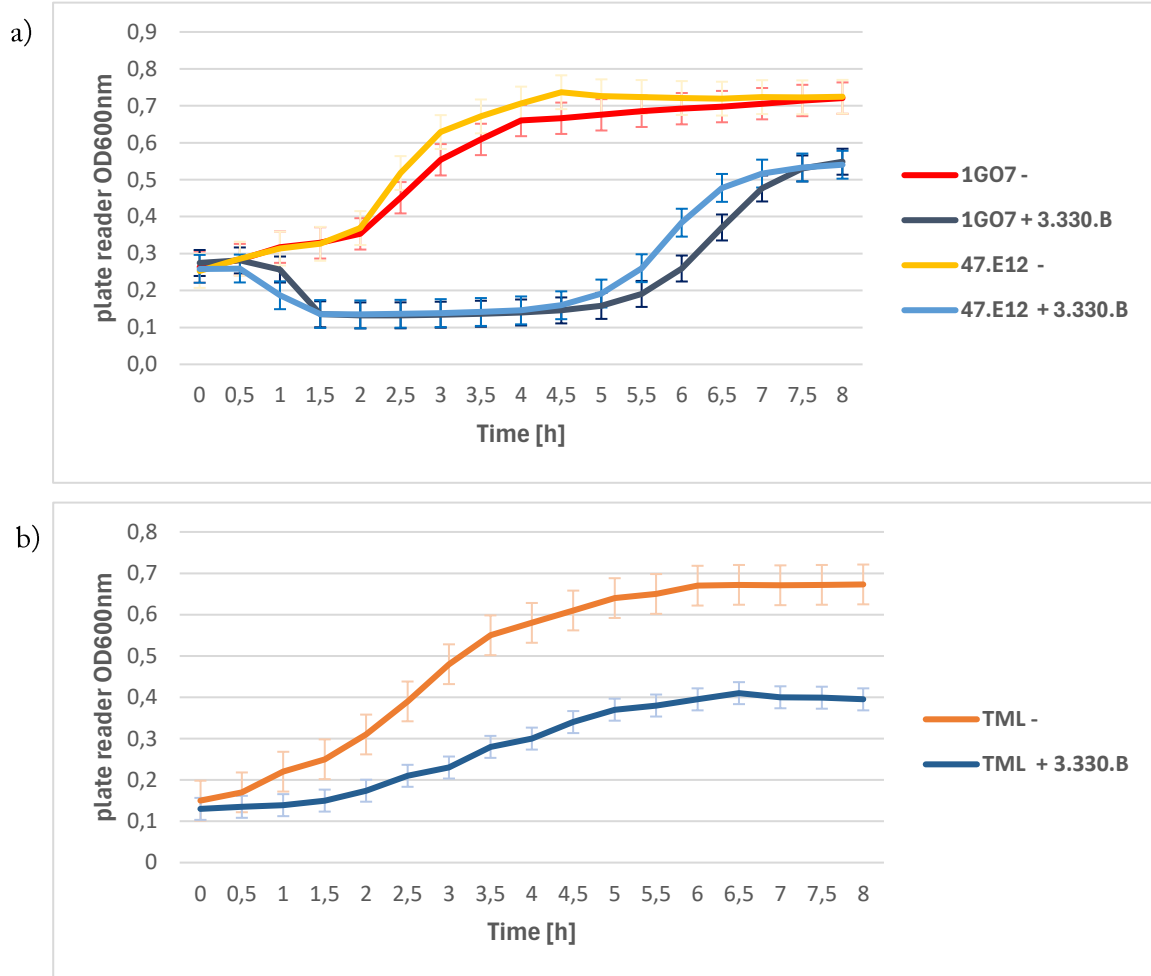


Figure 1.7: Growth dynamics of a) *V. cyclitrophicus* strains 1G07 and 10N.244.47.E12, b) of the transposon mutant library, following an infection with phage 3.330.B at a multiplicity of infection (MOI) of 100. Error bars of each graph are indicated in the corresponding color shade. Bacterial growth was monitored by measuring optical density at 600nm (OD600) over a time period of 8 hours using a Tecan Spark plate reader.

3.5 10N.239.311.G07 colonies carry phage 3.330.B DNA

To further investigate how the mutant strains might have acquired resistance, the presence of phage 3.330.B DNA within the surviving cells of the mutant library after phage selection was assessed. Colony PCRs were performed using primers, targeting phage 3.330.B. After PCR amplification, the products were analyzed in gel electrophoresis, all samples except the 1G07 wildtype colony were showing bands at the expected fragment size for all three primer pairs

tested, indicating the presence of phage genomic DNA in these cells (Figure 1.8). Suggesting, that the cells had not acquired resistance through the transposon insertions, but rather due to the fact that phage 3.330.B shows prophage like behavior and seems to be present inside the host cells.

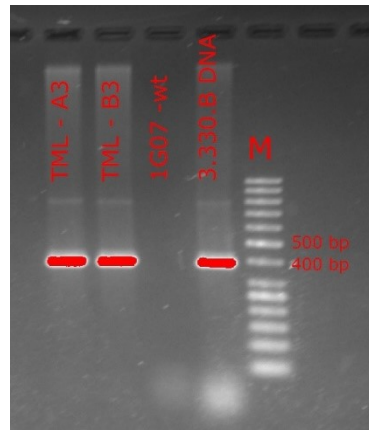


Figure 1.8: 2% agarose gel + GelRed stain, run at 120 V for 40 min, marker 1 kb GeneRuler. Colony PCR using primers detecting phage 3.330.B. Lane 2 and 3 colonies of mutant strains, lane 4 wildtype 1G07 colony, lane 5 phage 3.330.B DNA as control.

All mutant library strains (TML) were tested in a colony PCR screen for the presence of phage 3.330.B DNA. Results showed that at least 84% of the mutant strains carry the phage 3.330.B DNA (Supplementary Figure S 2.3, Table S 1.6). The genome of the wildtype strain 1G07 (JBFSRN000000000) was screened for an inserted phage 3.330.B, leading to no hits at all, but a second potential prophage was found within the strain's genome (position: contig 4 – base 86877 to 100142; 13266 bases in size) (Supplementary Figure S 2.4). Interesting to note at this point is the fact that in the course of phage stock preparation of phage 3.330.B, two different plaque morphologies were consistently observed (Supplementary Figure S 2.5). Suggesting that the resulting phage preparation is not phenotypically uniform and may either comprise more than one phage(-like) entity or contain heterogeneity within a single phage population, that gives rise to distinct plaque phenotypes.

To further investigate how the phage DNA persists intracellularly, plasmid preparations of wildtype and mutant cultures were made. Those plasmid extractions were then again used as template in PCR reactions using the 3.330.B primers targeting for the phage DNA. The gel electrophoresis revealed a positive read out (Figure 1.9 a), nevertheless the wildtype 1G07

plasmid prep revealed host contamination in the hsp60 PCR control (Figure 1.9 b), the detection of 3.330.B-specific PCR products from plasmid-enriched extracts suggests that phage 3.330.B exists as a plasmid within its host cells, however co-purification of host genomic DNA limits interpretation.

To obtain higher DNA yields of the plasmids, plasmid midi-preps of the wildtype 1G07 and the mutant strain TML_B3 were made, to be used in an enzymatic digestion assay. The goal was to compare the observed fragment patterns to in silico predicted restriction profiles for phage 3.330.B, which is fully sequenced. The plasmid DNA was digested using the following restriction enzymes: BamHI, PvuII, NheI, SalI, NcoI, MluI, and XhoI, with the predicted cut sites ranging from 1 to 17 cuts per enzyme. However, the cutting patterns did not align with the expected fragment patterns (Supplementary Figure 2.5). Most lanes (BamHI through XhoI) display little to no digestion or single, high-molecular-weight bands, consistent with uncut or linearized DNA. Whereas enzymes like SalI, MluI and NcoI, which were expected to produce multiple fragments (17, 11 and 2 cuts respectively), also showed single large bands with no visible digestion products. The Exonuclease treatments included as control in the experiment (Exo III, DNase I and S1) partially degraded the DNA, suggesting it is accessible. Taken together, the restriction digests patterns did not align with the predicted 3.330.B profiles, so the episomal status of 3.330.B cannot be resolved on the basis of this experiment. Suggesting that the extracted DNA belongs to another plasmid. Or that the host contains multiple plasmids which might be more abundant than the phage episome, leading to a phage episome concentration that is insufficient for the digestion step.

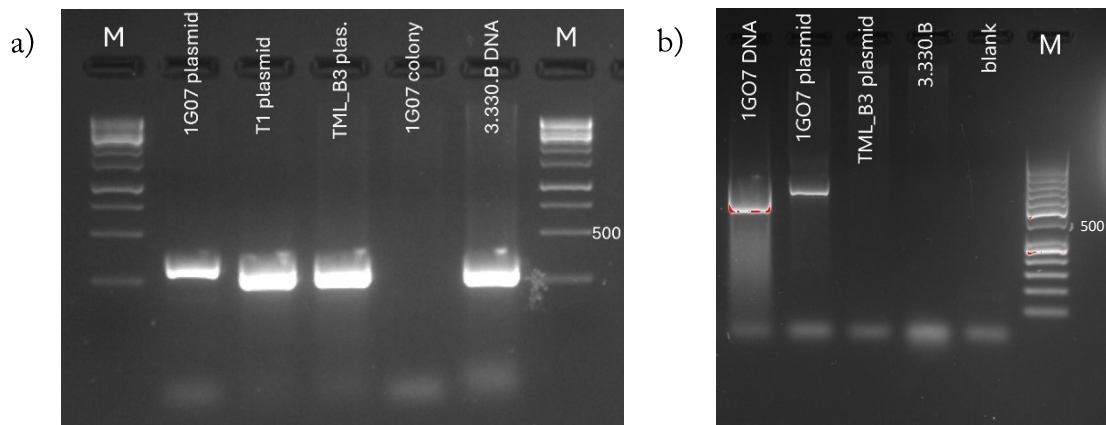


Figure 1.9: 3.330.B-diagnostic PCR - both gels run as 2% agarose gel, 120 V for 40 min, GelRed stained 20 min.; a) Marker 50 bp GeneRuler, 3.330.B PCR products, PCR templates: lane 2 – 4 contain the different plasmid preps, lane 5 1G07 as negative control, lane 6 phage 3.330.B extracted DNA. b) host contamination control: Marker 1 kb Gene ruler, hsp60 PCR products; PCR templates: lane 1 extracted DNA (host 1G07) as positive control, lane 2 and 3 plasmid preps, lane 4 phage 3.330.B extracted DNA as negative control, lane 5 as blank PCR reaction control.

3.6 Discovery and first characterization of a phage-inducing compound in *V. cyclithrophicus*

During the host-range assay of the 189 putatively resistant transposon mutagenesis strains, susceptibility to the same set of 76 phage from the cross-infection assay was assessed for the mutant strains. Induction of at least one temperate phage was observed on 38 of the plates (20% of the mutant strains (Table S1.6). Several tests were conducted to exclude contamination and to investigate a possible cause of the induction (Methods 2.10), different incubation temperatures as well as different salt concentrations (0.01M till 5M of NaCl) could be ruled out as trigger for the induction.

Soluble material was eluted from agar overlay plates of strain 1G07, that has been challenged with phages 3.330.B, 5.330.B and 7.330.B, by covering the plates with SM buffer and filtering the incubated supernatant. The supernatant was filtered through a 30 kDa centrifugal filter unit and passed through a 0.22 μ m sterile membrane to rule out intact phage particles and larger cell

debris. When reapplied on agar overlay plates of wildtype strain 1G07 or its mutant strains, the spotting of the extract led to lysis (Figure 1.10 a). Two single plaques from the agar overlay plates with the induced phage were picked (T9 A & B), phage stocks of those were generated and the genetic material was tested in a PCR reaction, using the 3.330.B primer pairs, revealing the induction of phage 3.330.B or close relatives in the plates (Figure 1.10 b). In this PCR reaction, the extract of the inducing agent was included, showing no positive signal for 3.330.B DNA within the filtrates.

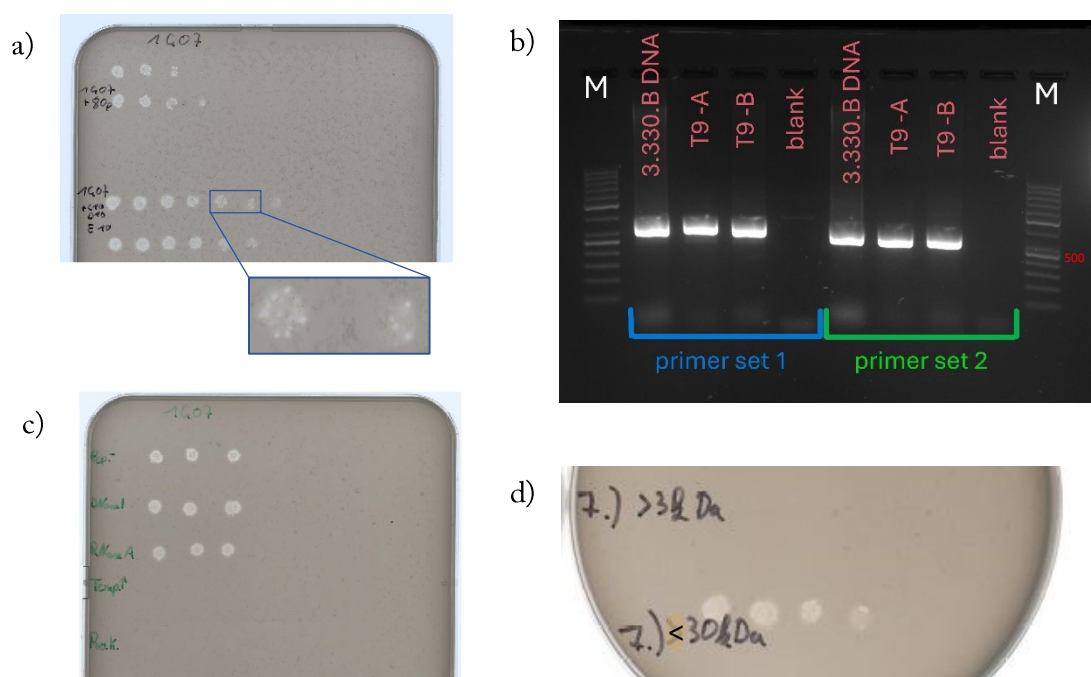


Figure 1.10: Characterization of phage inducing agent. a) 2 filtrates containing the inducing agent spotted in a dilution series on agar overlay plates of strain 1G07, each in duplicates – single plaques are visible in higher dilutions of the agent (zoomed in within the blue rectangle). b) 2% agarose gel + GelRed stain, run at 120 V for 40 min. 3.330.B PCR products analyzed, two different primer pairs were used – both targeting the phage 3.330.B. Two phage stocks, created from different plaques after spotting the inducing agent (T9 A and B). No-template controls were included in each PCR reaction (blank). c) Inducing agent activity test after enzymatic digestion. In the first row, the undigested agent was spotted as negative control. Followed by the digests / treatments with: DNase I, RNase A, 1 min at 100°C, Proteinase K. (heat inactivated), all spotted on agar overlay plates of strain 1G07. d) Inducing agent filtered through two different filters, > 3 kDa and < 30 kDa, spotted on agar overlay plates of strain 1G07.

To address the possible impact of the compound on other *V. cyclitrophicus* strains it was included in the cross-infection assay performed on the strains previously described and assessed by (Kreutter, 2024) (Methods 2.4.1) (Figure 1.5). Wherein the inducing compound exhibited broad growth inhibiting activity, lysing 139 out of 311 (45%) tested *V. cyclitrophicus* isolates.

Subsequent treatment of the inducing agent with RNase A, DNase I and Proteinase K indicated that only the digest with Proteinase K and or its heat denaturation step abolished the lytic activity of the compound (Figure 1.10 c), suggesting a proteinaceous or peptide-based nature of the active compound. The inducing agent is polar (remaining in the aqueous phase) and ranges in size between 3 – 30 kDa, consistent with small proteins, signaling peptides or large molecules (Figure 1.10 d).

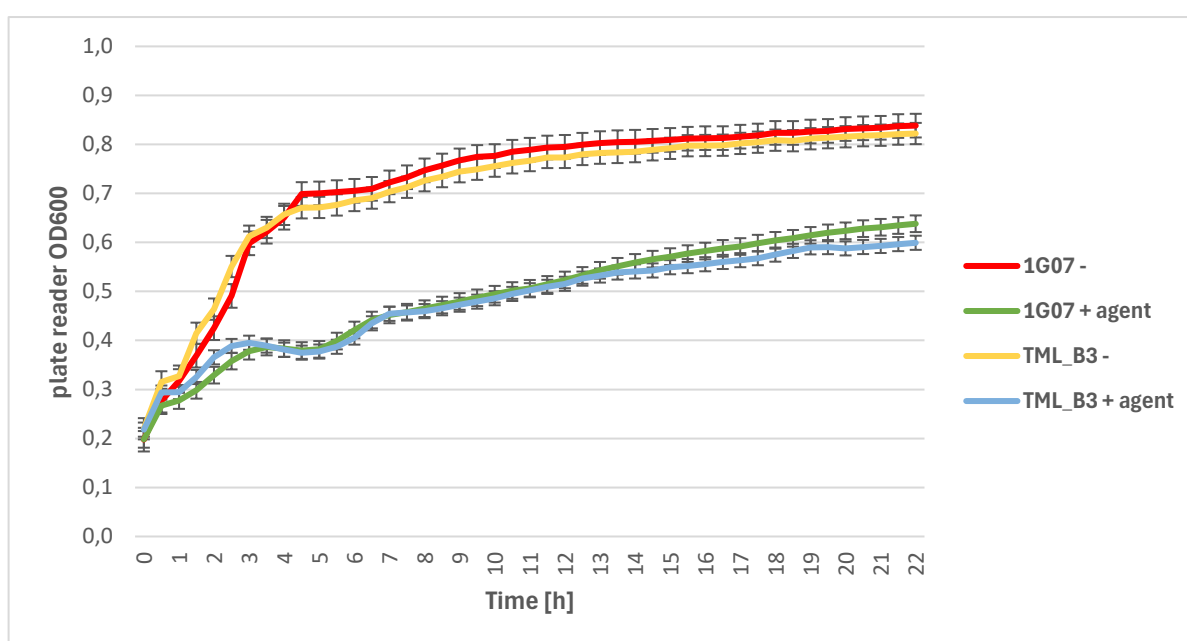


Figure 1.11: The inducing agent effecting growth of 1G07 and its mutant TML_B3 negatively. Growth displayed as optical density 600nm wavelength (OD600) of a Tecan Spark plate reader (y-axis), measured over time (hours) (x-axis), incubated at 25°C, at the lowest amplitude of orbital shaking. In green (1G07) and blue (TML_B3) the growth after the addition of the agent, while in red (1G07) and yellow (TML_B3) negative controls are shown. 5 biological replicates were used for both negative controls, while 25 replicates per strain challenged with the inducing agent were included.

Moreover, when applied to liquid cultures of strain 1G07 and its mutant library strain TML_B3, the filtrate suppressed bacterial growth (Figure 1.11) and, after incubating the culture with the inducing compound for several hours, phage particles could be extracted from the supernatant, causing single plaques when spotted on agar overlays of wildtype 1G07 again (Figure 1.12). The genetic material from the supernatant was extracted and a PCR with the 3.330.B primer pairs was performed, showing that the phage that was induced in the cells was 3.330.B or its close relatives (Figure 1.13). Together, these findings demonstrate that the inducing agent is capable of triggering prophage induction in liquid culture independent of prior phage exposure.

