Microbiology Spectrum
American Society for Microbiology Press

Cross-Regulation between Bacteria and Phages at a Posttranscriptional Level

SHOSHY ALTUVIA,[1] GISELA STORZ,[2] and KAI PAPENFORT[3]

[1]Department of Microbiology and Molecular Genetics, IMRIC, The Hebrew University-Hadassah Medical School, Jerusalem, Israel; [2]Division of Molecular and Cellular Biology, Eunice Kennedy Shriver National Institute of Child Health and Human Development, Bethesda, MD 20892; [3]Munich Center for Integrated Protein Science (CIPSM) at the Department of Microbiology, Ludwig-Maximilians-University of Munich, 82152 Martinsried, Germany

ABSTRACT The study of bacteriophages (phages) and prophages has provided key insights into almost every cellular process as well as led to the discovery of unexpected new mechanisms and the development of valuable tools. This is exemplified for RNA-based regulation. For instance, the characterization and exploitation of the antiphage CRISPR (clustered regularly interspaced short palindromic repeat) systems is revolutionizing molecular biology. Phage-encoded proteins such as the RNA-binding MS2 protein, which is broadly used to isolate tagged RNAs, also have been developed as valuable tools. Hfq, the RNA chaperone protein central to the function of many base-pairing small RNAs (sRNAs), was first characterized as a bacterial host factor required for Qβ phage replication. The ongoing studies of RNAs are continuing to reveal regulatory connections between infecting phages, prophages, and bacteria and to provide novel insights. There are bacterial and prophage sRNAs that regulate prophage genes, which impact bacterial virulence as well as bacterial cell killing. Conversely, phage- and prophage-encoded sRNAs modulate the expression of bacterial genes modifying metabolism. An interesting subcategory of the prophage-encoded sRNAs are sponge RNAs that inhibit the activities of bacterial-encoded sRNAs. Phages also affect posttranscriptional regulation in bacteria through proteins that inhibit or alter the activities of key bacterial proteins involved in posttranscriptional regulation. However, what is most exciting about phage and prophage research, given the millions of phage-encoded genes that have not yet been characterized, is the vast potential for discovering new RNA regulators and novel mechanisms and for gaining insight into the evolution of regulatory RNAs.

INTRODUCTION

The impact that the study of phages, both in their lytic form and as prophages integrated into bacterial chromosomes, has had on molecular biology and microbiology is hard to overstate. The ease of phage manipulation helped establish several of the central dogmas in molecular biology. For example, characterization of various phage DNA polymerases contributed to the understanding of replication (1, 2), and models of transcription regulation were greatly influenced by studies of *c*I, the phage λ repressor (3, 4). Phages also have continually provided important tools such as transduction, the phage-assisted movement of DNA from one bacterium to another, which has been an essential tool since the early years of molecular biology (5, 6). As another example, the development of chain termination DNA-sequencing approaches benefited from single-stranded DNA cloning vectors derived from phage M13 (7).

Received: 19 February 2018, **Accepted:** 4 April 2018, **Published:** 13 July 2018

Editors: Gisela Storz, Division of Molecular and Cellular Biology, Eunice Kennedy Shriver National Institute of Child Health and Human Development, Bethesda, MD; Kai Papenfort, Department of Biology I, Microbiology, LMU Munich, Martinsried, Germany

Citation: Altuvia S, Storz G, Papenfort K. 2018. Cross-regulation between bacteria and phages at a posttranscriptional level. *Microbiol Spectrum* 6(4):RWR-0027-2018. doi:10.1128/microbiolspec.RWR-0027-2018.

Correspondence: Shoshy Altuvia, shoshy.altuvia@mail.huji.ac.il; Gisela Storz, storzg@mail.nih.gov; Kai Papenfort, kai.papenfort@lmu.de

Aside from their benefits as models and tools, the study of phages is important given their enormous impact on bacterial genome evolution, both as prophages integrated into the genomes and through mechanisms related to their ability to transduce genes. For instance, ~10% of the genome of *Streptococcus pyogenes*, including several pathogenicity factors, is of prophage origin, whereas ~16% of the genetic information of *Escherichia coli* O157:H7 strain Sakai traces back to 18 prophages (8). Since some prophage sequences are similar, recombination between the integrated sequences can lead to chromosomal inversions and deletions. Phage sequences also can serve as precursors of new genes (9). Additionally, an estimated 10^{25} phage infections occur worldwide every second (10). There are many mechanisms by which gene transfer takes place during these infections. These include (i) specialized transduction, whereby DNA located adjacent to an integrated prophage is transferred after imprecise excision of a prophage; (ii) gene transfer agents, prophage-like elements that package random bacterial DNA but cannot package enough to enable the transmission of their own genes; and (iii) phage-inducible chromosomal islands, which hijack helper phages to assist in their high-efficiency transfer to neighboring bacteria (11, 12). In one medically important example, the *Staphylococcus aureus* pathogenicity islands, which produce superantigens, utilize phages for effective transduction (13).

The transferred DNA can dramatically modify the recipient organism by encoding a wide range of genes, including virulence factors, toxins, secretion systems, and regulators. For bacteria to survive, the expression of the prophages or other foreign genes must be integrated into existing regulatory circuits (14–16). The diversity of the gene products encoded by phages, together with the rapidity with which these genes are integrated and transferred, results in great evolutionary pressure on the phages, prophages, and bacteria, leading to rapid changes in both the gene products and the regulatory circuits.

All of these concepts—the value of studying phage-prophage-bacterial interactions, the impact of rapid evolution, and the interwoven regulatory circuits—are applicable to RNA-based regulation, as we will discuss in this review.

