Prophages and plasmids display opposite trends in the types of accessory genes they carry

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1.4 Keyword

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2. Abstract

Prophages and plasmids often possess accessory genes encoding bacterial functions. To uncover rules governing the arsenal of accessory genes prophages and plasmids carry, we compare prophages and plasmids regarding how frequently they carry antibiotic resistance genes (ARGs) and virulence factor genes (VFGs) in 21 pathogenic bacterial species. The results show that prophages

tend to carry VFGs more frequently than ARGs in three species, whereas plasmids tend to carry ARGs more frequently than VFGs in nine species. In the other species, prophage-borne or plasmid-borne ARGs and VFGs are barely detected. We suggest that phages and plasmids differentiate in the types of accessory gene they carry because phages typically kill host cells when they transmit to other cells, whereas plasmids do not.

3. Introduction

Mobile genetic elements (MGEs), such as phages and plasmids, often possess accessory genes encoding bacterial phenotypes that are not apparently integral to the replication and transmission of MGEs. For example, plasmids frequently possess various antibiotic resistance genes (ARGs) [1-3]. Phages and plasmids also possess virulence factor genes (VFGs) required for bacterial pathogenicity [4-8]. Mediating the horizontal transfer of accessory genes between bacteria, MGEs play important roles for the evolution of bacterial genomes and phenotypes [9, 10].

MGEs are parasites of bacteria. Thus, horizontal gene transfer (HGT) mediated by MGEs can be regarded as the genetic manipulation of hosts by parasites [11]. Given that MGEs are self-interested evolving entities, MGEs are expected to possess accessory genes that advantage themselves [12, 13]. For example, plasmids are considered to gain selective advantages from ARGs by improving the survival of their bacterial hosts in heterogeneous environments [13-16]. It has also been hypothesised that phages gain selective advantages from VFGs by modifying environments in which their bacterial hosts live [17].

What evolutionary rules govern the arsenal of accessory genes carried by MGEs [12, 13]? Such rules, if they exist, might reflect the different infection strategies of MGEs. For example, phages typically lyse host cells to transmit to other cells, whereas plasmids do not. Consequently, phages might not gain much of an advantage by carrying genes that improve the survival of bacteria, such as ARGs. To understand the rules governing HGT mediated by MGEs, it is thus beneficial to investigate whether different MGEs carry different types of accessory genes.

To address the above question, we consider an ongoing debate about phage-borne ARGs. While it is well established that plasmids frequently carry ARGs [1-3], how frequently phages carry ARGs is controversial [18]. Phages mediate HGT through multiple mechanisms, among which specialised transduction is the most similar to HGT mediated by plasmid [19]. In specialised transduction, phages transfer genes carried in their genomes. Therefore, specialised transduction is strictly coupled with the infectious transmission of phages, the coupling that is also entailed in plasmid conjugation [19]. Laboratory experiments have demonstrated that phages are capable of transferring ARGs to bacteria through specialised transduction [20]. However, the specialised

transduction of ARGs in nature has been scarcely documented [3, 21]. While metagenomic studies have detected ARGs in viral fractions of environmental DNA samples [22-25], other studies provide evidence suggesting that the detection of ARGs was due to the contamination of bacterial DNA in the viral fractions [26, 27]. Genomics studies have predicted a number of prophages—i.e., phage genomes inserted into bacterial chromosomes as a consequence of specialised transduction—carrying ARGs in the genomes of *Acinetobacter baumannii* [28], *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* [29] [see also [30]]. Also, a previous study has isolated 29 phages from wastewater, of which 15 carry ARGs, suggesting that phages frequently possess ARGs [31]. However, these results appear at odds with a recent comprehensive analysis of phage genomes in public databases, which shows that ARGs are carried by only 0.3% of phages [32]. Taken together, the existing studies present mixed messages about the frequency at which phages carry ARGs.

To investigate how frequently phages carry ARGs, here we compare the distributions of ARGs and VFGs between the prophages and plasmids of pathogenic bacteria by comprehensively analysing public databases. We consider prophages instead of phages to compare different MGEs belonging to the same bacterial genomes. Our approach is designed to mitigate two issues we consider to be involved in the computational analyses of ARGs encoded in prophages, which are not taken into account in previous studies [28-30]. First, the misidentification of prophages can cause systematic biases in the number of prophage-borne ARGs. For example, non-prophage regions can be misidentified as prophages, causing overestimation in the number of prophage-borne ARGs. Contrariwise, a true prophage can be missed, which leads to underestimation in the number of prophage-borne ARGs. To avoid these biases due to prophage prediction, we compare the number of prophage-borne ARGs to that of prophage-borne VFGs, where both numbers are expected to be biased by common factors so that the biases can be cancelled out. The second issue involved in the analysis of prophage-borne ARGs is a sampling bias in bacterial genomes, which can cause overestimation in the numbers of ARGs and VFGs owing to the double-counting of orthologous genes. The degree to which this bias occurs can depend on the types of gene. To correct this bias, we cluster all genes into putative orthologous groups based on sequence similarity and synteny conservation and count the numbers of putative orthologous groups of ARGs and VFGs (OGARGs and OGVFGs, respectively). Finally, to investigate a potential differentiation between prophages and plasmids, we also analyse the distributions of ARGs and VFGs in plasmids. The results suggest that prophages are biased towards carrying VFGs, whereas plasmids are biased towards carrying ARGs. However, in many species, both ARGs and VFGs are hardly detected in prophages and plasmids.