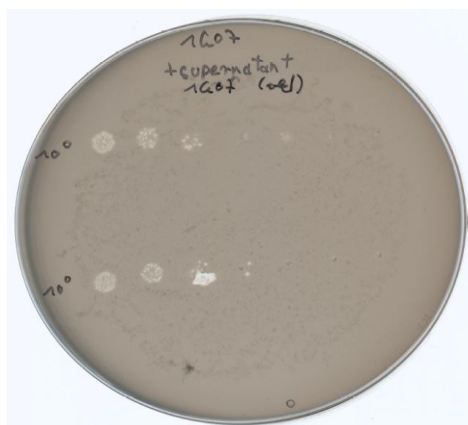


Figure 1.12: agar overlay plate of strain 1G07, were supernatant of the growth experiment of 1G07 + inducing agent was spotted on, as duplicate in tenfold serial dilution ranging from 10^0 till 10^{-6} - supernatant is able to lyse strain 1G07, causing the formation of single plaques

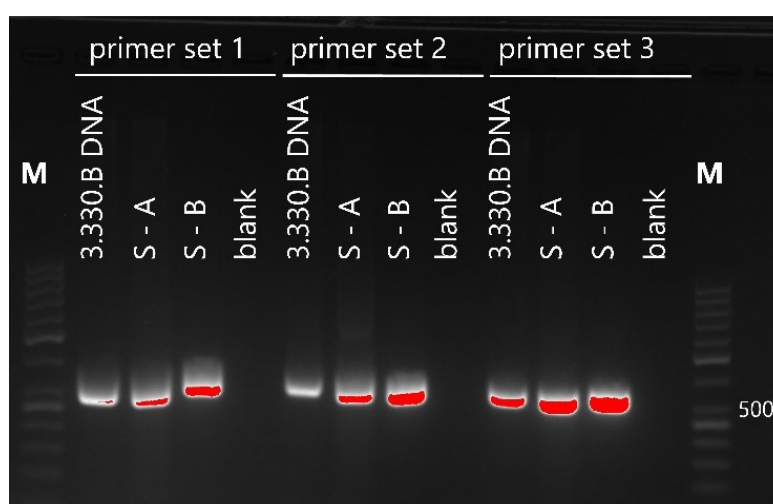


Figure 1.13: 2% agarose gel + GelRed stain, run at 120 V for 40 min, Marker 1 kb Generuler. 3.330.B PCR of the genetic material extracted from the supernatant (1G07 incubated with inducing agent in liquid culture). S-A (0.22 μ m filtered before extraction), S-B (was not filtered before extraction). No-template control added to all three reactions (blank).

To obtain sufficient quantities, with higher concentration of the phage-inducing compound for further biochemical characterization, the extraction protocol was optimized (Methods 2.10.3). Specifically, instead of applying the full set of 76 phages as in the cross-infection assays, only spotting the three closely related phages 3.330.B, 5.330.B and 7.330.B onto the agar overlays containing their host of isolation 1G07 increased the yield of the compound, which was quantified using serial dilution assays and defined by the highest dilution that still produced detectable plaques. These results indicate that these phages are the primary source or trigger of active agent production.

Discussion

4.1 Modular and sparse phage-host interaction networks in post-bloom *V. cyclitrophicus* populations.

The cross-infection assay performed on *Vibrio cyclitrophicus* isolates from day 244, occurring shortly after peak bloom day (day 239) within the Nahant time series, revealed a sharp decline in phage infectivity, reaching the absolute minimum at day 242 (Kaufmann et al. 2022; Kreutter 2024). The phage-host interaction matrix was highly modular and overall sparse, with phages only replicating in a small fraction (9%) of the bacterial isolates. Despite testing a genomically diverse set of phages (76 phages) in just 232 of the 44,477 (around 0.005%) phage-host combinations lysis was observed. Notably, the phages that exhibited comparatively broad host ranges among the day 244 isolates, infecting more than 10 different hosts (1.293.O, 1.215.A, 3.330.B, 5.330.B, 7.330.B) were also among the most broadly infective phages reported by Kreutter (2024) across several other sampling days (222, 232, 236, 237, 239, 247, 261 and 286). The repeated detection of these broadly infective phages throughout the different time points suggest that a subset of phages can consistently exploit host features that are conserved across many *V. cyclitrophicus* strains.

However, closer inspection revealed that three of the phages (3.330.B, 5.330.B, 7.330.B) seemed able to lyse over 90% of the isolates of day 244, but only at undiluted phage stock concentrations.

Since this lytic activity was not maintained at higher dilutions, the observed lysis was likely not phage-mediated infection but rather caused by cytotoxic components present in the crude lysates, such as bacterial debris, residual antimicrobial compounds or signaling molecules. These observations highlight the importance of interpreting low-dilution lysis in host range assays with care, paying close attention to the strength of the interactions as well as the morphology of the plaque/ inhibition zones, in order to interpret the interaction correctly and to distinguish between lysis from without and growth inhibition caused by bacteriocins. Such low-dilution artefacts, likely caused by bacteriocins, can otherwise lead to an overestimation of the host range and inaccurate ecological conclusions. The discovery of a probably phage-derived inducing agent extracted from lysed plates reproduced similar lysis patterns, excluding the phages themselves.

Except for the appearance of growth inhibition, when undiluted phage stocks of the three related phages 3.330.B, 5.330.B and 7.330.B, as well as the inducing agent were spotted, the apparent stability of host range patterns between this study and the earlier matrix (Kreutter 2024), despite different phage stock concentrations, indicate that most phage-host interactions are robust and reproducible. Nevertheless, the emergence of false-positive lysis, due to antimicrobial activities, at undiluted titers are demanding for a nuanced analytical pipeline, potentially combining cross-infection assays with another technique as validation step, since compounds like the inducing agent described earlier might display the same phenotype in agar overlay assays as phages. As an additional control, refining cross-infection data, a real-time fluorescent dye-based lysis assay can be included (Egido et al. 2023). This high-throughput method can distinguish true phage-induced cell death, marked by DNA release, from non-specific cytotoxic growth inhibitions.

Marine phage-host interactions are highly specific and play a central role in shaping microbial community structures and ecosystem functioning. It was shown that most phages only infect a narrow subset of bacterial hosts, limiting cross-infection across lineages (Kauffmann et al. 2022). This specificity structures microbial communities by controlling abundance and turnover of particular hosts, which in turn regulates nutrient cycling. Through host cell lysis, phages drive nutrient regeneration and carbon cycling via the viral shunt, positioning them as critical agents

in the global biogeochemical processes (Weitz & Wilhelm, 2012). Detailed phage-host interaction networks are therefore essential to advance our ecological understanding of microbial systems in marine environments.

In addition to their ecological relevance, phage-host interaction studies provide valuable insight for biotechnological innovation. The identification of generalist phages or temperate carriers offers promising avenues for microbiome engineering, targeted microbial control strategies, and the discovery of novel antimicrobial compounds (Nobrega et al. 2015; Altamirano & Barr 2019). Systematical charting interaction patterns, as performed through cross-infection assays, help to uncover resistance mechanisms and coevolutionary dynamics, thereby guiding the engineering of phages and phage-derived enzymes for potential antimicrobial applications. Moreover, when a sufficiently large and diverse set of phages is included, it could also provide indirect clues about host surface receptors, as consistent patterns of susceptibility or resistance may reflect shared receptor features across strains.

4.2 Limitation of transposon mutagenesis for receptor identification in temperate phages

To identify the receptor of phage 3.330.B, transposon mutagenesis on its host of isolation 10N.239.311.G07 was performed to generate a random insertion library. This approach aimed to disrupt host genes and after phage challenge, recover resistant mutants from the agar overlay plates. Selected mutants resistant to phage 3.330.B were sequenced to map the insertion sites, however the insertions were dispersed across the genome and did not converge on a specific gene or genomic region. Interestingly, the resistance screening revealed that 10% of the mutant strains were susceptible to the phages 1.043.O. and 1.080.O., whereas the wildtype strain wasn't. Extending the assay beyond the phages infecting the wildtype and including a broader phage panel may therefore provide an opportunity to uncover additional regulatory factors, such as receptor masking or changes in the host defense capacity. But also in those cases, the insertions sites were widely distributed along the host genome.

Despite repeated sequencing of the host genome, phage 3.330.B could not be detected as an integrated element. Subsequent plasmid analysis indicated that 3.330.B is likely a temperate phage which is being maintained episomally within the host. As such, rather than lysing its host, the phage persists intracellularly without killing the infected cells, making it impossible to recover resistant receptor mutants by this method. Since this screening strategy relies on the selection of non-lysed survivors, potential receptor-deficient mutants, making it incompatible with temperate phages.

Additionally, the receptor gene itself could be essential for the hosts viability, further complicating its identification through knockout-based approaches. Future efforts to resolve the receptor's identity should consider alternative strategies to pure phage selective methods, such as receptor-blocking assays using purified phage particles. Expressing and purifying recombinant receptor binding proteins to inhibit phage adsorption, thereby confirming receptor identity (Simpson et al. 2016), but since this is not a targeted approach a general idea of the receptor and the purified phage particle are needed. Alternatively, bioinformatic prediction with machine learning tools to predict putative receptor binding proteins could be applied, narrowing the search to a more manageable set instead of experimentally testing every structural gene (Boeckaerts et al. 2023). Coupling it with molecular work/cloning would allow for validation of the predictions. In the case of essentiality of the bacterial host's gene, the phage genome could be modified by introducing mutations into the predicted phage receptor-binding protein gene. The loss of infectivity of the modified phage or an altered host range, would support that the region is involved in receptor recognition. Conversely, mutations which do not impair infection could be used to refine the prediction models.

4.3 Episomal state of phage 3.330.B.

Another explanation for the fact that the interaction of phage 3.330.B and its host is not strictly lytic but rather lysogenic is that the phage genome may persist in the host episomally, as a circular or linear DNA molecule not integrated into the chromosome. This is supported by the

finding of the plasmid preparation analysis performed on the wildtype and mutant 1G07 strains, as well as by the fact that the 1G07 host genome does not even contain parts of the 3.330.B phage genome. Plasmid-like maintenance of prophage genomes has also been reported in *Vibrio*, including circular episomal prophages present in multiple copies per host cell (Chen et al., 2025). The phage is transcriptionally silent or partially expressed, allowing the host to survive and grow until conditions favor phage reactivation (Jover *et al.*, 2013). Restriction digests of the plasmid midi-preps from wildtype 1G07 and the mutant strain TML_B3 produced a band patterns that did not match the in silico-predicted restriction profiles of the phage 3.330.B. Across multiple enzymes, the digests shown on the gel were dominated by high-molecular-weight DNA, with little evidence of the fragmentation expected from the predicted cut-site distribution indicating that these digests did not provide confirmatory support for a 3.330.B-derived episome in the plasmid-enrichment. Given that the wildtype plasmid preparation also showed host genomic DNA contamination, the extracted DNA might be comprising a mixture of different DNA types, like multiple plasmids, or the digestions might be incomplete, such that the dominant DNA in the preparation was not resolving into the expected 3.330.B fragment pattern. Nevertheless, the observation that colonies surviving phage exposure can retain phage DNA while remaining susceptible upon re-challenge is consistent with a non-classical temperate association; however, the restriction digest data alone do not allow conclusions about the physical form of the phage DNA and additional approaches will be required to resolve its intracellular state. Enabling horizontal gene transfer and promoting genetic diversity without imposing the cost of host genome integration or host lysis. Since their episomal persistence allows them to remain in bacterial populations across environmental fluctuations, potentially influencing microbial community structure, stress tolerance, and adaptive capacity over time. Examples of such phage episomes were previously described for instance by (Verheust, Jensen, Mahillon, 2003) where *Tectiviridae*, were found as linear plasmids in *Bacillus* species. Non-integrative temperate phages seem to be more widespread than previously thought, (Xue et al., 2015) surveyed marine *Vibrionaceae* populations and discovered many plasmid-like temperate phages to be present extrachromosomally. These episomes persist in free-living cells and were not integrated into the host genomes. The widespread presence of plasmid-like phages in free-

living marine *Vibrionaceae* (Xue et al. 2015) suggests that phage-like episomes may play a significant ecological role by acting as mobile genetic reservoirs in the marine ecosystem.

While the results presented in this thesis shed light on the persistence of phage 3.330.B DNA within its host cells, the experimental setup did not directly assess phage activity, such as ongoing replication or particle production. Given the temperate nature of phage 3.330.B and its suspected episome-like behavior, it remains uncertain whether the surviving bacteria maintain the phage in a state of dormancy, supporting low-level phage replication, or occasionally produce infectious particles. Especially in regard to the different growth behaviors of the wildtype 1G07 strain and the mutant library when challenged with phage 3.330.B, follow-up experiments such as plaque assays or phage titration from culture supernatants would offer a better insight and allow for better determination whether active phage release occurs, as well as the plating of washed cells. Likewise, quantitative PCR (qPCR) targeting phage genes could help distinguish between stable episomal maintenance and active phage replication, by monitoring phage genome copy numbers over time. Such data would provide a better picture whether phage 3.330.B exists in a true carrier state, as a silent lysogen, or engages in sporadic lytic cycles.

4.4 Insights into temperate phage activation from an unidentified inducing agent

The finding of a possibly short-peptide, polar, extracellular phage-inducing/growth inhibiting compound adds a new layer to phage-host interactions in marine *Vibrio*. The extractability and reproducible induction of the temperate phage 3.330.B suggests a form of phage-encoded signaling, or host-phage feedback mechanism. This compound might resemble the recently described viral communication systems, like for instance arbitrium (Erez Z. et al. 2017), though the function of our inducing compound appears to favor lytic activation, rather than suppression. But the concept of a small, secreted, phage-encoded peptide controlling phage developmental fate might also fit in our case. Given the possibility that our host strain *V. cyclitrophicus* 1G07 might carry at least one prophage in its genome, a possibility arises that these specific phages interact with the resident prophage, either through superinfection, induction or signaling crosstalk, thereby promoting the release of a compound involved in temperate phage activation.

The inducing agent could be a phage-encoded or prophage-associated product, whose synthesis or secretion is specifically triggered by encounter with the related phages 3.330.B, 5.330.B and 7.330.B. The specificity of this response might support the idea of coordinated communication or induction among phage and prophage elements within the same host range. Similarly coordination via trans-acting anti-repressors in polylysogenic bacteria (Lemire et al. 2011), wherein small anti-repressor proteins encoded by one prophage could act on non-cognate repressors, triggering induction across genetically related prophages. Providing an example of prophage-prophage crosstalk enabling synchronized activation in polylysogens.

Alternatively, host-derived proteins or peptides could induce the temperate phage. Proteinaceous toxins can induce prophages via the SOS response. Like for instance the small host-produced genotoxin Colibactin, which triggers prophage induction through RecA-mediated SOS activation across multiple bacterial hosts (Silpe et al. 2022). Or acting via a non-DNA-damaging mechanism, like the bacteriocin Lactociccin972 (Madera et al. 2009), inhibiting septum formation and inducing the lytic cycle of resident prophages in a concentration-dependent way. A recent study demonstrated that prophage induction in marine *Vibrio* can also be triggered by host-derived metabolites, specifically a peptide deformylase inhibitor produced during interbacterial antagonism, which selectively activates prophages in competing strains without relying on SOS induction (Chen et al. 2025). Those findings support a concept of an inducing agent extracted from phage-infected *Vibrio* agar overlays that may be acting through analogous induction and growth inhibition mechanisms, potentially as a secreted peptide or bacteriocin-like factor.

But above all the results from the cross-infection assay, wherein the inducing agent isolated from a *V. cyclitrophicus* strain itself, showed a widespread lytic activity, being able to lyse roughly 45% of the tested *V. cyclitrophicus* strains. The killing spectrum is consistent with the typical behavior of host-derived bacteriocins or tailocins, which mostly exhibit a narrow target range, but as described often exclude the producing strain and its close relatives due to immunity proteins or tightly regulated production mechanisms (Riley & Wertz, 2002; Wall, 2016). Whereas our producing strain is not immune to the inducing agent itself, indicating more towards a phage-

encoded or prophage-mediated compound involved in coordinated induction of temperate phages, since also for the production/ extraction of the inducing compound an infection by phage 3.330.B and or its relatives is necessary. Originating from a strain that is likely to carry another prophage, harboring a lytic activity that affects a wide subset of closely related strains, raises the possibility that the compound functions as a phage-induced signaling molecule or lytic effector. Moreover, the wide lytic activity on a strain-level suggests that the compound engages in intraspecies regulation or competitive interactions, potentially favoring the spread of certain prophage elements or the selective killing of non-immune subpopulations during bloom conditions. This is particularly relevant for marine microbial ecosystems, in which temperate phages are abundant and episomal or inducible prophages have a significant contribution to host fitness and phage-host coevolution (Xue et al. 2015; Brum et al. 2015). Analogous to bacterial quorum sensing, these mechanisms may allow phages to sense local population density or the physiological state of their host community and coordinate decisions between lysis and lysogeny.

Conclusion

This study contributes to a more detailed understanding of the interactions between temperate phages and marine *Vibrio cyclitrophicus* populations and highlights how phage-host outcomes in natural systems may be shaped by narrow compatibility patterns as well as inducible behaviors. In the cross-infection assays, productive lysis was observed for only a small fraction of the tested phage-host combinations, supporting the view that phage-host interactions in this setting are highly strain specific, with susceptibility varying even among closely related hosts.

A key outcome of this work is the indication that the interaction between phage 3.330.B and its host does not fully align with a simplified binary model of either efficient host killing or stable chromosomal integration. The detection of phage DNA in surviving colonies without an accompanying, stable resistance phenotype, together with the ability to recover phage activity under inducing conditions, is compatible with a non-classical temperate association, potentially involving episomal maintenance and/or unstable lysogeny. While the underlying mechanism remains unresolved, the persistence of phage DNA without a clear resistance/ lysis outcome offers a plausible explanation for why the transposon-based receptor screening was not informative in this system.

Finally, we discovered a transferable, extracellular inducing agent that could be recovered from agar overlay plates and that reproducibly triggered 3.330.B-associated phage activity. Although the molecular identity and mechanism of action of this inducing factor remains unclear, its activity was observed both on agar and in liquid culture, indicating that phage induction can be mediated by this diffusible component under these experimental conditions. Future work should focus on determining the biochemical nature of this factor and establish how it promotes phage induction, as well as clarifying the lifestyle of phage 3.330.B. More broadly, incorporating inducible behavior of temperate phages into ecological frameworks may improve our abilities to interpret and predict phage impact on bacterial population dynamics and to evaluate potential applications of phage-derived processes in the environmental and biotechnological context.

Supplementary Figures

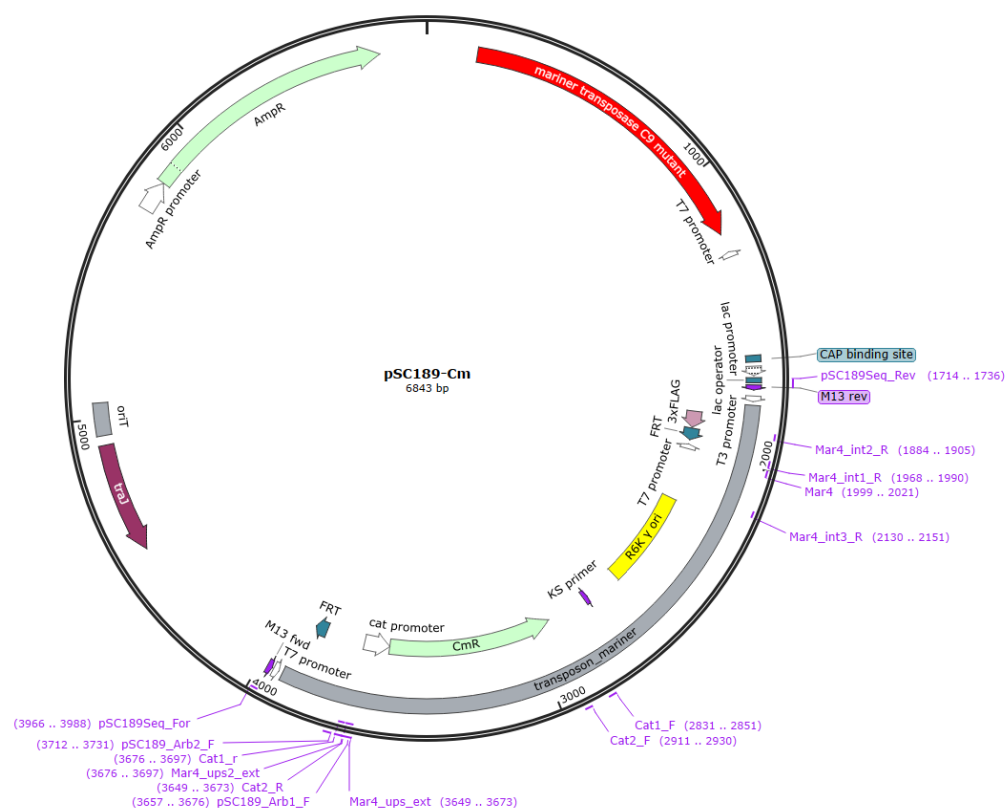


Figure S 2.1: Plasmid map of the pSC189-Cm suicide vector encoding the hyperactive C9 mariner transposase.

