

Phages of Listeria offer novel tools for diagnostics and biocontrol

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Historically, bacteriophages infecting their hosts have perhaps been best known and even notorious for being a nuisance in dairy-fermentation processes. However, with the rapid progress in molecular microbiology and microbial ecology, a new dawn has risen for phages. This review will provide an overview on possible uses and applications of *Listeria* phages, including phage-typing, reporter phage for bacterial diagnostics, and use of phage as biocontrol agents for food safety. The use of phage-encoded enzymes such as endolysins for the detection and as antimicrobial agent will also be addressed. Desirable properties of candidate phages for biocontrol will be discussed. While emphasizing the enormous future potential for applications, we will also consider some of the intrinsic limitations dictated by both phage and bacterial ecology.

Keywords: bacteriophage, tools, diagnostics, typing, biocontrol, endolysins

INTRODUCTION

Bacteriophages affect the world in numerous ways. They represent parasites of bacteria, without own metabolism, relying on the host cell to provide energy and resources for their own replication. In terms of quantity, phages are the most abundant self-replicating entities on our planet, and outnumber their hosts by a factor of at least 10:1. This results in an estimated population of 10³⁰–10³¹ phage particles existing on the planet at any given time (Wommack and Colwell, 2000). In order to maintain this number, an estimated 10²⁵ infections happen every second (Pedulla et al., 2003). In any environment where bacteria play an important role it therefore stands to reason that bacteriophage will have an impact on that environment. In the worlds' oceans and seas cyanobacteria play a vital role in primary production and most work focusing on ecological impact of phages has focused on their role in nutrient cycles. However, it should be obvious that, next to protozoa, phages are the only natural predators of bacteria and thus play an essential role in controlling bacterial populations everywhere. Bacteriophages also influence human lives in various other ways. Wherever bacteria are used in fermentation processes, be it for food or production of other compounds, phages can affect the end-result by infecting and lysing the desired bacteria. In the biological sciences, bacteriophages have been instrumental in building our understanding of fundamental genetic principles, such as the concept of the operon, functioning of promoters and the restriction-modification, one of the most valuable and versatile tools in molecular biology. Phages can contribute to the virulence of bacterial pathogens in two ways. General transduction is a process where instead of phage-DNA host-DNA is packaged into infectious phage-like particles and this host DNA is subsequently injected into a susceptible host where it may integrate into the chromosome through homologous recombination. Whenever this transduced DNA contains virulence genes the infected bacteria can have altered virulence. Although other strategies for survival and replication exist, most phages can be separated into temperate or virulent phages. The latter are often termed lytic or strictly lytic as well. This lifestyle involves obligate production of new phages after infection resulting in lysis of the host and release of progeny phage. Temperate phages can do this but alternatively they can integrate their genetic information into the host chromosome. Lysogenic conversion is the phenomenon where temperate phages alter the virulence of the infected host after DNA integration. Examples of bacteria that rely on phage (genes) for their full pathogenic potential are Vibrio cholera, which is only pathogenic when it the cholera toxin is introduced by phage CTX¢, the diphtheria toxin of Corynebacterium diphteriae is also encoded by a phage, and shiga-toxin production in Enterobactericeae originates from genes on temperate phages integrated into the genomes of these bacteria (Freeman, 1951; Smith et al., 1983; Waldor and Mekalanos, 1996). Many more examples can be found in the literature. Lastly, phages have long been used in medical applications. Phage-typing has long been employed to conduct epidemiological studies of bacterial infection.

