Microbiology and Infectious Disease

Prophage regulation of *Shewanella fidelis* 3313 motility and biofilm formation: implications for gut colonization dynamics in *Ciona robusta*

Reviewed Preprint
v1 • January 6, 2025
Not revised

Ojas Natarajan, Susanne L Gibboney, Morgan N Young, Shen Jean Lim, Felicia Nguyen, Natalia Pluta, Celine GF Atkinson, Assunta Liberti, Eric D Kees, Brittany A Leigh, Mya Breitbart, Jeffrey A Gralnick, Larry J Dishaw

Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States • College of Marine Science, University of South Florida, Tampa FL, United States • Biomedical Sciences Program, University of South Florida, Tampa FL, United States • Department of Cell Biology, Microbiology, and Molecular Biology, University of South Florida, Tampa FL, United States • Stazione Zoologica Anton Dohrn, Naples, Italy • BioTechnology Institute, University of Minnesota, St. Paul, MN, United States • Plant and Microbial Biology, University of Minnesota, St. Paul, MN, United States

eLife Assessment

This **valuable** study presents findings linking prophage carriage to lifestyle regulation in the marine bacterium Shewanella fidelis, with potential implications for niche occupation within a host (Ciona robusta) and mediation of host immune responses. The study leverages a unique animal model system that offers distinct advantages in identifying select phenotypes to present generally **solid** evidence that supports findings relating to the impact of a prophage on host-microbe interaction. Understanding the role of integrated lysogenic phages in bacterial fitness, both within a host and in the environment, is a significant concept in bacterial eco-physiology, potentially contributing to the success of certain strains.

https://doi.org/10.7554/eLife.103107.1.sa3

Abstract

Lysogens, bacteria that contain viruses (prophages) integrated into their genomes, are abundant in the gut of animals. Prophages often influence bacterial traits; however, the influence of prophages on the gut microbiota-host immune axis in animals remains poorly understood.Here, we investigate the influence of the prophage SfPat on *Shewanella fidelis* 3313, a persistent member of the gut microbiome of the model marine tunicate, *Ciona robusta*. Establishment of a SfPat deletion mutant (ΔSfPat) reveals the influence of this prophage on bacterial physiology *in vitro* and during colonization of the *Ciona* gut. *In vitro*, deletion of SfPat reduces *S. fidelis* 3313 motility and swimming while increasing biofilm formation. To understand the *in vivo* impact of these prophage-induced changes in bacterial traits, we exposed metamorphic stage 4 *Ciona* juveniles to wildtype (WT) and ΔSfPat strains.

During colonization, ΔSfPat localizes to distinct areas of the gut compared to the WT strain. We tested the differential expression of various regulators of cyclic-di-GMP, a secondary signaling molecule known to mediate biofilm formation and motility. The pdeB gene, which encodes a bacterial phosphodiesterase known to influence biofilm formation and motility by degrading cyclic-di-GMP, is upregulated in the WT strain but not in ΔSfPat when examined *in vivo*. Expression of the *Ciona* gut immune effector, VCBP-C, is enhanced during colonization by ΔSfPat compared to the WT strain; however, VCBP-C binding to the WT strain does not promote the excision of SfPat in an SOS-dependent pathway. Our findings suggest that SfPat influences host perception of this important colonizing commensal and highlights the significance of investigating interkingdom dynamics between prophages, bacteria, and their animal hosts to better understand the gut microbiota-host immune axis.

Introduction

An epithelial layer with a mucus-rich surface lines the gastrointestinal tract (or gut) of animals. This dynamic environment is a primary interface between host immunity, symbiotic microbes, and dietary antigens Li et al. (2015); Johansson et al. (2011). During colonization of the gut, bacteria encounter physical, chemical, and biological forces. They must compete for nutrients and niche space while managing the stress of digestive enzymes and host immune factors Duncan et al. (2021); Harrington et al. (2021); Hornung et al. (2018); Moran et al. (2019). Gut-colonizing bacteria also encounter bacteriophages (phages), or viruses that infect bacteria Mirzaei and Maurice (2017); e.g., over 10^{12} viruses have been estimated in the human gut Shkoporov and Hill (2019).

Phages display both lytic and temperate lifestyles. While the former impacts bacterial community dynamics through lysis, the effect of temperate phages on bacterial communities, especially those associated with animals, remains poorly understood. Conventionally, temperate phages integrate into bacterial genomes as prophages and remain 'dormant' until an external trigger activates them to enter the lytic cycle Lwoff (1953); Boling et al. (2020); Howard-Varona et al. (2017); these bacteria are considered 'lysogenized' and referred to as lysogens Lwoff (1953); Howard-Varona et al. (2017). Prophages often encode accessory genes that can influence bacterial traits and behaviors Mills et al. (2013). These genes can encode virulence factors, antibiotic resistance genes, and those that provide superinfection exclusion, thereby protecting their bacterial hosts from infections by related phages Bondy-Denomy and Davidson (2014). Based on the site of integration, prophages can also impact the expression of bacterial genes Aziz et al. (2005). Bacterial lysogens exist in every environment Jiang and Paul (1998); Silveira et al. (2021); Leigh et al. (2018) and are particularly prevalent in the microbiomes of diverse animals Kim and Bae (2018); Shkoporov and Hill (2019).

Prophage induction results in bacterial lysis and can be mediated by various stressors, including antibiotics and inflammatory processes Allen et al. (2011); Banks et al. (2003); Diard et al. (2017); Fang et al. (2017); Garcia-Russell et al. (2009); Maiques et al. (2006); Nanda et al. (2015); Wang et al. (2010); Zhang et al. (2000). Because prophages can influence phenotypes of their bacterial hosts such as biofilm formation Nanda et al. (2015), understanding the impact of lysogens in animal microbiomes is becoming a research priority Fortier and Sekulovic (2013); Hu et al. (2021); Lin et al. (1999). In the gut, biofilms that associate with host mucus may benefit the host by enhancing epithelial barriers against pathogenic invasion Swidsinski et al. (2007). Integration of prophages into bacterial genomes may impart functional changes that could be important in surface colonization. For example, in *E. coli* K-12, integrating the Rac prophage into a tRNA thioltransferase region disrupts biofilm functions Liu et al. (2015); deleting this prophage decreases resistance to antibiotics, acids, and oxidative stress. Some of

these traits may be affected by prophage-specific genes Wang et al. (2010). Prophages have also been shown to influence biofilm life cycles in Pseudomonas aeruginosa Gödeke et al. (2011); Rice et al. (2009).

Lysogenized *Shewanella* species colonize the gut of *Ciona robusta*, an ascidian collected in Southern California waters ***Dishaw et al. (2014b)***; Leigh et al. (2017) and referred to here as *Ciona*. Tu-nicates like *Ciona* are a subphylum (Tunicata) of chordates that are well-established invertebrate model systems for studies of animal development Chiba et al. (2004); Davidson (2007); Liu et al. (2006) and are now increasingly leveraged for gut immune and microbiome studies Liberti et al. (2021). Armed with only innate immunity, *Ciona* maintains stable gut bacterial and viral communities ***Dishaw et al. (2014b)***; Leigh et al. (2018) despite continuously filtering microbe-rich seawater. Previous efforts to define gut immunity in *Ciona* revealed the presence of a secreted immune effector, the variable immunoglobulin (V-Ig) domain-containing chitin-binding protein, or VCBP, that likely plays important roles in shaping the ecology of the gut microbiome by binding bacteria and fungi (as well as chitin-rich mucus) on opposing functional domains Dishaw et al. (2011); Liberti et al. (2019). VCBP-C is one of the best-studied VCBPs expressed in the stomach and intestines of *Ciona*, shown to bind bacteria *in vitro* and in the gut lumen Dishaw et al. (2016, 2011). Based on various *in vitro* and *in vivo* observations, it was proposed previously that VCBPs likely modulate bacterial settlement and/or biofilm formation Dishaw et al. (2016); Liberti et al. (2019, 2021). The potential influence of soluble immune effectors on host-bacterial-viral interactions is particularly interesting. However, the possibility that prophages may influence interactions between bacteria and secreted immune effectors like VCBPs remains to be explored.

Shewanella fidelis strain 3313 was isolated previously from the gut of *Ciona* and found to contain two inducible prophages, SfPat and SfMu Leigh et al. (2017). Furthermore, *in vitro* experiments demonstrated enhanced biofilm formation in *S. fidelis* 3313 in the presence of extracellular DNA (eDNA) that may originate from lytic phage activity Leigh et al. (2017). Other *Shewanella* species have previously demonstrated a link between phage-mediated lysis and biofilm formation Gödeke et al. (2011). For example, in *S. oneidensis* strain MR-1, Mu, and Lambda prophages enhance biofilm formation via eDNA released during prophage-induced lysis, with genomic DNA likely serving as a scaffold for biofilms Gödeke et al. (2011). Similarly, the P2 prophage of *S. putrefaciens* strain W3-18-1 influences biofilm formation via spontaneous induction at low frequencies, resulting in cell lysis and contributing eDNA that can mediate biofilm formation Liu et al. (2019).

Here, we set out to isolate and characterize the influence of the prophage, SfPat, on its host, *S. fidelis* 3313. Since the last description Leigh et al. (2017), the genome of *S. fidelis* 3313 was improved by combining long-read and short-read sequencing, which resulted in improved resolution of the genomic landscape within and around the prophages. A homologous recombination-based deletion strategy was designed to generate a deletion mutant (i.e., knockout) of SfPat. We report that deletion of SfPat results in reduced bacterial motility and increased biofilm formation *in vitro*. These changes in bacterial traits and behaviors are associated with the expression of genes regulating important signaling molecules and a corresponding impact on host immune gene expression during gut colonization in *Ciona* juveniles. Gut colonization experiments in laboratory-reared *Ciona* juveniles comparing wild-type (WT) and SfPat prophage knockout (ΔSfPat) mutant strains demonstrate that SfPat influences gut colonization outcomes, e.g., niche preference, and these effects are influenced by host gene expression The results reported herein reflect complex inter-kingdom interactions among prophages, bacterial hosts, and animal immune systems.

Results

Sequence verification of prophage deletion mutant strains

Colony PCR and single primer extension sequencing were both used to validate the prophage deletion, using primers EDK81/82 for SfPat (**Table 2**)(**Figure 1 a**). All recovered amplicon sizes were consistent with the predictions for SfPat deletion (**Figure 1 b**). The SfPat deletion (ΔSfPat) strain was named JG3862 (**Table 1**). Genome sequencing of the deletion mutant strain did not reveal the significant introduction of additional mutations or DNA modifications (**Figure 1 b**). The WT and Δ SfPat strains were then used for *in vitro* and *in vivo* experiments to understand the potential role of prophages in shaping *S. fidelis* 3313 colonization dynamics in the gut of *Ciona*.

Prophage deletion modulates biofilm formation and motility in *S. fidelis* 3313 *in vitro*

Deletion of SfPat from *S. fidelis* 3313 contributed to an overall increase in biofilm formation as quantified by crystal violet staining by at least 14% compared to WT strains (**Figure 2 a**). Conventionally, to form a biofilm, bacteria will settle and initiate stationary growth dynamics Watnick and Kolter (2000). We studied bacterial swimming on simple semi-solid media to determine if the prophages influenced motility and chemotaxis in *S. fidelis* 3313. Bacterial motility was measured by the spread diameter from a primary inoculation point after overnight incubation (**Figure 2 b**). The WT strain demonstrated a mean diameter of 8.21 mm, while ΔSfPat resulted in a decreased mean diameter of 4.04 mm, demonstrating reduced motility and increased biofilm formation.