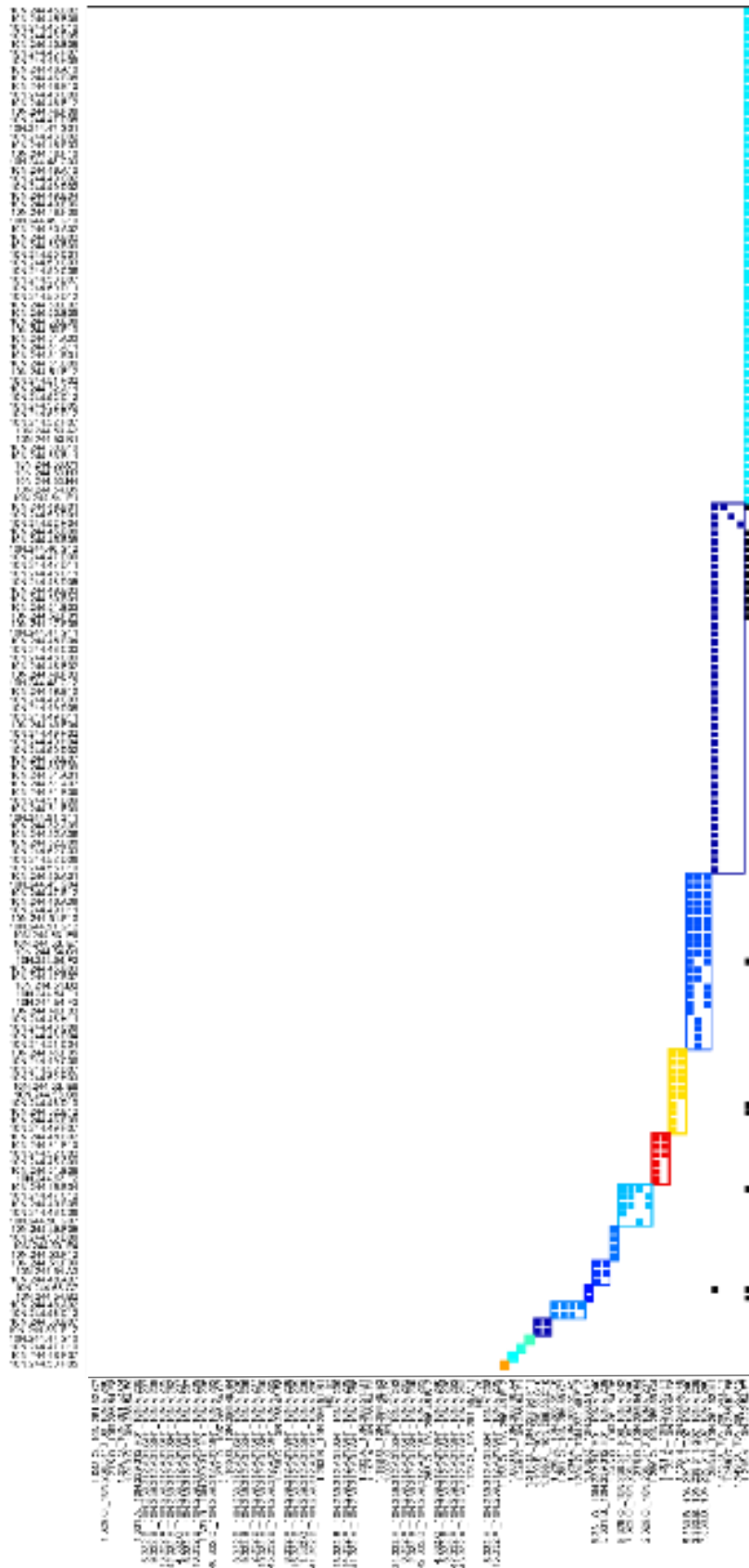


Figure S 2.2: Visualization of the modularity and nestedness of phage-host interaction network from post-bloom day 244. Lytic interactions are displayed as colored squares, whereas all the interactions without lysis are displayed white. On the y-axis are all the isolates, while all phages are sorted on the x-axis.

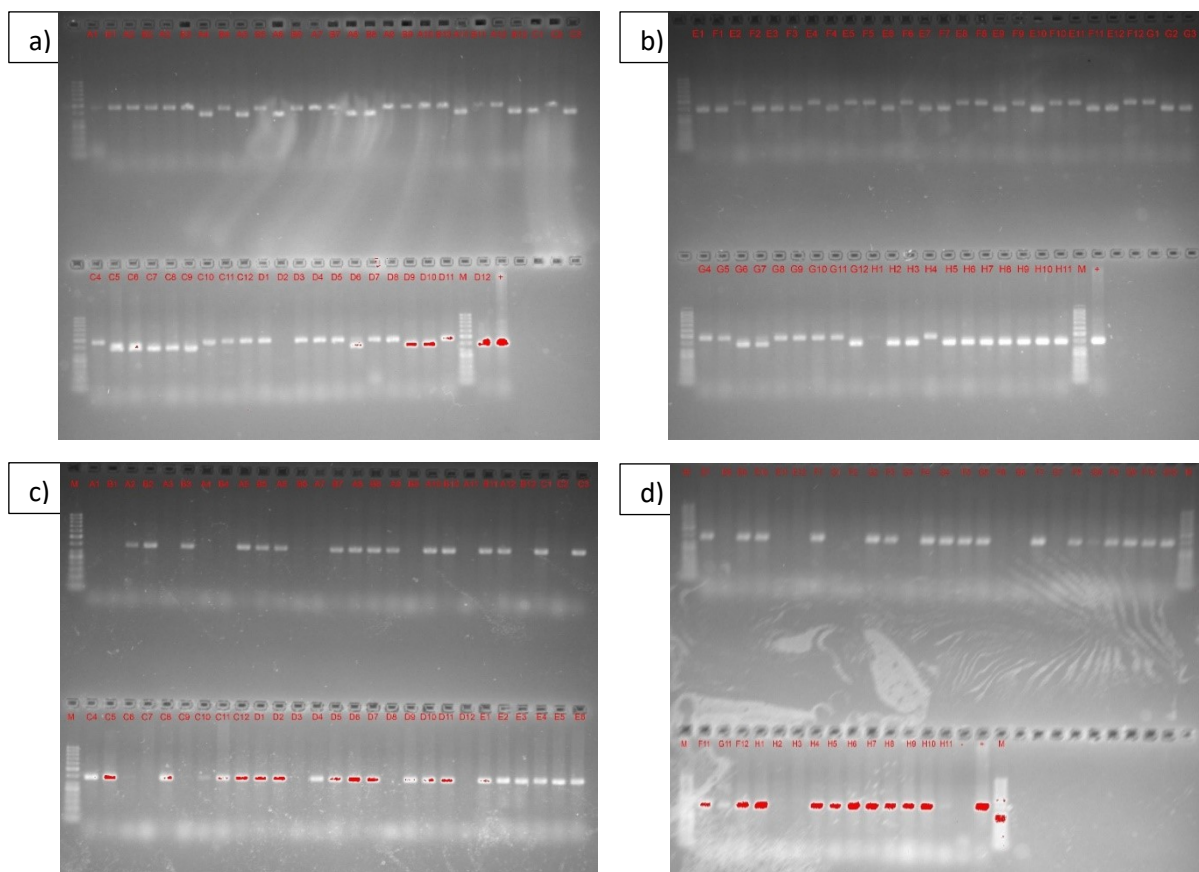


Figure S 2.3: 2% agarose gels, run 120V for 40min, marker 1kb GeneRuler. Colony 3.330.B PCR of the transposon mutagenesis strains. Gels a) and b) contain the strains from plate TML 1 (strains labelled according to their plate position). Gels c) and d) contain the strains from plate TML 2 (strains labelled according to their plate position).



Figure S 2.4: Prophage integrated into strain 10N.239.311.G07. The genome was annotated with RAST. The potential prophage location is marked by the two vertical bars, ranging from base 86877 to 100142 (13266 bases long) on contig 4.

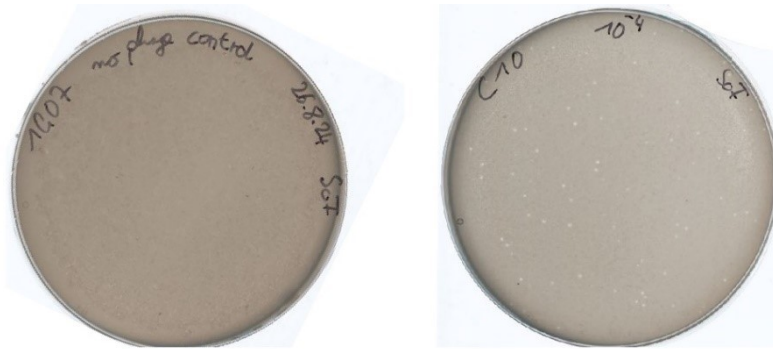


Figure S 2.5: Agar overlay of strain 10N.239.311.G07 and phage 3.330.B stock shows two different plaque morphologies. The plate on the left is the no phage control plate, where only 100ul of the host overnight culture were plated out. On the right plate 100ul of the stock dilution 10^{-4} (PPA.02370) were added additionally.

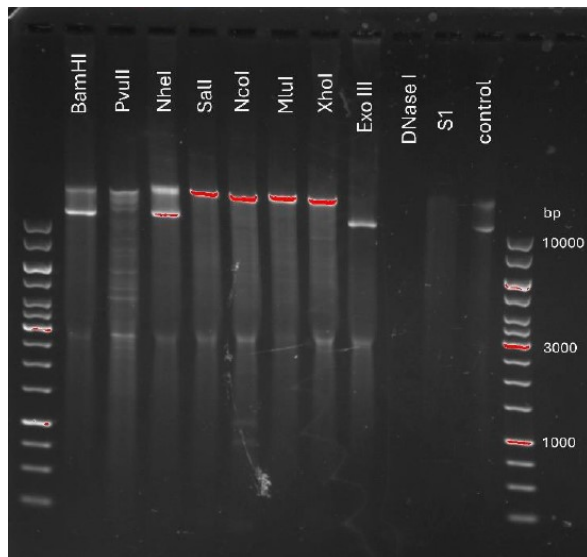


Figure S 2.6: 0.5% agarose gel + GelRed stain, run at 80V for 160min, marker 1kb GeneRuler. Enzymatic digests of the 1G07 plasmid midi prep. Lanes 2 to 8 contain the different restriction digests. Lane 9 Exonuclease III digest. Lane 10 contains the DNase I digest and in lane 11 the Nuclease S1 digest. In lane 12 the plasmid prep is added undigested as control. Predicted cuts of the restriction enzymes: BamHI – 2, PvuII – 2, NheI – 1, Sall – 17, NcoI – 2, MluI – 11, XhoI – 1.

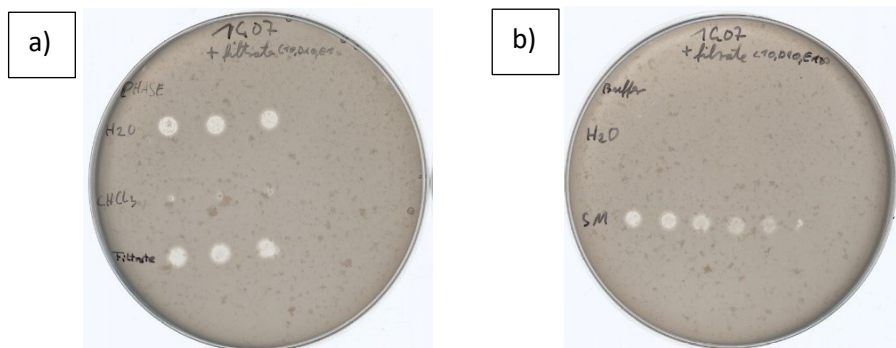


Figure S 2.7: Solubility of inducing agent. a) Inducing agent spotted on agar overlay of strain 1G07, after solubility testing, the filtrate itself is spotted as control (lowest row). b) inducing agent extracts with DEPC water and SM buffer spotted on agar overlay plates of strain 1G07.

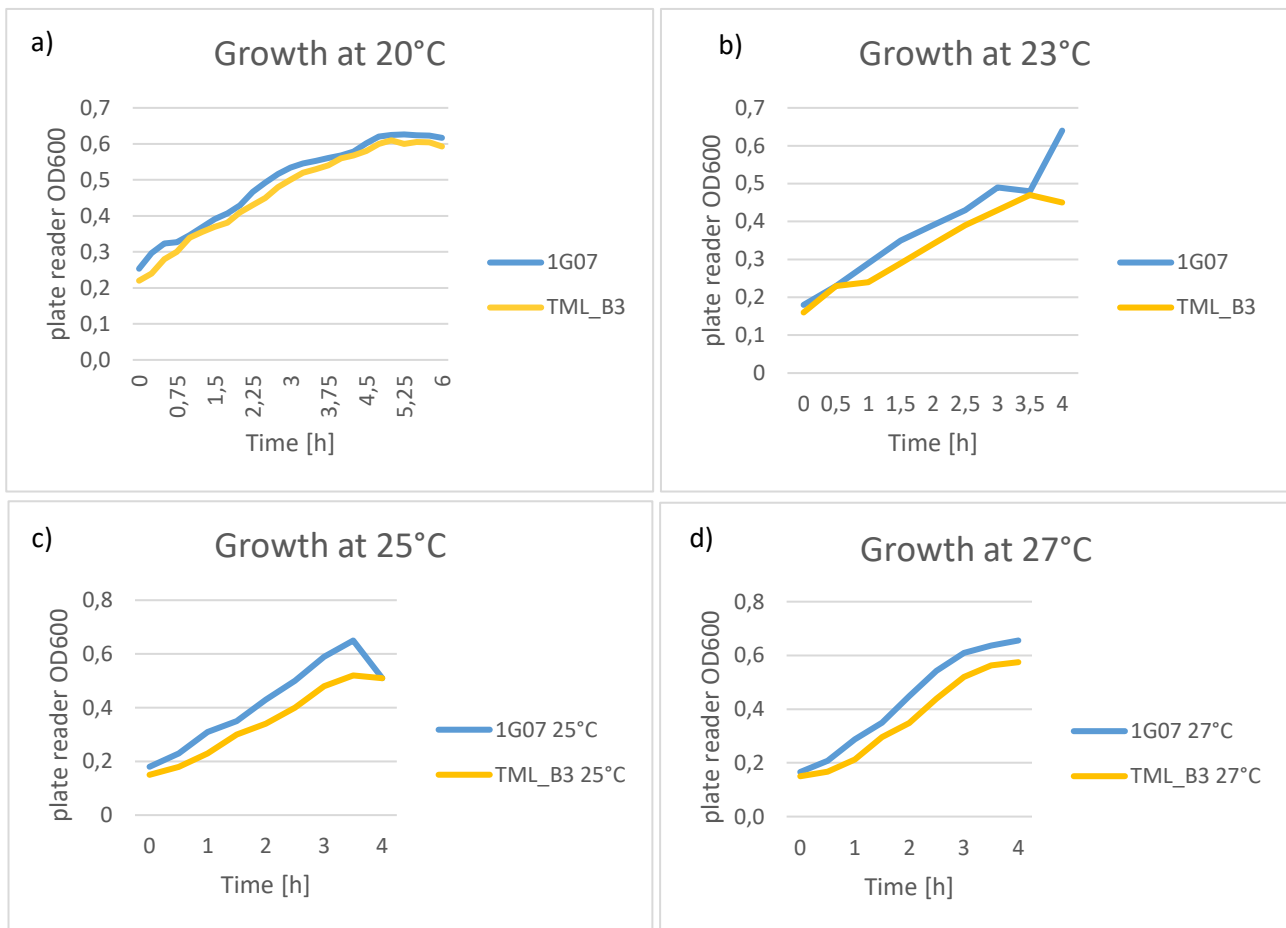


Figure S 2.8: Growth of strain 1G07 and its mutant strain TML_B3 at different incubation temperatures. Bacterial growth was monitored by measuring optical density at 600nm (OD600) every 15min, using a Tecan Spark plate reader. a) growth at 20°C, b) growth at 23°C, c) growth at 25°C, d) growth at 27°C.



Figure S 2.9: Controls to assess the origin and activity of the phage inducing agent. Supernatant from agar overlay plates of mutant strain T1 were filtered through >30kDa centrifugal filter units were only the following was spotted on: - MB 2216 medium (row 4) - 1 M PBS (row 5); Additionally, high-titer phage stocks were filtered the same way and spotted on the agar overlay plate. Phage 3.330.B (row 6) and Phage 8.332.B (row 7). As control the filtrates from agar overlay plate from 1G07 and T1 which were challenged with the set of 79phages were spotted (row 1 & 2).

Supplementary Tables

Table S 1.2: Morphology of Vibrionaceae isolates from day 244 on mTCBS agar plates, after purification.