Over the past two decades, there has been a huge revival of interest in studying phages, but for other reasons. The emergence and increase in antibiotic-resistant bacteria and the possibility of replacing chemical drugs with phage or phage-encoded enzymes has been one of the main driving forces behind this renaissance. The fundamental insights which the genomics era has provided us with also led to the development of various tools based on phages or their components. Phage protein based detection of bacteria is now commercially available in the form of Vidas UP® technology, which employs recombinant host recognition proteins for in vitro diagnostics (IVD) of Escherichia coli and Salmonella. Phages have also been considered and applied since many decades to treat bacterial infections. This practice was and still is most common in the former Soviet Union, and to this day, phage preparations to treat a variety of infections are still produced in the Republic of Georgia. In the Western world, phage products for biocontrol are currently being commercialized for agricultural applications and food applications. Phage-derived proteins have also been commercialized and a number of commercial companies are investigating phage or phage-derived products for use in medical applications. The following chapters will focus on the impact of phage studies on our understanding of the genus *Listeria* with emphasis on *Listeria monocytogenes* as well as phage-derived tools for the detection and biocontrol of this important foodborne pathogen.

THE GENUS Listeria

Listeria spp. are small Gram-positive, flagellated rods with a ubiquitous distribution in the environment. Their principle lifestyle is saprophytic and thus the bacteria are frequently associated with plant material. Nine species are currently recognized, and they are L. monocytogens, L. ivanovii, L. innocua, L. marthii, L. rocourtiae, L. seeligeri, L. welshimeri L. fleischmannii, and L. grayii. Most research has been undertaken with respect to the human pathogen L. monocytogenes (Glaser et al., 2001; Graves et al., 2010; Leclercq et al., 2010; Bertsch et al., 2013). In healthy individuals, the infection (termed listeriosis) often manifests itself as a gastroenteritis, but in the very young, old, pregnant, and immunocompromised (a risk group commonly referred to as YOPIs), the bacteria can penetrate the intestinal tract and cause systemic infections including the central nervous system, and stillbirth or abortion in pregnant women (Vázquez-Boland et al., 2001). The disease is caused by the consumption of food contaminated with L. monocytogenes. The bacterium is a psychrotroph and can grow at refrigeration temperatures, and tolerates a wide range of pH and salt concentrations, rendering even low contaminations at production level dangerous if the shelf life of the food is longer than a few days (Gandhi and Chikindas, 2007). Many countries have strict regulations on the number of L. monocytogenes cells that are allowed in a given food, and zero-tolerance policies are in place in the US and Oceania. Phage therapy of Listeriosis is of course no option, as the bacteria multiply as intracellular pathogens, and cannot be reached by phages. Even antibiotics to which the bacteria are usually highly sensitive need to be administered at relatively high doses over prolonged periods of time in order to establish sufficient intracellular concentration. However, phage can be used both for the detection of this pathogen, and in controlling their presence in food processing equipment and on ready-to-eat products.