THE CONTRIBUTION OF PHAGE BIOLOGY TO THE DEVELOPMENT OF TOOLS AND NEW CONCEPTS IN RNA-BASED REGULATION

The study of phages and the cross talk between phages and bacteria has led to a number of critical RNA-based tools for molecular biology. The most prominent tools come from the CRISPR (clustered regularly interspaced short palindromic repeat) phage defense systems, whose exploitation for genome engineering is changing molecular biology forever (17). A second class of important tools takes advantage of the high-affinity RNA-binding proteins encoded by phages. Probably the most widely utilized protein is the MS2 coat protein of the RNA phage R17, which binds a 19-nucleotide (nt) RNA hairpin, denoted MBS, with nanomolar affinity (18). MS2 and other phage RNA-binding proteins are employed in techniques that rely on these proteins for detecting and isolating correspondingly tagged RNAs in complex with their associated molecules (19).

The study of phages has also led to the identification of key factors of small RNA (sRNA)-based regulation. For example, the OOP RNA, encoded by DNA phage λ, was one of the first characterized sRNAs (20, 21). Studies of this antisense sRNA showed that it base-pairs with the *c*II-*O* mRNA, leading to degradation in a process involving RNase III (an endoribonuclease that recognizes double-stranded RNA) and possibly another RNases, ultimately resulting in decreased levels of the *c*II activator (20, 22). As another example, Hfq, critical to the function of base-pairing sRNAs in many bacteria, was first identified as a host factor required for RNA phage Qβ replication (23). In the Qβ context, Hfq has been proposed to alter the structure of the phage RNA, possibly allowing the 3′ end to be brought into the proximity of the replicase (24).

sRNAs REGULATING PROPHAGE-ENCODED VIRULENCE FACTORS

In pathogens, phage-mediated gene transfer has resulted in the acquisition of virulence genes. For example, the *Vibrio cholerae* toxin originates from the filamentous phage CTXΦ (25), and the emergence of new epidemic strains of *Salmonella enterica* has involved phages carrying virulence factors (26).

The role of regulatory sRNAs in the interplay of core genomic elements and the horizontally acquired virulence genes has been particularly well studied in *S. enterica*, a model for enteric infections. This bacterium utilizes specialized protein secretion systems encoded within *S. enterica* pathogenicity islands 1 and 2 (SPI-1 and SPI-2) to deliver effector proteins that manipulate mammalian cell signaling cascades (27). Several effectors, including SopE, SspH1, SseI, and SopE2, are encoded by phages or phage remnants (8, 26).

Two core *S. enterica* genome-encoded sRNAs that impact both core-encoded and horizontally acquired

virulence genes are SgrS and RprA. SgrS induction is triggered by the accumulation of nonmetabolizable, phosphorylated sugars in the cell. The SgrS role in responding to phosphosugar stress, repressing the synthesis of sugar transporters and increasing the level of a phosphatase, is conserved across several enteric bacteria (28). However, SgrS has broadened its regulatory repertoire in *S. enterica* to also repress expression of the horizontally acquired SopD effector protein (29). Phosphosugar induction of SgrS, with the concomitant repression of SopD, might help *Salmonella* adjust effector protein production to changes in carbon source availability during the infection process. The core-encoded sRNA RprA is induced by both the Rcs and Cpx two-component systems in response to cell envelope stress and activates the expression of the core-encoded stationary sigma factor σ^S. Like SgrS, RprA has broadened its selection of targets to include two prophage-derived transcripts of *S. enterica* (SL2594 and SL2705) and several mRNAs encoded by the virulence plasmid pSLT (30). Interestingly, RprA activation of *ricI*, one of the pSLT-encoded targets that inhibits plasmid transfer, involves regulation of both core-encoded (indirectly through the stationary-phase sigma factor σ^S, which activates *ricI* transcription) and horizontally acquired (directly through activation of *ricI* translation) genes.

In contrast to SgrS and RprA, two other *S. enterica* sRNAs that control the synthesis of prophage-encoded virulence factors are themselves encoded on horizontally acquired genes specific to *S. enterica*. The first of these, PinT, is strongly induced by the PhoPQ two-component system, a key regulator of *S. enterica* virulence, when the bacteria are internalized in the mammalian cells (31). By base-pairing with the corresponding mRNAs, PinT blocks further synthesis of the prophage-encoded SopE and SopE2 effectors, which are expressed early in infection to facilitate bacterial invasion. PinT also base-pairs with the mRNA that encodes Crp, the transcription factor that controls central carbon metabolism and activates transcription of genes encoding SPI-2 proteins. By regulating the temporal expression of both SPI-1 effectors and SPI-2 virulence genes, PinT facilitates *Salmonella*'s transition from an invasive state to a state capable of intracellular replication (Fig. 1A). Another *S. enterica* island-encoded sRNA, IsrM, is also expressed during infection and inhibits the production of other horizontally acquired genes, such as the SopA effector protein and HilE, a global regulator of SPI-1 transcription (32).

In two examples from other bacteria, both the sRNAs and their target genes were acquired together within a single horizontally transferred module (33). The AfaR sRNA of extraintestinal pathogenic *E. coli* is expressed from the intergenic region between the *afaABCD* and *afaE* transcription units, adjacent to a prophage locus encoding a family of afimbrial adhesins (34). AfaR base-pairs close to the *afaD* translational start site, promoting cleavage by RNase E (an endoribonuclease that recognizes single-stranded RNA and is part of the degradosome), thus reducing the production of AfaD VIII invasin protein while leaving *afaABC* unaffected (35). In another example from *V. cholerae*, the expression of the TarB sRNA from the horizontally acquired *Vibrio* pathogenicity island (VPI) is activated by the master virulence regulator ToxT (36). Upon its induction, TarB inhibits the expression of the VPI-encoded *tcpF* mRNA, which codes for an essential colonization factor of *V. cholerae* (37). It has been speculated that, similar to PinT, TarB helps to coordinate the timing of steps in the infection process by repressing TcpF expression prior to penetration of the mucous barrier of the small intestine.

sRNAs REGULATING PROPHAGE GENES ENCODING TOXINS

Prophages also encode proteins that are toxic to bacteria when synthesized at high levels. sRNA-based mechanisms have evolved to modulate expression of some of these prophage toxins. One example of indirect induction of a toxin involves *E. coli* OxyS, a conserved sRNA characterized early on (38). In fact, it was studies on OxyS that revealed that Hfq functions to facilitate base-pairing of *trans*-encoded sRNAs with their targets (39). Transcription of OxyS is induced by the OxyR transcription factor in response to hydrogen peroxide, and the sRNA was found to repress mutagenesis by an unknown mechanism (38). Only a limited number of OxyS targets, such as *fhlA*, were known (40), and none could explain the toxic phenotype of OxyS overexpression. To identify additional targets, a computational search for mRNAs encoded by essential genes that could base-pair with a predominantly single-stranded section of OxyS, a region encompassing point mutations known to exacerbate or suppress the toxic phenotype, was carried out (41). This approach led to the identification of *nusG*, encoding a vital transcription termination factor, as a target of OxyS. Mutational and probing experiments confirmed that OxyS base-pairs with the transcript and blocks NusG synthesis.