4. Methods

Our method is sketched in Figure 1.

4.1 Data acquisition

The three VFG databases, viz., VFDB (3685 genes in set A), Victors (5085 genes), and PATRIC_VF (1293 genes), were downloaded from the respective websites in December 2020 [33-35]. The VFGs in Victors were refined by removing those carried by non-bacterial pathogens or lacking NCBI protein GIs (4575 genes remained). Some VFGs in Victors were missing protein sequences, which were downloaded from Genbank based on their protein GIs [36]. All VFGs were pooled and clustered to remove redundancy with CD-HIT with the protein sequence identity threshold of 1.0 [37], resulting in a combined database of 7218 VFGs.

The genome assemblies with the 'Complete' status were downloaded from RefSeq in September 2021 with the following criteria [38]: a species had at least 60 complete genomes in RefSeq and at least 70 VFGs in the combined VFG database. These criteria resulted in 21 species of bacterial pathogens spanning three phyla, Actinobacteria, Firmicute, and Proteobacteria, as follows (numbers in brackets indicate the number of genomes examined in this study): *Acinetobacter baumannii* (275), *Bacillus anthracis* (99), *Bordetella pertussis* (562), *Brucella melitensis* (64), *Burkholderia pseudomallei* (126), *Campylobacter jejuni* (220), *Enterococcus faecalis* (64), *Escherichia coli* (1444), *Haemophilus influenzae* (92), *Helicobacter pylori* (225), *Klebsiella pneumoniae* (873), *Legionella pneumophila* (102), *Listeria monocytogenes* (263), *Mycobacterium tuberculosis* (285), *Neisseria meningitidis* (122), *Pseudomonas aeruginosa* (320), *Salmonella enterica* (996), *Staphylococcus aureus* (618), *Streptococcus agalactiae* (91), *Streptococcus pyogenes* (235), and *Vibrio cholerae* (99). The complete list of genomes analysed in this study is in Table S1.

4.2 Prophage prediction

Prophages were predicted with VIBRANT (version 1.2.1), which was selected for three reasons. First, VIBRANT has comparatively high performance as reported by a recent benchmark [39]. Second, it is a standalone tool, which can be run on local computers. Third, its algorithm is based on the similarity search of known phage proteins, which is suitable because our aim was to analyse known prophages rather than discover novel prophages. VIBRANT was run against the genomic nucleotide sequences with default parameters.

4.3 Plasmids

Contigs were considered as plasmids or chromosomes if they were annotated as such in the RefSeq assembly report files (in total, there were 9279 plasmid and 6607 chromosome contigs). Contigs annotated as 'Segment', 'Genome Segment', or 'Extrachromosomal Element' were ignored (3, 1, or 5 contigs, respectively).

4.4 ARG prediction

ARGs were predicted with AMRFinderPlus (version 3.10.5) and the core subset of the database (version 2021-09-11.1) with the organism option if possible [40]. AMRFinderPlus was run against translated coding sequences. The genes predicted by AMRFinderPlus as ARGs (i.e., "element subtype AMR") and not annotated as pseudo-genes in RefSeq were considered as ARGs (those predicted as "element subtype POINT", which contain point mutations associated with AR, were excluded).

4.5 VFG prediction

Every VFG in the combined VFG database was queried against every bacterial genome with BLASTP with E-value threshold of 1e-9 [41]. A gene in a bacterial genome (bacterial gene, for short) could match multiple VFGs in the combined VFG database, in which case the VFG with the highest bit-score was selected as the best match. A bacterial gene was considered as encoding VF if it met the following additional criteria: (i) it was not annotated as a pseudo-gene in RefSeq [38]; (ii) the BLASTP alignment between the bacterial gene and its best match VFG, if any, had at least 80% sequence identity and covers at least 80% of both the bacterial gene and the best match VFG; (iii) the species of the genome in which the bacterial gene resides was identical to the species in which the best match VFG resides [33-35].

4.6 Orthology prediction

Genes annotated in RefSeq were clustered into putative orthologous groups based on protein sequence similarity and synteny conservation, as follows. First, preliminary orthologous pairs of genes were identified between every pair of genomes within each species through all-against-all sequence similarity searches using ProteinOrtho version 6.0.25 (with DIAMOND ver. 2.0.6 [42]; E-value cut-off of 1e-5; minimum coverage of best alignments of 75%; minimum per-cent identity of best alignments of 25%; minimum reciprocal similarity of 0.95) [43]. ProteinOrtho defines a preliminary orthologous pair of genes as a reciprocal nearly-best hit (RNBH), as follows. A nearly-best hit (NBH) of a gene queried against a target genome is defined as a hit whose bit-score is not smaller by a factor f than that of the best hit. The value of f was 0.95, which is the default value of ProteinOrtho. If two genes are mutually NBH of each other, they form RNBH [43].

RNBHs obtained with ProteinOrtho were pruned based on synteny conservation with an in-house script, as follows. Let x and y be a pair of genes forming RNBH, and let X and Y be the genomic neighbours of x and y, respectively, where the genomic neighbour of a gene (denoted by z) is defined as a set of 21 genes consisting of ten genes upstream of z, ten genes downstream of z, and z itself (all contigs were assumed to be circular, and the orientation of genes were ignored). Let N_x and N_y be the number of genes in X and Y that form RNBHs with at least one gene in Y and X, respectively (note that a single gene in one genome can form RNBHs with multiple genes in another genome owing to tandem duplication). If both N_x and N_y are greater than ten (i.e., a majority of the genes in X

form RNBHs with the genes in *Y*, and *vice versa*), the RNBH formed by *x* and *y* was kept; otherwise, it was discarded [44].