The influence of prophages on *Ciona* gut colonization by *S. fidelis* 3313

Since swimming and biofilm formation behaviors also depend on quorum sensing mechanisms, changes in the expression levels of four genes regulating cyclic-di-GMP (*pleD*, *pilZ*, chitinase and *pdeB*) were measured by qPCR between WT and Δ SfPat. We found no significant change in the expression of these genes in bacteria recovered from 24-hour biofilms (*in vitro*) (**Figure 2 c** and Sup fig s1a). However, when these bacteria were introduced to metamorphic stage 4 (MS4) *Ciona* for 24 hours, the RT-qPCR revealed significant changes in the expression of pdeB (**Figure 2 c** and Sup fig s1a). The bacterial gene, *pdeB*, encodes a phosphodiesterase enzyme that degrades c-di-GMP and can serve as a negative regulator of motility, a positive regulator of biofilm formation, and a quorum sensing signal Chao et al. (2013). Colonizing WT *S. fidelis* 3313 demonstrated higher *pdeB* expression than the ΔSfPat mutant strain (**Figure 2c**).

Swimming and biofilm formation often facilitate bacterial colonization of a host. We investigated whether prophages could impact the ability of *S. fidelis* 3313 to colonize the *Ciona* gut. Colonization assays were performed on MS4 *Ciona* juveniles by exposing animals to either WT or ΔSfPat strains, repeating the experiments six times to account for diverse genetic backgrounds (**Figure 3 a** and **b**), i.e., using gametes from distinct outbred adults. After exposure to the bacterial strains, retention was estimated by recovering bacteria from animals and quantifying colony-forming units (cfu) at different time points. The ΔSfPat strain revealed a statistically insignificant 1.3-to-1.5-fold change in retention compared to the WT strain after 1 hour of bacterial exposure, a time point that mimics initial colonization (**Figure 3 a**). However, after 24 hours of exposure, WT was over two-fold retained in the gut than the ΔSfPat strain($p<0.05$) (**Figure 3 b**).

Table 1.

All *S. fidelis* 3313 strains are submitted under the BioProject *PRJNA 90327* on NCBI, Accession: SAMN31793880 ID:31793880

Organisms	Phenotype	Biosamples
JG4066	WT	SAMN317993881
JG3862	ΔSfPat	SAMN317993883

Table 2.

Primer sequences on S. flidelis 3313 used for generating Δ SfPat deletion suicide vector and for deletion verification

Primer ID	Sequence (5'-3')
EDK77	AAATGGATCCCGATCAGCCTGCTAGTTTATT
EDK78	ACGGAATAGGTTGAATGCGACTCAGGC
EDK79	TCGCATTCAACCTATTCCGTCATGTTTAGCC
EDK80	ACATGAGCTCGATGCAGATAAAGAGCCGTAAA
EDK81	GTTTATTTTGTGGCAATCGCA
EDK82	GGTAGCAGTGCTTAAACGAT

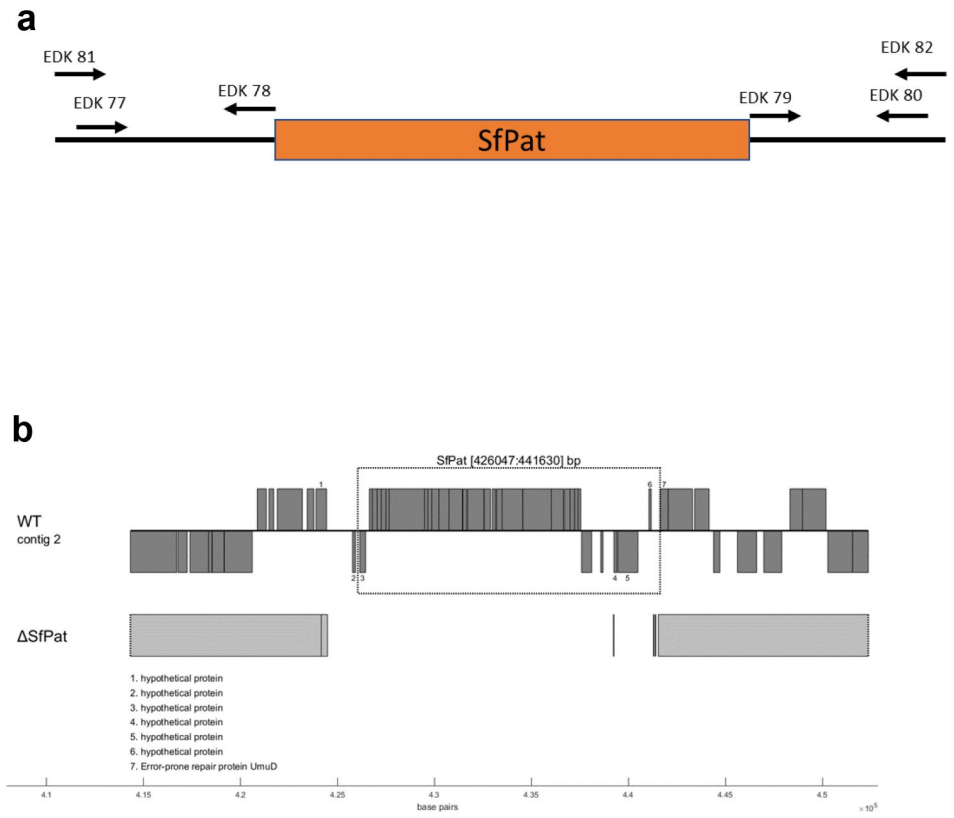

Figure 1.

General prophage deletion scheme. (a) location of upstream, downstream and flanking primers used in the deletion of SfPat, (b) Deletion of SfPat from *S. fidelis* 3313 identified after assembling Illumina sequenced genomes and mapping on to the improved WT genome.

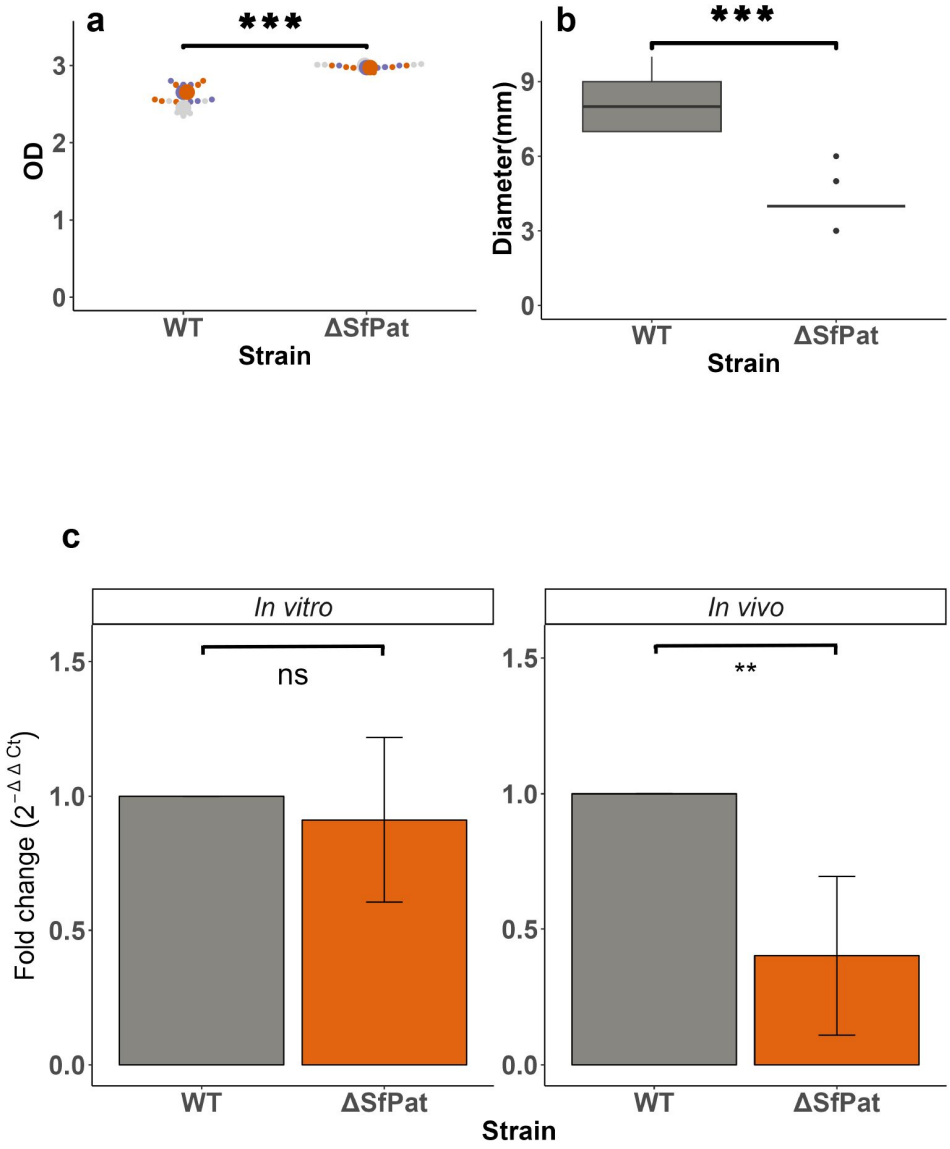

Figure 2.

Effects of prophages on biofilm and swimming in *S. fidelis* 3313. (a) Effect of prophages on *in vitro* biofilm formation over 24 hours quantified with crystal violet assay (n=3), (b) role of prophages in swimming (or chemotaxis) quantified as the diameter of spread on soft agar after 24-hours (n=6), and (c) fold-change of *pdeB* (with *Rho* as internal control) from 24-hour biofilm (*in vitro*) (n=4) and 24-hour *in vivo* (n=4). (*= p-value<0.05, **= p-value<0.01).

Figure 2—figure supplement 1. Supplemental Figure: (a) Cyclic di GMP regulators expression in WT and ΔSfPat *in vitro* after 24 hours of exposure (n=4), (b) Cyclic di GMP regulators expression in WT and ΔSfPat *in vivo* of *Ciona* MS4 after 24 hours of exposure (n=4).

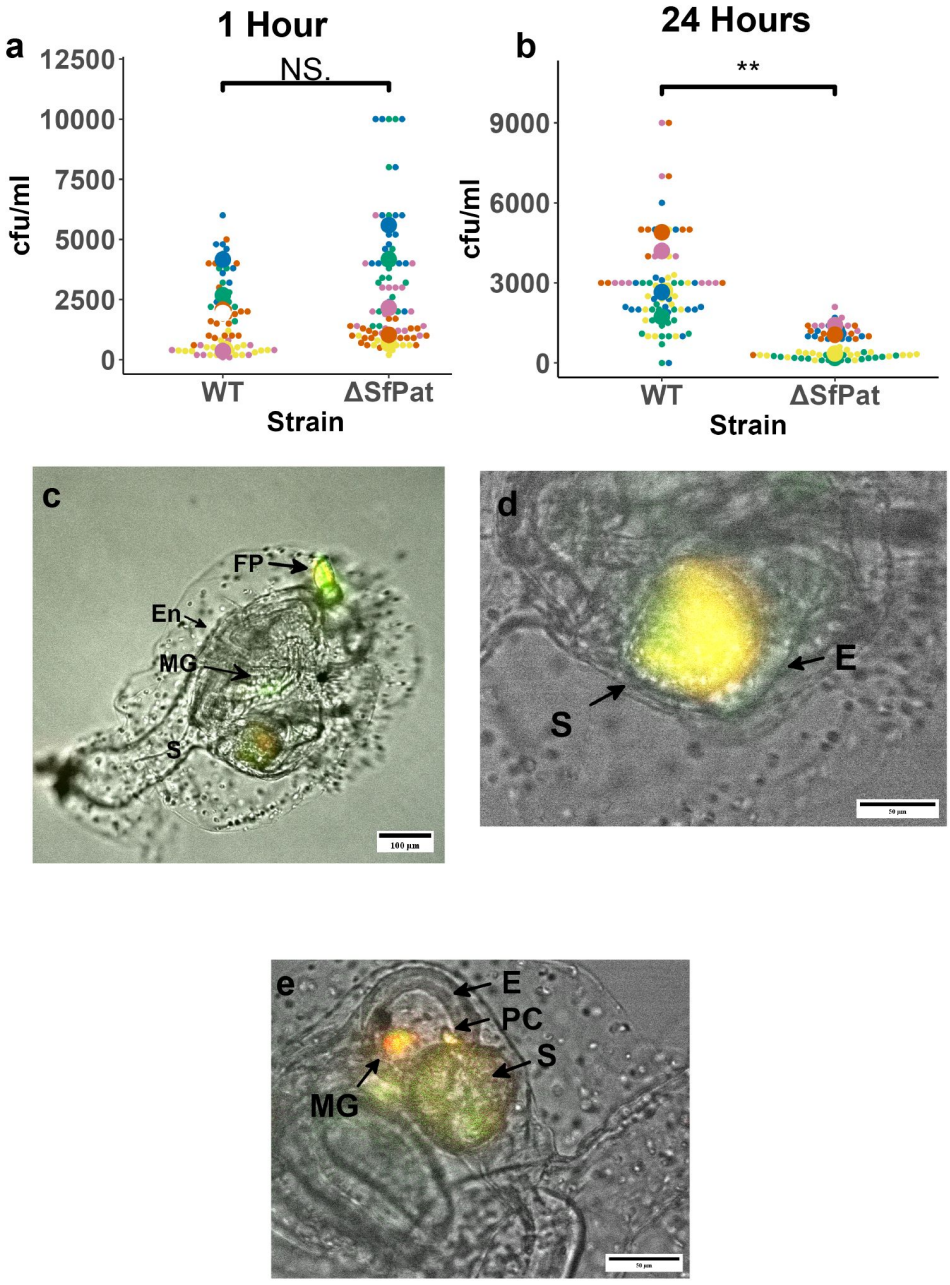

Figure 3.