Isolate ID	Morphology on mTCBS	Isolate ID	Morphology on mTCBS
10N.244.45.A1	2-3mm diameter, round, yellow (morp. 1)	10N.244.45.D6	morp.2
10N.244.45.B1	morp.1	10N.244.45.E6	morp.2
10N.244.45.C1	morp.1	10N.244.45.F6	morp.3
10N.244.45.D1	morp.1	10N.244.45.G6	morp.3
10N.244.45.E1	3mm diameter, round, dark green (morp. 2)	10N.244.45.H6	morp.2
10N.244.45.F1	morp.2	10N.244.45.A7	morp.3
10N.244.45.G1	morp.2	10N.244.45.B7	morp.2
10N.244.45.H1	morp.1	10N.244.45.C7	morp.3
10N.244.45.A2	morp.2	10N.244.45.D7	morp.3
10N.244.45.B2	3mm diameter, round, yellow brownish (morp.3)	10N.244.45.E7	morp.4
10N.244.45.C2	morp.2	10N.244.45.F7	morp.2
10N.244.45.D2	morp.3	10N.244.45.G7	morp.2
10N.244.45.E2	morp.3	10N.244.45.H7	morp.3
10N.244.45.F2	morp.3	10N.244.45.A8	morp.2
10N.244.45.G2	morp.3	10N.244.45.B8	morp.3
10N.244.45.H2	morp.3	10N.244.45.C8	morp.3
10N.244.45.A3	morp.2	10N.244.45.D8	morp.2
10N.244.45.B3	morp.3	10N.244.45.E8	morp.3
10N.244.45.C3	morp.2	10N.244.45.F8	morp.3
10N.244.45.D3	smeary, dark yellow (morp.4)	10N.244.45.G8	morp.3
10N.244.45.E3	morp.4	10N.244.45.H8	morp.2
10N.244.45.F3	morp.1	10N.244.45.A9	morp.3
10N.244.45.G3	morp.1	10N.244.45.B9	morp.3
10N.244.45.H3	morp.2	10N.244.45.C9	morp.3
10N.244.45.A4	morp.2	10N.244.45.D9	morp.2
10N.244.45.B4	morp.2	10N.244.45.E9	morp.3
10N.244.45.C4	morp.2	10N.244.45.F9	morp.3
10N.244.45.D4	morp.3	10N.244.45.G9	morp.3
10N.244.45.E4	morp.3	10N.244.45.H9	morp.3
10N.244.45.F4	morp.3	10N.244.45.A10	morp.2
10N.244.45.G4	morp.3	10N.244.45.B10	morp.2
10N.244.45.H4	morp.3	10N.244.45.C10	morp.3
10N.244.45.A5	morp.1	10N.244.45.D10	morp.2
10N.244.45.B5	morp.2	10N.244.45.E10	morp.3
10N.244.45.C5	morp.1	10N.244.45.F10	morp.2
10N.244.45.D5	morp.1	10N.244.45.G10	morp.2
10N.244.45.E5	morp.1	10N.244.45.H10	morp.2
		10N.244.45.A11	morp.2
		10N.244.45.B11	morp.3
		10N.244.45.C11	morp.2
		10N.244.45.D11	morp.3

10N.244.45.F5	morp.1
10N.244.45.G5	morp.1
10N.244.45.H5	morp.1
10N.244.45.A6	morp.2
10N.244.45.B6	morp.2
10N.244.45.C6	morp.2
10N.244.45.C12	morp.2
10N.244.45.D12	morp.1
10N.244.45.E12	morp.1
10N.244.45.F12	morp.1
10N.244.45.G12	morp.2
10N.244.46.A1	morp.1
10N.244.46.B1	morp.2
10N.244.46.C1	morp.1
10N.244.46.D1	morp.1
10N.244.46.E1	morp.2
10N.244.46.F1	morp.1
10N.244.46.G1	morp.1
10N.244.46.H1	morp.1
10N.244.46.A2	morp.3
10N.244.46.B2	morp.3
10N.244.46.C2	morp.3
10N.244.46.D2	morp.3
10N.244.46.E2	morp.3
10N.244.46.F2	morp.3
10N.244.46.G2	morp.3
10N.244.46.H2	morp.1
10N.244.46.A3	morp.3
10N.244.46.B3	morp.3
10N.244.46.C3	morp.3
10N.244.46.D3	morp.3
10N.244.46.E3	morp.3
10N.244.46.F3	morp.3
10N.244.46.G3	morp.3
10N.244.46.H3	morp.3
10N.244.46.A4	morp.3
10N.244.46.B4	morp.2
10N.244.46.C4	morp.2
10N.244.46.D4	morp.2
10N.244.46.E4	morp.2
10N.244.46.F4	morp.2
10N.244.46.G4	morp.2
10N.244.46.H4	morp.2
10N.244.46.A5	morp.2
10N.244.46.B5	morp.2
10N.244.46.C5	morp.2
10N.244.46.D5	morp.2
10N.244.46.E5	morp.2
10N.244.46.F5	morp.2
10N.244.46.G5	morp.2

10N.244.45.E11	morp.3
10N.244.45.F11	morp.3
10N.244.45.G11	morp.3
10N.244.45.H11	morp.2
10N.244.45.A12	morp.3
10N.244.45.B12	morp.2
10N.244.46.D6	morp.2
10N.244.46.E6	morp.2
10N.244.46.F6	morp.2
10N.244.46.G6	morp.2
10N.244.46.H6	morp.2
10N.244.46.A7	morp.2
10N.244.46.B7	morp.2
10N.244.46.C7	morp.2
10N.244.46.D7	morp.2
10N.244.46.E7	morp.2
10N.244.46.F7	morp.2
10N.244.46.G7	morp.2
10N.244.46.H7	morp.2
10N.244.46.A8	morp.2
10N.244.46.B8	morp.3
10N.244.46.C8	morp.3
10N.244.46.D8	morp.3
10N.244.46.E8	morp.3
10N.244.46.F8	morp.3
10N.244.46.G8	morp.3
10N.244.46.H8	morp.3
10N.244.46.A9	morp.3
10N.244.46.B9	morp.3
10N.244.46.C9	morp.3
10N.244.46.D9	morp.3
10N.244.46.E9	morp.3
10N.244.46.F9	morp.3
10N.244.46.G9	morp.3
10N.244.46.H9	morp.3
10N.244.46.A10	morp.3
10N.244.46.B10	morp.3
10N.244.46.C10	morp.3
10N.244.46.D10	morp.3
10N.244.46.E10	morp.3
10N.244.46.F10	morp.3
10N.244.46.G10	morp.3
10N.244.46.H10	morp.3
10N.244.46.A11	morp.3
10N.244.46.B11	morp.3
10N.244.46.C11	morp.3
10N.244.46.D11	morp.3
10N.244.46.E11	morp.3
10N.244.46.F11	morp.3
10N.244.46.G11	morp.3

10N.244.46.H5	morp.2
10N.244.46.A6	morp.2
10N.244.46.B6	morp.2
10N.244.46.C6	morp.2
10N.244.46.D12	morp.3
10N.244.46.E12	morp.3
10N.244.46.F12	morp.3
10N.244.46.G12	morp.3
10N.244.47.A1	morp.1
10N.244.47.B1	morp.3
10N.244.47.C1	morp.3
10N.244.47.D1	morp.3
10N.244.47.E1	morp.3
10N.244.47.F1	morp.3
10N.244.47.G1	morp.3
10N.244.47.H1	morp.3
10N.244.47.A2	morp.3
10N.244.47.B2	morp.3
10N.244.47.C2	morp.3
10N.244.47.D2	morp.3
10N.244.47.E2	morp.3
10N.244.47.F2	morp.3
10N.244.47.G2	morp.3
10N.244.47.H2	morp.3
10N.244.47.A3	morp.3
10N.244.47.B3	morp.3
10N.244.47.C3	morp.3
10N.244.47.D3	morp.3
10N.244.47.E3	morp.3
10N.244.47.F3	morp.3
10N.244.47.G3	morp.3
10N.244.47.H3	morp.3
10N.244.47.A4	morp.3
10N.244.47.B4	morp.3
10N.244.47.C4	morp.3
10N.244.47.D4	morp.3
10N.244.47.E4	morp.3
10N.244.47.F4	morp.3
10N.244.47.G4	morp.3
10N.244.47.H4	morp.3
10N.244.47.A5	morp.2
10N.244.47.B5	morp.2
10N.244.47.C5	morp.2
10N.244.47.D5	morp.2
10N.244.47.E5	morp.2
10N.244.47.F5	morp.2
10N.244.47.G5	morp.2
10N.244.47.H5	morp.2
10N.244.47.A6	morp.2
10N.244.47.B6	morp.2

10N.244.46.H11	morp.3
10N.244.46.A12	morp.3
10N.244.46.B12	morp.3
10N.244.46.C12	morp.3
10N.244.47.E6	morp.2
10N.244.47.F6	morp.2
10N.244.47.G6	morp.2
10N.244.47.H6	morp.2
10N.244.47.A7	morp.2
10N.244.47.B7	morp.2
10N.244.47.C7	morp.2
10N.244.47.D7	morp.2
10N.244.47.E7	morp.2
10N.244.47.F7	morp.2
10N.244.47.G7	morp.2
10N.244.47.H7	morp.2
10N.244.47.A8	morp.2
10N.244.47.B8	morp.2
10N.244.47.C8	morp.2
10N.244.47.D8	morp.2
10N.244.47.E8	morp.2
10N.244.47.F8	morp.2
10N.244.47.G8	morp.2
10N.244.47.H8	5-6mm diameter, round, dark yellow (morp. 5)
10N.244.47.A9	morp.5
10N.244.47.B9	morp.5
10N.244.47.C9	morp.5
10N.244.47.D9	morp.5
10N.244.47.E9	morp.5
10N.244.47.F9	morp.5
10N.244.47.G9	morp.5
10N.244.47.H9	morp.5
10N.244.47.A10	morp.5
10N.244.47.B10	morp.5
10N.244.47.C10	morp.5
10N.244.47.D10	morp.5
10N.244.47.E10	morp.5
10N.244.47.F10	morp.5
10N.244.47.G10	morp.5
10N.244.47.H10	morp.5
10N.244.47.A11	morp.5
10N.244.47.B11	morp.5
10N.244.47.C11	morp.5
10N.244.47.D11	morp.5
10N.244.47.E11	morp.5
10N.244.47.F11	morp.5
10N.244.47.G11	morp.5
10N.244.47.H11	morp.5
10N.244.47.A12	morp.5

10N.244.47.C6	morp.2
10N.244.47.D6	morp.2
10N.244.47.D12	morp.5
10N.244.47.E12	morp.5
10N.244.47.F12	morp.5
10N.244.47.G12	morp.5
10N.244.48.A1	morp.5
10N.244.48.B1	morp.5
10N.244.48.C1	morp.5
10N.244.48.D1	morp.5
10N.244.48.E1	morp.2
10N.244.48.F1	morp.5
10N.244.48.G1	morp.5
10N.244.48.H1	morp.5
10N.244.48.A2	morp.5
10N.244.48.B2	morp.5
10N.244.48.C2	morp.5
10N.244.48.D2	morp.5
10N.244.48.E2	morp.5
10N.244.48.F2	morp.5
10N.244.48.G2	morp.5
10N.244.48.H2	morp.5
10N.244.48.A3	morp.5
10N.244.48.B3	morp.5
10N.244.48.C3	morp.5
10N.244.48.D3	morp.5
10N.244.48.E3	morp.5
10N.244.48.F3	morp.5
10N.244.48.G3	morp.5
10N.244.48.H3	morp.5
10N.244.48.A4	morp.5
10N.244.48.B4	morp.5
10N.244.48.C4	morp.5
10N.244.48.D4	morp.5
10N.244.48.E4	morp.5
10N.244.48.F4	5-6mm diameter, round, green (morp. 6)
10N.244.48.G4	morp.5
10N.244.48.H4	morp.6
10N.244.48.A5	morp.6
10N.244.48.B5	morp.5
10N.244.48.C5	morp.5
10N.244.48.D5	morp.5
10N.244.48.E5	morp.5
10N.244.48.F5	morp.5
10N.244.48.G5	morp.5
10N.244.48.H5	morp.5
10N.244.48.A6	morp.6
10N.244.48.B6	morp.5
10N.244.48.C6	morp.5

10N.244.47.B12	morp.5
10N.244.47.C12	morp.5
10N.244.48.D6	morp.5
10N.244.48.E6	morp.5
10N.244.48.F6	morp.5
10N.244.48.G6	morp.5
10N.244.48.H6	morp.5
10N.244.48.A7	morp.5
10N.244.48.B7	morp.5
10N.244.48.C7	morp.5
10N.244.48.D7	morp.5
10N.244.48.E7	morp.5
10N.244.48.F7	morp.5
10N.244.48.G7	morp.5
10N.244.48.H7	morp.6
10N.244.48.A8	morp.6
10N.244.48.B8	morp.5
10N.244.48.C8	morp.5
10N.244.48.D8	morp.6
10N.244.48.E8	morp.5
10N.244.48.F8	morp.5
10N.244.48.G8	morp.6
10N.244.48.H8	morp.5
10N.244.48.A9	morp.5
10N.244.48.B9	morp.5
10N.244.48.C9	morp.5
10N.244.48.D9	morp.5
10N.244.48.E9	morp.5
10N.244.48.F9	morp.5
10N.244.48.G9	morp.5
10N.244.48.H9	morp.5
10N.244.48.A10	morp.5
10N.244.48.B10	morp.5
10N.244.48.C10	morp.5
10N.244.48.D10	morp.5
10N.244.48.E10	morp.5
10N.244.48.F10	morp.5
10N.244.48.G10	morp.5
10N.244.48.H10	morp.5
10N.244.48.A11	morp.5
10N.244.48.B11	morp.5
10N.244.48.C11	morp.5
10N.244.48.D11	morp.5
10N.244.48.E11	morp.5
10N.244.48.F11	morp.5
10N.244.48.G11	morp.5
10N.244.48.H11	morp.6
10N.244.48.A12	morp.5
10N.244.48.B12	morp.5
10N.244.48.C12	morp.5

10N.244.48.D12	morp.5
10N.244.48.E12	morp.5
10N.244.48.F12	morp.5
10N.244.48.G12	morp.5
10N.244.49.A1	morp.5
10N.244.49.B1	morp.5
10N.244.49.C1	morp.5
10N.244.49.D1	morp.2
10N.244.49.E1	morp.2
10N.244.49.F1	morp.2
10N.244.49.G1	morp.5
10N.244.49.H1	morp.5
10N.244.49.A2	morp.5
10N.244.49.B2	morp.5
10N.244.49.C2	morp.5
10N.244.49.D2	morp.5
10N.244.49.E2	morp.5
10N.244.49.F2	morp.5
10N.244.49.G2	morp.6
10N.244.49.H2	morp.5
10N.244.49.A3	morp.6
10N.244.49.B3	morp.5
10N.244.49.C3	morp.5
10N.244.49.D3	morp.6
10N.244.49.E3	morp.5
10N.244.49.F3	morp.5
10N.244.49.G3	morp.5
10N.244.49.H3	morp.5
10N.244.49.A4	morp.5
10N.244.49.B4	morp.5
10N.244.49.C4	morp.5
10N.244.49.D4	morp.5
10N.244.49.E4	morp.5
10N.244.49.F4	morp.5
10N.244.49.G4	morp.5
10N.244.49.H4	morp.5
10N.244.49.A5	morp.5
10N.244.49.B5	morp.5
10N.244.49.C5	morp.2
10N.244.49.D5	morp.5
10N.244.49.E5	morp.5
10N.244.49.F5	morp.5
10N.244.49.G5	morp.5
10N.244.49.H5	morp.6
10N.244.49.A6	morp.2
10N.244.49.B6	morp.5
10N.244.49.C6	morp.5
10N.244.49.D6	morp.5
10N.244.49.A12	morp.5
10N.244.49.B12	morp.5

10N.244.49.E6	morp.5
10N.244.49.F6	morp.5
10N.244.49.G6	morp.5
10N.244.49.H6	morp.5
10N.244.49.A7	morp.5
10N.244.49.B7	morp.5
10N.244.49.C7	morp.5
10N.244.49.D7	morp.2
10N.244.49.E7	morp.5
10N.244.49.F7	morp.5
10N.244.49.G7	morp.5
10N.244.49.H7	morp.5
10N.244.49.A8	morp.5
10N.244.49.B8	morp.5
10N.244.49.C8	morp.5
10N.244.49.D8	morp.5
10N.244.49.E8	morp.5
10N.244.49.F8	morp.5
10N.244.49.G8	morp.5
10N.244.49.H8	morp.5
10N.244.49.A9	morp.5
10N.244.49.B9	morp.5
10N.244.49.C9	morp.5
10N.244.49.D9	morp.5
10N.244.49.E9	morp.5
10N.244.49.F9	morp.5
10N.244.49.G9	morp.4
10N.244.49.H9	morp.5
10N.244.49.A10	morp.5
10N.244.49.B10	morp.5
10N.244.49.C10	morp.5
10N.244.49.D10	morp.6
10N.244.49.E10	morp.5
10N.244.49.F10	morp.5
10N.244.49.G10	morp.5
10N.244.49.H10	morp.5
10N.244.49.A11	morp.5
10N.244.49.B11	morp.5
10N.244.49.C11	morp.5
10N.244.49.D11	5mm diameter, round and concave, yellow (morp. 7)
10N.244.49.E11	morp.5
10N.244.49.F11	morp.5
10N.244.49.G11	5mm diameter, round and flat, yellow (morp. 8)
10N.244.49.H11	morp.5
10N.244.50.B6	morp.5
10N.244.50.C6	morp.5

10N.244.49.C12	morp.5
10N.244.49.D12	morp.5
10N.244.49.E12	morp.6
10N.244.49.F12	morp.6
10N.244.49.G12	morp.5
10N.244.50.A1	morp.5
10N.244.50.B1	morp.5
10N.244.50.C1	morp.5
10N.244.50.D1	morp.5
10N.244.50.E1	morp.2
10N.244.50.F1	morp.5
10N.244.50.G1	morp.5
10N.244.50.H1	morp.5
10N.244.50.A2	morp.5
10N.244.50.B2	morp.5
10N.244.50.C2	morp.6
10N.244.50.D2	morp.5
10N.244.50.E2	morp.5
10N.244.50.F2	morp.5
10N.244.50.G2	morp.5
10N.244.50.H2	morp.5
10N.244.50.A3	morp.1
10N.244.50.B3	morp.2
10N.244.50.C3	morp.2
10N.244.50.D3	morp.1
10N.244.50.E3	morp.1
10N.244.50.F3	morp.1
10N.244.50.G3	morp.1
10N.244.50.H3	morp.1
10N.244.50.A4	morp.1
10N.244.50.B4	morp.1
10N.244.50.C4	morp.1
10N.244.50.D4	morp.1
10N.244.50.E4	morp.1
10N.244.50.F4	morp.1
10N.244.50.G4	morp.1
10N.244.50.H4	morp.2
10N.244.50.A5	morp.1
10N.244.50.B5	morp.1
10N.244.50.C5	morp.1
10N.244.50.D5	morp.1
10N.244.50.E5	morp.1
10N.244.50.F5	morp.5
10N.244.50.G5	morp.5
10N.244.50.H5	morp.5
10N.244.50.A6	morp.5
10N.244.50.B12	morp.5
10N.244.50.C12	morp.5
10N.244.50.D12	morp.5
10N.244.50.E12	morp.5

10N.244.50.D6	morp.5
10N.244.50.E6	morp.4
10N.244.50.F6	morp.5
10N.244.50.G6	morp.5
10N.244.50.H6	morp.5
10N.244.50.A7	morp.5
10N.244.50.B7	morp.5
10N.244.50.C7	morp.5
10N.244.50.D7	morp.5
10N.244.50.E7	morp.5
10N.244.50.F7	morp.5
10N.244.50.G7	morp.5
10N.244.50.H7	morp.5
10N.244.50.A8	morp.6
10N.244.50.B8	morp.5
10N.244.50.C8	morp.5
10N.244.50.D8	morp.5
10N.244.50.E8	morp.5
10N.244.50.F8	morp.5
10N.244.50.G8	morp.5
10N.244.50.H8	morp.5
10N.244.50.A9	morp.2
10N.244.50.B9	morp.1
10N.244.50.C9	morp.1
10N.244.50.D9	morp.1
10N.244.50.E9	morp.1
10N.244.50.F9	morp.5
10N.244.50.G9	morp.5
10N.244.50.H9	morp.5
10N.244.50.A10	morp.2
10N.244.50.B10	morp.1
10N.244.50.C10	morp.1
10N.244.50.D10	morp.1
10N.244.50.E10	morp.1
10N.244.50.F10	morp.1
10N.244.50.G10	morp.1
10N.244.50.H10	morp.1
10N.244.50.A11	morp.1
10N.244.50.B11	morp.1
10N.244.50.C11	morp.1
10N.244.50.D11	morp.1
10N.244.50.E11	morp.1
10N.244.50.F11	morp.7
10N.244.50.G11	morp.5
10N.244.50.H11	morp.5
10N.244.50.A12	morp.5
10N.244.51.C6	morp.5
10N.244.51.D6	morp.5
10N.244.51.E6	morp.5
10N.244.51.F6	morp.5

10N.244.50.F12	morp.5
10N.244.50.G12	morp.5
10N.244.51.A1	morp.4
10N.244.51.B1	morp.1
10N.244.51.C1	morp.6
10N.244.51.D1	morp.5
10N.244.51.E1	morp.7
10N.244.51.F1	morp.5
10N.244.51.G1	morp.5
10N.244.51.H1	morp.5
10N.244.51.A2	morp.6
10N.244.51.B2	morp.5
10N.244.51.C2	morp.6
10N.244.51.D2	morp.5
10N.244.51.E2	morp.7
10N.244.51.F2	morp.5
10N.244.51.G2	morp.5
10N.244.51.H2	morp.5
10N.244.51.A3	morp.5
10N.244.51.B3	morp.6
10N.244.51.C3	morp.5
10N.244.51.D3	morp.5
10N.244.51.E3	morp.5
10N.244.51.F3	morp.5
10N.244.51.G3	morp.5
10N.244.51.H3	morp.7
10N.244.51.A4	morp.5
10N.244.51.B4	morp.5
10N.244.51.C4	morp.5
10N.244.51.D4	morp.5
10N.244.51.E4	morp.5
10N.244.51.F4	morp.5
10N.244.51.G4	morp.5
10N.244.51.H4	morp.5
10N.244.51.A5	morp.5
10N.244.51.B5	morp.6
10N.244.51.C5	morp.1
10N.244.51.D5	morp.1
10N.244.51.E5	morp.1
10N.244.51.F5	morp.1
10N.244.51.G5	morp.1
10N.244.51.H5	morp.1
10N.244.51.A6	morp.5
10N.244.51.B6	morp.5
10N.244.51.C12	morp.5
10N.244.51.D12	morp.5
10N.244.51.E12	morp.5
10N.244.51.F12	morp.5
10N.244.51.G12	morp.5
10N.244.52.A1	morp.5