Finally, the pruned RNBHs were clustered into putative orthologous groups with the spectral clustering algorithm implemented in ProteinOrtho version 6.0.25 (minimum algebraic connectivity of 0.1; exact step 3; minimum number of species of 0; purity of 1e-7) [43].

4.7 Classification of orthologous gene groups

A gene (VFG or ARG) was considered as encoded in a prophage if the entire gene is included within a genomic region predicted as a prophage.

An orthologous group of genes was considered to be encoded in a prophage residing in a chromosome (chromosomal prophage, for short), a prophage residing in a plasmid (plasmidic prophage), or a plasmid if the majority of the genes belonging to the group were in chromosomal prophages, plasmidic prophages, or plasmids, respectively (the cases of ties were ignored). Orthologous groups in plasmidic prophages were classified separately from those in chromosomal prophages or plasmids, for two reasons. First, it was ambiguous whether they should be regarded as encoded by plasmids, prophages, or both. Second, plasmidic prophages potentially represent a distinct class of mobile genetic elements called phage-plasmids [45].

An orthologous group of genes was considered as an ARG or VFG if the majority of the genes belonging to the group were predicted as ARGs or VFGs, respectively. The majority rule was used because a subset of genes in OGARG or OGVFG could be predicted as non-ARGs or non-VFGs, respectively, owing to sequence divergence. However, for most orthologous groups of ARGs and VFGs, all genes in a group were predicted as either ARGs or VFGs. Moreover, no orthologous group contained both ARGs and VFGs.

5. Results

5.1 Prophage prediction

To examine the distribution of ARGs in prophages, we computationally predicted prophages using VIBRANT [46] and ARGs using AMRFinderPlus [40] in the genomes of 21 pathogenic bacterial species downloaded from the RefSeq database [38] (Methods; Tables S1 and S2). To avoid double-counting orthologous ARGs in different genomes, we clustered all genes into putative orthologous groups based on sequence similarity and synteny conservation (Methods). We then counted the number of

orthologous groups of ARGs (OGARGs) encoded in the predicted prophages, distinguishing between prophages residing in bacterial chromosomes and prophages residing in plasmids (chromosomal prophage and plasmidic prophage, respectively, for short). This distinction was made because it was ambiguous whether ARGs in plasmidic prophages should be regarded as encoded in prophages, plasmids, or both [plasmidic prophages potentially represent phage-plasmids, which are a separate class of MGEs from typical phages and plasmids [45]]. The result shows that a few to several prophage-borne OGARGs were detected in ten of the 21 examined species (Tables 1 and S3).

To probe the precision of the above prediction, we manually examined whether predicted prophages carrying ARG contained at least one phage-structure gene (e.g., phage baseplate, capsid, portal, tail, tail fibre, tail sheath, tail assembly, head-tail connector, and tail tape measure) according to the RefSeq annotation. Although this criterion cannot perfectly distinguish true prophages from false ones, it allows us to split the predicted prophages into those enriched with true prophages and those enriched with false prophages, allowing us to probe the precision of the prophage prediction. The result of the examination shows that 24 out of 29 (i.e., 83% of) chromosomal prophages carrying ARGs contained phage-structure genes, whereas seven out of 18 (i.e., 39% of) plasmidic prophages carrying ARGs contained phage-structure genes (Table S4). This result means that 28 out of 33 (i.e., 85% of) OGARGs in chromosomal prophages are in prophages carrying phage-structure genes, whereas nine out of 21 (i.e., 43% of) OGARGs in plasmidic prophages are in prophages carrying phage-structure genes (Table 1; note that the number of prophages carrying ARGs is smaller than that of prophage-borne ARGs because one prophage can carry multiple ARGs). This result suggests that the precision of VIBRANT is acceptable for chromosomal prophages.

During the manual examination, we noticed that a subset of plasmidic prophages carrying ARGs also carried genes encoding integron integrases according to the RefSeq annotation (Tables S4). Moreover, these prophages have a higher frequency of lacking phage-structure genes than those without integron integrase genes (IIGs, for short). Specifically, seven out of ten (i.e., 70% of) prophages carrying both ARGs and IIGs lack phage-structure genes, whereas nine out of 37 (i.e., 24% of) prophages carrying ARGs and lacking IIGs lack phage-structure genes. VIBRANT predicted that the genes annotated by RefSeq as IIGs matched phage integrase genes, which are typical components of phage genomes. However, the RefSeq annotation implies that proteins encoded by these genes are more similar to integron integrases than phage integrases because the RefSeq annotation considers a broader set of protein families than does VIBRANT [38, 46]. Therefore, the above result suggests that about a half of the prophages carrying ARGs and lacking phage-structure genes might have arisen from the misidentification of integrons as prophages [see also [47]].