The influence of SfPat prophage on gut colonization in *Ciona*. (a) colonization of MS4 juvenile gut by WT and ΔSfPat after one hour of exposure to strains (n=3). (b) after 24 hours of exposure (n=6). MS4 juveniles reveal differential colonization of WT and ΔSfPat after one hour of exposure (c-e), where WT strain stained with BacLight Green (c) is seen localized in the lower esophagus to anterior stomach, while the ΔSfPat deletion strain, stained with BacLight Red, localized to the hindgut, while (d) the WT stained with BacLight Red is seen localized mostly as a fecal pellet in the center of the stomach while ΔSfPat stained in the same way prefers to adhere to the stomach folds. The WT strain, stained in BacLight Red (e), also prefers to localize within the pyloric cecum (En = Endostyle, E= Esophagus, S= Stomach, MG= Mid Gut, HG = Hind Gut, PC = Pyloric Cecum)
Figure 3—figure supplement 1. Supplemental Figure 3: WT stained in BacLight Red exposed to Ciona MS4 for one hour c) ΔSfPat stained in BacLight Red exposed to Ciona MS4 for one hour. d) ΔfPat stained in BacLight Green exposed to *Ciona* MS4 for one hour

To visualize the localization of WT and ΔSfPat mutant strains in the gut, MS4 Ciona juveniles were exposed for one hour to BacLight Green-stained WT and BacLight Red-stained ΔSfPat strain variants and vice versa (**Figure 3 c-e**). The one-hour time point reflects changes in the initial colo-nization of juveniles. These experiments revealed differential localization to the stomach epithelial folds by the WT and ΔSfPat mutant strains. The WT strain typically prefers to occupy the pyloric cecum and the posterior portion of the esophagus and entrance into the stomach (**Figure 3d** and **e**, Supp fig s3a and s3b). The ΔSfPat was seen to colonize the walls of the stomach during co-colonization (**Figure 3d**). The ΔSfPat mutant was also found to colonize the stomach and intestines and less of the esophagus (Supp fig s3 c and s3d). These studies reveal spatial and temporal differences in colonization by differentially lysogenized strains of *S. fidelis* 3313.

Host immune discrimination and impact on lysogenized bacteria

Host immunity also plays an important role in shaping gut homeostasis. Distinct microbes and their antigens and/or metabolites can elicit host immune responses (Rooks and Garrett (2016)). To determine if the *Ciona* immune system discriminates among *S. fidelis* 3313 strains differing only in the presence or absence of the SfPat prophage, we examined the expression patterns of a secreted immune effector, VCBP-C, among juvenile MS4 during intestinal colonization. Under normal healthy conditions, VCBP-C is expressed and secreted by the gut epithelium and can bind (and opsonize) bacteria within the gut lumen (Dishaw et al. (2011)) and influence biofilms *in vitro* (Dishaw et al. (2016)). After one hour of exposure to the *S. fidelis* 3313 WT and mutant strains, changes were detected in the expression of VCBP-C. Up-regulation of VCBP-C was noted when juveniles were exposed to ΔSfPat mutant strains of *S. fidelis* 3313, compared to the WT strain (**Figure 4 a**) by qPCR($p<0.05$). Expression of other innate immune genes were evaluated after 24hrs of exposure to the strains; however, statistically significant responses were likely obscured by host genetic diversity. (**Figure 4 b**).

Since the presence of SfPat influences host VCBP-C responses, we investigated whether the binding of VCBP-C to bacterial cell surfaces could influence prophage gene expression. *S. fidelis* 3313 was grown in MA in vitro for 24 hours in the presence or absence of 50μg/ml of recombinant VCBP-C(Dishaw et al. (2016)). RNA was extracted from the biofilms, and gene expression among SfPat open reading frames was monitored, as well as the SOS response regulators, *lexA* and *recA*, in *S. fidelis* 3313. Interaction of VCBP-C with the WT strain was found to suppress the expression of the structural phage protein P5 of SfPat (**Figure 5**). It was noted that VCBP-C did not significantly alter the expression of *lexA* and *recA*, indicators of the SOS pathway (**Figure 5**). This reveals that VCBP-C binding to the surface of the *S. fidelis* 3313 strain may not influence prophage structural genes via conventional SOS responses.

Discussion

In this report, we utilize a phage-deletion strategy to study the influence of a prophage (SfPat) on a gut symbiont (*S. fidelis* 3313) of the model invertebrate, *Ciona robusta*. Deletion of SfPat prophage from *S. fidelis* 3313 revealed phage-mediated disruption of colonization dynamics. We find that the SfPat prophage increases swimming behavior while reducing biofilm formation in the WT. These different bacterial phenotypes influence host immune responses in a manner consistent with influences on gut colonization dynamics. Our identification of a prophage that interferes with biofilm formation in a *Shewanella* strain contrasts other reports, which show that presence of prophages helps in biofilm formation by lysis and subsequent eDNA in the biofilms. (Gödeke et al. (2011); Liu et al. (2019)). Our study is the first to implicate phage-included change in motility for *Shewanella* spp, and it indicates that prophages can impact their hosts by modulating traits through diverse mechanisms. For example, some prophages have also been shown to also influence motility in *Pseudomonas aeruginosa* (Tsao et al. (2018)).

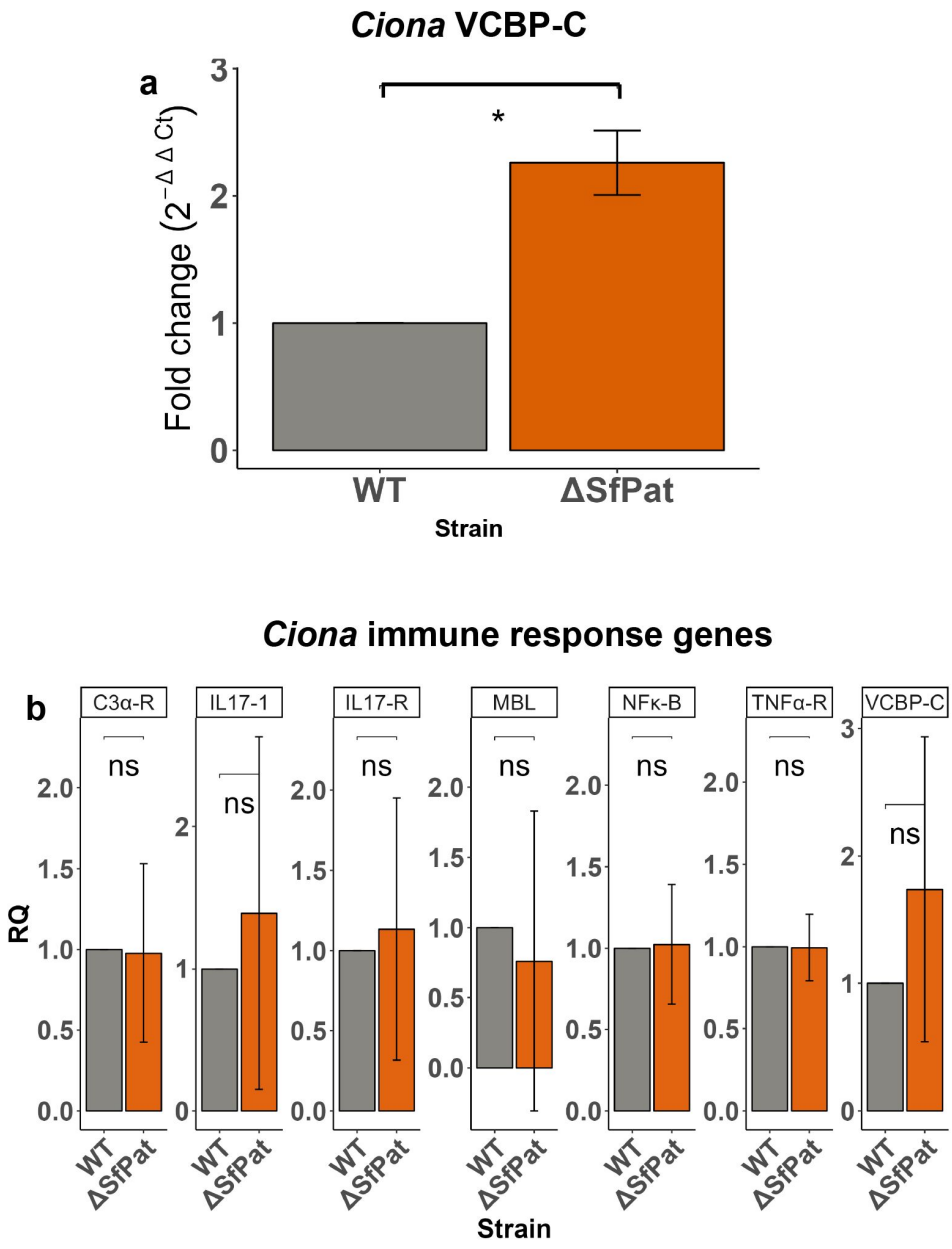

Figure 4.

The influence of prophages on host gene expression. (a) VCBP-C gene expression in MS4 juveniles after one hour of exposure to *S. fidelis* 3313 strains (n=4), (b) Survey of additional innate immune gene expression in MS4 juveniles after 24-hour exposure to WT or ΔSfPat mutant strains (n=3). Actin is the internal control. (*= p-value<0.05, **= p-value<0.01.).

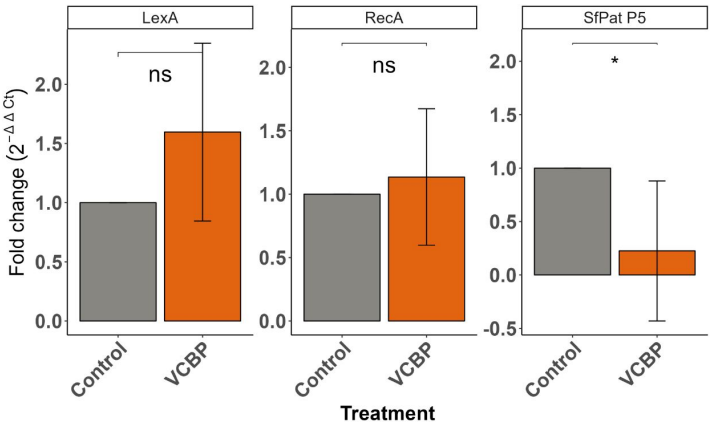

Figure 5.