BACTERIOPHAGES OF Listeria

Listeria phages have been isolated from several of sources, including sewage plants, silage, food processing environments, and from lysogenic strains (Loessner and Busse, 1990; Hodgson, 2000; Kim et al., 2008; Arachchi et al., 2013). In total, some 500 phages specifically infecting *Listeria* have been identified, while only a limited number has been fully characterized on the molecular and genomic level (Loessner et al., 2000; Zimmer et al., 2003; Carlton et al., 2005; Dorscht et al., 2009; Schmuki et al., 2012). Phages have been reported to be able to infect other species. These studies revealed extensive mosaicism between many *Listeria* phages. All known *Listeria* phages belong to the order *Caudovirales*, which are tailed viruses with double stranded DNA. Podoviruses feature very short tails, while myoviruses have long, non-flexible contractile tail and siphoviruses have long, flexible tails. While members of both the Siphoviridae and Myoviridae are common, no Podoviridae infecting Listeria have yet been found and reported. The majority of the described phage are temperate, being able to integrate into the host genome. In fact, many Listeria strains are lysogenic, sometimes carrying multiple prophages, while most also harbor defective prophages. Many Listeria strains produce and release so-called monocins, which represent defective prophages, often recognized as lytic particles resembling phage tail structures (Zink et al., 1994, 1995). As in other bacteria, exposure to DNAdamaging agents such as UV light or Mitomycin C can induce the lytic cycle and lead to production of infective phage (Loessner, 1991). Listeria temperate phages generally display narrow host ranges, infecting only a small percentage of strains. This is in part caused by homoimmunity, i.e., resistance to a particular phage based on presence of a compatible repressor protein encoded by the same or a related phage within the bacterial cell. It is also noteworthy that the temperate phages of *Listeria* appear to be largely serovar-specific. It has been shown that this is based upon cell wall ligands, which the temperate phages recognize and attach to infect their hosts. They are serovar-specific sugar substituents of the polyribitol-phosphate teichoic acids on the Listeria cell wall (Wendlinger et al., 1996). In contrast, the large virulent phages such as A511 have been shown to use the cell-wall peptidoglycan backbone itself as a primary receptor (Wendlinger et al., 1996; Habann et al., 2014). Phages specifically infecting the different major serovar groups (1/2, 4, 5, and 6) have been identified, while no phages for L. monocytogenes serovar 3 or L. grayii strains have yet been found. Very little data exist on phenotype conversion or alteration following lysogenization. A recent study shows that prophage integration into the Listeria comK gene hinders cells escaping from macrophage phagosomal environments. In this case, the prophage may be excised during intracellular growth without generating progeny phage, integrity of *comK* is reconstituted, and following a cascade of events triggered by the ComK protein, the bacteria can eventually escape (Rabinovich et al., 2012). Another study shows that cells which harbor a phage integrated into comK display enhanced persistence and higher cell densities under meat processing plant conditions compared to strains lacking the phages. However, no explanation is offered and the underlying mechanisms causing this phenomenon remain obscure (Verghese et al., 2011). The less frequent virulent phages of Listeria fall into three groups. The large (~140 kb) Myoviruses P100 and A511 (Carlton et al., 2005; Klumpp et al., 2008) feature exceptionally broad host ranges, while the smaller siphoviruses P35 and P40 (around 40 kb) and the recently described, slightly larger (70 kb) phage designated P70 (Dorscht et al., 2009; Schmuki et al., 2012) still infect most members of given serovar groups. Virulent phages, i.e., those that will always kill their host cells are of course most useful when phage-based biocontrol is the aim. In contrast, generalized transducing phages, even though they may feature a virulent lifestyle such as P35 (Hodgson, 2000), are not desirable for application in biocontrol because they may tranfer genetic material, including virulence factors from one strain to another (Hagens and Loessner, 2010). Preferred are members of a specific group of the large, virulent myoviruses closely related to P100 and A511, which have been isolated from sources in Europe, the US and New Zealand (Zink and Loessner, 1992; Carlton et al., 2005; Kim et al., 2008; Bigot et al., 2011; Arachchi et al., 2013).

The natural property of phage to specifically target and kill bacterial cells of a certain species or genus has been fairly well exploited with respect to Listeria. As mentioned above, phage therapy of L. monocytogenes infections is not possible. However, prevention of the disease by anti-Listeria control measures during and after food processing is highly effective and desirable. Phages used for biocontrol purposes should be virulent and feature a broad host range, i.e., infect and kill as many target strains as possible. They must also be unable to transduce, and should ideally be propagated on a non-pathogenic production strain, or alternatively needs to be purified from the bacterial lysate. As of now, two Listeria phage products are commercially available: a broad host range myovirus is marketed as "ListexTM P100," and was granted GRAS (Generally Recognized As Safe) status by FDA and USDA in 2007 for use in all food products. Several studies have demonstrated its efficacy in foods such as cheese, RTE (ready to eat) meats and poultry, fruits, vegetables, and smoked fish, either alone or in combination with a growth limiting antimicrobial (Carlton et al., 2005; Soni and Nannapaneni, 2010a; Soni et al., 2010, 2012; Chibeu et al., 2013; Oliveira et al., 2014). Another study showed its efficacy on stainless steel surfaces, achieving more than five logs bacterial kill (Soni and Nannapaneni, 2010b). Another study used phage A511, closely related to P100, and confirmed its effectiveness in various RTE foods and surface ripenend soft cheeses (Guenther et al., 2009; Guenther and Loessner, 2011). Another product is termed "ListShield," and is also FDA and USDA approved. It consist of a cocktail of several phages, and its efficacy was investigated in two studies using fresh-cut produce in combination with the bacteriocin Nisin and as a spray application on honey-dew melons (Leverentz et al., 2003, 2004). An alternative approach to suspended phage is directed immobilization of the viral particles on cellulose membranes, which has been proposed as a possible intervention strategy against Listeria on packaging material (Anany et al., 2011).