5.2 Prophages carry significantly more VFGs than ARGs in multiple species

To compare the frequencies of ARGs to those of VFGs in chromosomal prophages, we used BLASTP [41] to search bacterial genomes for VFGs collected from VFDB [33], Victors [34] and PATRIC_VF [35] (Methods). We counted the number of orthologous groups of VFGs (OGVFGs, for short) encoded in the predicted prophages (Tables 1 and S5). The number of OGVFGs cannot directly be compared to that of OGARGs because we have no *a priori* reason to expect that bacteria possess an equal number of VFGs and ARGs. Thus, we instead compared the relative frequencies of OGVFGs and OGARGs against the genomic background (see Figure 1 for the illustration of what we did). Specifically, we performed binomial tests under the null hypothesis that the relative frequencies of OGARGs and OGVFGs in the chromosomal prophages of each species are the same as those of all OGARGs and OGVFGs in the genomes of the respective species. In this test, we included prophages lacking phage-structure genes for fairness because prophages carrying VFGs were too numerous to be manually examined (however, we found that none of the prophages carrying VFGs carried IIG, which suggests that the prophages carrying VFGs do not contain false positives arising from integron misidentification). Also, we corrected P values using the Holm–Bonferroni method to control the family-wise error rate of all the statistical tests conducted in this study [48, 49]. The results of the tests indicate that the relative frequencies of OGARGs and OGVFGs in chromosomal prophages are significantly different from those of respective genomic backgrounds in the following three species (Figure 2): *E. coli* (Gammaproteobacteria), *S. enterica* (Gammaproteobacteria), and *S. aureus* (Firmicute). In all these species, chromosomal prophages carry VFGs more frequently than ARGs. The remaining 18 species, where significant biases were not detected, can be grouped into three categories: the one species where a large number of prophage-borne VFGs were detected, but a bias was not significant (*S. pyogenes*), the eight species where only a small number of prophage-borne ARGs or VFGs were detected (*A. baumannii*, *B. anthracis*, *H. influenzae*, *K. pneumoniae*, *N. meningitidis*, *P. aeruginosa*, *S. agalactiae*, and *V. cholerae*), the six species where no prophage-borne ARG and VFG were detected (*B. pertussis*, *B. melitensis*, *B. pseudomallei*, *C. jejuni*, *E. faecalis*, *L. pneumophila*), and the three species where prophages were rarely or hardly detected (*H. pylori*, *L. monocytogenes*, and *M. tuberculosis*) (Table 1 and Figure 2). The paucity or absence of prophage-borne ARGs and VFGs could be due to the limited sensitivity of the prophage prediction tool. However, a large number of prophages were predicted in the second and third categories of species. Therefore, if the prophage prediction tool missed prophages carrying ARGs or VFGs in these species, those prophages are likely to be distinct from the currently known phages. Taken together, the above results suggest that phages tend to carry ARGs less frequently than VFGs if they carry a sufficient number of ARGs or VFGs; however, in many bacterial species, they carry little or no ARGs and VFGs.

5.3 Plasmids carry more ARGs than VFGs in many of species

To compare prophages to plasmids, we counted the number of OGARGs and OGVFGs encoded in plasmids (Table 2). We then performed binomial tests under the null hypothesis that the relative frequencies of OGARGs and OGVFGs in the plasmids of each species are the same as those of all OGARGs and OGVFGs in the genomes of the respective species. The results of the tests indicate that

the relative frequencies of OGARGs and OGVFGs in plasmids are significantly different from those of the genomic background in nine out of the 21 examined species (Figure 3). In all these species, plasmids are biased towards carrying ARGs more frequently than VFGs. These species include six species of Gammaproteobacteria (*A. baumannii*, *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *S. enterica*, and *V. cholerae*), one species of Epsilonproteobacteria (*C. jejuni*), and two species of Firmicutes (*E. faecalis* and *S. aureus*). The remaining 12 species, where significant biases were not detected, can be grouped into three categories: the four species where plasmids are hardly present (*B. pertussis*, *B. melitensis*, *M. tuberculosis*, and *N. meningitidis*), the seven species where plasmids are rare, and plasmid-borne ARGs and VFGs were barely detected (*B. pseudomallei*, *H. influenzae*, *H. pylori*, *L. pneumophila*, *L. monocytogenes*, *S. agalactiae*, and S. pyogenes), and the one species where plasmids carry more VFGs than ARGs, but a bias was not significant (*B. anthracis*). Taken together, the above results suggest that plasmids tend to carry ARGs more frequently than VFGs if they carry a sufficient number of VFGs or ARGs, with a possible exception of *B. anthracis*; however, in several species, plasmids barely carry VFGs and ARGs.

6. Discussion

The results presented above indicate that prophages tend to carry VFGs more frequently than ARGs in three of the 21 examined species. In most of the other species, prophage-borne ARGs and VFGs were hardly detected. In contrast, plasmids carry ARGs more frequently than VFGs in nine of the 21 examined species. In most of the other species, plasmid-borne ARGs and VFGs were barely detected. Taken together, these results indicate that prophages and plasmids display opposite trends if they carry a sufficient number of VFGs or ARGs: prophages are biased towards carrying VFGs, whereas plasmids toward carrying ARGs. This difference between phages and plasmids led us to formulate the following hypothesis to test for future (Figure 4): Temperate phages do not gain much benefit from carrying ARGs because if their hosts are in danger, they can abandon their hosts and seek new ones [50-54]. In contrast, both phages and plasmids can benefit from VFGs because VFGs can accelerate bacterial replication by making bacteria exploit their hosts more aggressively [17].