Lysogen gene expression in response to host immune effector binding. Gene expression of SfPat structural protein p5, *recA* and *lexA* of WT strain grown as a 24-hour biofilm while exposed to 50 µg/ml VCBP-C. Rho is the internal control (n=4). (*= p-value<0.05).

Figure 5—figure supplement 1. Supplemental Figure 2: Rho is the most stable gene across strains when tested in vitro (n=3)

SfPat in *S. fidelis* 3313 appears to have a variable influence on bacterial retention in the gut of *Ciona*. As feeding is initiated in MS4 *Ciona* juveniles, food (or bacteria in the environment, natural or artificially introduced) accumulates in the gastrointestinal tract and on average takes about 45 minutes to begin exiting the anus and atrial siphon as fecal pellets. Thus, we monitored and compared transit and retention of introduced bacteria in the gut of MS4 juveniles at one and 24 hrs after introduction. SfPat deletion reveals a prophage-mediated influence on gut localization and retention. For example, within one hour of exposure, fecal pellets begin to form in the stomach that are enriched for the WT *S. fidelis* 3313; however, the WT strain then appears to be retained in the posterior portion of the esophagus (just before the entrance into the stomach) as well as in the pyloric cecum (which is a small outpouching just ventral and posterior to the stomach). However, the ΔSfPat mutant strain appears to adhere and colonize the stomach folds and the intestines and not the esophagus. The overall retention of the two strains did not vary significantly within one hour of colonization. However, after 24hrs, the retention of the WT strain was significantly greater than that of ΔSfPat despite the continued feeding behavior of the MS4 juveniles. The increase in pdeB activity of the WT *in vivo* (**Figure 5**) might indicate that the secondary messenger, cyclic di GMP, may be degraded in the WT, leading to increased biofilm formation and reduced motility(Jenal and Malone (2006)). Thus, the presence of SfPat influences niche preference and retention.

In addition to host genetics obscuring the influence of phages on colonization of the gut, other biophysical factors that include host immune effectors play crucial and often silent roles in influencing bacterial settlement dynamics. For example, human secretory immunoglobulin A (SIgA) has been shown to enhance and often favor settlement of bacteria both *in vitro* and *in vivo* (Bollinger et al. (2006); Thomas and Parker (2010); Pratt and Kolter (1998); Donaldson et al. (2018)), raising a basic question as to whether this phenomenon is more widespread among other secretory immune effectors present in mucosal environments of animals (***Dishaw et al. (2014a)***). We speculate that while prophages likely impact the behavior of lysogenized bacteria in ways that can influence colonization dynamics, interaction with VCBP-C on the mucosal surface of the *Ciona* gut likely further influences settlement behaviors (Dishaw et al. (2016, 2014a)). Importantly, we show here that the influence of the SfPat prophage on bacterial physiology leads to a reduced expression of *Ciona* VCBP-C in the first hours of colonization (an indicator of initial contact of bacteria to a juvenile gut). It remains to be shown if prophages stimulate the production of a bacterial metabolite with immunomodulatory properties or if the host immune system responds to differences in bacterial behaviors or traits, as suggested in the ΔSfPat deletion mutant.

Metagenomic sequencing of gut microbes from healthy humans has revealed that temperate lifestyles are prevalent among phages from these ecosystems (Minot et al. (2011, 2013); Reyes et al. (2010)), an observation also made in the *Ciona* gut (Leigh et al. (2018)). Various environmental triggers, such as UV light and mutagenic agents like mitomycin C, have been shown to induce a switch from the temperate to lytic cycle via the SOS response, a cell-wide response to DNA damage that can promote survival (Weinbauer and Suttle (1999)). Since, VCBP-C is an immune molecule in the gut that can interact with bacteria, it could influence prophage induction. However, we find that VCBP-C binding on the surface of WT *S. fidelis* 3313 leads to a reduction in the expression of an important SfPat structural protein P5, suggesting a limitation in SfPat induction in the presence of VCBP-C. No significant changes in lexA/recA expression were observed upon VCBP-C exposure/binding, suggesting a lack of SOS response when exposed to this immune effector. The various mechanisms by which prophages shape colonization behaviors among gut bacteria of animals remain unclear. While the data reported here are only based on one bacterial strain that colonizes the *Ciona* gut, we find that WT *S. fidelis* colonize the gut with reduced activation of VCBP-C gene expression compared to ΔSfPat, a trait that may be important in shaping colonization outcomes. We speculate that these observations are more widely applicable since lysogens are so abundant in animal microbiomes. Under normal conditions, VCBP-C protein is present in copious amounts and tethered to chitin-rich mucus lining the gut, as revealed by immunohisto-chemical staining (Dishaw et al. (2016)). Therefore, overexpression of VCBP-C is

not necessarily helpful, and can correspond to the induction of additional inflammatory responses, including an overproduction of mucus. Thus, regulation of the production of additional VCBP-C likely serves important roles influencing colonization dynamics.

Since colonization of animal mucosal surfaces is an ancient process (***Dishaw et al. (2014b)***), prophages and their integration into bacterial genomes have likely evolved to provide fitness benefits in often challenging environments like the gut lumen. Determining the role of animal immunity and prophages in these exchanges is of broad interest. Immune effectors like VCBPs, which undoubtedly possess broad specificities, can bind a range of bacterial hosts; however, it remains to be shown if they bind lysogenized bacteria with different affinities than their prophage-free counterparts. Prophages can also be induced to generate lytic particles that can influence gut microbiome structure, serving as an indirect form of protection for the host Wang et al. (2010); Barr et al. (2013). Prophages can also contribute to the transfer of virulence factors (Nanda et al. (2015); Wagner and Waldor (2002)). Retention of lysogens may be preferred if the prophages provide competitive fitness and retention in the gut. Since lysogens are integral in animal development, immunity, and metabolism(Fraune and Bosch (2010)), there is a transkingdom interplay required for survival, a snapshot of which is shown here.

Methods and Materials

Culture and growth conditions

S. fidelis 3313 used in this study was originally isolated from the gut of *Ciona robusta* obtained from Mission Bay, CA, USA, as previously described Leigh et al. (2017). The bacterium was cultured using Difco marine agar 2216 (MA) (Fisher Scientific, Hampton, NH) and marine broth (MB) at room temperature. Subsequent genetic manipulations were performed on strains grown in LB/MB, which consists of a mixture of 75% LB (Lysogeny Broth, Fisher Scientific, Hampton, NH) and 25% MB. Strains are listed in **Table 1**.

Prophage deletion

SfPat was targeted for deletion from *S. fidelis* 3313 using homologous recombination methods adapted from Saltikov and Newman (2003) to produce knockout mutant strains. First, a pSMV3 suicide vector Saltikov and Newman (2003) was designed with 700 bp regions corresponding to the upstream and downstream sequence of the prophage (**Table 2**). These flanking regions were amplified and ligated using overlap extension PCR, then directionally inserted into the vector with the restriction enzymes BamHI and SacI (**Table 3**) ***Bryksin (2010)***. Plasmid conjugation was then performed by inoculating a colony of *S. fidelis* 3313 into a culture of *E. coli* containing the desired suicide vector on an LB/MB agar plate for two hours. Illumina sequencing (MiGS, University of Pittsburgh) confirmed the deletion of SfPat and the evaluation of any additional genetic changes or mutations (Figure s1a).

S. fidelis crystal violet biofilm assay

WT and ΔSfPat strains were cultured in MB overnight at RT and then diluted to 10^7 cfu/ml in MB. The cultures were brought to a 2 ml final volume of MB in 12-well dishes and incubated at RT for 24 hours to examine biofilm development. Each variable was tested in technical duplicate. Biofilms were quantified by crystal violet staining as previously described Liberti et al. (2022). Briefly, supernatants were aspirated after 24-hour incubation, and the biofilms were dried and stained with 0.1% crystal violet for 10 mins. The stained biofilms were then gently washed with deionized water, and the amount of biofilm produced was quantified as the intensity of the stain (oD_{570}) after biofilm bound crystal violet was extracted from the biofilm with 30% acetic acid. All biofilm assays were performed at least in triplicates.

Plasmids	Genotype	Source/ Reference
UQ950	*E. coli* DH5α λ(pir) host for cloning; F^{-} Δ (argF^{-}ac)169 Φ 80dlacZ58(Δ M15) glnV44(AS) rfbD1 gyrA96(NalR) recA1 endA1 spoT1 thi^{-}1 hsdR17 deoR Λ pir $^{+}$	***Saltikov and Newman* (*2003*)**
pSMV3−Δ SfPat	pSMV3 with 778 bp upstream and 779 bp downstream of flanking regions of SfPat	This study

Table 3.

Plasmids used in the study

Motility assay

Soft-agar overlay motility assays were carried out in 12-well dishes to compare swimming behaviors Wolfe and Berg (1989); Kearns (2010) overnight at RT and then inoculated onto the center of soft agar (containing LB/MB and 0.5% low-melt agarose) and incubated at RT overnight. The results were recorded as the distance traveled (in millimeters) from the inoculation zone. Each variable was tested in duplicate. Two perpendicular distances from the inoculation zone were recorded and averaged for each well.

Ciona mariculture

The *in vivo* colonization experiments were performed on animals reared under conditions termed "semi-germ-free" (SGF), which include minimal exposure to marine microbes. SGF conditions include animals harvested under conventional approaches Cirino et al. (2002) but permanently maintained in 0.22 µm-filtered, conditioned artificial seawater (cASW), handled with gloves, and lids only carefully removed for water/media changes. cASW is prepared by conditioning ASW made with Instant Ocean™ in an in-house sump-aquarium system containing live rock, growth lights, and sediment from San Diego, California; salinity is maintained at 32-34 parts per thousand (or grams per liter). Compared to germ-free Leigh et al. (2016) or SGF, conventionally-reared (CR) includes a step-up exposure to 0.7µm-filtered cASW that increases exposure to marine bacteria during development. The SGF approach is considered an intermediate method of rearing that includes minimal exposures to microbial signals during development (unpublished observations). The animals were reared at 20 $^{\circ}$C from larval to juvenile stages. The *Ciona* were collected from Mission Bay, California in order to produce juvenile organisms for each biological replicate. These wild-harvested animals provide a wider genetic diversity compared to traditional model systems, where genetic diversity has been reduced or eliminated through controlled breeding practices.

Gut colonization assays

Both bacterial strains were grown overnight at RT in MB and diluted to 10^7 cfu/ml in cASW after repeated washes. Metamorphic stage 4 (MS4) animals reared in six-well dishes in cASW were exposed to 5 ml of 10^7 cfu/ml bacteria in each well for one hour or 24 hours, respectively. MS4 animals are considered part of the 1st ascidian stages (post-settlement stages 1-6, whereas stages 7-8 and onwards are 2nd ascidian stages and reflect young adult animals). MS4 juveniles can be identified as having a pair of protostigmata, or gill slits, on each side of the animal (Chiba et al. (2004)). These juveniles first initiate feeding via newly developed and opened siphons; before this, the gut remains closed, and the interior lumen is unexposed to the outside world. Following this initial exposure or colonization, for various time intervals, the plates were rinsed multiple times with cASW and replaced with fresh cASW. Ten juveniles were chosen randomly for each treatment, pooled, and homogenized with a plastic pestle; live bacteria were counted by performing serial dilutions and enumerating colony-forming units (cfu) via spot-plating assays (***Gaudy Jr et al. (1963)***; Miles et al. (1938)). Each graphed data represents a biological replicate dataset from genetically distinct/ diverse backgrounds of *Ciona* (represented by separate live animal collection and spawning events). Statistical significance was calculated using the Wilcoxon t-test by pooling data across six genetically diverse biological replicates. Live bacteria in the gut were visualized using BacLight stains and previously described fluorescently labeled bacteria Moran et al. (2019). For BacLight staining, 1 ml of bacterial cultures were grown overnight at RT, pelleted, washed twice with cASW, and stained with 4 µl of BacLight Red (Invitrogen Cat no B35001) or BacLight Green (Invitrogen Cat no B35000) for 15 mins in the dark. The cultures were stained with alternate dyes in different replicates to get unbiased data from changes in fluorescence. The stained cultures were washed twice with cASW, and then diluted to 10^7 cfu/ml with cASW. MS4 animals were grown in 6-well dishes were then exposed to 5 ml of this culture. Bacteria in the gut of animals were visualized after one hour on a Leica DMI 6000B stereoscope

with a CY5 fluorescent filter for BacLight Red and GFP filter for BacLight Green; and imaged-captured with a Hamamatsu ORCAII camera (model C10600-10B-H) and processed with the MetaMorph 7.10.4 imaging suite (Molecular Devices, Downingtown, PA).