TOOLS BASED ON Listeria PHAGE

Table 1 lists several Listeria phage-derived applications. The first widely used application was in phage typing. This is an inexpensive, low-tech and relatively quick tool to differentiate strains in epidemiological and microbial source-tracking studies. While being increasingly replaced by modern and more sophisticated molecular methods, it is yet not likely to become completely obsolete because of its simplicity and low cost. Phage typing had a prominent role in demonstrating food to be the primary cause of listeriosis in humans (Fleming et al., 1985). A number of different phage sets were developed (Audurier et al., 1979, 1984; Rocourt et al., 1985; McLauchlin et al., 1986; Loessner and Busse, 1990; Loessner, 1991; Estela and Sofos, 1993; Gerner-Smidt et al., 1993; van der Mee-Marquet et al., 1997). However, since Listeria serovar 3 strains appear resistant to phage infection, not all isolates can be typed. However, almost all strains that occur in foodborne outbreaks feature either serovar 1/2 or 4b, and are mostly susceptible to phage infection and can therefore generally be differentiated using phage typing (van der Mee-Marquet et al., 1997). Transducing phages, while not suited for biocontrol purposes, have been used to transfer genetic traits from one strain to another, allowing genetic manipulation and phenotype investigations (Freitag, 2000; Hodgson, 2000). Lauer and coworkers provided specific E. coli/Listeria shuttle vectors designed to integrate into the Listeria chromosome after transformation. Here, site-specific integration by Listeria phage integrase has been employed to mediate single-copy, selection-free integration of genes placed on the vectors. As a proof of concept, the approach allowed successful complementation of actA and hly knockouts (Lauer et al., 2002). Derivatives of the initial pPL2 vector have

Table 1 Listeria phage-derived tools.	Application	Reference
Large sets of different phages (broad and narrow host range) Single phages or cocktails (broad host range)	Phage typing Biocontrol (targeted killing in foods)	Audurier et al. (1979, 1984), Rocourt et al. (1985), McLauchlin et al. (1986), Loessner and Busse (1990), Loessner (1991), Estela and Sofos (1993), Gerner-Smidt et al. (1993), van der Mee-Marquet et al. (1997) Leverentz et al. (2003, 2004), Carlton et al. (2005), Guenther and Loessner (2011), Guenther et al. (2009), Soni et al. (2010, 2012), Soni and Nannapaneni (2010a), Chibeu et al. (2013),Oliveira et al.
Departer phases (bread best renge)	Disgnastics (datastics)	(2014)
Reporter phages (broad host range) Phage endolysins and functional domains	Diagnostics (detection) Diagnostics	Loessner et al. (1996, 1997), Hagens et al. (2011) Kretzer et al. (2007), Schmelcher et al. (2010), Walcher et al. (2010), Tolba et al. (2012)
Phage tail fibers Endolysins and modified endolysins	Immobilization and detection Antimicrobial	Junillon et al. (2012), Habann et al. (2014) Fischetti (2010), Schmelcher et al. (2012)
Phage integrase genes	Site-specific integration vectors	Lauer et al. (2002)

since been used in many studies addressing *L. monocytogenes* phenotypes and virulence properties, have been successfully employed to monitor promoter activity in *in vivo* infection studies (Lenz and Portnoy, 2002; Lenz et al., 2003; Grundling et al., 2004; Bron et al., 2006), and were fundamental in elucidating the mechanisms of L-form formation in *L. monocytogenes* (Dell'Era et al., 2009).