The results described above, however, do not mean that plasmids rarely carry VFGs or that prophages always carry VFGs. For example, in *K. pneumoniae*, plasmids carry ARGs more frequently than VFGs; nevertheless, plasmids carry a large number of VFGs (viz., 96 out of 372 orthologous groups), whereas prophages carry none (Tables 1 and 2). A similar, yet less striking, pattern is seen in *E. faecalis*. Given that many prophages are predicted in these species (Table 1, Figure 2), the absence of prophage-borne VFGs is unlikely to be merely due to the limited sensitivity of the prophage detection tool. By contrast, in *S. aureus* and *S. pyogenes*, prophages carry greater numbers of VFGs than do plasmids (Tables 1 and 2). This heterogeneity in the distribution of VFGs suggests that plasmids and prophages play variable roles in the pathogenicity of different bacterial species.

The absolute numbers of prophage-borne ARGs reported in this study need to be interpreted with caution because of the limited sensitivity and precision of the prophage prediction tool. In particular, these numbers do not necessary indicate that prophages are devoid of ARGs in many bacterial species since prophages carrying ARGs could have been missed. However, the conclusion of this study does not directly depend on the absolute numbers of prophage-borne ARGs because it is based on comparison between the relative frequencies of prophage-borne ARGs and VFGs.

Regarding the limitations of prophage prediction tools, it is pertinent to discuss a discrepancy between our result and the result of Kondo et al. (2021) with respect to *P. aeruginosa* [29]. While we found no prophage-borne ARGs in *P. aeruginosa*, Kondo et al. (2021) reports that more than 10% of *P. aeruginosa* genomes possess prophage-borne ARGs [29]. The important difference between Kondo et al. (2021) and our study is that they used different tools for prophage prediction: Kondo et al. (2021) uses PHASTER [55], whereas we used VIBRANT [46]. To investigate the cause of the above discrepancy, we manually examined the 11 prophages described in Kondo et al. (2021) that carry ARGs and are predicted as "intact" by PHASTER in *P. aeruginosa* [29]. We found that the examined prophages could be grouped into two categories (Table S6). In the first group (five prophages), both VIBRANT and PHASTER predicted prophages in almost the same genomic locations. However, PHASTER predicts longer genomic regions including ARGs as prophages, whereas VIBRANT predicted shorter regions excluding ARGs. We do not know which prophage boundaries are more accurate. In the second group (6 prophages), prophages were predicted only by PHASTER. These prophages, however, contained no phage-structure genes. Although they contained phage-related genes, such as integrase, transposase, and protease, these genes are not exclusively associated with phages. Moreover, PHASTER annotated tellurium resistance proteins, TerD, as virion structural proteins in three prophages in the second group, which is likely to be erroneous. These findings suggest that the second group of the prophages could be false positives. Prophages predicted as "incomplete" or "questionable" by PHASTER are less likely to be true than those predicted as "intact". Taken together, the above results suggest that the frequency of prophage-borne ARGs in *P. aeruginosa* is potentially underestimated in our study and overestimated in Kondo et al. (2021) owing to the limitations of the prophage prediction tools.

In interpreting the results obtained in this study, we assumed that ARGs and VFGs found within prophages were carried by phage genomes. However, these genes could have been inserted into pre-exiting inactivated prophages (i.e., inserted after lysogeny). Although this possibility cannot be completely excluded, the following evidence suggests that not all ARGs and VFGs are inserted into pre-existing inactivated prophages. A previous study has shown that ARGs and VFGs are found in the genomes of temperate phages (which are thus not prophages) and that these genes are hardly found in the genomes of virulent phages [32]. This result would not be expected if all ARGs and VFGs were inserted into pre-existing inactivated prophages. More important, we do not have an *a priori* expectation that VFGs are more likely to be inserted into pre-existing prophages than ARGs. In the absence of such an expectation, our results are likely to be robust to post-hoc insertions of ARGs

and VFGs because they are based on comparison between the relative frequencies of ARGs and VFGs.

That phages do not possess ARGs does not necessarily mean that phages do not mediate the horizontal transfer of ARGs because they can mediate HGT even if their genomes do not contain ARGs. Phages mediate HGT through three known mechanisms: specialised, generalised, and lateral transduction [19, 56, 57]. In specialised transduction (the focus of this study), a transferred gene constitutes a part of a phage genome [19]. By contrast, in generalised and lateral transduction, a transferred gene is originally encoded in bacterial DNA, which is encapsulated into phage particles and subsequently transferred to other cells [19, 56, 57]. Thus, phages can mediate the horizontal transfer of ARGs even if their genomes do not contain ARGs.

In conclusion, the results presented above lend support to the hypothesis that MGEs differ in the functional categories of accessory genes they carry depending on their infection strategies.

7. Author statements

7.1 Conflicts of interest

The authors declare that there are no conflicts of interest.

7.2 Funding information

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8. Tables and figures

Table 1. Numbers of predicted prophages per genome (SD, standard deviation), and number of orthologous groups of antibiotic resistance genes (OGARGs) predicted by AMRFinderPlus in genomes

(total), predicted plasmidic prophages, and predicted chromosomal prophages. Numbers in brackets are for OGARGs in prophages containing at least one phage-structure gene.