NusG inhibits the production of toxic gene products encoded on horizontally acquired genomic elements, including the *rac* prophage, which carries the *kilR* gene

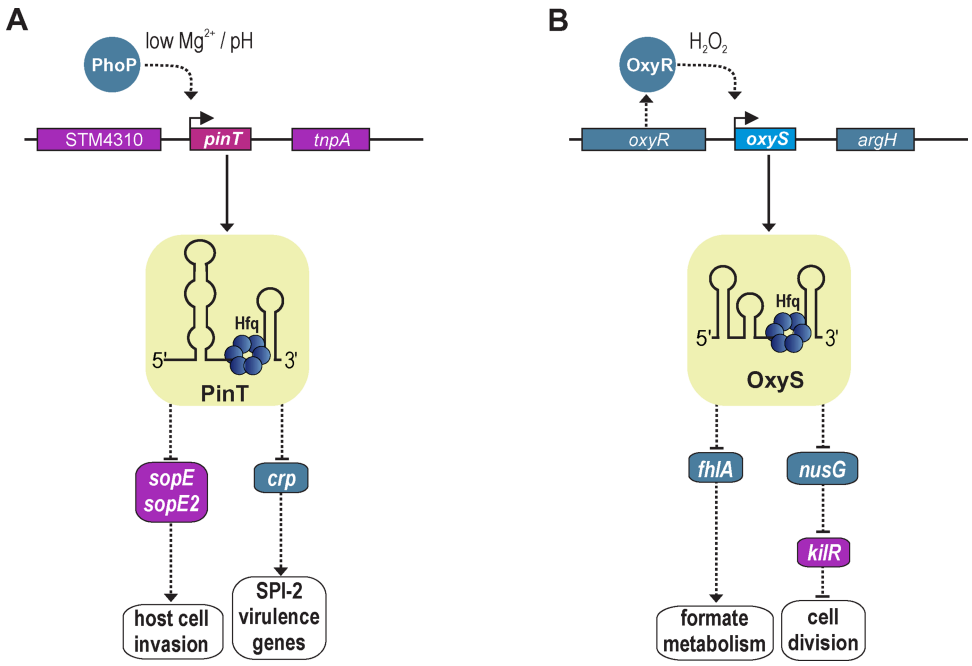

FIGURE 1 Repression of both prophage- and bacterial-encoded mRNAs by sRNAs encoded by horizontally acquired elements and the bacterial core genome. (A) Following host-cell invasion, the prophage-encoded sRNA PinT (purple) is activated by the core genome-encoded transcription factor PhoP (blue). PinT is an Hfq-binding sRNA that regulates multiple target genes through direct base-pairing. These include the mRNAs of the two horizontally acquired effector proteins, SopE and SopE2, as well as the core genome-encoded *crp* mRNA. The Crp protein acts as an activator of SPI-2 (intracellular) virulence genes of *S. enterica*. (B) The core genome-encoded (blue) OxyS sRNA is activated by the OxyR transcription factor under conditions of oxidative stress. OxyS associates with Hfq to regulate at least two targets: the mRNA encoding the FhlA transcription regulator of formate metabolism and the transcript encoding NusG, an important transcription termination factor. OxyS repression of NusG, which normally blocks expression of the prophage-encoded (purple) KilR protein together with the Rho termination factor, results in increased production of KilR, which transiently inhibits cell division.

(42–44). The KilR protein blocks cell division by interfering with the function of FtsZ, which forms the tubulin-like ring required for division (45, 46). Consistent with the model that OxyS repression of NusG results in cell killing by KilR, the effects of OxyS overexpression on cell viability and cell elongation were decreased in a strain lacking the KilR toxin. Given that the OxyS-mediated antimutator phenotype was similarly lost in the *kilR* mutant strain, it seemed plausible that induction of OxyS results in a transient reduction of NusG production, which consequently increases KilR expression from the *rac* prophage and triggers temporary growth arrest (Fig. 1B). The growth arrest, like cell cycle checkpoints in response to DNA damage in eukaryotic cells, allows for DNA repair before normal growth is resumed.

An example of an sRNA that indirectly induces expression of a toxic protein is IsrK, encoded by Gifsy-1 prophage of *Salmonella* (47). The *isrK* promoter directs the synthesis of two distinct RNA species: a short IsrK sRNA and a long mRNA, which encodes an open reading frame of unknown function (*orf45*) and an antirepressor (*anrP*) but is translationally inactive. IsrK sRNA base-pairs with the translationally inactive *orf45-anrP* mRNA to increase translation of the antirepressor protein, AnrP. AnrP in turn activates the transcription of the prophage-encoded antiterminator AntQ. Increased levels of AntQ protein globally impact bacterial transcription termination, leading to growth arrest and ultimately cell death.

A more direct way of controlling toxin production and cell growth is exemplified by *cis*-encoded antisense RNAs that base-pair directly with the toxin mRNAs transcribed from the opposite DNA strand. While a significant number of these classic so-called type I toxin-antitoxin systems are known to be encoded by plasmids and the core bacterial genome, they are also found in

phage and prophage sequences (48). We speculate that large numbers of *cis*-encoded antitoxin sRNAs remain to be characterized. For example, a distinct antisense transcript detected in *E. coli* is encoded opposite the *ymfL* gene of the lambdoid prophage e14 (49) and may silence expression of the protein. While the function of YmfL is currently unknown, overexpression of this region of e14 leads to cell filamentation (44). In a slightly different variation, the RalA sRNA is encoded in *trans*, downstream of the toxic *ralR* gene of the *rac* prophage, but shares 16 nt of complementarity and can block synthesis of the RalR endonuclease in an Hfq-dependent manner (50). Many other examples of *trans*-encoded sRNAs controlling toxin production are anticipated.