Gene expression studies

To determine if the *Ciona* innate immune system can recognize and respond to unique mutant strains, which differ only in the presence or absence of prophages, candidate immune response markers were tested using reverse transcription quantitative PCR (RT-qPCR). RNA was extracted using the RNA XS kit (Macherey-Nagel, Cat no 740902) from MS4 *Ciona* juveniles that underwent gut colonization. Complementary DNA (cDNA) synthesis was performed with oligo-dT primers and random hexamers using the First Strand cDNA Synthesis Kit (Promega Cat no A5000) following the manufacturer's instructions. The amplification was set with the qPCR kit (Promega Cat no A6000) and carried out on an ABI7500 with an initial melting temperature of 95°C for 2 mins and 40 cycles of 95°C for 15 sec and 60°C for 1 min. The innate immune responses tested and their primers are reported in **Table 4**. Results from four distinct biological replicates are presented. Each replicate includes pooled *Ciona* juveniles from at least two wells of a 6-well dish. *Ciona* actin was referenced as an endogenous control. Data was analyzed using ΔΔCT method ***Pfaffl*(*2001*)** and the ABI7500 software suite. To understand bacterial genes that are differentially regulated due to the presence of prophages, bacterial gene expression was studied *in vitro* and *in vivo*. The bacterial strains were cultivated in six-well dishes using the same methodology described for biofilm assays. To understand if the host immune molecule VCBP-C induced prophages, WT was cultured in six-well dishes as described in the biofilm section in the presence or absence of 50 µg/ml VCBP-C Dishaw et al. (2016). After 24 hours, the supernatant was discarded for both experiments, and RNA from the biofilm was extracted using the Zymo Research Direct-zol kit. cDNA synthesis was carried out with random hexamers primers, and qPCR was carried out as described above. Targeted bacterial genes are described in (**table 5**). Rho was identified as the most stable reference gene using RefFinder, which utilizes Bestkeeper, GeNorm, Normfinder, and comparative ΔΔ CT methods (**Figure 5** supplement 1) Andersen et al. (2004); ***Pfaffl*(*2001*)**; Vandesompele et al. (2002); Watnick and Kolter (2000).

Statistical analysis and data visualization

Statistical analysis and data visualization were carried out in R, version 4.2 ***Team (2021)***. Data were plotted with ggplot 3.3.5 Kassambara (2020); the Beeswarm plot was constructed using ggbeeswarm 0.6 ***Eklund (2021)***. Beeswarm plots and statistics for motility assays were calculated using replicate averages Lord et al. (2020). Statistical significance was calculated using ggsignif package 0.6.3 or ggpubr0.4.0 Kassambara (2020); ***Constantin (2021)***. If the data were found to be normally distributed by Shapiro's test, then significance was calculated using an unpaired t-test. The Wilcoxon signed-rank test was used to calculate the significance of non-parametric data.

Author contributions

O.N. designed, executed, and analyzed experiments and wrote and edited the manuscript, S.L.G., N.P., C.G.F.A., F.N, A.L., and E.D.K performed experiments and provided feedback and approved the manuscript, M.N.Y., S.J.L., and B.A.L. performed genome sequence analysis, assembly, and provided feedback and approved the manuscript, M.B. and J.A.G. helped interpret data, provided feedback and approved the manuscript, and L.J.D, helped design experiments, interpret data, and helped write, edit and approve the manuscript.

Table 4.

Ciona Genes targeted and the necessary reverse transcription-qPCR primers

Gene	Function	Genbank accession no.	Primer (5'-3')	Reference
VCBP-C-Fwd	Secreted immune effector in the gut	HQ324151	AGACCAACGCCAACACAGTA	*Liberti et al.* (*2018*)
VCBP-C-Rev			CCCCATACATTGCAGCATTTC	
Actin–Fwd	Cytoskeletal actin	AJ297725	CCCAAATCATGTTCGAAACC	*Liberti et al.* (*2018*)
Actin-Rev	**Reference gene**		ACACCATCACCACTGTCGAA	
IL17-1-Fwd	Interleukin 17	NM_001129875.1	AGGTTAAGAATCCCTATGGTGC	*Liberti et al.* (*2023*)
IL17-1-Rev			CAAAGGCACAGACGCAAAGG	
IL17-1R-Fwd	Interleukin 17 Receptor	NM_001245045	TGTTGGCATGAGTGTTCGGT	
IL17-1R-Rev			AGTTGGTTCTGCCCCAAAGT	
NFκ-B-Fwd		NM_001078304	TGTCGCTTGTCGTCATGGAA	*Liberti et al.* (*2023*)
NFκ-B-Rev			AACACCCAAGACCGTCGAAA	
TNFα-R-Fwd	Tumor Necrosis Factor	NM_001128107	TTCAGAAAGATTGGACGACGA	*Liberti et al.* (*2023*)
TNFα-R-Rev			TCGTTTAGAAATGCTGCTGTGG	
C3A-R-Fwd		NM_001078552	TTGTAAGCTGGCACAAGGTGT	This study
C3A-R-Rev			GACCGTAGTCTGGTAGAGGTC	
MBL-Fwd	Mannose Binding Lectin	NM_001167707.2	TTATTGATGGGAAAGTTTGGT	This study
MBL-Rev			TAACATCTCTGTTCTTGGGTC	

Table 5.

S. fidelis 3313 Genes targeted and the necessary reverse transcription-qPCR primers

Gene	Function	Genbank accession no.	Primer (5'-3')	Reference
pleD-Fwd	Regulates production of cyclic di-GMP	NZ_KI912459.1	CTCTTCACCGCCACTTCTT	This study
pleD-Rev			GGTGTGGTCTCTTATGCCTATC	
Chitinase-Fwd	Chitin utilization gene	NF027718.3	CAGTGTAGCTAAGTCGTCATC	This study
Chitinase-Rev			CGCCAACCAGTGCTTTATTG	
pilZ-Fwd	Type IV Pilus control protein	NZ_JADX01000014.1	TGGCAAGGTCGTTTGGATTA	This study
pilZ-Rev			AGGCAAGCTCACTGGAAAG	
pdeB-Fwd	Phosphodiesterase	NF012772.3	GCATCAGGGCTCTTACCAATAG	This study
pdeB-Rev			GAGGCGGTGATCCTTACAGATA	
recA-Fwd	Bacterial recombinase	NZ_KI912459.1	CGTAGTGGTGCGGTAGATGT	This study
recA-Rev			CGCATTGCTTGGCTCATCAT	
lexA-Fwd	Regulator of recombinase	NZ_JADX01000011.1	TGACCCAGCTATGTTCCGCC	This study
lexA-Rev			GCTCAACCTTGTGTACGGCG	
Rho-Fwd	**Bacterial reference gene**	NZ_JADX01000026.1	CACGTACAAGTTGCCGAAATG	This study
Rho-Rev			CAAGACGGGTGATAGAGTCAAG	

Funding

This project was supported by NSF IOS-1456301 (L.J.D. and M.B.), NSF MCB-1817308 (L.J.D), NSF IOS-2226050/51 (L.J.D. and J.G.), internal awards from the MCOM Deans Office, Ann, and Andrew Hines Endowed Chair in Molecular Genetics, and the USF Institute for Microbiomes to L.J.D. W also got funding through an NSF GRFP award to B.A.L., and a New Investigator Award to O.N. by USF.

Acknowledgements

The authors acknowledge the expertise of Gary W. Litman and John P. Cannon for expert feedback and guidance on earlier efforts of the project.

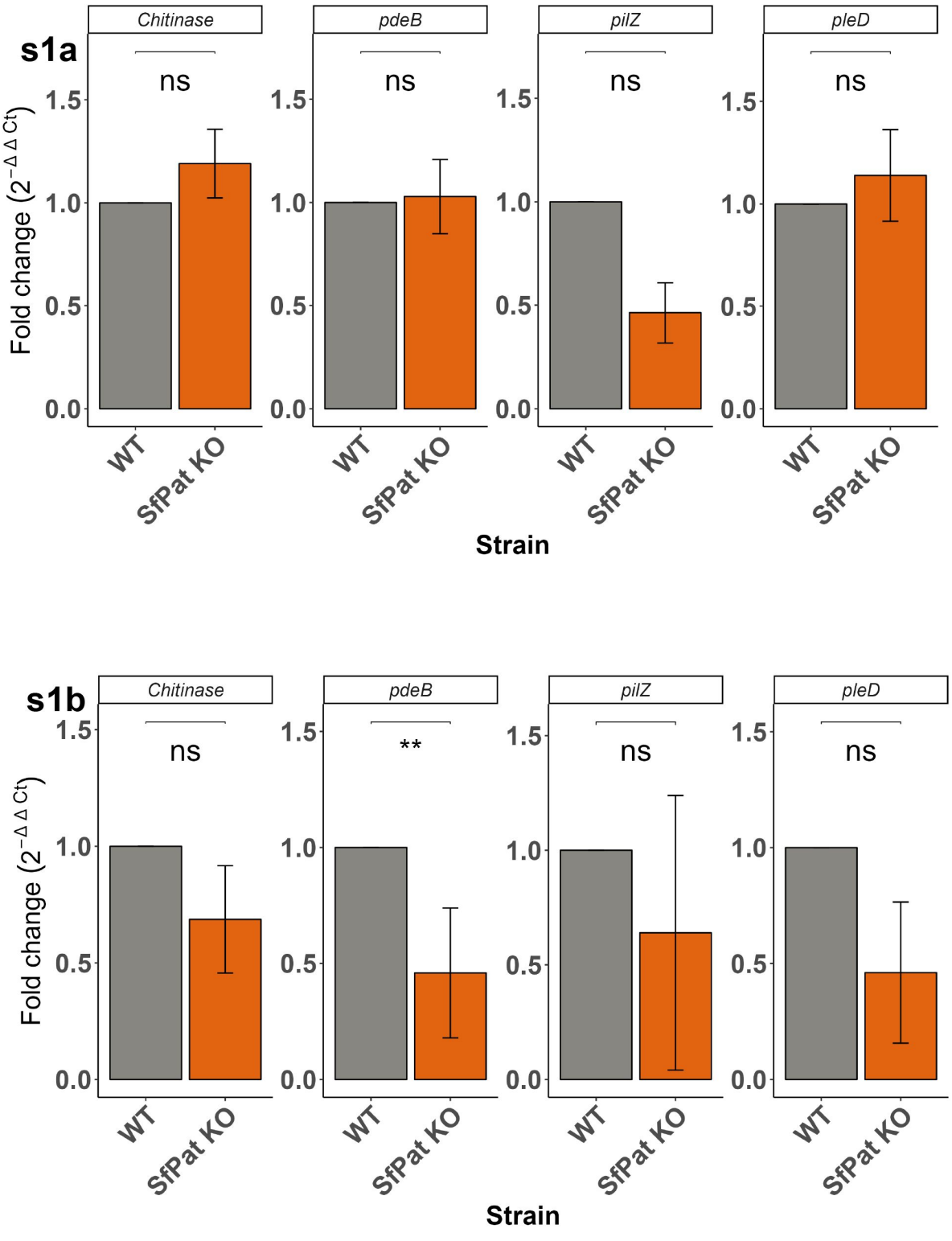

Figure 2—figure supplement 1.