10N.244.51.G6	morp.5
10N.244.51.H6	morp.5
10N.244.51.A7	morp.5
10N.244.51.B7	morp.5
10N.244.51.C7	morp.5
10N.244.51.D7	morp.5
10N.244.51.E7	morp.5
10N.244.51.F7	morp.5
10N.244.51.G7	morp.5
10N.244.51.H7	morp.5
10N.244.51.A8	morp.5
10N.244.51.B8	morp.5
10N.244.51.C8	morp.5
10N.244.51.D8	morp.5
10N.244.51.E8	morp.5
10N.244.51.F8	morp.5
10N.244.51.G8	morp.5
10N.244.51.H8	morp.5
10N.244.51.A9	morp.5
10N.244.51.B9	morp.5
10N.244.51.C9	morp.5
10N.244.51.D9	morp.5
10N.244.51.E9	morp.5
10N.244.51.F9	morp.5
10N.244.51.G9	morp.5
10N.244.51.H9	morp.5
10N.244.51.A10	morp.5
10N.244.51.B10	morp.5
10N.244.51.C10	smeary, green (morp.9)
10N.244.51.D10	morp.5
10N.244.51.E10	morp.5
10N.244.51.F10	morp.5
10N.244.51.G10	morp.5
10N.244.51.H10	morp.5
10N.244.51.A11	morp.5
10N.244.51.B11	morp.2
10N.244.51.C11	morp.5
10N.244.51.D11	morp.5
10N.244.51.E11	morp.6
10N.244.51.F11	morp.5
10N.244.51.G11	morp.5
10N.244.51.H11	morp.4
10N.244.51.A12	morp.5
10N.244.51.B12	morp.5
10N.244.52.D6	morp.1
10N.244.52.E6	morp.1
10N.244.52.F6	morp.1
10N.244.52.G6	morp.1
10N.244.52.H6	morp.1
10N.244.52.A7	morp.1

10N.244.52.B1	morp.5
10N.244.52.C1	morp.5
10N.244.52.D1	morp.5
10N.244.52.E1	morp.5
10N.244.52.F1	morp.5
10N.244.52.G1	morp.5
10N.244.52.H1	morp.5
10N.244.52.A2	morp.5
10N.244.52.B2	morp.5
10N.244.52.C2	morp.5
10N.244.52.D2	morp.5
10N.244.52.E2	morp.5
10N.244.52.F2	morp.5
10N.244.52.G2	morp.5
10N.244.52.H2	morp.5
10N.244.52.A3	morp.5
10N.244.52.B3	morp.5
10N.244.52.C3	morp.5
10N.244.52.D3	morp.5
10N.244.52.E3	morp.5
10N.244.52.F3	morp.5
10N.244.52.G3	morp.7
10N.244.52.H3	morp.1
10N.244.52.A4	morp.1
10N.244.52.B4	morp.1
10N.244.52.C4	morp.1
10N.244.52.D4	morp.1
10N.244.52.E4	morp.2
10N.244.52.F4	morp.1
10N.244.52.G4	morp.1
10N.244.52.H4	morp.1
10N.244.52.A5	morp.1
10N.244.52.B5	morp.2
10N.244.52.C5	morp.1
10N.244.52.D5	morp.1
10N.244.52.E5	morp.1
10N.244.52.F5	morp.1
10N.244.52.G5	morp.1
10N.244.52.H5	morp.1
10N.244.52.A6	morp.1
10N.244.52.B6	morp.2
10N.244.52.C6	morp.1
10N.244.52.D12	morp.2
10N.244.52.E12	morp.5
10N.244.52.F12	morp.2
10N.244.52.G12	morp.5
10N.244.53.A1	morp.5
10N.244.53.B1	morp.5
10N.244.53.C1	morp.5
10N.244.53.D1	morp.5

10N.244.52.B7	morp.1
10N.244.52.C7	morp.9
10N.244.52.D7	morp.1
10N.244.52.E7	morp.1
10N.244.52.F7	morp.1
10N.244.52.G7	morp.1
10N.244.52.H7	morp.1
10N.244.52.A8	morp.2
10N.244.52.B8	morp.1
10N.244.52.C8	morp.2
10N.244.52.D8	morp.2
10N.244.52.E8	morp.2
10N.244.52.F8	morp.1
10N.244.52.G8	morp.1
10N.244.52.H8	morp.1
10N.244.52.A9	morp.1
10N.244.52.B9	morp.1
10N.244.52.C9	morp.1
10N.244.52.D9	morp.5
10N.244.52.E9	morp.5
10N.244.52.F9	morp.5
10N.244.52.G9	morp.5
10N.244.52.H9	morp.5
10N.244.52.A10	morp.5
10N.244.52.B10	morp.5
10N.244.52.C10	morp.5
10N.244.52.D10	morp.5
10N.244.52.E10	morp.5
10N.244.52.F10	morp.5
10N.244.52.G10	morp.5
10N.244.52.H10	morp.5
10N.244.52.A11	morp.5
10N.244.52.B11	morp.5
10N.244.52.C11	morp.5
10N.244.52.D11	morp.5
10N.244.52.E11	morp.5
10N.244.52.F11	morp.5
10N.244.52.G11	morp.5
10N.244.52.H11	morp.6
10N.244.52.A12	morp.6
10N.244.52.B12	morp.5
10N.244.52.C12	morp.5
10N.244.53.E6	morp.5
10N.244.53.F6	morp.6
10N.244.53.G6	morp.5
10N.244.53.H6	morp.6
10N.244.53.A7	morp.6
10N.244.53.B7	morp.5
10N.244.53.C7	morp.5
10N.244.53.D7	morp.5

10N.244.53.E1	morp.5
10N.244.53.F1	morp.6
10N.244.53.G1	morp.5
10N.244.53.H1	morp.5
10N.244.53.A2	morp.6
10N.244.53.B2	morp.6
10N.244.53.C2	morp.5
10N.244.53.D2	morp.6
10N.244.53.E2	morp.5
10N.244.53.F2	morp.5
10N.244.53.G2	morp.6
10N.244.53.H2	morp.5
10N.244.53.A3	morp.5
10N.244.53.B3	morp.5
10N.244.53.C3	morp.5
10N.244.53.D3	morp.5
10N.244.53.E3	morp.5
10N.244.53.F3	morp.5
10N.244.53.G3	morp.5
10N.244.53.H3	morp.5
10N.244.53.A4	morp.5
10N.244.53.B4	morp.5
10N.244.53.C4	morp.5
10N.244.53.D4	morp.5
10N.244.53.E4	morp.5
10N.244.53.F4	morp.5
10N.244.53.G4	morp.5
10N.244.53.H4	morp.5
10N.244.53.A5	morp.5
10N.244.53.B5	morp.6
10N.244.53.C5	morp.5
10N.244.53.D5	morp.5
10N.244.53.E5	morp.5
10N.244.53.F5	morp.5
10N.244.53.G5	morp.6
10N.244.53.H5	morp.6
10N.244.53.A6	morp.6
10N.244.53.B6	morp.6
10N.244.53.C6	morp.6
10N.244.53.D6	morp.6
10N.244.53.E12	morp.1
10N.244.53.F12	morp.1
10N.244.53.G12	morp.2
10N.244.54.A1	morp.2
10N.244.54.B1	morp.1
10N.244.54.C1	morp.2
10N.244.54.D1	morp.1
10N.244.54.E1	morp.1
10N.244.54.F1	morp.1
10N.244.54.G1	morp.1

10N.244.53.E7	morp.5
10N.244.53.F7	morp.5
10N.244.53.G7	morp.5
10N.244.53.H7	morp.6
10N.244.53.A8	morp.5
10N.244.53.B8	morp.5
10N.244.53.C8	morp.5
10N.244.53.D8	morp.5
10N.244.53.E8	morp.5
10N.244.53.F8	morp.5
10N.244.53.G8	morp.6
10N.244.53.H8	morp.5
10N.244.53.A9	morp.6
10N.244.53.B9	morp.6
10N.244.53.C9	morp.1
10N.244.53.D9	morp.1
10N.244.53.E9	morp.1
10N.244.53.F9	morp.1
10N.244.53.G9	morp.1
10N.244.53.H9	morp.2
10N.244.53.A10	morp.1
10N.244.53.B10	morp.1
10N.244.53.C10	morp.1
10N.244.53.D10	morp.1
10N.244.53.E10	morp.1
10N.244.53.F10	morp.1
10N.244.53.G10	morp.1
10N.244.53.H10	morp.1
10N.244.53.A11	morp.1
10N.244.53.B11	morp.1
10N.244.53.C11	morp.2
10N.244.53.D11	morp.1
10N.244.53.E11	morp.1
10N.244.53.F11	morp.2
10N.244.53.G11	morp.2
10N.244.53.H11	morp.1
10N.244.53.A12	morp.1
10N.244.53.B12	morp.2
10N.244.53.C12	morp.1
10N.244.53.D12	morp.2
10N.244.54.D3	morp.2
10N.244.54.E3	morp.2
10N.244.54.F3	morp.1
10N.244.54.G3	morp.2
10N.244.54.H3	morp.1
10N.244.54.A4	morp.1
10N.244.54.B4	morp.1
10N.244.54.C4	morp.1
10N.244.54.D4	morp.2
10N.244.54.E4	morp.1

10N.244.54.H1	morp.2	10N.244.54.F4	morp.1
10N.244.54.A2	morp.2	10N.244.54.G4	morp.1
10N.244.54.B2	morp.1	10N.244.54.H4	morp.2
10N.244.54.C2	morp.1	10N.244.54.A5	morp.1
10N.244.54.D2	morp.1	10N.244.54.B5	morp.1
10N.244.54.E2	morp.2	10N.244.54.C5	morp.2
10N.244.54.F2	morp.1	10N.244.54.D5	morp.1
10N.244.54.G2	morp.1	10N.244.54.E5	morp.1
10N.244.54.H2	morp.2	10N.244.54.F5	morp.1
10N.244.54.A3	morp.1	10N.244.54.G5	morp.1
10N.244.54.B3	morp.2	10N.244.54.H5	morp.1
10N.244.54.C3	morp.1		

Table S 1.3: List of all isolated *V. cyclitrophicus* host strains from day 244

Isolate IDs

10N.244.45.A01	10N.244.45.G06	10N.244.46.G10	10N.244.47.G09	10N.244.48.E09
10N.244.45.A07	10N.244.45.G08	10N.244.46.G12	10N.244.47.G10	10N.244.48.E10
10N.244.45.A12	10N.244.45.G09	10N.244.46.H01	10N.244.47.G11	10N.244.48.E11
10N.244.45.B01	10N.244.45.H01	10N.244.46.H03	10N.244.47.G12	10N.244.48.E12
10N.244.45.B02	10N.244.45.H02	10N.244.46.H09	10N.244.47.H01	10N.244.48.F03
10N.244.45.B03	10N.244.45.H04	10N.244.46.H11	10N.244.47.H10	10N.244.48.F06
10N.244.45.B06	10N.244.45.H05	10N.244.47.A05	10N.244.48.A02	10N.244.48.F07
10N.244.45.B08	10N.244.45.H07	10N.244.47.A07	10N.244.48.A04	10N.244.48.F08
10N.244.45.B09	10N.244.45.H09	10N.244.47.A08	10N.244.48.A07	10N.244.48.F10
10N.244.45.B11	10N.244.46.A02	10N.244.47.A11	10N.244.48.A08	10N.244.48.F11
10N.244.45.C01	10N.244.46.A03	10N.244.47.A12	10N.244.48.A09	10N.244.48.F12
10N.244.45.C05	10N.244.46.A04	10N.244.47.B04	10N.244.48.A11	10N.244.48.G03
10N.244.45.C08	10N.244.46.A09	10N.244.47.B07	10N.244.48.A12	10N.244.48.G06
10N.244.45.C09	10N.244.46.A10	10N.244.47.B10	10N.244.48.B02	10N.244.48.G07
10N.244.45.C10	10N.244.46.A12	10N.244.47.B12	10N.244.48.B04	10N.244.48.G09
10N.244.45.D01	10N.244.46.B01	10N.244.47.C02	10N.244.48.B08	10N.244.48.G11
10N.244.45.D02	10N.244.46.B02	10N.244.47.C06	10N.244.48.B11	10N.244.48.G12
10N.244.45.D03	10N.244.46.B07	10N.244.47.C08	10N.244.48.C01	10N.244.48.H02
10N.244.45.D04	10N.244.46.B08	10N.244.47.C09	10N.244.48.C03	10N.244.48.H03
10N.244.45.D05	10N.244.46.B09	10N.244.47.C10	10N.244.48.C04	10N.244.48.H04
10N.244.45.D07	10N.244.46.B10	10N.244.47.C12	10N.244.48.C06	10N.244.48.H06
10N.244.45.D09	10N.244.46.C02	10N.244.47.D04	10N.244.48.C07	10N.244.48.H10
10N.244.45.D11	10N.244.46.C06	10N.244.47.D07	10N.244.48.C08	10N.244.49.A01
10N.244.45.D12	10N.244.46.C07	10N.244.47.D08	10N.244.48.C09	10N.244.49.A04
10N.244.45.E02	10N.244.46.C09	10N.244.47.D09	10N.244.48.C10	10N.244.49.A05
10N.244.45.E03	10N.244.46.C11	10N.244.47.D10	10N.244.48.C11	10N.244.49.A07

10N.244.45.E04	10N.244.46.C12	10N.244.47.D11	10N.244.48.C12	10N.244.49.A08
10N.244.45.E05	10N.244.46.D03	10N.244.47.D12	10N.244.48.D02	10N.244.49.A10
10N.244.45.E07	10N.244.46.D09	10N.244.47.E02	10N.244.48.D04	10N.244.49.A12
10N.244.45.E08	10N.244.46.D10	10N.244.47.E05	10N.244.48.D05	10N.244.49.B01
10N.244.45.E10	10N.244.46.D12	10N.244.47.E11	10N.244.48.D06	10N.244.49.B02
10N.244.45.E11	10N.244.46.E03	10N.244.47.E12	10N.244.48.D07	10N.244.49.B03
10N.244.45.E12	10N.244.46.E09	10N.244.47.F04	10N.244.48.D09	10N.244.49.B04
10N.244.45.F03	10N.244.46.E10	10N.244.47.F08	10N.244.48.D10	10N.244.49.B05
10N.244.45.F04	10N.244.46.E12	10N.244.47.F09	10N.244.48.D11	10N.244.49.B06
10N.244.45.F05	10N.244.46.F01	10N.244.47.F10	10N.244.48.D12	10N.244.49.B07
10N.244.45.F11	10N.244.46.F03	10N.244.47.F12	10N.244.48.E02	10N.244.49.B08
10N.244.45.G02	10N.244.46.F08	10N.244.47.G01	10N.244.48.E03	10N.244.49.B09
10N.244.45.G03	10N.244.46.F11	10N.244.47.G04	10N.244.48.E04	10N.244.49.B10
10N.244.45.G04	10N.244.46.G02	10N.244.47.G06	10N.244.48.E07	10N.244.49.B11
10N.244.45.G05	10N.244.46.G03	10N.244.47.G07	10N.244.48.E08	10N.244.49.B12
10N.244.49.C01	10N.244.49.H10	10N.244.50.E12	10N.244.51.B09	10N.244.51.G06
10N.244.49.C02	10N.244.49.H11	10N.244.50.F02	10N.244.51.B10	10N.244.51.G08
10N.244.49.C03	10N.244.50.A01	10N.244.50.F03	10N.244.51.B12	10N.244.51.G09
10N.244.49.C04	10N.244.50.A02	10N.244.50.F04	10N.244.51.C02	10N.244.51.G10
10N.244.49.C06	10N.244.50.A04	10N.244.50.F05	10N.244.51.C03	10N.244.51.G11
10N.244.49.C07	10N.244.50.A06	10N.244.50.F07	10N.244.51.C04	10N.244.51.G12
10N.244.49.C09	10N.244.50.A08	10N.244.50.F08	10N.244.51.C05	10N.244.51.H01
10N.244.49.C11	10N.244.50.A12	10N.244.50.F09	10N.244.51.C06	10N.244.51.H02
10N.244.49.C12	10N.244.50.B01	10N.244.50.F10	10N.244.51.C07	10N.244.51.H03
10N.244.49.D01	10N.244.50.B02	10N.244.50.F11	10N.244.51.D02	10N.244.51.H04
10N.244.49.D02	10N.244.50.B03	10N.244.50.F12	10N.244.51.D03	10N.244.51.H05
10N.244.49.D04	10N.244.50.B04	10N.244.50.G03	10N.244.51.D04	10N.244.51.H06
10N.244.49.D05	10N.244.50.B05	10N.244.50.G04	10N.244.51.D05	10N.244.51.H07
10N.244.49.D08	10N.244.50.B07	10N.244.50.G05	10N.244.51.D06	10N.244.51.H09
10N.244.49.D11	10N.244.50.B09	10N.244.50.G07	10N.244.51.D07	10N.244.51.H10
10N.244.49.E02	10N.244.50.B10	10N.244.50.G08	10N.244.51.D08	10N.244.52.A01
10N.244.49.E03	10N.244.50.B11	10N.244.50.G09	10N.244.51.D09	10N.244.52.A03
10N.244.49.E04	10N.244.50.B12	10N.244.50.G10	10N.244.51.D10	10N.244.52.A05
10N.244.49.E05	10N.244.50.C01	10N.244.50.G11	10N.244.51.D11	10N.244.52.A06
10N.244.49.E06	10N.244.50.C02	10N.244.50.G12	10N.244.51.D12	10N.244.52.A07
10N.244.49.E07	10N.244.50.C03	10N.244.50.H01	10N.244.51.E01	10N.244.52.A09
10N.244.49.E10	10N.244.50.C06	10N.244.50.H02	10N.244.51.E02	10N.244.52.A10
10N.244.49.E11	10N.244.50.C07	10N.244.50.H03	10N.244.51.E03	10N.244.52.A11
10N.244.49.F02	10N.244.50.C08	10N.244.50.H05	10N.244.51.E04	10N.244.52.B01
10N.244.49.F03	10N.244.50.C09	10N.244.50.H06	10N.244.51.E05	10N.244.52.B02
10N.244.49.F04	10N.244.50.C10	10N.244.50.H07	10N.244.51.E06	10N.244.52.B06
10N.244.49.F05	10N.244.50.C11	10N.244.50.H09	10N.244.51.E07	10N.244.52.B07
10N.244.49.F07	10N.244.50.C12	10N.244.50.H10	10N.244.51.E08	10N.244.52.B08
10N.244.49.F08	10N.244.50.D01	10N.244.50.H11	10N.244.51.E09	10N.244.52.B09