PROPHAGE sRNAs REGULATING TRANSCRIPTS ENCODED ON THE CORE GENOME

Given their sophisticated regulatory networks and the concise genomes, it is not surprising that phages and also prophages encode sRNAs (33, 51). These sRNAs are being found not only to regulate phage and prophage genes but also to modulate the expression of genes transcribed from the core genome (Table 1). One of the earliest sRNAs to be discovered in *E. coli* is DicF, an sRNA processed from a polycistronic transcript of the defective lambdoid prophage Qin/Kim (52). Expression of the transcript, which also encodes five small proteins (YdfA, YdfB, YdfC, DicB, and YdfD), is under the control of a *c*I-like repressor (53). The DicF sRNA accumulates as two isoforms in the cell (Fig. 2A). RNase E-mediated processing of the polycistronic transcript generates the 5′ end of both, while alternative Rho-independent transcription termination and RNase III-mediated processing produce the 53-nt and 72-nt variants, respectively (54).

Of the proteins encoded on the polycistronic RNA, only the DicB protein has been reported to have a biological function. The protein interacts with MinC and ZipA and thereby inhibits FtsZ polymerization and consequently cell division (55, 56). Overproduction of the DicF sRNA similarly inhibits cell division, in this case by pairing with the *ftsZ* mRNA to repress translation initiation (57, 58). Consistent with this base-pairing role, DicF associates with the Hfq chaperone *in vivo* (59) and *in vitro* (60).

Two recent studies revealed possible metabolic functions for DicF. High levels of DicF inhibit the expression of metabolic genes encoding a transcription factor involved in D-xylose degradation (*xylR*), pyruvate kinase A (*pykA*), and a mannose transporter (*manX*) (57, 61). While repression of *xylR* requires the DicF 5′ end, repression of *ftsZ* and *manX* involves the very 3′ end of DicF (57, 61), which is unusual for Hfq-mediated base-pairing interactions (62) and might suggest an alternative mechanism of gene regulation. Indeed, rather than sequestering the *manX* ribosome binding site (RBS)

TABLE 1 Examples of posttranscriptional cross-regulation between bacteria and phages

Species	Phage	sRNA	Bacterial target	Bacterial/phage process affected	Reference(s)
Prophage sRNAs regulating transcripts encoded on the core genome					
E. coli	Qin	DicF	*ftsZ*	Cell division	57, 58
			xylR, pykA, manX	Metabolism	57, 61
E. coli	Degraded prophage	EcsR2	*ansB*	Fumarate production	64, 65
EHEC	SpLE1	Esr41	*fliC*	Motility	66, 67
			cirA, bfr, chuA	Iron metabolism	68
Prophage sRNAs regulating sRNAs encoded on the core genome					
EHEC	Sp5	AgvB	GcvB	Niche colonization in cattle	66
	Sp10, SP11	AsxR	FnrS	Iron release from heme	66
Phage sRNAs regulating transcripts encoded on the core genome					
E. coli	PA-2	IpeX	*ompC*	Porin regulation	73
E. coli	Φ24B	24B_1	*d_ant*	Phage production	79
P. aeruginosa	PAK_P3	sRNA2	TψC-tRNA loop	Translation	82
Phage proteins impacting host posttranscriptional regulation					
E. coli	T4	SrD	RNase E	Bacterial RNA decay	85
E. coli	T7	0.7	RNase E	Phage RNA stabilization	86
E. coli	T7	0.7	RNase III	Phage RNA maturation	87
P. aeruginosa	ΦKZ	Dip	RNase E	Phage RNA stabilization	88