	prophage (SD)	OGARG			OGVFG		
		total	prophage		total	prophage	
			plasmidic	chromosomal		plasmidic	chromosomal
A. baumannii	4.3 (1.7)	455	0	4 (4)	48	0	0
B. anthracis	4.1 (0.6)	17	0	1 (1)	39	0	0
B. pertussis	1.9 (0.3)	0	0	0	95	0	0
B. melitensis	1.0 (0.3)	1	0	0	183	0	0
B. pseudomallei	2.2 (1.3)	3	0	0	192	0	0
C. jejuni	1.1 (1.2)	65	0	0	480	0	0
E. faecalis	3.8 (1.8)	179	2 (0)	0	114	1	0
E. coli	7.1 (3.8)	3041	9 (7)	9 (9)	18019	6	1590
H. influenzae	3.0 (1.4)	7	0	0	161	0	1
H. pylori	0.2 (0.5)	6	0	0	285	0	0
K. pneumoniae	4.5 (2.1)	1473	7 (2)	7 (7)	372	0	0
L. pneumophila	0.1 (0.3)	5	0	0	773	0	0
L. monocytogenes	2.5 (1.3)	5	0	0	172	0	0
M. tuberculosis	0 (0.1)	4	0	0	997	0	0
N. meningitidis	1.9 (0.6)	4	0	0	123	0	1
P. aeruginosa	4.5 (2.7)	543	0	0	526	0	2
S. enterica	3.9 (1.8)	826	2 (0)	0	1844	2	64
S. aureus	3.5 (1.3)	423	0	6 (2)	217	0	28
S. agalactiae	2.0 (1.0)	46	0	1 (1)	71	0	0
S. pyogenes	3.1 (1.5)	28	0	3 (3)	103	0	48
V. cholerae	1.5 (1.2)	101	1 (0)	2 (1)	251	1	5

400 **Table 2**. Numbers of plasmids per genome (SD, standard deviation), and numbers of orthologous
401 groups of virulence factor genes (OGVFGs) and those of antibiotic resistance genes (OGARGs) in
402 genomes (total) and plasmids.

	Plasmid (SD)	OGARG		OGVFG	
		total	plasmid	total	plasmid
A. baumannii	1.7 (1.6)	455	195	48	0
B. anthracis	1.5 (0.9)	17	1	39	14
B. pertussis	0.0 (0.0)	0	0	95	0
B. melitensis	0.0 (0.0)	1	0	183	0
B. pseudomallei	0.1 (0.3)	3	0	192	0
C. jejuni	0.3 (0.6)	65	21	480	9
E. faecalis	1.4 (1.4)	179	127	114	24
E. coli	2.0 (1.9)	3041	2397	18019	2452
H. influenzae	0.0 (0.1)	7	1	161	0
H. pylori	0.2 (0.4)	6	0	285	0
K. pneumoniae	3.4 (2.2)	1473	1274	372	96
L. pneumophila	0.3 (0.5)	5	1	773	0
L. monocytogenes	0.2 (0.5)	5	0	172	1
M. tuberculosis	0.0 (0.0)	4	0	997	0
N. meningitidis	0.0 (0.0)	4	0	123	0
P. aeruginosa	0.2 (0.6)	543	128	526	3
S. enterica	1.1 (1.2)	826	638	1844	46
S. aureus	0.8 (1.0)	423	182	217	9
S. agalactiae	0.0 (0.1)	46	1	71	0
S. pyogenes	0.0 (0.2)	28	3	103	0
V. cholerae	0.1 (0.4)	101	36	251	0

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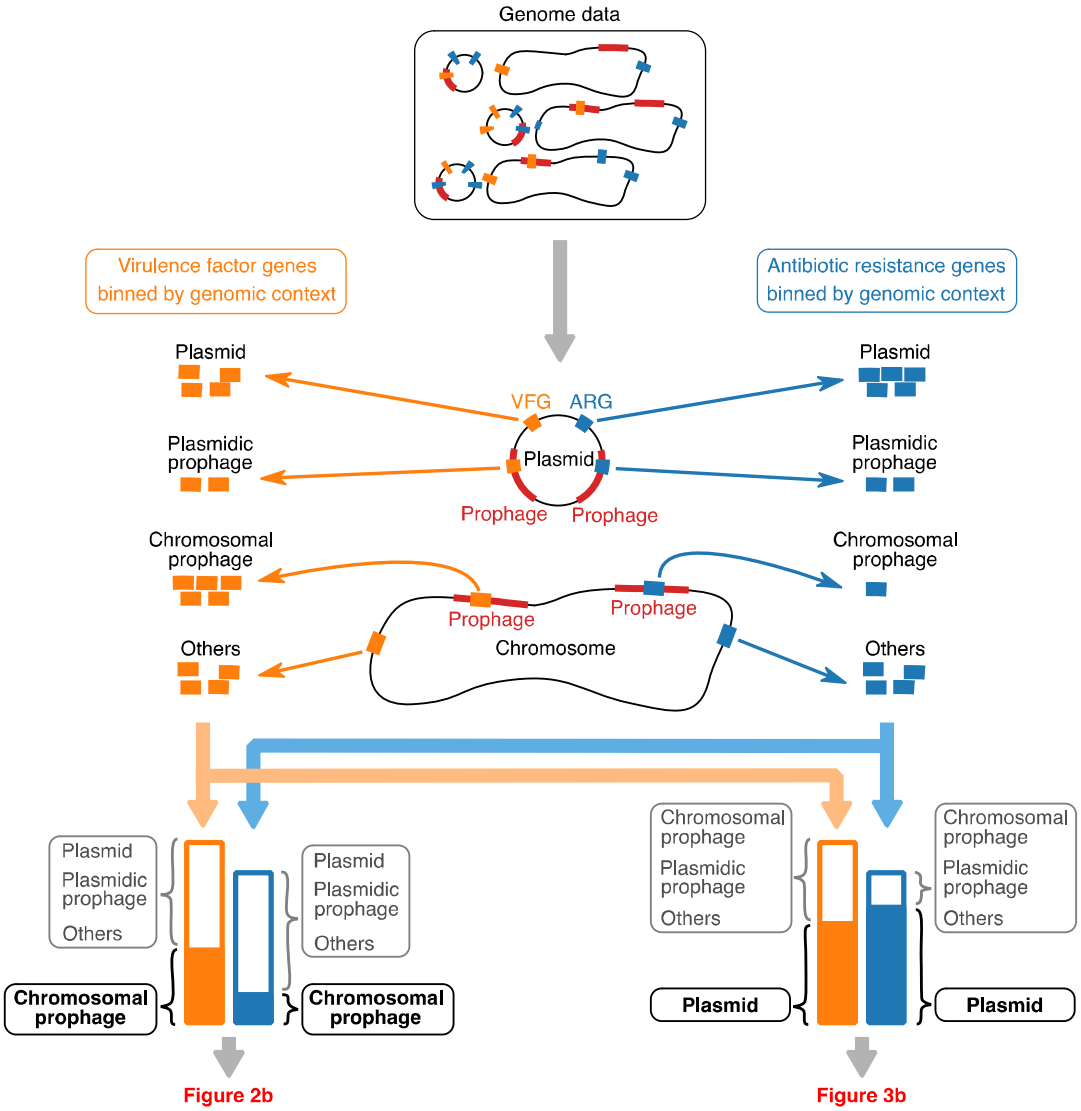