10N.244.49.F09	10N.244.50.D02	10N.244.51.A01	10N.244.51.E10	10N.244.52.B10
10N.244.49.F10	10N.244.50.D07	10N.244.51.A03	10N.244.51.F02	10N.244.52.B11
10N.244.49.G03	10N.244.50.D08	10N.244.51.A04	10N.244.51.F03	10N.244.52.B12
10N.244.49.G04	10N.244.50.D10	10N.244.51.A05	10N.244.51.F04	10N.244.52.C01
10N.244.49.G05	10N.244.50.D11	10N.244.51.A06	10N.244.51.F05	10N.244.52.C02
10N.244.49.G06	10N.244.50.D12	10N.244.51.A07	10N.244.51.F06	10N.244.52.C03
10N.244.49.G08	10N.244.50.E02	10N.244.51.A08	10N.244.51.F08	10N.244.52.C04
10N.244.49.G10	10N.244.50.E03	10N.244.51.A10	10N.244.51.F09	10N.244.52.C05
10N.244.49.G11	10N.244.50.E04	10N.244.51.A11	10N.244.51.F10	10N.244.52.C06
10N.244.49.G12	10N.244.50.E05	10N.244.51.A12	10N.244.51.F11	10N.244.52.C08
10N.244.49.H01	10N.244.50.E06	10N.244.51.B01	10N.244.51.F12	10N.244.52.C09
10N.244.49.H02	10N.244.50.E07	10N.244.51.B02	10N.244.51.G01	10N.244.52.C10
10N.244.49.H03	10N.244.50.E08	10N.244.51.B04	10N.244.51.G02	10N.244.52.C11
10N.244.49.H04	10N.244.50.E09	10N.244.51.B06	10N.244.51.G03	10N.244.52.C12
10N.244.49.H07	10N.244.50.E10	10N.244.51.B07	10N.244.51.G04	10N.244.52.D02
10N.244.49.H09	10N.244.50.E11	10N.244.51.B08	10N.244.51.G05	10N.244.52.D03
10N.244.52.D04	10N.244.52.G04	10N.244.53.B7	10N.244.53. E9	10N.244.53.H10
10N.244.52.D05	10N.244.52.G06	10N.244.53.B8	10N.244.53.E10	10N.244.53.H11
10N.244.52.D06	10N.244.52.G07	10N.244.53.B10	10N.244.53.E11	10N.244.54.A3
10N.244.52.D07	10N.244.52.G08	10N.244.53.B11	10N.244.53.E12	10N.244.54.A4
10N.244.52.D08	10N.244.52.G09	10N.244.53.C1	10N.244.53.F2	10N.244.54.B1
10N.244.52.D11	10N.244.52.G11	10N.244.53.C2	10N.244.53.F3	10N.244.54.B2
10N.244.52.D12	10N.244.52.G12	10N.244.53.C5	10N.244.53.F5	10N.244.54.B4
10N.244.52.E02	10N.244.52.H02	10N.244.53.C7	10N.244.53.F6	10N.244.54.B5
10N.244.52.E03	10N.244.52.H03	10N.244.53.C8	10N.244.53.F7	10N.244.54.C1
10N.244.52.E05	10N.244.52.H04	10N.244.53.C10	10N.244.53.F8	10N.244.54.C2
10N.244.52.E06	10N.244.52.H05	10N.244.53.C12	10N.244.53.F9	10N.244.54.C3
10N.244.52.E07	10N.244.52.H06	10N.244.53.D1	10N.244.53.F10	10N.244.54.C4
10N.244.52.E11	10N.244.52.H07	10N.244.53.D2	10N.244.53.F12	10N.244.54.D1
10N.244.52.E12	10N.244.52.H08	10N.244.53.D3	10N.244.53.G2	10N.244.54.D2
10N.244.52.F01	10N.244.52.H09	10N.244.53.D4	10N.244.53.G3	10N.244.54.D5
10N.244.52.F02	10N.244.52.H10	10N.244.53.D5	10N.244.53.G4	10N.244.54. E1
10N.244.52.F03	10N.244.53.A1	10N.244.53.D7	10N.244.53.G5	10N.244.54. E5
10N.244.52.F04	10N.244.53.A2	10N.244.53.D8	10N.244.53.G6	10N.244.54.F1
10N.244.52.F05	10N.244.53.A4	10N.244.53.D9	10N.244.53.G7	10N.244.54.F2
10N.244.52.F07	10N.244.53.A5	10N.244.53.D11	10N.244.53.G8	10N.244.54.F3
10N.244.52.F08	10N.244.53.A9	10N.244.53. E1	10N.244.53.G9	10N.244.54.F4
10N.244.52.F09	10N.244.53.A11	10N.244.53. E2	10N.244.53.G10	10N.244.54.F5
10N.244.52.F10	10N.244.53.A12	10N.244.53. E4	10N.244.53.H1	10N.244.54.G1
10N.244.52.F11	10N.244.53.B1	10N.244.53. E5	10N.244.53.H2	10N.244.54.G2
10N.244.52.G01	10N.244.53.B3	10N.244.53. E6	10N.244.53.H3	10N.244.54.G5
10N.244.52.G02	10N.244.53.B4	10N.244.53. E7	10N.244.53.H4	10N.244.54.H5
10N.244.52.G03	10N.244.53.B5	10N.244.53. E8		

Table S 1.4: List of all phages used in the cross infection assays

Layout position	Phage stock (PPA.)	Short ID	Fullname
A2	PPA.02378	15.332.A.	15.332.A._10N.239.312.A01.SH1_10N.V.239
A3	PPA.02386	8.332.A.	8.332.A._10N.239.312.A01.SH1_10N.V.238
A4	PPA.02397		
A5	PPA.02032	5.331.B.	5.331.B._10N.239.31.JE.2H01
A6	PPA.02168	1.149.O.	1.149.O._10N.286.55.A12
A7	PPA.02347	1.173.O.	1.173.O._10N.261.55.A11
A8	PPA.02355	1.243.O.	1.243.O._10N.261.54.B5
A9	PPA.02363	1.284.A.	1.284.A._10N.286.55.A5
A10	PPA.02007	7.329.O.	7.329.O._10N.239.31.JE.1F08
B1	PPA.02371	43.332.A.	43.332.A._10N.239.312.A01.SH1_10N.V.262
B2	PPA.02379	47.332.A.	47.332.A._10N.239.312.A01.SH1_10N.V.282
B3	PPA.02387	8.332.B.	8.332.B._10N.239.312.A01.SH1_10N.V.238
B4	PPA.02398	4.332.O.	4.332.O._10N.239.312.A01.SH1_10N.V.240
B5	PPA.02039	8.331.O.	8.331.O._10N.239.31.JE.2H01
B6	PPA.02178	1.253.O.	1.253.O._10N.286.45.B12
B7	PPA.02348	1.178.O.	1.178.O._10N.286.45.E12
B8	PPA.02356	1.248.O.	1.248.O._10N.286.54.F1
B9	PPA.02364	1.286.O.	1.286.O._10N.286.55.C4
B10	PPA.02008	8.329.O.	8.329.O._10N.239.31.JE.1F08
C1	PPA.02372	42.332.D.	42.332.D._10N.239.312.A01.SH1_10N.V.282
C2	PPA.02380	2.332.B.	2.332.B._10N.239.312.A01.SH1_10N.V.239
C3	PPA.02388	8.332.A.	8.332.A._10N.239.312.A01.SH1_10N.V.282
C4	PPA.02399	34.332.A.	34.332.A._10N.239.312.A01.SH1_10N.V.242
C5	PPA.02049	1.007.O.	1.007.O._10N.261.55.F9
C6	PPA.02219	1.186.O.	1.186.O._10N.286.49.E3
C7	PPA.02349	1.197.A.	1.197.A._10N.286.54.F2
C8	PPA.02357	1.263.A.	1.263.A._10N.286.51.B1
C9	PPA.02365	1.287.O.	1.287.O._10N.286.55.C7
C10	PPA.02370	3.330.B.	3.330.B._10N.239.31.JE.1G07
D1	PPA.02373	41.332.A.	41.332.A._10N.239.312.A01.SH1_10N.V.288
D2	PPA.02381	14.332.A.	14.332.A._10N.239.312.A01.SH1_10N.V.239
D3	PPA.02389	13.332.B.	13.332.B._10N.239.312.A01.SH1_10N.V.239
D4	PPA.02400		
D5	PPA.02144	1.122.B.	1.122.B._10N.286.46.F8
D6	PPA.02222	1.204.O.	1.204.O._10N.222.46.F12
D7	PPA.02350	1.199.A.	1.199.A._10N.286.55.C10
D8	PPA.02358	1.263.B.	1.263.B._10N.286.51.B1
D9	PPA.02229	1.215.A.	1.215.A._10N.222.54.F7

D10	PPA.02017	5.330.B.	5.330.B._10N.239.31.JE.1G07
E1	PPA.02374	41.332.B.	41.332.B._10N.239.312.A01.SH1_10N.V.288
E2	PPA.02382	1.332.O.	1.332.O._10N.239.312.A01.SH1_10N.V.236
E3	PPA.02393	15.332.B.	15.332.B._10N.239.312.A01.SH1_10N.V.239
E4	PPA.02401	8.332.A.	8.332.A._10N.239.312.A01.SH1_10N.V.238
E5	PPA.02145	1.122.A.	1.122.A._10N.286.46.F8
E6	PPA.02225	1.256.O.	1.256.O._10N.286.45.F8
E7	PPA.02351	1.199.B.	1.199.B._10N.286.55.C10
E8	PPA.02359	1.265.O.	1.265.O._10N.286.52.F6
E9	PPA.02390	45.332.B.	45.332.B._10N.239.312.A01.SH1_10N.V.282
E10	PPA.02021	7.330.B.	7.330.B._10N.239.31.JE.1G07
F1	PPA.02375	10.332.A.	10.332.A._10N.239.312.A01.SH1_10N.V.239
F2	PPA.02383	2.332.B.	2.332.B._10N.239.312.A01.SH1_10N.V.237
F3	PPA.02394	12.332.B.	12.332.B._10N.239.312.A01.SH1_10N.V.239
F4	PPA.02325	8.332.B.	8.332.B._10N.239.312.A01.SH1_10N.V.238
F5	PPA.02153	1.105.O.	1.105.O._10N.286.49.B4
F6	PPA.02226	1.273.O.	1.273.O._10N.286.54.C7
F7	PPA.02352	1.201.B.	1.201.B._10N.286.55.F1
F8	PPA.02360	1.275.O.	1.275.O._10N.286.54.E11
F9	PPA.02391	40.332.C.	40.332.C._10N.239.312.A01.SH1_10N.V.282
F10	PPA.02025	1.331.B.	1.331.B._10N.239.31.JE.2H01
G1	PPA.02376	10.332.B.	10.332.B._10N.239.312.A01.SH1_10N.V.239
G2	PPA.02384	6.332.A.	6.332.A._10N.239.312.A01.SH1_10N.V.237
G3	PPA.02395	4.332.O.	4.332.O._10N.239.312.A01.SH1_10N.V.237
G4	PPA.02002	2.329.O.	2.329.O._10N.239.31.JE.1F08
G5	PPA.02159	1.106.O.	1.106.O._10N.286.51.F7
G6	PPA.02228	1.289.A.	1.289.A._10N.286.55.E8
G7	PPA.02353	1.214.O.	1.214.O._10N.222.54.F11
G8	PPA.02361	1.276.O.	1.276.O._10N.286.54.E4
G9	PPA.02392	42.332.A.	42.332.A._10N.239.312.A01.SH1_10N.V.282
G10	PPA.02367	1.080.O.	1.080.O._10N.286.48.A4
H1	PPA.02377	13.332.A.	13.332.A._10N.239.312.A01.SH1_10N.V.239
H2	PPA.02385	9.332.B.	9.332.B._10N.239.312.A01.SH1_10N.V.238
H3	PPA.02396	5.332.B.	5.332.B._10N.239.312.A01.SH1_10N.V.237
H4	PPA.02024	1.331.A.	1.331.A._10N.239.31.JE.2H01
H5	PPA.02167	1.013.O.	1.013.O._10N.286.54.F9
H6	PPA.02231	1.293.O.	1.293.O._10N.261.52.E1
H7	PPA.02354	1.236.O.	1.236.O._10N.261.52.C4
H8	PPA.02362	1.278.O.	1.278.O._10N.286.54.E8
H9	PPA.02001	1.329.O.	1.329.O._10N.239.31.JE.1F08
H10	PPA.02368	1.043.O.	1.043.O._10N.261.52.C7

Table S 1.5: Interactions between *V. cyclitrophicus* hosts from day 244 and phages from the Nahant collection, that were identified in the cross infection assay. (lytic interaction marked in red, might be caused by inducing agent, rather than the phages)

Host	No lysis	Lysis	Single plaques / LI
10N.244.45.A01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.A07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.A12	X		
10N.244.45.B01	X		
10N.244.45.B02		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No
10N.244.45.B03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.B06		1.215.A.	No
10N.244.45.B08		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.45.B09		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.45.B11	X		
10N.244.45.C01	X		
10N.244.45.C05	X		
10N.244.45.C08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.C09		1.286.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.C10		1.215.A.	No
10N.244.45.D01	X		
10N.244.45.D02	X		
10N.244.45.D03	X		
10N.244.45.D04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.D05		1.215.A.	No
10N.244.45.D07	X		
10N.244.45.D09	X		
10N.244.45.D11	X		
10N.244.45.D12	X		
10N.244.45.E02	X		
10N.244.45.E03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.E04	X		
10N.244.45.E05	X		
10N.244.45.E07	X		
10N.244.45.E08		1.215.A.	No
10N.244.45.E10	X		
10N.244.45.E11	X		
10N.244.45.E12	X		
10N.244.45.F03	X		
10N.244.45.F04	X		
10N.244.45.F05		1.122.B., 1.122.A.	No
10N.244.45.F11	X		

10N.244.45.G02	X		
10N.244.45.G03	X		
10N.244.45.G04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.G05	X		
10N.244.45.G06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.G08	X		
10N.244.45.G09	X		
10N.244.45.H01	X		
10N.244.45.H02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.45.H04	X		
10N.244.45.H05	X		
10N.244.45.H07		3.330.B., 1.215.A., 5.330.B., 7.330.B	1.215.A - yes
10N.244.45.H09		3.330.B., 1.215.A., 5.330.B., 7.330.B	No
10N.244.46.A02	X		
10N.244.46.A03	X		
10N.244.46.A04	X		
10N.244.46.A09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.A10		1.215.A.	No
10N.244.46.A12	X		
10N.244.46.B01		Prophage was induced	Yes
10N.244.46.B02	X		
10N.244.46.B07	X		
10N.244.46.B08		3.330.B., 1.215.A., 5.330.B., 7.330.B	1.215.A - yes
10N.244.46.B09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.B10		3.330.B., 1.215.A., 5.330.B., 7.330.B	1.215.A - yes
10N.244.46.C02	X	3.330.B., 1.215.A., 5.330.B., 7.330.B	No
10N.244.46.C06		8.329.O.	No
10N.244.46.C07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.C09		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A - yes
10N.244.46.C11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.C12		1.284.A., 1.287.O., 1.289.A.	No
10N.244.46.D03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.D09	X		
10N.244.46.D10		3.330.B., 1.215.A., 5.330.B., 1.122.A., 7.330.B	1.215.A - yes
10N.244.46.D12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.E03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.E09		3.330.B., 5.330.B., 1.122.A., 7.330.B.	No
10N.244.46.E10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.E12		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No
10N.244.46.F01	X		
10N.244.46.F03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.F08		3.330.B., 1.215.A., 5.330.B., 7.330.B	No
10N.244.46.F11	X		

10N.244.46.G02	X		
10N.244.46.G03	X		
10N.244.46.G10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.G12		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.46.H01	X		
10N.244.46.H03	X		
10N.244.46.H09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.46.H11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.A05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.A07	X		
10N.244.47.A08	X		
10N.244.47.A11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.A12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.B04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.B07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.B10	X		
10N.244.47.B12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.C02	X		
10N.244.47.C06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.C08	X		
10N.244.47.C09	X		
10N.244.47.C10	X		
10N.244.47.C12		7.329.O., 8.329.O., 3.330.B., 5.330.B., 7.330.B., 2.329.O.	No
10N.244.47.D04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.D07	X		
10N.244.47.D08		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A - yes
10N.244.47.D09		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.47.D10	X		
10N.244.47.D11		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.47.D12	X		
10N.244.47.E02	X		
10N.244.47.E05	X		
10N.244.47.E11	X		
10N.244.47.E12		3.330.B., 5.330.B., 7.330.B.	Yes
10N.244.47.F04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.F08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.F09		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.47.F10	X		
10N.244.47.F12	X		
10N.244.47.G01		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes

10N.244.47.G04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.G06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.G07	X		
10N.244.47.G09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.47.G10		1.214.O.	No
10N.244.47.G11		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.47.G12		3.330.B., 5.330.B., 7.330.B.	
10N.244.47.H01	X		
10N.244.47.H10		1.248.O., 3.330.B., 5.330.B., 7.330.B.	1.248.O. - yes
10N.244.48.A02		1.284.A., 1.287.O., 3.330.B., 1.204.O., 5.330.B., 7.330.B., 1.289.A.	No
10N.244.48.A04	X		
10N.244.48.A07		8.331.O.	No
10N.244.48.A08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.A09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.A11	X		
10N.244.48.A12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.B02		1.286.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B.	No
10N.244.48.B04		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.48.B08	X		
10N.244.48.B11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C03		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.48.C04	X		
10N.244.48.C06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C09		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.48.C10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.C11		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.48.C12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.D02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.48.D04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.D05		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.48.D06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.D07	X		
10N.244.48.D09	X		
10N.244.48.D10	X		
10N.244.48.D11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.D12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.E02		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No

10N.244.48.E03		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.48.E04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.E07		3.330.B., 5.330.B., 7.330.B., 1.080.O.	No
10N.244.48.E08	X		
10N.244.48.E09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.E10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.E11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.E12	X		
10N.244.48.F03		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.48.F06	X		
10N.244.48.F07	X		
10N.244.48.F08	X		
10N.244.48.F10		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.48.F11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.F12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.G03		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.48.G06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.48.G07	X		
10N.244.48.G09	X		
10N.244.48.G11	X		
10N.244.48.G12		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.48.H02	X		
10N.244.48.H03	X		
10N.244.48.H04	X		
10N.244.48.H06	X		
10N.244.48.H10	X		
10N.244.49.A01	X		
10N.244.49.A04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.A05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.A07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.A08	X		
10N.244.49.A10		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.49.A12	X		
10N.244.49.B01		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.275.O., 1.293.O.	1.215.A - yes
10N.244.49.B02	X		
10N.244.49.B03		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.B04		7.329.O., 8.329.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.276.O.	No
10N.244.49.B05		7.329.O., 8.329.O., 2.329.O.	No
10N.244.49.B06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.B07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.B08		3.330.B., 5.330.B., 7.330.B.	No

10N.244.49.B09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.B10		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.B11	X		
10N.244.49.B12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.C01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.C02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.49.C03		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.C04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.C06		1.122.B., 1.122.A.	No
10N.244.49.C07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.C09	X		
10N.244.49.C11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.C12	X		
10N.244.49.D01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.D02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.49.D04	X		
10N.244.49.D05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.D08		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.D11		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.E02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.E03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.E04		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.49.E05	X		
10N.244.49.E06		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.49.E07	X		
10N.244.49.E10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.E11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.F02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.F03	X		
10N.244.49.F04		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.F05	X		
10N.244.49.F07	X		
10N.244.49.F08		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.49.F09		1.243.O.	No
10N.244.49.F10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.G03	X		
10N.244.49.G04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.G05	X		
10N.244.49.G06	X		
10N.244.49.G08	X		
10N.244.49.G10		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.49.G11	X		
10N.244.49.G12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.H01	X		

10N.244.49.H02		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.H03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.49.H04		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.49.H07		3.330.B., 5.330.B., 1.122.A., 7.330.B.	No
10N.244.49.H09	X		
10N.244.49.H10	X		
10N.244.49.H11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.A01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.A02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.A04	X		
10N.244.50.A06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.A08	X		
10N.244.50.A12	X		
10N.244.50.B01		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.50.B02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.B03	X		
10N.244.50.B04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.B05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.B07		3.330.B., 1.199.A., 5.330.B., 1.199.B., 7.330.B.	1.199.A. and 1.199.B. - yes
10N.244.50.B09		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.B10	X		
10N.244.50.B11	X		
10N.244.50.B12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.C01		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.50.C02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.C03		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.50.C06		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.C07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.C08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.C09	X		
10N.244.50.C10	X		
10N.244.50.C11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.C12	X		
10N.244.50.D01		3.330.B., 5.330.B., 1.265.O., 7.330.B., 1.293.O.	No
10N.244.50.D02		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.50.D07		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.D08		1.243.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.D10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.D11		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.D12		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.50.E02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes

10N.244.50.E03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.E04	X		
10N.244.50.E05		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.E06	X		
10N.244.50.E07		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.50.E08		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.E09		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.50.E10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.E11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.E12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.F02	X		
10N.244.50.F03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.F04	X		
10N.244.50.F05	X		
10N.244.50.F07	X		
10N.244.50.F08	X		
10N.244.50.F09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.F10		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.50.F11	X		
10N.244.50.F12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.G03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.G04	X		
10N.244.50.G05	X		
10N.244.50.G07		3.330.B., 5.330.B., 7.330.B., 1.276.O.	No
10N.244.50.G08	X		
10N.244.50.G09	X		
10N.244.50.G10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.G11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.G12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.H01	X		
10N.244.50.H02	X		
10N.244.50.H03	X		
10N.244.50.H05		1.178.O., 3.330.B., 5.330.B., 7.330.B.	1.178.O. - yes
10N.244.50.H06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.H07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.50.H09	X		
10N.244.50.H10	X		
10N.244.50.H11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.A01		1.293.O.	No
10N.244.51.A03		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.51.A04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.A05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.A06	X		
10N.244.51.A07		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No