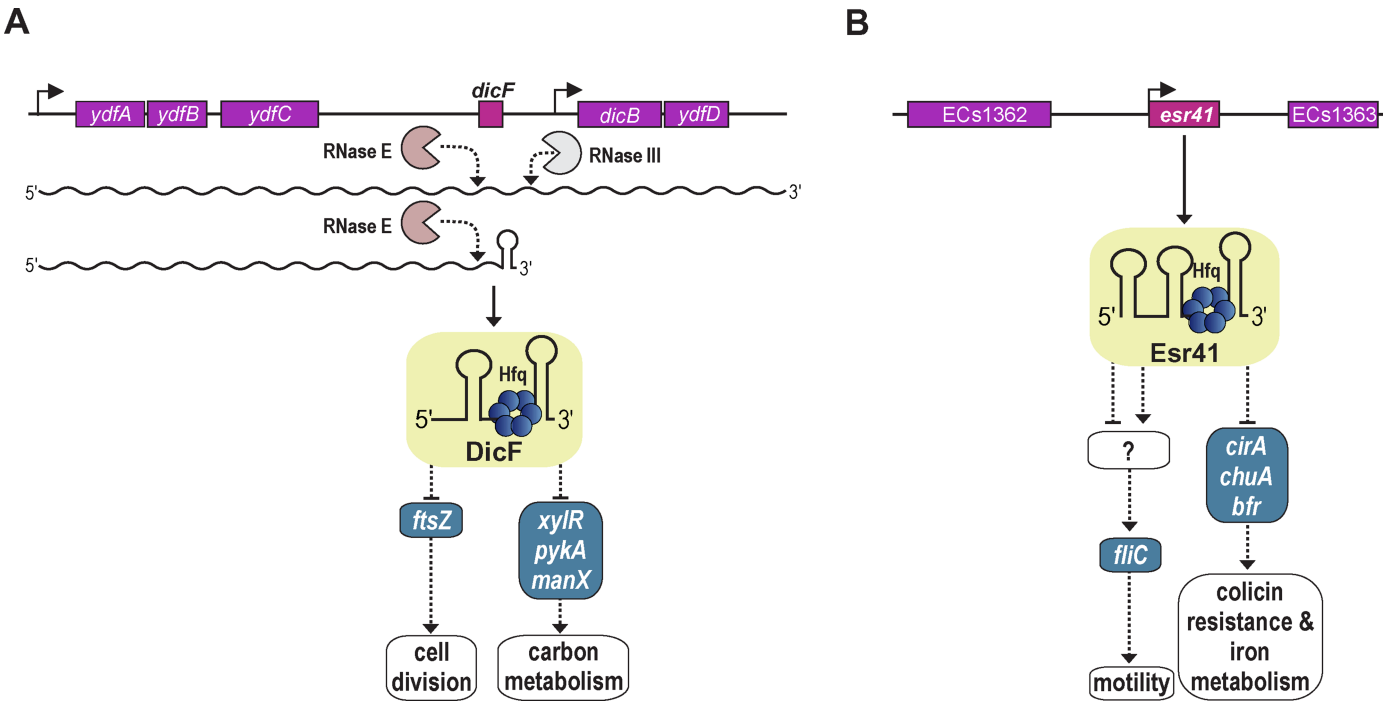

FIGURE 2 Prophage-encoded sRNAs that regulate the expression of host genes. (A) The prophage-encoded (purple) sRNA DicF is processed from a polycistronic transcript by RNase E, and, for the second DicF isoform, by RNase III. DicF associates with Hfq to repress synthesis of the core genome-encoded (blue) FtsZ protein, required for cell division, as well as XylR, PykA, and ManX, all involved in carbon metabolism. (B) Esr41 is a prophage-encoded (purple) sRNA that binds Hfq to inhibit translation of the core genome-encoded (blue) *cirA*, *chuA*, and *bfr* mRNAs. The gene products of the mRNAs are involved in iron metabolism, and repression of *cirA* results in colicin resistance. Esr41 also leads to increased motility by upregulation of FliC; however, the molecular mechanism underlying this process has not yet been determined.

directly, base-pairing of DicF with the *manX* coding sequence recruits Hfq to the RBS to inhibit translation initiation (61). Whether DicF affects metabolic fluxes as a consequence is currently unknown; however, another link between DicF and metabolism comes from the report that DicF is stabilized by enolase under anaerobic conditions (63). Enolase is central to the glycolytic pathway and is also part of the degradosome complex, which is key for bulk RNA turnover in *E. coli* and related organisms.

Degraded prophage genes are the sources of the *E. coli* EcsR2 and *Salmonella* SesR2 sRNAs (64). Whereas very little is known about the biological function of SesR2, posttranscriptional gene regulation by EcsR2 has been studied in *E. coli*. The sRNA is expressed at low levels from the *yagU-ykgJ* intergenic region, and phylogenetic analysis suggests that the sRNA originated from a vestigial phage gene (65). Two independent experimental approaches revealed that the mRNA for a periplasmic L-asparaginase (*ansB*) is a direct interaction partner of EcsR2 and suggested that base-pairing with *ansB* requires an unstructured and conserved sequence element in the center of the sRNA. Because of its recent appearance in the *E. coli* genome, EcsR2 is considered a "young" sRNA and could therefore serve as a model to study sRNA evolution in bacteria.

As discussed above, horizontal gene transfer, especially through infecting phages and lysogens, has a major impact on the evolution of pathogenic microbes. The sRNAs encoded on these virulence-related prophages were previously often overlooked; however, they are now being recognized as a source of posttranscriptional regulators. One such example is Esr41/EcOnc14 (66) from the Sakai prophage-like element (SpLE1) of enterohemorrhagic *E. coli* (EHEC) (Fig. 2B). Esr41 is ~70 nt long and was initially found to stimulate flagellin (*fliC*) expression, and consequently motility, when expressed from a multicopy plasmid (67). It is currently not known if this phenotype requires base-pairing of Esr41 with the *fliC* mRNA or rather is an indirect effect involving additional factors.

A recent study applying CLASH (cross-linking, ligation, and sequencing of hybrids) to RNase E revealed multiple direct interaction partners of Esr41 in EHEC (68). Three mRNAs encoding an iron-siderophore complex uptake receptor (*cirA*), bacterioferritin (*bfr*), and outer membrane heme receptor (*chuA*) were confirmed to form duplexes with Esr41. In all three cases, base-pairing with Esr41 involved the RBS of the target mRNA, suggesting that Esr41 inhibits translation initiation (68). These findings were confirmed at the phenotypic level by showing that Esr41 overexpression renders *E. coli* resistant to pore-forming colicin 1A, which enters the cell through the CirA receptor. Additionally, EHEC cells deficient for *esr41* gained a fitness advantage in iron-limited medium, which might be attributable to derepression of iron transporters in the mutant (68). It is interesting to note that some of the Esr41 targets overlap with validated interaction partners of the core-encoded RyhB sRNA, and that RyhB paralogs have been discovered in the horizontally acquired elements of other enteric pathogens such as *S. enterica* (69).

PROPHAGE sRNAs REGULATING THE ACTIVITY OF CORE GENOME-ENCODED sRNAs

It has become clear that the activities of sRNAs themselves can be regulated by other RNAs, often referred to as "sponge RNAs," that base-pair with and block the activities of the target sRNA. Prophage examples of this type of sponge RNAs have now also been found through studies of Hfq-binding sRNAs in EHEC (66). In this study, transcripts that bound to Hfq were identified upon UV-induced cross-linking of the RNAs to affinity-tagged Hfq, followed by isolation of Hfq and deep sequencing. A surprising finding from this study was that very short sRNAs of 51 to 60 nt encoded by lambdoid prophages were among the most frequently recovered sRNAs. The sRNAs were found to be encoded in similar locations in eight different prophages, and the four most abundant transcripts carry variable 5′ regions of 14 to 18 nt together with highly conserved 3′ regions of 42 nt, which encompass a Rho-independent terminator.