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406 Figure 1. Schematic drawing of what we did in this study. For simplicity, clustering of orthologous
407 genes is omitted from depiction (see Methods).

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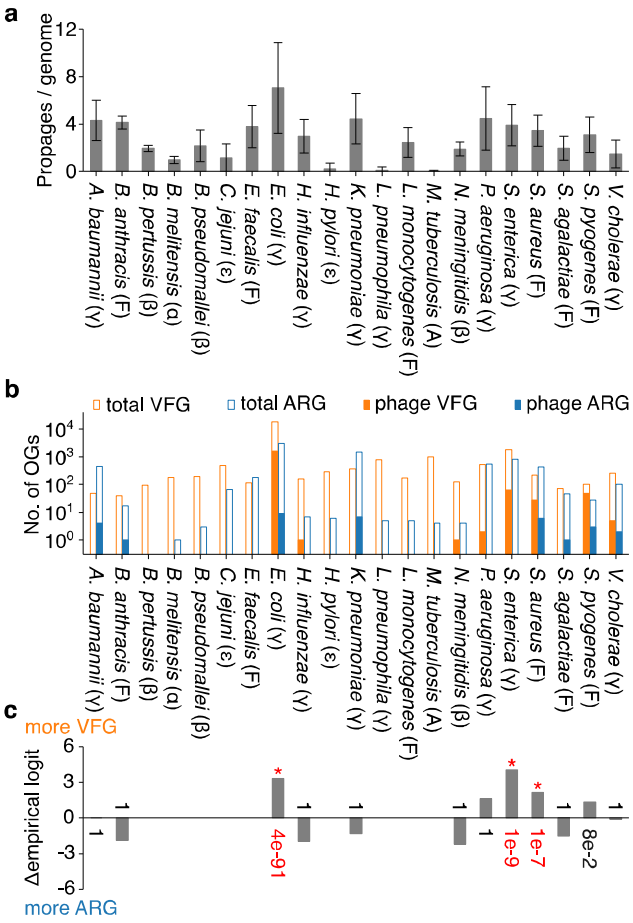

Figure 2. **a** Average number of prophages per genome and standard deviation. **b** Numbers of orthologous groups of virulence factor genes (OGVFGs) and antibiotic resistance genes (OGARGs) in prophages (filled bars) and genomes (open bars). Symbols in brackets indicate taxonomic groups: Actinobacteria (A), Firmicute (F), Alphaproteobacteria (α), Betaproteobacteria (β), Epsilonproteobacteria (ε), and Gammaproteobacteria (γ). **c** Degree of bias towards carrying VFGs more frequently than ARGs. Negative values indicate opposite bias (zero indicates no bias). Difference between empirical logits (denoted as Δempirical logit) is defined as $\log([a+0.5]/[b+0.5]) - \log([c+0.5]/[d+0.5])$, where a and b are numbers of OGVFGs and OGARGs in prophages, respectively (filled bars in a), and c and d are numbers of all OGVFGs and OGARGs in genomes, respectively (open bars in a). Numbers next to bars are P values of two-sided binomial test under null hypothesis that a and b are numbers drawn from binomial distribution with probabilities $c/(c+d)$ and $d/(c+d)$, respectively (corrected by the Holm–Bonferroni method). Asterisks and red numbers indicate that P values are less than or equal to 0.05.