10N.244.51.A08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.A10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.A11		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.51.A12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.B01		1.215.A	No
10N.244.51.B02	X		
10N.244.51.B04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.B06		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.51.B07	X		
10N.244.51.B08		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.51.B09	X		
10N.244.51.B10	X		
10N.244.51.B12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.C02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.C03	X		
10N.244.51.C04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.C05	X		
10N.244.51.C06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.C07	X		
10N.244.51.D02	X		
10N.244.51.D03		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.51.D04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D08	X		
10N.244.51.D09		1.293.O.	No
10N.244.51.D10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.D12	X		
10N.244.51.E01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E03		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.51.E04	X		
10N.244.51.E05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E07		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E08		1.286.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.E10		1.286.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B.	No
10N.244.51.F02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.F03		3.330.B., 5.330.B., 7.330.B.	No

10N.244.51.F04	X		
10N.244.51.F05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.F06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.F08	X		
10N.244.51.F09		5.331.B., 8.331.O.	No
10N.244.51.F10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.F11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.F12		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.51.G01	X		
10N.244.51.G02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.G03	X		
10N.244.51.G04	X		
10N.244.51.G05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.G06	X		
10N.244.51.G08	X		
10N.244.51.G09		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.G10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.G11		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.51.G12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.H01	X		
10N.244.51.H02		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.51.H03		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.H04	X		
10N.244.51.H05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.H06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.51.H07	X		
10N.244.51.H09	X		
10N.244.51.H10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.A01		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.A03	X		
10N.244.52.A05		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.52.A06		3.330.B., 5.330.B., 7.330.B., 1.293.O.	1.293.O. - yes
10N.244.52.A07	X		
10N.244.52.A09	X		
10N.244.52.A10	X		
10N.244.52.A11		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.52.B01	X		
10N.244.52.B02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.B06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.B07	X		
10N.244.52.B08		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.52.B09	X		
10N.244.52.B10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.B11	X		

10N.244.52.B12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.C01	X		
10N.244.52.C02		1.286.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B.	1.286.O. - yes
10N.244.52.C03		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.52.C04	X		
10N.244.52.C05	X		
10N.244.52.C06	X		
10N.244.52.C08	X		
10N.244.52.C09	X		
10N.244.52.C10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.C11	X		
10N.244.52.C12		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.52.D02	X		
10N.244.52.D03	X		
10N.244.52.D04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.D05		1.215.A	1.215.A - yes
10N.244.52.D06		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.52.D07		3.330.B., 1.122.B., 5.330.B., 1.215.A, 7.330.B., 1.122.A.	No
10N.244.52.D08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.D11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.D12		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.52.E02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.E03	X		
10N.244.52.E05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.E06	X		
10N.244.52.E07	X		
10N.244.52.E11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.E12		1.215.A., 1.122.A.	No
10N.244.52.F01		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A - yes
10N.244.52.F02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.F03	X		
10N.244.52.F04	X		
10N.244.52.F05	X		
10N.244.52.F07	X		
10N.244.52.F08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.F09	X		
10N.244.52.F10	X		
10N.244.52.F11	X		
10N.244.52.G01	X		
10N.244.52.G02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.G03	X		

10N.244.52.G04		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.G06	X		
10N.244.52.G07	X		
10N.244.52.G08	X		
10N.244.52.G09	X		
10N.244.52.G11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.G12	X		
10N.244.52.H02		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.H03		3.330.B., 1.122.B., 5.330.B., 1.122.A., 7.330.B.	No
10N.244.52.H04		1.149.O., 3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.52.H05		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.H06		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.H07		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.52.H08		3.330.B., 5.330.B., 7.330.B.	No
10N.244.52.H09	X		
10N.244.52.H10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.A1		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.A2		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.A4	X		
10N.244.53.A5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.A9	X		
10N.244.53.A11	X		
10N.244.53.A12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.B1		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.B3		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.B4	X		
10N.244.53.B5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.B7		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.B8	X		
10N.244.53.B10		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.B11		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.C1		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.C2	X		
10N.244.53.C5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.C7	X		
10N.244.53.C8		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.C10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.C12		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.D1	X		
10N.244.53.D2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.D3	X		
10N.244.53.D4		3.330.B., 5.330.B., 7.330.B.	No

10N.244.53.D5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.D7	X		
10N.244.53.D8		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.D9		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.D11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E1	X		
10N.244.53. E2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E4		1.243.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E6		3.330.B., 5.330.B., 7.330.B.	Yes
10N.244.53. E7		3.330.B., 5.330.B., 7.330.B.	Yes
10N.244.53. E8		3.330.B., 1.122.B., 5.330.B., 1.122.A., 7.330.B.	No
10N.244.53. E9		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E10		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E11		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53. E12		3.330.B., 1.199.A., 5.330.B., 1.199.B., 7.330.B.	No
10N.244.53.F2		1.286.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F3		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F5	X		
10N.244.53.F6		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F7		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F8		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F9		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.F10	X		
10N.244.53.F12		1.243.O., 3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G3		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G4		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G6		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G7		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.106.O., 1.293.O.	1.215.A - yes
10N.244.53.G8		3.330.B., 1.122.B., 5.330.B., 1.122.A., 7.330.B.	No
10N.244.53.G9		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.G10	X		
10N.244.53.H1	X		
10N.244.53.H2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.53.H3		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.53.H4		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A - yes
10N.244.53.H10		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No
10N.244.53.H11	X		

10N.244.54.A3		5.331.B., 8.331.O.	No
10N.244.54.A4	X		
10N.244.54.B1		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.B2		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.106.O.	No
10N.244.54.B4		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.B5		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.54.C1		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.C2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.C3		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.C4	X		
10N.244.54.D1	X		
10N.244.54.D2		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.D5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54. E1		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No
10N.244.54. E5	X		
10N.244.54.F1		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.F2		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.215.A. - yes
10N.244.54.F3		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.F4		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.F5		3.330.B., 5.330.B., 7.330.B.	No
10N.244.54.G1	X		
10N.244.54.G2	X		
10N.244.54.G5	X		
10N.244.54.H5	X		

Table S 1.6: Interactions between *V. cyclitrophicus* hosts from days 222, 232, 236, 237, 239, 247, 261, 286, and phages from the Nahant collection, as well as the inducing agent.

Host	No lysis	Lysis	Single plaques / LI	Inducing agent
10N.222.45.C8		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.222.45.E8		1.215.A., 1.275.O., 1.293.O.	1.215.A. and 1.293.O. - yes	No
10N.222.46.A10		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	1.215.A. - yes	Yes
10N.222.46.B11		1.186.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.273.O., 1.293.O.	1.215.A., 1.293.O. and 1.273.O. - yes	No
10N.222.46.B4		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.46.B5		1.178.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B.,	1.178.O. and 1.215.A. - yes	Yes
10N.222.46.E12		1.284.A., 1.287.O., 1.204.O., 1.289.A.	1.287.O., 1.204.O.	No

10N.222.46.F1		1.286.O., 3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.46.F12		1.284.A., 1.286.O., 1.287.O., 1.204.O., 1.289.A., 1.293.O.	1.204.O. and 1.289.A. - yes	No
10N.222.49.A1		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.49.C11		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.222.49.E12		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.49.E3		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.51.C10		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.A10		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.A11		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.A2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.A7		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - yes	Yes
10N.222.54.B10		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.B4		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.C12		1.243.O., 3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.E1		1.286.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B.	No	No
10N.222.54.E10		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.E11		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.E12		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.222.54.E7		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.54.F1		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No	No
10N.222.54.F11		1.197.A., 2.329.O., 1.106.O., 1.289.A., 1.214.O., 1.276.O., 1.331.A., 1.013.O., 1.293.O.	1.214.O., 1.013.O. and 1.293.O. - Yes	No
10N.222.54.F4	X			
10N.222.54.F7		1.215.A., 1.275.O., 1.293.O.	1.215.A. - Yes	No
10N.222.55.A12		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.55.A7		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.222.55.A9		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.55.B2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.55.C3		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.55.C4		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.222.55.C5		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No	No
10N.222.55.E11		1.173.O., 1.286.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.201.B.	1.286.O. - Yes	No
10N.232.45.A2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.A3	X			
10N.232.45.B1		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.B11		1.293.O.	No	No
10N.232.45.B3		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.C1		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.C3	X			
10N.232.45.D1		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.D3		3.330.B., 5.330.B., 7.330.B.	No	Yes

10N.232.45.E1		1.293.O., 3.330.B., 5.330.B., 1.265.O., 7.330.B.	No	No
10N.232.45.E11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	No
10N.232.45.E12		1.293.O.	No	No
10N.232.45.E3	X			
10N.232.45.F2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.F3		1.215.A.	1.215.A. - Yes	No
10N.232.45.G1	X			
10N.232.45.G2	X			
10N.232.45.H2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.45.H3		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.46.A2	X			
10N.232.46.A3		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.232.46.B2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.46.C2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.46.D2		1.186.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.273.O., 1.293.O.	1.215.A. - Yes	Yes
10N.232.46.E4	X			
10N.232.46.F1		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.46.F2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.232.46.G1	X			
10N.232.46.H1		1.253.O., 1.293.O.	1.253.O. and 1.293.O. - yes	No
10N.232.46.H2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.45.B12	X			
10N.236.45.C12		1.253.O., 1.293.O.	No	No
10N.236.45.D12	X			
10N.236.45.E12	X			
10N.236.45.F12	X			
10N.236.46.A1	X			
10N.236.46.A2		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.46.C1		3.330.B., 1.122.B., 5.330.B., 1.122.A., 7.330.B.	No	Yes
10N.236.46.C2		5.331.B., 8.331.O., 1.331.B., 1.331.A.	No	No
10N.236.46.D2		1.186.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.273.O., 1.293.O.	1.215.A. - Yes	No
10N.236.46.E1		1.215.A.	No	No
10N.236.46.E2	X			
10N.236.46.F1	X			
10N.236.46.F2	X			
10N.236.46.H1		1.253.O., 1.293.O.	1.253.O. and 1.293.O. - Yes	No
10N.236.47.A10	X			
10N.236.47.B10		1.286.O., 1.201.B.		
10N.236.47.B11		1.173.O., 3.330.B., 5.330.B., 7.330.B., 1.293.O.	1.173.O. - Yes	Yes
10N.236.47.B8		1.215.A.	No	No

10N.236.47.B9		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.47.C10		1.243.O., 3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.47.C8		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.47.C9		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.47.D8		3.330.B., 5.330.B., 7.330.B., 1.293.O.	1.293.O. - Yes	Yes
10N.236.47.D9	X			
10N.236.47.E8	X			
10N.236.47.F10		5.331.B., 8.331.O.	No	No
10N.236.47.F7		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.236.47.F8	X			
10N.236.47.G7	X			
10N.236.47.G8		1.173.O., 3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.236.47.H8		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.237.312.A05		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.237.312.A09		3.330.B., 5.330.B., 7.330.B., 1.293.O.	1.293.O. - Yes	Yes
10N.237.312.B04		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.237.312.B10		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	No
10N.237.312.C05		3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.237.312.C08		3.330.B., 5.330.B., 7.330.B., 1.293.O.	1.293.O. - Yes	Yes
10N.237.312.C11		5.331.B., 8.331.O.,		
10N.237.312.D05	X			
10N.237.312.D10		3.330.B., 5.330.B., 7.330.B., 1.276.O.	No	No
10N.237.312.D11		3.330.B., 5.330.B., 7.330.B.	No	No
10N.237.312.E09		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	No
10N.237.312.E11		1.293.O.	1.293.O. - Yes	No
10N.237.312.G08		3.330.B., 5.330.B., 7.330.B.	No	No
10N.239.311.A05		1.215.A.	No	No
10N.239.311.A09	X			
10N.239.311.B02		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	No
10N.239.311.B03	X			
10N.239.311.B10		3.330.B., 1.122.B., 1.215.A., 5.330.B., 1.122.A., 7.330.B.	No	Yes
10N.239.311.B11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No	No
10N.239.311.C11		5.331.B., 8.331.O., 1.331.B.	No	No
10N.239.311.D05	X			
10N.239.311.D07	X			
10N.239.311.E01		1.122.B., 1.215.A., 1.122.A., 1.105.O.		
10N.239.311.E03	X			
10N.239.311.E06		1.178.O., 3.330.B., 5.330.B., 7.330.B.	No	No
10N.239.311.F08		7.329.O., 8.329.O., 1.122.A., 2.329.O., 1.278.O., 1.329.O., 1.043.O.	7.329.O., 8.329.O., 2.329.O. and 1.043.O. - Yes	No
10N.239.311.G07		3.330.B., 5.330.B., 7.330.B.	Yes	Yes
10N.239.311.G11	X			

10N.239.311.H11		3.330.B., 5.330.B., 7.330.B.	No	No
10N.239.312.A01		15.332.A., 8.332.A., 5.331.B., 1.149.O., 43.332.A., 47.332.A., 8.332.B., 4.332.O., 8.331.O., 1.253.O., 42.332.D., 2.332.B., 8.332.A., 34.332.A., 1.007.O., 41.332.A., 14.332.A., 13.332.B., 1.122.B., 41.332.B., 1.332.O., 15.332.B., 8.332.A., 1.122.A., 1.265.O., 45.332.B., 10.332.A., 2.332.B., 12.332.B., 8.332.B., 1.105.O., 40.332.C., 10.332.B., 6.332.A., 4.332.O., 42.332.A., 1.080.O., 13.332.A., 9.332.B., 5.332.B.	15.332.A., 8.332.A., 47.332.A., 8.332.B., 4.332.O., 42.332.D., 34.332.A., 41.332.A., 14.332.A., 13.332.B., 41.332.B., 1.332.O., 15.332.B., 8.332.A., 45.332.B., 10.332.A., 2.332.B., 12.332.B., 8.332.B., 40.332.C., 10.332.B., 6.332.A., 4.332.O., 42.332.A., 13.332.A., 9.332.B., 5.332.B.	No
10N.239.312.B09		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	No
10N.239.312.D01		3.330.B., 5.330.B., 7.330.B.,	No	No
10N.239.312.G01		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.239.312.H01		5.331.B., 4.332.O., 8.331.O., 1.253.O., 1.007.O., 45.332.B., 8.332.B., 40.332.C., 1.331.B., 5.332.B., 1.331.A., 1.013.O.	5.331.B., 8.331.O., 1.331.B., 1.331.A. - yes	Yes
10N.239.312.H11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.247.310.01	X			
10N.247.310.22	X			
10N.247.310.38		3.330.B., 5.330.B., 7.330.B.,	No	No
10N.247.310.82	X			
10N.247.310.87	X			
10N.247.310.92		1.293.O.	No	No
10N.247.310.95	X			
10N.247.310.97		1.215.A.		
10N.247.311.43	X			
10N.247.311.45		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.247.311.58	X			
10N.247.311.62	X			
10N.247.311.81		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.247.311.82		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.247.311.85	X			
10N.247.311.86		3.330.B., 5.330.B., 7.330.B.,	No	No
10N.247.311.87		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.45.A3		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No	Yes
10N.261.45.C10	X			
10N.261.45.E6		1.215.A., 1.293.O.	No	No
10N.261.45.E7	X			
10N.261.45.F7		1.293.O.	1.293.O. - Yes	No

10N.261.46.A5	X			
10N.261.46.F9	X			
10N.261.48.A6		1.293.O.	No	No
10N.261.48.C10		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.48.C2	X			
10N.261.48.E11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.261.48.F2		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.48.F6		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.51.A5		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.261.51.B10		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.51.F10		1.293.O.	No	No
10N.261.51.F5		8.332.A., 1.007.O., 1.122.B., 1.204.O., 1.122.A., 1.105.O.	1.122.B. and 1.122.A. - Yes	No
10N.261.52.C4		47.332.A., 8.331.O., 34.332.A., 1.263.B., 1.215.A., 1.256.O., 1.289.A., 1.214.O., 1.013.O., 1.293.O., 1.236.O., 1.278.O., 1.329.O.	1.215.A. and 1.236.O. - Yes	No
10N.261.52.E1		1.215.A., 1.289.A., 1.013.O., 1.293.O., 1.236.O.	1.215.A. and 1.236.O. - Yes	No
10N.261.54.A3		1.215.A., 1.293.O.	No	No
10N.261.54.A7		1.215.A.	1.215.A. - Yes	No
10N.261.54.B10		1.215.A.	No	No
10N.261.54.B11	X			
10N.261.54.B12	X			
10N.261.54.B3	X			
10N.261.54.B5		1.243.O., 1.284.A., 7.329.O., 1.275.O.	No	No
10N.261.54.B8	X			
10N.261.54.C12	X			
10N.261.54.C2		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No	Yes
10N.261.54.C5		1.215.A.	1.215.A. - Yes	No
10N.261.54.C8		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.261.54.C9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.54.E2		1.284.A., 1.287.O., 3.330.B., 1.204.O., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.261.54.E5		5.331.B., 7.329.O., 8.331.O., 1.248.O., 1.286.O., 8.329.O., 1.186.O., 1.263.A., 1.215.A., 1.201.B.	1.215.A. - Yes	No
10N.261.54.E8		3.330.B., 5.330.B., 7.330.B., 1.275.O., 1.293.O.	No	Yes
10N.261.54.E9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.54.F1		1.243.O., 1.248.O., 1.197.A., 1.263.A., 1.215.A.	1.248.O. and 1.215.A. - Yes	No
10N.261.54.F11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	No	Yes
10N.261.54.F12		1.243.O., 3.330.B., 5.330.B., 7.330.B.,	1.243.O. - Yes	Yes
10N.261.54.F2		3.330.B., 5.330.B., 7.330.B.,	No	Yes

10N.261.54.F7		1.215.A., 1.275.O.	No	No
10N.261.54.F8		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.54.F9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.A1		1.215.A., 1.293.O.	No	No
10N.261.55.A11		1.149.O., 1.173.O., 1.253.O., 1.331.A., 1.293.O.	1.173.O., 1.331.A. and 1.293.O. - Yes	No
10N.261.55.A5		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.261.55.A6		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.B1		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.B11		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.B4		3.330.B., 5.330.B., 7.330.B., 1.293.O.	No	No
10N.261.55.B6		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.B7		3.330.B., 5.330.B., 1.122.A., 7.330.B., 1.105.O.	No	Yes
10N.261.55.B9	X			
10N.261.55.C4		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.E10		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.E3		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.E6	X			
10N.261.55.F1		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.261.55.F11		3.330.B., 5.330.B., 7.330.B., 1.276.O., 1.278.O.	1.276.O. - Yes	No
10N.261.55.F3	X			
10N.261.55.F7	X			
10N.261.55.F9		1.149.O., 4.332.O., 34.332.A., 1.007.O., 1.122.B., 1.122.A., 1.293.O.	1.007.O. - Yes	No
10N.286.45.A5		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.45.B12		1.253.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.253.O. and 1.215.A. - Yes	Yes
10N.286.45.B7	X			
10N.286.45.C2	X			
10N.286.45.C6	X			
10N.286.45.E12		1.178.O., 1.248.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.178.O. - Yes	Yes
10N.286.45.F4	X			
10N.286.45.F6		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.45.F7		1.122.A., 1.293.O.	1.122.A. – Yes	No
10N.286.45.F8		3.330.B., 5.330.B., 1.122.A., 7.330.B., 1.293.O.	1.122.A. – Yes	Yes
10N.286.46.B3	X			
10N.286.46.B5		1.215.A.	No	No
10N.286.46.B6	X			
10N.286.46.C8	X			
10N.286.46.E9		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.286.46.F8		4.332.O., 3.330.B., 1.122.B. 5.330.B., 1.122.A., 7.330.B.	1.122.A. and 1.122.B. - Yes	Yes