Two of the abundant sRNAs, AsxR and AgvB, were characterized in more detail and found to act as "anti-sRNAs" or sponges against the core genome-encoded FnrS and GcvB sRNAs, respectively (Table 1). Transcriptomic studies examining the consequences of short-term overexpression of AsxR showed that AsxR increases the levels of the *chuAS* mRNA (encoding a heme outer membrane receptor and a heme oxygenase, respectively). These effects were at the posttranscriptional level, but the lack of homology between AsxR and the *chuAS* mRNA did not support a mechanism involving direct base-pairing. Instead, complementarity was observed between the 5′ end of AsxR and the FnrS sRNA, whose expression is highest under anaerobic conditions (70). FnrS does base-pair with and repress *chuAS* translation. Thus, by titrating the negative regulator FnrS and promoting its decay, AsxR indirectly promotes expression of *chuAS*, and potentially other FnrS target genes. AgvB, similarly, was found to alleviate GcvB sRNA-mediated repression of the *dpp* mRNA (encoding a dipeptide transporter). GcvB is highly conserved among the enterobacteria and controls a large regulon of genes coding for amino acid and peptide transporters (71). The 5′ end of AgvB is partially complementary to the conserved R1 seed region by which GcvB recognizes most of its targets, and base-pairing of AgvB with this region antagonizes its function (66). Interestingly, the core-encoded sRNA SroC uses a similar mechanism to counteract GcvB function (Fig. 3) (72). However, different from AgvB, SroC base-pairs with two distinct sequence elements to achieve GcvB degradation. It is worth noting that *E. coli* O157 strain Sakai encodes two copies of *agvB*, which might act additively to curtail GcvB function.

As for other examples discussed thus far, expression of these prophage sponge sRNAs was proposed to impact EHEC virulence. Thus, repression of FnrS, which conceivably is upregulated in the microaerobic environments of the gastrointestinal tract, by AsxR (expressed from the same prophage as Shiga toxin-2), would lead to increased synthesis of heme utilization proteins of benefit in the low iron environment of the infected mammalian cell.

PHAGE sRNAs REGULATING EXPRESSION OF TRANSCRIPTS ENCODED BY THE CORE GENOME

Similar to prophage sRNAs, sRNAs of infecting phages can control core genome expression (Table 1). One example is the IpeX sRNA, transcribed downstream of the *lc* porin gene of phage PA-2. An identical sequence is also present on the genome of the cryptic phage *qsr* (DLP12). Infection of *E. coli* with PA-2 results in the reduction of OmpC production (73), which was attributed to IpeX activity since IpeX overexpression from a plasmid also inhibits OmpC and OmpF production in *E. coli* (74). However, the absence of convincing se-

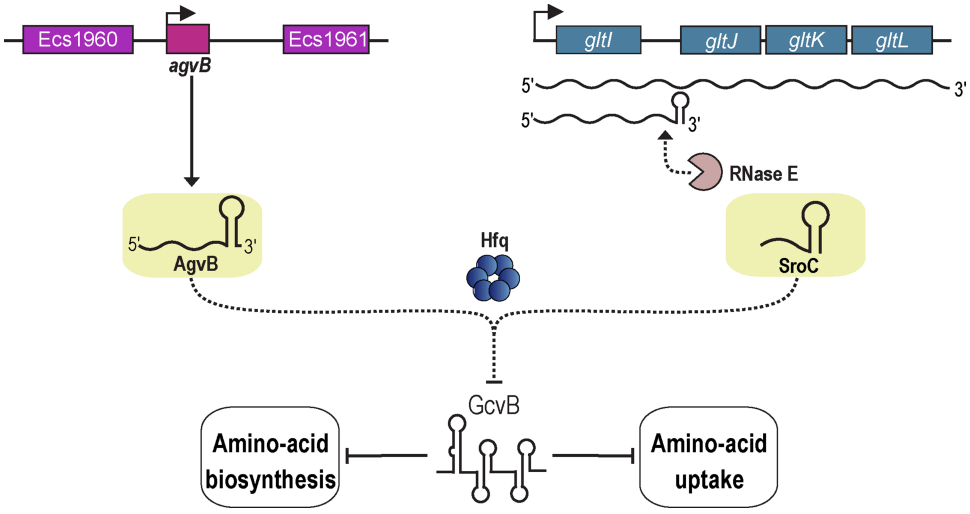

FIGURE 3 Prophage-encoded and core genome-encoded sRNAs that act as sponges to block the activities of core-encoded sRNAs. The prophage-encoded (purple) AgvB sRNA, as well as the core genome-encoded sRNA (blue) SroC use Hfq to base-pair with the GcvB sRNA to inhibit the function of the GcvB global regulator of amino acid uptake and metabolism. SroC is generated from RNase E-mediated endonucleolytic processing of a polycistronic transcript, while AgvB is transcribed from a freestanding gene.

quence complementarity between IpeX and *ompC* suggests that regulation might require additional factors. Similar to DicF, IpeX production was reported to require processing from a larger transcript, a feature that has now been reported for several other sRNAs from diverse microbes (75–78).

An unusual phage-derived sRNA is 24B_1, encoded on the genome of the Shiga toxin-converting phage Φ24B. Different from the bacterial sRNAs described above, 24B_1 is processed from an ~80-nt precursor and accumulates as a transcript of only ~20 nt in the cell (79). As such, 24B_1 has been suggested to resemble the ubiquitous eukaryotic microRNAs (80), a class of posttranscriptional regulators proposed to also exist in bacteria (81). Deletion of 24B_1 from the Φ24B genome has multiple effects on the physiology of the phage, including more efficient prophage induction, increased phage production, and differential bacterial cell adsorption (79). The molecular mechanisms underlying these phenotypes are yet to be discovered, and it will be interesting to explore if these microRNA-sized transcripts also work through base-pairing with mRNA targets or employ alternative regulatory mechanisms.