Supplemental Figure: (a) Cyclic di GMP regulators expression in WT and ΔSfPat *in vitro* after 24 hours of exposure (n=4), (b) Cyclic di GMP regulators expression in WT and ΔSfPat *in vivo* of *Ciona* MS4 after 24 hours of exposure (n=4).

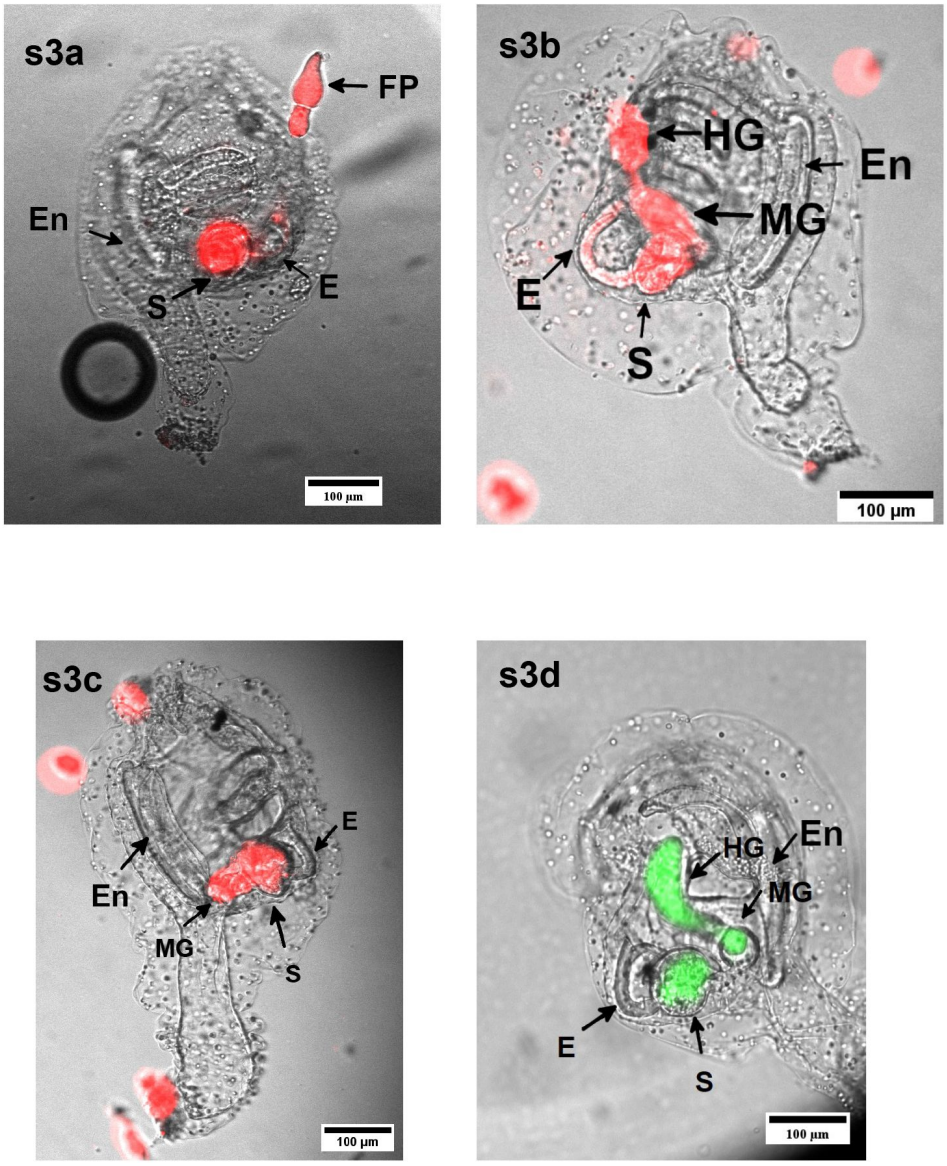

Figure 3—figure supplement 1.

Supplemental Figure 3: WT stained in BacLight Red exposed to Ciona MS4 for one hour c) ΔSfPat stained in BacLight Red exposed to Ciona MS4 for one hour. d) ΔfPat stained in BacLight Green exposed to *Ciona* MS4 for one hour

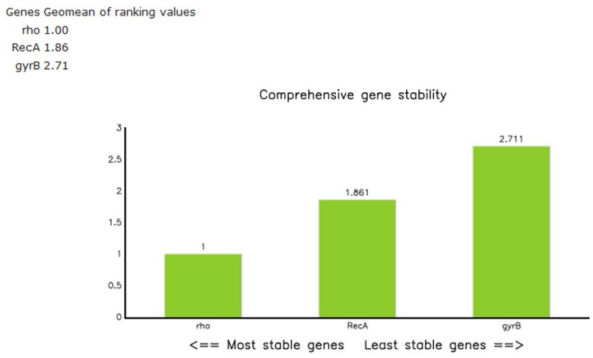

Figure 5—figure supplement 1.

Supplemental Figure 2: Rho is the most stable gene across strains when tested in vitro (n=3)

References

Allen HK, Looft T, Bayles DO, Humphrey S, Levine UY, Alt D, Stanton TB (2011) **Antibiotics in feed induce prophages in swine fecal microbiomes** *MBio*

Andersen CL, Jensen JL, Ørntoft TF (2004) **Normalization of real-time quantitative reverse transcription-PCR data: a model-based variance estimation approach to identify genes suited for normalization, applied to bladder and colon cancer data sets** *Cancer research* **64**:5245–5250

Aziz RK, Edwards RA, Taylor WW, Low DE, McGeer A, Kotb M. (2005) **Mosaic prophages with horizontally acquired genes account for the emergence and diversification of the globally disseminated M1T1 clone of Streptococcus pyogenes** *Journal of bacteriology* **187**:3311–3318

Banks DJ, Lei B, Musser JM (2003) **Prophage induction and expression of prophage-encoded virulence factors in group A Streptococcus serotype M3 strain MGAS315** *Infect Immun* **71**:7079–86

Barr JJ *et al.* (2013) **Bacteriophage adhering to mucus provide a non-host-derived immunity** *Proc Natl Acad Sci U S A* **110**:10771–6 https://doi.org/10.1073/pnas.1305923110

Boling L *et al.* (2020) **Dietary prophage inducers and antimicrobials: toward landscaping the human gut microbiome** *Gut Microbes* **11**:721–734 https://doi.org/10.1080/19490976.2019.1701353

Bollinger RR, Everett ML, Wahl SD, Lee YH, Orndorff PE, Parker W. (2006) **Secretory IgA and mucin-mediated biofilm formation by environmental strains of Escherichia coli: role of type 1 pili** *Mol Immunol* **43**:378–87 https://doi.org/10.1016/j.molimm.2005.02.013

Bondy-Denomy J, Davidson AR (2014) **When a virus is not a parasite: the beneficial effects of prophages on bacterial fitness** *Journal of microbiology* **52**:235–242

Anton Bryksin I, Matsumura V (2010) **Overlap extension PCR cloning: a simple and reliable way to create recombinant plasmids** *BioTechniques* **48**:463–465 https://doi.org/10.2144/000113418

Chao L, Rakshe S, Leff M, Spormann AM (2013) **PdeB, a Cyclic Di-GMP-Specific Phosphodiesterase That Regulates Shewanella oneidensis MR-1 Motility and Biofilm Formation** *Journal of Bacteriology* **195**:3827–3833 https://doi.org/10.1128/jb.00498-13

Chiba S, Sasaki A, Nakayama A, Takamura K, Satoh N. (2004) **Development of Ciona intestinalis juveniles (through 2nd ascidian stage)** *Zoolog Sci* **21**:285–98 https://doi.org/10.2108/zsj.21.285

Cirino P, Toscano A, Caramiello D, Macina A, Miraglia V, Monte A (2002) **Laboratory culture of the ascidian Ciona intestinalis(L.): a model system for molecular developmental biology research. University of Chicago** *Marine Biological Laboratory*

Ahlmann-Eltze Constantin I (2021) **Patil, ggsignif: R Package for Displaying Significance Brackets for 'ggplot2'** *PsyArXiV* https://doi.org/10.31234/osf.io/7awm6

Davidson B. (2007) **Ciona intestinalis as a model for cardiac development** *Seminars in Cell & Developmental Biology* **18**:16–26 https://doi.org/10.1016/j.semcdb.2006.12.007

Diard M *et al.* (2017) **Inflammation boosts bacteriophage transfer between Salmonella spp** *Science* **355**:1211–1215 https://doi.org/10.1126/science.aaf8451

Dishaw LJ, Cannon JP, Litman GW, Parker W. (2014) **Immune-directed support of rich microbial communities in the gut has ancient roots** *Dev Comp Immunol* https://doi.org/10.1016/j.dci.2014.06.011

Dishaw LJ *et al.* (2014) **The gut of geographically disparate Ciona intestinalis harbors a core microbiota** *PLoS One* **9** https://doi.org/10.1371/journal.pone.0093386

Dishaw LJ, Leigh B, Cannon JP, Liberti A, Mueller MG, Skapura DP, Karrer CR, Pinto MR, De Santis R, Litman GW (2016) **Gut immunity in a protochordate involves a secreted immunoglobulin-type mediator binding host chitin and bacteria** *Nat Commun* **7** https://doi.org/10.1038/ncomms10617

Dishaw LJ, Giacomelli S, Melillo D, Zucchetti I, Haire RN, Natale L, Russo NA, De Santis R, Litman GW, Pinto MR (2011) **A role for variable region-containing chitin-binding proteins (VCBPs) in host gut–bacteria interactions** *Proceedings of the National Academy of Sciences* **108**:16747–16752 https://doi.org/10.1073/pnas.1109687108

Donaldson GP *et al.* (2018) **Gut microbiota utilize immunoglobulin A for mucosal colonization** *Science* https://doi.org/10.1126/science.aaq0926

Duncan K, Carey-Ewend K, Vaishnava S. (2021) **Spatial analysis of gut microbiome reveals a distinct ecological niche associated with the mucus layer** *Gut Microbes* **13** https://doi.org/10.1080/19490976.2021.1874815

Aron Eklund J (2021) **Trimble, The Bee Swarm Plot, an Alternative to Stripchart**

Fang Y, Mercer RG, McMullen LM, Ganzle MG (2017) **Induction of Shiga Toxin-Encoding Prophage by Abiotic Environmental Stress in Food** *Appl Environ Microbiol* **83** https://doi.org/10.1128/AEM.01378-17

Fortier LC, Sekulovic O. (2013) **Importance of prophages to evolution and virulence of bacterial pathogens** *Virulence* **4**:354–65 https://doi.org/10.4161/viru.24498

Fraune S, Bosch TC (2010) **Why bacteria matter in animal development and evolution** *Bioessays* **32**:571–580

Garcia-Russell N, Elrod B, Dominguez K. (2009) **Stress-induced prophage DNA replication in Salmonella enterica serovar Typhimurium** *Infect Genet Evol* **9**:889–95 https://doi.org/10.1016/j.meegid.2009.05.017

Gaudy A, Abu-Niaaj F, Gaudy E. (1963) **Statistical study of the spot-plate technique for viable-cell counts** *Applied microbiology* **11**:305–309

Gödeke J, Paul K, Lassak J, Thormann KM (2011) **Phage-induced lysis enhances biofilm formation in Shewanella oneidensis MR-1** *The ISME Journal* **5**:613–626 https://doi.org/10.1038/ismej.2010.153

Harrington V, Lau L, Seddu K, Suez J. (2021) **Ecology and Medicine Converge at the Microbiome-Host Interface** *mSystems* https://doi.org/10.1128/mSystems.00756-21

Hornung B, Martins Dos Santos VAP, Smidt H, Schaap PJ (2018) **Studying microbial functionality within the gut ecosystem by systems biology** *Genes Nutr* **13** https://doi.org/10.1186/s12263-018-0594-6

Howard-Varona C, Hargreaves KR, Abedon ST, Sullivan MB (2017) **Lysogeny in nature: mechanisms, impact and ecology of temperate phages** *The ISME journal* **11**:1511–1520