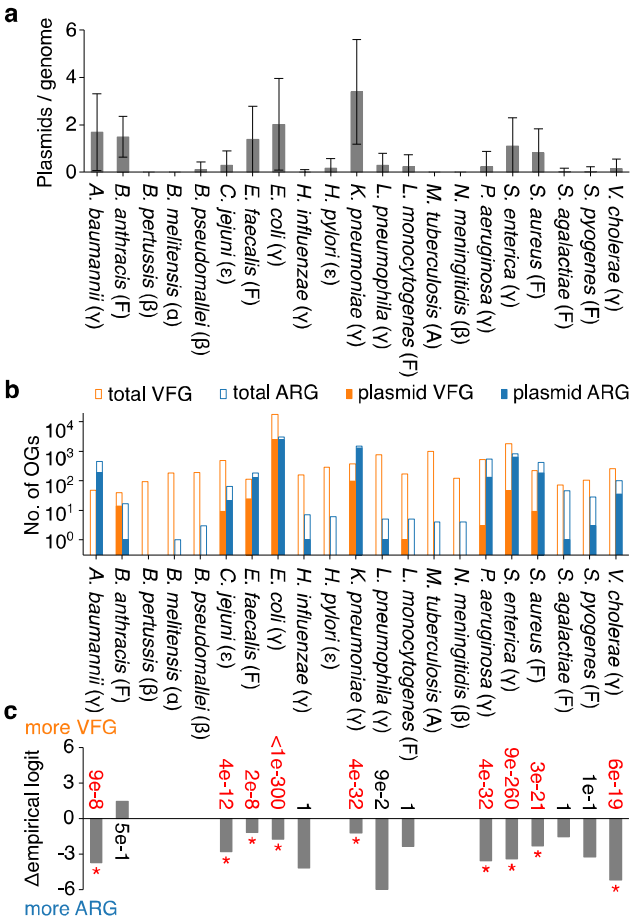

Figure 3. **a** Average number of plasmids per genome and standard deviation. **b** Numbers of orthologous groups of virulence factor genes (OGVFGs) and antibiotic resistance genes (OGARGs) in plasmids (filled bars) and genomes (open bars). Symbols in brackets indicate phyla: Actinobacteria (A), Firmicute (F), Alphaproteobacteria (α), Betaproteobacteria (β), Epsilonproteobacteria (ε), and Gammaproteobacteria (γ). **c** Degree of bias towards carrying VFGs more frequently than ARGs. Negative values indicate opposite bias (zero indicates no bias). Difference between empirical logits (denoted as Δempirical logit) is defined as $\log([a+0.5]/[b+0.5]) - \log([c+0.5]/[d+0.5])$, where a and b are numbers of OGVFGs and OGARGs in prophages, respectively (filled bars in a), and c and d are numbers of all OGVFGs and OGARGs in genomes, respectively (open bars in a). Numbers next to bars are P values of two-sided binomial test under null hypothesis that a and b are numbers drawn from binomial distribution with probabilities $c/(c+d)$ and $d/(c+d)$, respectively (corrected by the Holm–Bonferroni method). Asterisks and red numbers indicate that P values are less than or equal to 0.05.

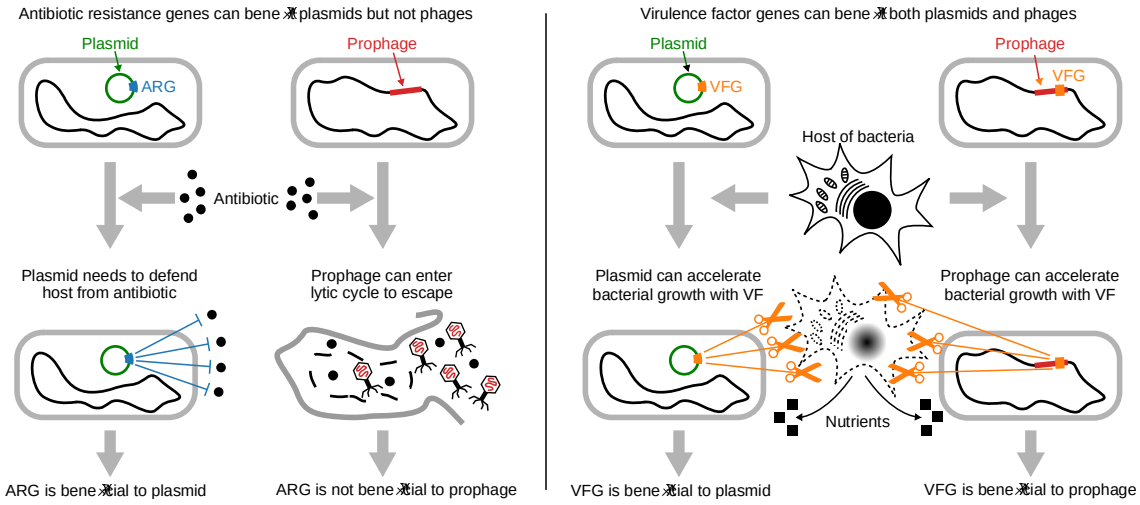

Figure 4. Schematic drawing of hypothesis formulated based on our results. Plasmids gain benefit from carrying ARG because they cannot abandon their hosts and thus need to minimise death of bacteria. However, temperate phages do not gain much benefit from carrying ARGs because if their hosts are in danger, they can abandon their hosts by entering lytic cycles and seek new hosts. In contrast, both plasmids and phages can benefit from VFGs because VFGs can enhance growth of bacteria by causing bacteria to exploit their hosts more aggressively.

9. Supplementary information

Supplementary files can be downloaded from
https://www.biorxiv.org/content/10.1101/2022.07.21.500938v1

Table S1: List of all genome assemblies used in this study.

Table S2: List of all prophages predicted by VIBRANT.

Table S3: List of all orthologous groups of antibiotic resistance genes.

Table S4: Information about all prophages manually examined.

Table S5: List of all orthologous groups of virulence factor genes.

Table S6: List of prophages that are described in Kondo et al. (2021) and manually examined in this study.

In-house scripts

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