10N.286.48.C5		7.329.O., 8.329.O., 2.329.O., 1.278.O., 1.329.O., 1.043.O.	7.329.O., 8.329.O., 2.329.O., 1.329.O. - Yes	No
10N.286.48.E2		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.48.E9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.A12	X			
10N.286.49.A5		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.B1		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.B11		3.330.B., 5.330.B., 7.330.B., 1.080.O., 1.043.O.	1.080.O. and 1.043.O. - Yes	Yes
10N.286.49.B4		1.007.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.105.O.	1.105.O. - Yes	Yes
10N.286.49.B7		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.B9	X			
10N.286.49.C10		1.215.A.	No	No
10N.286.49.E10		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.E3		1.178.O., 1.186.O., 1.197.A., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.273.O., 1.293.O.	1.186.O. and 1.293.O.	Yes
10N.286.49.F10		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.49.F4		3.330.B., 5.330.B., 7.330.B., 1.080.O.	No	Yes
10N.286.51.A5		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.51.B1		1.178.O., 1.197.A., 1.263.A., 1.215.A., 1.265.O., 1.293.O.	1.263.A. and 1.215.A. - Yes	No
10N.286.51.C11		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.51.E10		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.286.51.F7		3.330.B., 5.330.B., 7.330.B., 1.106.O., 1.293.O.	No	Yes
10N.286.51.F9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.52.A2		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.52.A7		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.52.C10		1.186.O., 1.106.O., 1.080.O., 1.293.O., 1.329.O., 1.043.O.	1.080.O., 1.293.O. and 1.043.O. - Yes	No
10N.286.52.C9	X			
10N.286.52.F6		1.263.B., 1.199.B., 1.265.O., 45.332.B.	1.265.O. - Yes	No
10N.286.54.A2		1.178.O., 1.197.A., 1.276.O., 1.080.O., 1.278.O.	1.276.O.	No
10N.286.54.A4	X			
10N.286.54.C11		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.54.C12		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.54.C7		1.186.O., 1.256.O., 1.273.O., 1.289.A.	1.273.O. - Yes	No
10N.286.54.E11		1.215.A., 1.265.O., 1.275.O., 40.332.C., 6.332.A., 1.293.O.	1.215.A. and 1.275.O. - Yes	No
10N.286.54.E3	X			

10N.286.54.E4		1.178.O., 1.186.O., 1.197.A., 1.263.A., 3.330.B., 5.330.B., 7.330.B., 1.275.O., 1.080.O., 1.278.O.	1.276.O. - Yes	Yes
10N.286.54.E5		8.332.A., 1.243.O., 8.332.B., 4.332.O., 1.286.O., 2.332.B., 3.330.B., 1.199.A., 5.330.B., 1.332.O., 1.199.B., 45.332.B., 7.330.B., 2.332.B., 8.332.B., 40.332.C., 42.332.A., 1.080.O., 1.329.O., 1.043.O.	1.080.O. and 1.043.O. - Yes	No
10N.286.54.E6	X			
10N.286.54.E8		1.173.O., 1.197.A., 1.287.O., 1.236.O., 1.278.O., 1.329.O.	1.173.O. and 1.197.A. - Yes	No
10N.286.54.F11		3.330.B., 1.215.A., 5.330.B., 7.330.B.	1.215.A. - Yes	Yes
10N.286.54.F2		1.197.A., 3.330.B., 5.330.B., 7.330.B.	No	Yes
10N.286.54.F4		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.54.F9		1.197.A., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.214.O., 1.276.O., 1.013.O.	1.214.O. and 1.013.O. - Yes	Yes
10N.286.55.A10		1.215.A.	No	No
10N.286.55.A11		1.215.A.	1.215.A. - Yes	No
10N.286.55.A12		1.149.O., 3.330.B., 1.204.O., 5.330.B., 7.330.B., 1.293.O.	No	Yes
10N.286.55.A3		1.253.O., 1.286.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B., 1.275.O.	No	Yes
10N.286.55.A4	X			
10N.286.55.A5		1.284.A., 7.329.O., 8.329.O., 1.287.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A., 1.293.O.	1.284.A., 1.287.O. and 1.289.A. - Yes	Yes
10N.286.55.A6		1.284.A., 7.329.O., 1.286.O., 8.329.O., 1.287.O., 3.330.B., 1.204.O., 1.263.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A., 1.214.O., 1.276.O., 1.293.O.	No	Yes
10N.286.55.A8		1.284.A., 7.329.O., 1.286.O., 8.329.O., 1.263.A., 1.287.O., 1.204.O., 1.289.A., 1.214.O., 1.276.O.	No	No
10N.286.55.B10		1.284.A., 7.329.O., 1.287.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A., 1.293.O.	1.284.A. - Yes	Yes
10N.286.55.B11	X			
10N.286.55.B12		1.197.A., 1.122.B., 1.204.O., 1.199.A., 1.263.B., 1.256.O., 1.199.B., 1.265.O., 45.332.B.	1.199.A. and 1.199.B. - Yes	No
10N.286.55.B3		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.B4		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.080.O., 1.043.O.	No	Yes
10N.286.55.B6		1.284.A., 7.329.O., 1.286.O., 8.329.O., 1.263.A., 1.287.O., 1.204.O., 3.330.B.,	No	Yes

		1.215.A., 5.330.B., 45.332.B., 7.330.B., 1.289.A., 1.214.O., 1.276.O		
10N.286.55.B7		1.284.A., 7.329.O., 1.286.O., 8.329.O., 1.263.A., 1.287.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A., 1.214.O., 1.276.O	No	Yes
10N.286.55.B8		1.284.A., 1.286.O., 1.287.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A.,	1.284.A. and 1.287.O. - Yes	No
10N.286.55.B9		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.C10		1.197.A., 1.122.B., 1.204.O., 1.199.A., 1.263.B., 1.256.O., 1.199.B., 1.265.O., 45.332.B., 8.332.B.	1.199.A. and 1.199.B. - Yes	No
10N.286.55.C3		1.243.O., 1.286.O., 1.199.A., 1.199.B., 1.080.O., 1.329.O., 1.043.O.	1.080.O. and 1.043.O.	No
10N.286.55.C4		1.286.O., 1.287.O., 1.273.O.	1.286.O. - Yes	No
10N.286.55.C7		1.284.A., 1.287.O., 3.330.B., 5.330.B., 7.330.B., 1.289.A.	1.284.A., 1.287.O. and 1.289.A.	Yes
10N.286.55.C8		1.284.A., 7.329.O., 1.286.O., 8.329.O., 1.287.O., 1.215.A., 1.289.A., 1.214.O.	1.289.A. - Yes	No
10N.286.55.E11		1.293.O.	No	No
10N.286.55.E2	X			
10N.286.55.E4	X			
10N.286.55.E6		1.253.O., 3.330.B., 5.330.B., 7.330.B., 1.293.O	1.253.O. - Yes	Yes
10N.286.55.E7		3.330.B., 1.215.A., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.E8		1.284.A., 1.287.O., 3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.289.A.	1.284.A., 1.287.O. and 1.289.A. - Yes	Yes
10N.286.55.F1		1.286.O., 8.329.O., 3.330.B., 5.330.B., 7.330.B., 1.201.B.,	1.201.B. - Yes	Yes
10N.286.55.F10		3.330.B., 1.215.A., 5.330.B., 7.330.B., 1.293.O., 1.278.O.	No	Yes
10N.286.55.F11		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.F12		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.F2		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.F3		3.330.B., 5.330.B., 7.330.B.,	No	Yes
10N.286.55.F4		3.330.B., 5.330.B., 7.330.B., 1.293.O	No	Yes
10N.286.55.F6		3.330.B., 5.330.B., 7.330.B.,	No	No
10N.286.55.F7		1.284.A., 7.329.O., 1.178.O., 1.248.O., 1.287.O., 3.330.B., 1.204.O., 5.330.B., 7.330.B., 1.273.O., 1.289.A., 1.276.O.	No	Yes

Table S 1.7: Interactions between the mutant strains of the transposon mutant library phages from the Nahant collection (Set of 76 phages)

Strain	No lysis	Lysis	Phage induction	3.330.B PCR
1G07 (wt)		3.330.B., 5.330.B., 7.330.B.	Yes	No
T 1		Temperate phage induction	Yes	Yes
T 2		Temperate phage induction	Yes	Yes
T 3	X		No	Yes
T 4	X		No	Yes
T 5		1.043.O., 1.080.O.	No	Yes
T 6		1.043.O., 1.080.O.	No	Yes
T 7		Temperate phage induction	Yes	Yes
T 8		3.330.B., 5.330.B., 7.330.B.	No	Yes
T 9		Temperate phage induction	Yes	Yes
T 10	X		No	Yes
T 11		Temperate phage induction	Yes	Yes
T 12		Temperate phage induction	Yes	No
T 13		Temperate phage induction	Yes	Yes
T 14	X		No	Yes
T 15	X		No	Yes
T 16	X		No	Yes
T 17		1.043.O., 1.080.O.	No	Yes
T 18		1.043.O., 1.080.O.	No	Yes
T19		Temperate phage induction	Yes	Yes
T 20		1.080.O.	No	Yes
T 21		1.043.O., 1.080.O.	No	Yes
T 22	X		No	Yes
T 23		3.330.B., 5.330.B., 7.330.B.	No	Yes
T 24	X		No	Yes
T 25	X		No	Yes
T 26		Temperate phage induction	Yes	Yes
T 27		1.043.O., 1.080.O.	No	Yes
T 28		Temperate phage induction	Yes	Yes
T 29	X			Yes
T 30	X			Yes
T 31	X			Yes
T 32		1.043.O., 1.080.O.	No	Yes
T 33	X		No	Yes
T 34		Temperate phage induction	Yes	Yes
T 35	X		No	Yes
T 36	X		No	Yes
T 37		Temperate phage induction	Yes	Yes
T 38		Temperate phage induction	Yes	Yes
T 39	X		No	Yes

T 40		Temperate phage induction	Yes	Yes
T 41	X		No	Yes
T 42	X		No	Yes
T 43		Temperate phage induction	Yes	Yes
T 44		Temperate phage induction	Yes	Yes
T 45		3.330.B., 5.330.B., 7.330.B.	Yes	Yes
T 46	X		No	Yes
T 47	X		No	Yes
T 48	X		No	Yes
T 49	X		No	Yes
T 50		Temperate phage induction	Yes	Yes
T 51	X		No	Yes
T 52		Temperate phage induction	Yes	Yes
T 53		3.330.B., 5.330.B., 7.330.B.	No	Yes
T 54	X		No	Yes
T 55	X		No	Yes
T 56	X		No	Yes
T 57		1.043.O., 1.080.O.	No	Yes
T 58	X		No	Yes
T 59	X		No	Yes
T 60	X		No	Yes
T 61		Temperate phage induction	Yes	Yes
T 62		Temperate phage induction	Yes	Yes
T 63	X		No	Yes
T 64	X		No	Yes
T 65	X		No	Yes
T 66				Yes
T 67	X		No	Yes
T 68		Temperate phage induction	Yes	Yes
T 69		Temperate phage induction	Yes	Yes
T 70				Yes
T 71				Yes
T 72		Temperate phage induction	Yes	Yes
T 73		Temperate phage induction	Yes	Yes
T 74	X		No	Yes
T 75	X		No	Yes
T 76	X		No	Yes
T 77	X		No	Yes
T 78	X		No	Yes
T 79	X		No	Yes
T 80	X		No	Yes
T 81		Temperate phage induction	Yes	Yes
T 82		Temperate phage induction	Yes	Yes
T 83	X		No	Yes

T 84	X		No	Yes
T 85	X		No	Yes
T 86	X		No	Yes
T 87	X		No	Yes
T 88	X		No	Yes
T 89		Temperate phage induction	Yes	Yes
T 90	X		No	Yes
T 91	X		No	Yes
T 92		Temperate phage induction	Yes	Yes
T 93	X		No	Yes
T 94	X		No	Yes
T 95	X		No	Yes
T 96	X		No	No
T 97	X		No	No
T 98	X		No	Yes
T 99	X		No	Yes
T 100	X		No	Yes
T 101	X		No	Yes
T 102	X		No	No
T 103	X		No	Yes
T 104		1.043.O., 1.080.O.	No	Yes
T 105	X		No	Yes
T 106	X		No	No
T 107		Temperate phage induction	Yes	Yes
T 108	X		No	Yes
T 109		1.043.O., 1.080.O.	No	No
T 110	X		No	Yes
T 111	X		No	No
T 112	X		No	No
T 113	X		No	Yes
T 114	X		No	Yes
T 115	X		No	No
T 116	X		No	Yes
T 116	X		No	Yes
T 117	X		No	Yes
T 118		Temperate phage induction	Yes	No
T 119	X		No	No
T 120	X		No	No
T 121	X		No	No
T 122	X		No	Yes
T 123	X		No	Yes
T 124	X		No	Yes
T 125		3.330.B., 5.330.B., 7.330.B.	No	Yes
T 126		Temperate phage induction	Yes	Yes

T 127	X		No	Yes
T 128		1.043.O., 1.080.O.	No	Yes
T 129		1.043.O., 1.080.O.	No	Yes
T 130	X		No	Yes
T 131	X		No	Yes
T 132		1.043.O., 1.080.O.	No	Yes
T 133	X		No	Yes
T 134	X		No	Yes
T 135		Temperate phage induction	Yes	Yes
T 136		1.043.O., 1.080.O.	No	Yes
T 137	X		No	No
T 138	X		No	Yes
T 139	X		No	Yes
T 140		Temperate phage induction	Yes	Yes
T 141		Temperate phage induction	Yes	No
T 142		3.330.B., 5.330.B., 7.330.B.	No	No
T 143		1.043.O., 1.080.O.	No	Yes
T 144	X		No	No
T 145	X		No	Yes
T 146	X		No	No
T 147	X		No	Yes
T 148		1.043.O., 1.080.O.	No	Yes
T 149	X		No	Yes
T 150	X		No	No
T 151	X		No	Yes
T 152	X		No	Yes
T 153	X		No	Yes
T 154		1.043.O., 1.080.O.	No	Yes
T 155	X		No	No
T 156	X		No	No
T 157	X		No	Yes
T 158		3.330.B., 5.330.B., 7.330.B.	No	Yes
T 159	X		No	Yes
T 160		Temperate phage induction	Yes	Yes
T 161	X		No	No
T 162	X		No	No
T 163	X		No	Yes
T 164	X		No	Yes
T 165		Temperate phage induction	Yes	Yes
T 166	X		No	Yes
T 167	X		No	Yes
T 168	X		No	Yes
T 169	X		No	Yes
T 170	X		No	Yes

T 171	X		No	Yes
T 172	X		No	Yes
T 173	X		No	Yes
T 174	X		No	Yes
T 175	X		No	Yes
T 176	X		No	No
T 177	X		No	Yes
T 178	X		No	Yes
T 179	X		No	Yes
T 180	X		No	No
T 181		1.043.O., 1.080.O.	No	Yes
T 182	X		No	Yes
T 183	X		No	No
T 184		1.043.O., 1.080.O.	No	Yes
T 185		Temperate phage induction	Yes	No
T 186	X		No	Yes
T 187	X		No	No
T 188	X		No	No
T 189	X		No	Yes

Table S 1.8: Annotated disrupted genes in clones from the transposon mutagenesis library of strain 10N.239.312.1G07

Clone ID	Annotation disrupted gene	contig
TML_B3	LSU rRNA	3
T 94	Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly	1
T 95	hypothetical protein CDS	3
T 96	TRAP type uncharacterized transporter system, fused permease component	1
T 97	Not annotated	/
T 98	Putative cell envelope opacity-associated protein A	3
T 99	Not annotated	/
T 100	DNA polymerase III beta subunit	2
T 101	general secretion pathway protein M	1
T 102	mobile element protein	1
T 103	SSU rRNA	1
T 104	Glutathione reductase	1
T 105	Not annotated	/
T 106	Not annotated	/
T 107	TRAP transporter solute receptor, TAXI family precursor	1

T 108	TRAP type uncharacterized transporter system, fused permease component	1
T 109	TRAP type uncharacterized transporter system, fused permease component	1
T 110	hypothetical protein CDS	1
T 111	End of Redox-sensitive transcriptional activator Sox CDS, beginning of hypothetical protein CDS	1
T 112	Putative preQ0 transporter YhhQ	1
T 113	Not annotated	/
T 114	ATPase superfamily protein YifB/ComM, associated with DNA recombination	1
T 115	Aspartate carbomoyltransferase regulatory chain (PyrI)	3
T 116	Retron-type RNA-directed DANN polymerase	2
T 117	5-methyltetrahydrofolate-homocysteine - methyltransferase	1
T 118	Not annotated	/
T 119	Not annotated	/
T 120	transposase and inactivated derivative	1
T 121	SSU rRNA	1
T 122	Not annotated	/
T 123	Not annotated	/
T 124	SSU rRNA	1
T 125	Inner membrane protein YihY, formerly thought to be Rnase BN	1
T 126	site-specific recombinase, phage integrase family CDS	3
T 127	transcription accessory protein	1
T 128	hypothetical protein CDS	3
T 129	Not annotated	/
T 130	Not annotated	/
T 131	Trk potassium uptake system protein TrkH	1
T 132	Not annotated	/
T 133	tRNA-Glu-TTC; tRNA-Lys-TTT; tRNA-Val-TAC	1
T 134	SSU rRNA	1
T 135	LSU rRNA	3
T 136	2',3'-cyclic-nucleotide 2'-phosphodiesterase	3
T 137	LSU rRNA	1
T 138	Not annotated	/
T 139	Not annotated	/
T 140	LSU rRNA	5
T 141	putative Na/H antiporter	1
T 142	tRNA-Gln-TTG; tRNA-Leu-TAG; tRNA-Met-CAT	1
T 143	Trk potassium uptake system protein TrkH	1
T 144	tRNA-Gln-TTG	1
T 145	Oxidoreductase, short-chain dehydrogenase/reductase family	2
T 146	Gamma-glutamyltranspeptidase	1
T 147	hypothetical protein CDS	3
T 148	OMPH PHOPR Porin-like protein H precursor CDS	3
T 149	site-specific recombinase, phage integrase family CDS	3
T 150	Oxaloacetate decarboxylase pump, beta chain	3

T 151	Protein of unknown function - DUF484 CDS	5
T 152	SSU rRNA	5
T 153	Guanylate kinase	1
T 154	SSU rRNA	1
T 155	general secretion pathway protein N	1
T 156	hypothetical protein CDS	3
T 157	Shikimate 5-dehydrogenase I alpha	1
T 158	LSU rRNA	1
T 159	Not annotated	/
T 160	LSU rRNA	3
T 161	intergenic region between YefM protein and Nucleotidyltransferase	1
T 162	Sodium:alanine symporter family protein	1
T 163	diguanylate cyclase/ phosphodiesterase (GGDEF& EAL domains) with PAS/PAC sensor	1
T 164	Not annotated	/
T 165	LSU rRNA	1
T 166	Type IV pilus biogenesis protein PilP	3
T 167	LSU ribosomal protein L14p	3
T 168	Not annotated	/
T 169	general secretion pathway protein N	1
T 170	LSU rRNA	2
T 171	Inner membrane protein YihY, formerly thought to be Rnase BN	1
T 172	Antitoxin of toxin-antitoxin stability system, StbD family	1
T 173	Phosphoenolpyruvate-protein phosphotransferase of PTS system	3
T 174	hypothetical protein CDS	1
T 175	Cytosol aminopeptidase PepA	3
T 176	Nucleoside-diphosphate sugar epimerase/dehydratase	1
T 177	Translation elongation factor G paralog	3
T 178	Not annotated	/
T 179	Oxidoreductase, short-chain dehydrogenase/reductase family	2
T 180	Cytosol aminopeptidase PepA	3
T 181	Oligopeptidase A	1
T 182	Prolyl endopeptidase	2
T 183	GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 6.3.5.2)	1
T 184	Not annotated	/
T 185	LSU rRNA	2
T 186	hypothetical protein CDS	3
T 187	Retron-type RNA-directed DNA polymerase	2
T 188	cell division integral membrane protein, YggT and half-length relatives	3
T 189	Retron-type RNA-directed DNA polymerase	2

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