Hu J, Ye H, Wang S, Wang J, Han D. (2021) **Prophage Activation in the Intestine: Insights Into Functions and Possible Applications** *Front Microbiol* **12** https://doi.org/10.3389/fmicb.2021.785634

Jenal U, Malone J. (2006) **Mechanisms of Cyclic-di-GMP Signaling in Bacteria** *Annual Review of Genetics* **40**:385–407 https://doi.org/10.1146/annurev.genet.40.110405.090423

Jiang SC, Paul JH (1998) **Significance of Lysogeny in the Marine Environment: Studies with Isolates and a Model of Lysogenic Phage Production** *Microbial Ecology* **35**:235–243 https://doi.org/10.1007/s002489900079

Johansson ME, Larsson JM, Hansson GC (2011) **The two mucus layers of colon are organized by the MUC2 mucin, whereas the outer layser is a legislator of host-microbial interactions** *Proc Natl Acad Sci U S A* **108**:4659–65 https://doi.org/10.1073/pnas.1006451107

Kassambara A (2020) **ggpubr: 'ggplot2' Based Publication Ready Plots**

Kearns DB (2010) **A field guide to bacterial swarming motility** *Nat Rev Microbiol* **8**:634–44 https://doi.org/10.1038/nrmicro2405

Kim MS, Bae JW (2018) **Lysogeny is prevalent and widely distributed in the murine gut microbiota** *The ISME Journal* **12**:1127–1141 https://doi.org/10.1038/s41396-018-0061-9

Leigh BA, Liberti A, Dishaw LJ (2016) **Generation of Germ-Free Ciona intestinalis for Studies of Gut-Microbe Interactions** *Front Microbiol* **7** https://doi.org/10.3389/fmicb.2016.02092

Leigh B, Karrer C, Cannon JP, Breitbart M, Dishaw LJ (2017) **Isolation and characterization of a Shewanella phage–host system from the gut of the tunicate, Ciona intestinalis** *Viruses* **9**

Leigh BA, Djurhuus A, Breitbart M, Dishaw LJ (2018) **The gut virome of the protochordate model organism, Ciona intestinalis subtype A** *Virus Research* **244**:137–146 https://doi.org/10.1016/j.virusres.2017.11.015

Li H *et al.* (2015) **The outer mucus layer hosts a distinct intestinal microbial niche** *Nat Commun* **6** https://doi.org/10.1038/ncomms9292

Liberti A, Cannon JP, Litman GW, Dishaw LJ (2019) **A Soluble Immune Effector Binds Both Fungi and Bacteria via Separate Functional Domains** *Front Immunol* **10** https://doi.org/10.3389/flmmu.2019.00369

Liberti A, Pollastro C, Pinto G, Illiano A, Marino R, Amoresano A, Spagnuolo A, Sordino P. (2023) **Transcriptional and proteomic analysis of the innate immune response to microbial stimuli in a model invertebrate chordate** *Front Immunol* **14** https://doi.org/10.3389/flmmu.2023.1217077

Liberti A, Leigh BA, Graham Z, Natarajan O, Dishaw LJ (2022) **In: Rast J, Buckley K, editors** *A Role for Secreted Immune Effectors in Microbial Biofilm Formation Revealed by Simple In Vitro Assays* New York, NY: Springer US :127–140 https://doi.org/10.1007/978-1-0716-1944-5_9

Liberti A, Natarajan O, Atkinson CGF, Sordino P, Dishaw LJ (2021) **Reflections on the Use of an Invertebrate Chordate Model System for Studies of Gut Microbial Immune Interactions** *Frontiers in Immunology* **12** https://doi.org/10.3389/flmmu.2021.642687

Liberti A, Zucchetti I, Melillo D, Skapura D, Shibata Y, De Santis R, Pinto MR, Litman GW, Dishaw LJ (2018) **Chitin protects the gut epithelial barrier in a protochordate model of DSS-induced colitis** *Biology Open* **7** https://doi.org/10.1242/bio.029355

Lin W, Fullner KJ, Clayton R, Sexton JA, Rogers MB, Calia KE, Calderwood SB, Fraser C, Mekalanos JJ (1999) **Identification of a Vibrio cholerae RTX toxin gene cluster that is tightly linked to the cholera toxin prophage** *Proceedings of the National Academy of Sciences* **96**:1071–1076 https://doi.org/10.1073/pnas.96.3.1071

Liu LP, Xiang JH, Dong B, Natarajan P, Yu KJ, Cai NE (2006) **Ciona intestinalis as an emerging model organism: Its regeneration under controlled conditions and methodology for egg dechorionation** *Journal of Zhejiang University SCIENCE B* **7**:467–474 https://doi.org/10.1631/jzus.2006.b0467

Liu X, Li Y, Guo Y, Zeng Z, Li B, Wood TK, Cai X, Wang X. (2015) **Physiological Function of Rac Prophage During Biofilm Formation and Regulation of Rac Excision in Escherichia coli K-12** *Scientific Reports* **5** https://doi.org/10.1038/srep16074

Liu X, Tang K, Zhang D, Li Y, Liu Z, Yao J, Wood TK, Wang X. (2019) **Symbiosis of a P2-family phage and deep-sea Shewanella putrefaciens** *Environmental Microbiology* **21**:4212–4232 https://doi.org/10.1111/1462-2920.14781

Lord SJ, Velle KB, Mullins RD, Fritz-Laylin LK (2020) **SuperPlots: Communicating reproducibility and variability in cell biology** *Journal of Cell Biology* **219**

Lwoff A. (1953) **Lysogeny** *Bacteriological reviews* **17**:269–337

Maiques E, Ubeda C, Campoy S, Salvador N, Lasa I, Novick RP, Barbe J, Penades JR (2006) **beta-lactam antibiotics induce the SOS response and horizontal transfer of virulence factors in Staphylococcus aureus** *J Bacteriol* **188**:2726–9 https://doi.org/10.1128/JB.188.7.2726-2729.2006

Miles AA, Misra S, Irwin J. (1938) **The estimation of the bactericidal power of the blood** *Epidemiology & Infection* **38**:732–749

Mills S, Shanahan F, Stanton C, Hill C, Coffey A, Ross RP (2013) **Movers and shakers: influence of bacteriophages in shaping the mammalian gut microbiota** *Gut Microbes* **4**:4–16 https://doi.org/10.4161/gmic.22371

Minot S, Bryson A, Chehoud C, Wu GD, Lewis JD, Bushman FD (2013) **Rapid evolution of the human gut virome** *Proc Natl Acad Sci U S A* **110**:12450–5 https://doi.org/10.1073/pnas.1300833110

Minot S, Sinha R, Chen J, Li H, Keilbaugh SA, Wu GD, Lewis JD, Bushman FD (2011) **The human gut virome: interindividual variation and dynamic response to diet** *Genome Res* **21**:1616–25 https://doi.org/10.1101/gr.122705.111

Mirzaei MK, Maurice CF (2017) **Ménage à trois in the human gut: interactions between host, bacteria and phages** *Nature Reviews Microbiology* **15**:397–408 https://doi.org/10.1038/nrmicro.2017.30

Moran NA, Ochman H, Hammer TJ (2019) **Evolutionary and ecological consequences of gut microbial communities** *Annu Rev Ecol Evol Syst* **50**:451–475 https://doi.org/10.1146/annurev-ecolsys-110617-062453

Nanda AM, Thormann K, Frunzke J. (2015) **Impact of spontaneous prophage induction on the fitness of bacterial populations and host-microbe interactions** *J Bacteriol* **197**:410–9 https://doi.org/10.1128/JB.02230-14

Pfaff MW (2001) **A new mathematical model for relative quantification in real-time RT-PCR** *Nucleic Acids Res* **29** https://doi.org/10.1093/nar/29.9.e45

Pratt LA, Kolter R. (1998) **Genetic analysis of Escherichia coli biofilm formation: roles of flagella, motility, chemotaxis and type I pili** *Mol Microbiol* **30**:285–93

Reyes A, Haynes M, Hanson N, Angly FE, Heath AC, Rohwer F, Gordon JI (2010) **Viruses in the faecal microbiota of monozygotic twins and their mothers** *Nature* **466**:334–8 https://doi.org/10.1038/nature09199

Rice SA, Tan CH, Mikkelsen PJ, Kung V, Woo J, Tay M, Hauser A, McDougald D, Webb JS, Kjelleberg S. (2009) **The biofilm life cycle and virulence of Pseudomonas aeruginosa are dependent on a filamentous prophage** *The ISME Journal* **3**:271–282 https://doi.org/10.1038/ismej.2008.109

Rooks MG, Garrett WS (2016) **Gut microbiota, metabolites and host immunity** *Nature Reviews Immunology* **16**:341–352 https://doi.org/10.1038/nri.2016.42

Saltikov CW, Newman DK (2003) **Genetic identification of a respiratory arsenate reductase** *Proceedings of the National Academy of Sciences* **100**:10983–10988 https://doi.org/10.1073/pnas.1834303100

Shkoporov AN, Hill C. (2019) **Bacteriophages of the Human Gut: The "Known Unknown" of the Microbiome** *Cell Host & Microbe* **25**:195–209 https://doi.org/10.1016/j.chom.2019.01.017

Silveira CB, Luque A, Rohwer F. (2021) **The landscape of lysogeny across microbial community density, diversity and energetics** *Environmental Microbiology* **23**:4098–4111 https://doi.org/10.1111/1462-2920.15640

Swidsinski A, Loening-Baucke V, Theissig F, Engelhardt H, Bengmark S, Koch S, Lochs H, Dorffel Y. (2007) **Comparative study of the intestinal mucus barrier in normal and inflamed colon** *Gut* **56**:343–50 https://doi.org/10.1136/gut.2006.098160

Team RC, R : A language and environment for statistical computing (2021) **R Team**

Thomas AD, Parker W. (2010) **Cultivation of epithelial-associated microbiota by the immune system** *Future Microbiol* **5**:1483–92 https://doi.org/10.2217/fmb.10.108

Tsao YF, Taylor VL, Kala S, Bondy-Denomy J, Khan AN, Bona D, Cattoir V, Lory S, Davidson AR, Maxwell KL (2018) **Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes** *Journal of Bacteriology* **200**:e00189–18 https://doi.org/10.1128/JB.00189-18

Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F. (2002) **Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes** *Genome biology* **3**:1–12

Wagner PL, Waldor MK (2002) **Bacteriophage control of bacterial virulence** *Infect Immun* **70**:3985–93

Wang X, Kim Y, Ma Q, Hong SH, Pokusaeva K, Sturino JM, Wood TK (2010) **Cryptic prophages help bacteria cope with adverse environments** *Nat Commun* **1** https://doi.org/10.1038/ncomms1146

Watnick P, Kolter R. (2000) **Biofilm, city of microbes** *Journal of bacteriology* **182**:2675–2679

Weinbauer MG, Suttle CA (1999) **Lysogeny and prophage induction in coastal and offshore bacterial communities** *Aquatic Microbial Ecology* **18**:217–225 https://doi.org/10.3354/ame018217

Wolfe AJ, Berg HC (1989) **Migration of bacteria in semisolid agar** *Proc Natl Acad Sci U S A* **86**:6973–7 https://doi.org/10.1073/pnas.86.18.6973

Zhang X, McDaniel AD, Wolf LE, Keusch GT, Waldor MK, Acheson DW (2000) **Quinolone antibiotics induce Shiga toxin-encoding bacteriophages, toxin production, and death in mice** *J Infect Dis* **181**:664–70 https://doi.org/10.1086/315239

Author information

Ojas Natarajan
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States
ORCID iD: 0000-0001-7887-2640

Susanne L Gibboney
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States

Morgan N Young
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States

Shen Jean Lim
College of Marine Science, University of South Florida, Tampa FL, United States
ORCID iD: 0000-0003-4578-5318

Felicia Nguyen
Biomedical Sciences Program, University of South Florida, Tampa FL, United States

Natalia Pluta[†]
Biomedical Sciences Program, University of South Florida, Tampa FL, United States