Unconventional types of gene regulation might also be employed by sRNA1 and sRNA2, which are expressed from the genome of the PAK_P3 phage infecting *Pseudomonas aeruginosa* (82). Both sRNAs accumulate as ~100-nt transcripts and are differentially regulated during the infection process, with expression peaking during late stages of infection. Although complementarity between sRNA2 and bacterial tRNAs has been noted, it again is not clear if sRNA1 and sRNA2 function by base-pairing and whether the true targets are of bacterial and/or phage origin.

Phage- and prophage-encoded sRNA-sized transcripts have now been detected in the transcriptomes of other microbes, including relevant pathogens such as *Mycobacterium* and *Listeria* species (83, 84). These sRNAs await functional characterization, which will be key to understanding their biological functions during phage replication.

PHAGE PROTEINS IMPACTING HOST POSTTRANSCRIPTIONAL REGULATION

To promote their own proliferation, phages have evolved a multitude of mechanisms to exploit the core bacterial machineries, increasing the expression of phage genes while limiting the expression of bacterial genes. The mechanisms include using and modifying bacterial RNA polymerases and, as we will discuss next, the bacterial machinery for degrading RNA (Table 1). For example, infection of *E. coli* by T4 phage results in rapid degradation of bacterial mRNAs. Consequently, bacterial gene expression ceases while the associated generation of ribonucleotides and free ribosomes facilitates transcription and translation of T4 genes (85). A 29-kDa phage protein denoted Srd (due to its similarity with RpoD)

was suggested to be responsible for the differential degradation. The association of Srd and RNase E *in vivo*, the involvement of Srd in the turnover of the unrelated bacterial mRNAs *lpp* and *ompA*, and the importance of Srd to phage proliferation led to the suggestion that Srd stimulates RNase E activity, thus leading to rapid bacterial RNA degradation (85).

Unlike T4, the phage T7 achieves differential RNA stability by inhibiting RNase E. The protein kinase domain of gene *0.7* of T7 phage phosphorylates RNase E and the associated RNA helicase RhlB, which results in the stabilization of mRNAs that are synthesized by T7 RNA polymerase but not those synthesized by *E. coli* RNA polymerase, by mechanisms that to our knowledge are not yet understood (86). Phosphorylation by the phage T7 gp0.7 kinase conversely has been reported to stimulate the activity of RNase III (87).

A more recent study showed that the activity of the *P. aeruginosa* RNA degradosome is inhibited by Gp37/Dip (degradosome interacting protein) encoded by the unusually large phage ΦKZ. Structural studies revealed that acidic patches on the convex outer surface of Dip contact two RNA-binding sites on RNase E, thus preventing RNAs from being bound and degraded by the RNA degradosome (88). The three different phage proteins mentioned, Srd, gp0.7, and Dip, modulate RNase E by very different mechanisms. As the RNA degradation machinery is central to bacterial and phage growth and is broadly conserved, we propose that there are other phage proteins engaged in modulating RNase activity by additional mechanisms that remain to be identified.

VAST POTENTIAL TO IDENTIFY NEW RNA-BINDING PROTEINS, REGULATORY RNAs, AND UNIQUE FUNCTIONS

In general, one aspect of phage and prophage biology that is particularly exciting, also for investigators studying regulatory RNAs, is the vast numbers of unknown genes encoded by these elements. There are estimates of 10^{31} phage particles worldwide (89). Although some phage genes are similar and functionally conserved, the number of potential genes encoded by this many phages is incomprehensible. These worldwide estimates likely even underestimate the number of phages with either single-stranded RNA or double-stranded RNA genomes, or those that dominate unique environments, as these classes may not be identified by standard phage isolation and genomic sequencing approaches (90, 91), or are underannotated because of their divergence from more well-characterized phages (92). One of the few characterized single-stranded RNA phages is the enterobacterial phage Qβ, whose study led to the discovery of Hfq (23). There is no doubt many of the as-yet uncharacterized genes and activities required for the proliferation of these viruses have RNA-related functions. It is worth noting that all of the examples mentioned here come from only three phage taxa (*Caudovirales*, *Inoviridae*, and *Leviviridae*), while virtually nothing is known about RNA-mediated processes for cystoviruses, plasmaviruses, tectiviruses, and microviruses, as well as the viruses that infect archaeal cells.

Likely there are a number of uncharacterized protein families encoded by phages or prophages or by bacterial genomes to modulate phage functions that carry out activities similar to those that are already known. For instance, for organisms that do not have recognizable RNA chaperone proteins such as Hfq, an analogous activity may be found among other proteins that are required for phage replication. Similarly, there is likely to be plethora of unidentified phage- and prophage-encoded sRNAs with standard base-pairing functions. Given the size of the phage metagenome, surprisingly few phage regulatory RNAs, such as the λ OOP and PA-2 IpeX sRNAs (20), have been characterized. The expectation is that there are many such sRNA regulators, especially since sRNA regulators might provide a selective advantage given that phage genomes are small and genes are densely packed. Structured RNAs encoded by phages and prophages, such as the *cis*-acting BOXA and BOXB RNA structures of phage λ and the PUT RNAs of HK022 phage, have long been known to impact transcription elongation (93). Other structured regions of phage and prophage transcripts undoubtedly will be found to have roles in transcription antitermination or additional phage functions, similar to the structured internal ribosome entry site elements required for translation of eukaryotic RNA viruses (94). Some of these elements may bind proteins or tRNAs or molecules like T-box RNAs or riboswitches. It is also possible that the structured sequences are sources for sRNA species cleaved from the longer transcripts.

In addition to uncovering different permutations of known mechanisms, the study of phage and prophage RNAs and their associated proteins could lead to the discovery of unexpected new mechanisms. There still are no known homologs for many phage-encoded proteins. Proteins that are conserved across multiple phage species (core genes) are probably required for phage propagation and thus likely impact conserved bacterial processes, while those that are only present in a more limited number of species (accessory genes) may have

predominantly regulatory roles. The characterization of proteins in both categories may uncover new RNA-based mechanisms. It is also worth noting that some of the largest noncoding RNAs of uncharacterized function, such as the GOLLD and ROOL RNAs, are encoded by phages and prophages (95, 96). Since their size and predicted structural complexity rival those of ribosomes, there are expectations that these large RNAs may have novel ribozyme activities.