Rapid and efficient detection of a Listeria contamination is critical with respect to food safety, and for compliance of food production with regulations concerning the presence of L. monocytogenes in foods and on food-contact surfaces. The high specificity of phages combined with the fact that viruses only multiply in viable and active host cells has sparked the development of phage amplification-based assays for the detection of various pathogens, including Listeria. One possible use is measuring an increase of Listeria phages after incubation with a contaminated sample (Bakulov et al., 1984). However, genetically modified reporter phages carrying a gene encoding an easy-to-measure product or activity offer more interesting and versatile alternatives. The reporter gene product will only be made following successful phage infection and gene expression. Listeria reporter phage A511::luxAB transduces a *luxAB* gene fusion coding for bacterial luciferase (Loessner et al., 1996), and its efficacy in rapid detection of low-level Listeria contaminations from various foods has been demonstrated (Loessner et al., 1997). The same phage was used to construct A511::celB, featuring a thermophilic glycosidase of Pyrococcus furiosus. Reporter genes from thermophiles feature an exceptional ease-of-use, and allow a wide range of substrates and assay formats to choose from (Hagens et al., 2011).

Rather than employing complete phages as antimicrobials and for diagnostics, proteins and peptides from phage may also be used for this purpose. Phage-encoded cell-wall-hydrolyzing enzymes are particularly useful. In order to digest the bacterial cell wall prior to release of phage progeny, most phages produce a class of enzymes termed endolysins. These enzymes feature a two-domain structure with an N-terminal catalytic domain and a C-terminal cell wall-binding domain (CBD) that binds with high affinity to cell wall-associated ligands, in order to direct the catalytic activity to its target site, and at the same time prevent collateral damage and lysis of yet uninfected potential host cells (Loessner et al., 1995). Such endolysin peptidoglycan hydrolases have a huge potential as antimicrobial reagents against Gram-positive pathogens, which has been reviewed elsewhere (Fischetti, 2010; Schmelcher et al., 2012). Yet, application of Listeria phage endolysins as highly specific antimicrobial agent in foods is hampered by the specific requirements of these enzymes, in terms of pH and salt concentration. Endolysins from Listeria phages can, however, be useful for removing Listeria occurring on food-contact surfaces and in biofilms.

Due to the high binding affinity and specificity of the endolysin CBD, these protein domains have been explored and used as versatile tools for diagnostics and identification of *Listeria*. Studies have shown that CBDs immobilized on paramagnetic beads are very effective in order to separate target cells from dilute suspensions, and the technique can be elegantly combined with different secondary diagnostic steps (Kretzer et al., 2007; Walcher et al., 2010). A recent study investigated detection of *Listeria* cells using electrochemical impedance spectroscopy (EIS), which can measure bacteria captured by the CBD molecules immobilized on a gold screen printed electrode (SPE; Tolba et al., 2012). Differently colored fluorescent proteins fused to CBDs with different recognition and binding spectra allow for rapid and multiplexed detection and differentiation of *Listeria* strains by fluorescence microscopy (Schmelcher et al., 2010). As an alternative approach, *Listeria* phage tail fiber proteins coupled to a solid support can also be used to bind target cells for primary enrichment and subsequent detection (Junillon et al., 2012).

In summary, the past years have demonstrated that phages infecting *Listeria* and other bacteria (Hagens and Loessner, 2010) provide us with numerous novel tools for various interesting approaches. The evolution of molecular microbiology and genetic engineering as technology platform, together with insights into phage biology, have been combined in interesting ways, and it is likely that this process will continue and more tools harnessing the properties and incredible biological specificity of bacterial viruses will be developed and available in the future.

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