[†]Present address: Uniformed Services University of Health Sciences, Bethesda, MD, USA;

Celine GF Atkinson[¶]
Department of Cell Biology, Microbiology, and Molecular Biology, University of South Florida, Tampa FL, United States

[¶]Present address: School of Dentistry, University of Washington, Seattle, USA;

Assunta Liberti
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States, Stazione Zoologica Anton Dohrn, Naples, Italy
ORCID iD: 0000-0001-9097-2871

Eric D Kees[††]
BioTechnology Institute, University of Minnesota, St. Paul, MN, United States
ORCID iD: 0000-0002-8258-9933

[††]Present address: Cargill Corporation, Wayzata, MN

Brittany A Leigh[‡‡]
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States, College of Marine Science, University of South Florida, Tampa FL, United States
ORCID iD: 0000-0001-5668-9925

[‡‡]Present address: LifeSci Communications, New York and Boston

Mya Breitbart
College of Marine Science, University of South Florida, Tampa FL, United States
ORCID iD: 0000-0003-3210-2899

Jeffrey A Gralnick
BioTechnology Institute, University of Minnesota, St. Paul, MN, United States, Plant and Microbial Biology, University of Minnesota, St. Paul, MN, United States
ORCID iD: 0000-0001-9250-7770

Larry J Dishaw
Dept Pediatrics, Morsani College of Medicine, University of South Florida, Tampa FL, United States, Biomedical Sciences Program, University of South Florida, Tampa FL, United States, Department of Cell Biology, Microbiology, and Molecular Biology, University of South Florida, Tampa FL, United States
ORCID iD: 0000-0002-2705-4573

For correspondence: ldishaw@usf.edu

Editors

Reviewer #1 (Public review):

Summary:

The manuscript aims to elucidate the impact of a prophage within the genome of Shewanella fidelis on its interaction with the marine tunicate Ciona robusta. The authors made a deletion mutant of S. fidelis that lacks one of its two prophages. This mutant exhibited an enhanced biofilm phenotype, as assessed through crystal violet staining, and showed reduced motility. The authors examined the effect of prophage deletion on several genes that could modulate cyclic-diGMP levels. While no significant changes were observed under in vitro conditions, the gene for one protein potentially involved in cyclic-diGMP hydrolysis was overexpressed during microbe-host interactions. The mutant was retained more effectively within a one-hour timeframe, whereas the wild-type (WT) strain became more abundant after 24 hours. Fluorescence microscopy was used to visualize the localization patterns of the two strains, which appeared to differ. Additionally, a significant difference in the expression of one immune protein was noted after one hour, but this difference was not evident after 23 hours. An effect of VCBC-C addition on the expression of one prophage gene was also observed.

Strengths:

I appreciate how the authors integrate diverse expertise and methods to address questions regarding the impact of prophages on gut microbiome-host interactions. The chosen model system is appropriate, as it allows for high-throughput experimentation and the application of simple imaging techniques.

Weaknesses:

My primary concern is that the manuscript primarily describes observations without providing insight into the molecular mechanisms underlying the observed differences. It is particularly unclear how the presence of the prophage leads to the phenotypic changes related to bacterial physiology and host-microbe interactions. Which specific prophage genes are critical, or is the insertion at a specific site in the bacterial genome the key factor? While significant effects on bacterial physiology are reported under in vitro conditions, there is no clear attribution to particular enzymes or proteins. In contrast, when the system is expanded to include the tunicate, differences in the expression of a cyclic-diGMP hydrolase become apparent. Why do we not observe such differences under in vitro conditions, despite noting variations in biofilm formation and motility? Furthermore, given that the bacterial strain possesses two prophages, I am curious as to why the authors chose to target only one and not both.

Regarding the microbe-host interaction, it is not clear why the increased retention ability of the prophage deletion strain did not lead to greater cell retention after 24 hours, especially since no differences in the immune response were observed at that time point.

Concerning the methodological approach, I am puzzled as to why the authors opted for qPCR instead of transcriptomics or proteomics. The latter approaches could have provided a broader understanding of the prophage's impact on both the microbe and the host.

https://doi.org/10.7554/eLife.103107.1.sa2

Reviewer #2 (Public review):

Summary:

In the manuscript, "Prophage regulation of Shewanella fidelis 3313 motility and biofilm formation: implications for gut colonization dynamics in Ciona robusta", the authors are experimentally investigating the idea that integrated viruses (prophages) within a bacterial colonizer of the host Ciona robusta affect both the colonizer and the host. They found a prophage within the Ciona robusta colonizing bacterium Shewanella fidelis 3313, which affected both the bacteria and host. This prophage does so by regulating the phosphodiesterase gene pdeB in the bacterium when the bacterium has colonized the host. The prophage also regulates the activity of the host immune gene VCBP-C during early bacterial colonization. Prophage effects on both these genes affect the precise localization of the colonizing bacterium, motility of the bacterium, and bacterial biofilm formation on the host. Interestingly, VCBP-C expression also suppressed a prophage structural protein, creating a tripartite feedback loop in this symbiosis. This is exciting research that adds to the emerging body of evidence that prophages can have beneficial effects not only on their host bacteria but also on how that bacteria interacts in its environment. This study establishes the evolutionary conservation of this concept with intriguing implications of prophage effects on tripartite interactions.

Strengths:

This research effectively shows that a prophage within a bacterium colonizing a model ascidian affects both the bacterium and the host in vivo. These data establish the prophage effects on bacterial activity and expand these effects to the natural interactions within the host animal. The effects of the prophage through deletion on a suite of host genes are a strength, as shown by striking microscopy.

Weaknesses:

Unfortunately, there are abundant negative data that cast some limitations on the interpretation of the data. That is, examining specific gene expression has its limitations, which could be avoided by global transcriptomics of the bacteria and the host during colonization by the prophage-containing and prophage-deleted bacteria (1 hour and 24 hours). In this way, the tripartite interactions leading to mechanism could be better established.

Impact:

The authors are correct to speculate that this research can have a significant impact on many animal microbiome studies, since bacterial lysogens are prevalent in most microbiomes. Screening for prophages, determining whether they are active, and "curing" the host bacteria of active prophages are effective tools for understanding the effects these mobile elements have on microbiomes. There are many potential effects of these elements in vivo, both positive and negative, this research is a good example of why this research should be explored.

Context:

The research area of prophage effects on host bacteria in vitro has been studied for decades, while these interactions in combination with animal hosts in vivo have been recent. The significance of this research shows that there could be divergent effects based on whether the study is conducted in vitro or in vivo. The in vivo results were striking. This is particularly so with the microscopy images. The benefit of using Ciona is that it has a translucent body which allows for following microbial localization. This is in contrast to mammalian studies where following microbial localization would either be difficult or near impossible.

https://doi.org/10.7554/eLife.103107.1.sa1

Reviewer #3 (Public review):

In this manuscript, Natarajan and colleagues report on the role of a prophage, termed SfPat, in the regulation of motility and biofilm formation by the marine bacterium Shewanella fidelis. The authors investigate the in vivo relevance of prophage carriage by studying the gut occupation patterns of Shewanella fidelis wild-type and an isogenic SfPat- mutant derivative in a model organism, juveniles of the marine tunicate Ciona robusta. The role of bacterial prophages in regulating bacterial lifestyle adaptation and niche occupation is a relatively underexplored field, and efforts in this direction are appreciated.

While the research question is interesting, the work presented lacks clarity in its support for several major claims, and, at times, the authors do not adequately explain their data.

Major concerns:

(1) Prophage deletion renders the SfPat- mutant derivative substantially less motile and with a higher biofilm formation capacity than the WT (Fig. 2a-b). The authors claim the mutant is otherwise isogenic to the WT strain upon sequence comparison of draft genome sequences (I'll take the opportunity to comment here that GenBank accessions are preferable to BioSample accessions in Table 1). Even in the absence of secondary mutations, complementation is needed to validate functional associations (i.e., phenotype restoration). A strategy for this could be phage reintegration into the mutant strain (PMID: 19005496).

(2) The authors claim that the downshift in motility (concomitant with an upshift in biofilm formation) is likely mediated by the activity of c-di-GMP turnover proteins. Specifically, the authors point to the c-di-GMP-specific phosphodiesterase PdeB as a key mediator, after finding lower transcript levels for its coding gene in vivo (lines 148-151, Fig. 2c), and suggesting higher activity of this protein in live animals (!)(line 229). I have several concerns here:
(2.1) Findings shown in Fig. 2a-b are in vitro, yet no altered transcript levels for pdeB were recorded (Fig. 2c). Why do the authors base their inferences only on in vivo data?
(2.2) Somewhat altered transcript levels alone are insufficient for making associations, let alone solid statements. Often, the activity of c-di-GMP turnover proteins is local and/or depends on the activation of specific sensory modules - in the case of PdeB, a PAS domain and a periplasmic sensor domain (PMID: 35501424). This has not been explored in the manuscript, i.e., specific activation vs. global alterations of cellular c-di-GMP pools (or involvement of other proteins, please see below). Additional experiments are needed to confirm the involvement of PdeB. Gaining such mechanistic insights would greatly enhance the impact of this study.
(2.3) What is the rationale behind selecting only four genes to probe the influence of the prophage on Ciona gut colonization by determining their transcript levels in vitro and in vivo? If the authors attribute the distinct behavior of the mutant to altered c-di-GMP homeostasis, as may be plausible, why did the authors choose those four genes specifically and not, for example, the many other c-di-GMP turnover protein-coding genes or c-di-GMP

effectors present in the S. fidelis genome? This methodological approach seems inadequate to me, and the conclusions on the potential implication of PdeB are premature.

(3) The behavior of the WT strain and the prophage deletion mutant is insufficiently characterized. For instance, how do the authors know that the higher retention capacity reported for the WT strain with respect to the mutant (Fig. 3b) is not merely a consequence of, e.g., a higher growth rate? It would be worth investigating this further, ideally under conditions reflecting the host environment.

(4) Related to the above, sometimes the authors refer to "retention" (e.g., line 162) and at other instances to "colonization" (e.g., line 161), or even adhesion (line 225). These are distinct processes. The authors have only tracked the presence of bacteria by fluorescence labeling; adhesion or colonization has not been assessed or demonstrated in vivo. Please revise.

(5) The higher CFU numbers for the WT after 24 h (line 161) might also indicate a role of motility for successful niche occupation or dissemination in vivo. The authors could test this hypothesis by examining the behavior of, e.g., flagellar mutants in their in vivo model.

(6) The endpoint of experiments with a mixed WT-mutant inoculum (assumedly 1:1? Please specify) was set to 1 h, I assume because of the differences observed in CFU counts after 24 h. In vivo findings shown in Fig. 3c-e are, prima facie, somewhat contradictory. The authors report preferential occupation of the esophagus by the WT (line 223), which seems proficient from evidence shown in Fig. S3. Yet, there is marginal presence of the WT in the esophagus in experiments with a mixed inoculum (Fig. 3d) or none at all (Fig. 3e). Likewise, the authors claim preferential "adhesion to stomach folds" by the mutant strain (line 225), but this is not evident from Fig. 3e. In fact, the occupation patterns by the WT and mutant strain in the stomach in panel 3e appear to differ from what is shown in panel 3d. The same holds true for the claimed "preferential localization of the WT in the pyloric cecum," with Fig. 3d showing a yellow signal that indicates the coexistence of WT and mutant.

(7) In general, and especially for in vivo data, there is considerable variability that precludes drawing conclusions beyond mere trends. One could attribute such variability in vivo to the employed model organism (which is not germ-free), differences between individuals, and other factors. This should be discussed more openly in the main text and presented as a limitation of the study. Even with such intrinsic factors affecting in vivo measurements, certain in vitro experiments, which are expected, in principle, to yield more reproducible results, also show high variability (e.g., Fig. 5). What do the authors attribute this variability to?

(8) Line 198-199: Why not look for potential prophage excision directly rather than relying on indirect, presumptive evidence based on qPCR?

https://doi.org/10.7554/eLife.103107.1.sa0