INSIGHTS INTO THE EVOLUTION OF RNA-BASED REGULATION FROM PHAGES AND PROPHAGES

Given the evolutionary constraints imposed on the interactions between bacteria, phages, and prophages, especially during phage-mediated horizontal gene transfer, the phage-bacteria interplay is an attractive system for studying the evolution of regulatory RNAs, a relatively unexplored topic (97). Interestingly, early studies noted that the genes encoding the *E. coli* CyaR and *Salmonella* SdsR/RyeB correspond to phage attachment or integration sites (98, 99) due to features that are not yet understood but are possibly shared with tRNA genes given that they also frequently overlap attachment sites (100). As already mentioned, the *E. coli* EcsR2 and *Salmonella* SesR2 sRNAs appear to have evolved from degraded prophage genes (65). Further comparisons among genomes should lead to additional examples and better understanding of the origin and evolution of regulatory RNAs.

The bacteria-phage/prophage systems are also useful for examining the evolution of base-pairing between sRNAs and new mRNA targets. For example, if the main role of OxyS sRNA-mediated repression of *nusG* translation is to promote induction of the prophage KilR, which brings about cell stasis and allows DNA damage repair (41), did this base-pairing only evolve in bacteria that carry the *rac* prophage? OxyS is fairly broadly conserved; did OxyS pairing with mRNAs encoding other proteins affecting cell stasis evolve in organisms without the *rac* prophage? Similar questions are relevant for horizontally acquired targets such as *sopD*, which is repressed by SgrS. Interestingly, while SgrS effectively represses *sopD*, the sRNA does not repress the homolog *sopD2*, although the sequence with potential to base-pair with SgrS only differs by one nucleotide (29). Regions of base-pairing between sRNAs and their targets generally are relatively short, and frequently single nucleotide differences can make or break an interaction and therefore gene regulation, but the rules for productive versus nonproductive base-pairing still are not well understood. Beyond base-pairing-based regulation, comparisons of structured RNA elements across phage species should give insights into the evolution of these features. Given the strong selective forces, only those nucleotides or secondary or tertiary structures that are essential for regulation will be maintained.

Finally, phage- and prophage-associated regulatory RNAs could be useful systems for exploring the evolution of the protein requirements for RNA function. While many bacterial sRNAs require Hfq for function, ProQ and other proteins with a FinO domain have recently been shown to facilitate sRNA-target mRNA pairing in some bacteria (101). Genes encoding potential FinO domain proteins have been discovered in genomes of many phages, and ligands of *Salmonella* ProQ include several phage-associated sRNAs (102). Future experiments will show if phage- or prophage-specific functions of ProQ exist and how these are integrated into the intrinsic gene regulatory networks orchestrated by Hfq and ProQ. A related issue is how many phage base-pairing sRNAs even require RNA chaperones for function. Conceivably, some phage-associated sRNAs, which evolved as *cis*-acting regulators, subsequently adapted to control expression of bacterial genes in *trans* without a requirement for a chaperone protein. Indeed, the Gifsy-1 IsrK sRNA does not require Hfq for function (47).

TAPPING INTO THE PHAGE AND PROPHAGE GOLD MINE OF RNA REGULATION

What are the best approaches to tap into the potential provided by phage and prophage genes? As the transcriptomes of more and more organisms are being determined, it will be critical to annotate the transcripts originating from phage or prophage sequences. This also is true for studies in which RNAs that associate with particular proteins or base-pair with specific RNAs are determined by deep sequencing. Computational searches to identify phage and prophage genes that encode RNAs with predicted secondary structures similar to known regulatory RNAs or proteins with known RNA binding motifs, as well as genes that are syntenic with other genes encoding RNAs or proteins with known functions in RNA metabolism, could also be productive. Likely this will require iterative searches with each newly identified homolog, as was carried out to find phage-encoded transcripts with Y-RNA-like structures and homologs of Ro60 RNA-binding proteins (103). Regardless of the method for identification, detailed functional char-

acterization of phage/prophage regulatory RNAs and RNA-binding proteins will be required to uncover their roles in phage and host physiology.

The expanding and unforeseen biological functions and molecular mechanisms uncovered by the studies of phage/prophage regulatory RNAs are expected to lead to new tools in biotechnology as well as advances in synthetic biology and phage therapy. For example, the large burst sizes and sometimes promiscuous replication mechanisms have made phages useful tools for mutational analysis, and they are now being exploited for directed evolution experiments (104). Either alone or assisted by computational predictions, phages might be used to evolve RNAs with dedicated biological functions or to construct synthetic gene regulatory circuits (105, 106). Finally, phages might be used as a potential treatment to change the human microbiome. In light of the rapidly worsening problem of multidrug-resistant bacterial pathogens, phage-directed antimicrobial therapies are currently experiencing a renaissance (107). Clinical applications of phage therapeutics require a thorough understanding of phage-controlled gene regulatory mechanisms, including RNA-based regulation (108). Thus, the continued characterization of the intricate and sophisticated RNA-based regulatory systems controlling phages and their cross talk with bacteria promises to be a fruitful direction for research for many years to come.

ACKNOWLEDGMENTS

We thank K. Fröhlich, S. Gottesman, and S. Krishnamurthy for comments on the manuscript. Work in the lab of S.A. is supported by GIF (G-1311-416.13/2015); the Israel Science Foundation founded by the Israel Academy of Sciences and Humanities (711/13); the Israel Centers of Research Excellence (ICORE), Chromatin and RNA (1796/12); and DIP (AM 441/1-1 SO 568/1-1); work in the lab of G.S. is supported by the Intramural Program of the Eunice Kennedy Shriver National Institute of Child Health and Human Development; and work in the lab of K.P. is supported by DFG (Exc114-2, GRK2062, SPP2002, PA2820/1, and TRR174), the Human Frontiers Science Program (CDA00024/2016-C), GIF (G-2411-416.13/2016), and the European Research Council (StG-758212).

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