

Common Preconditions for Safe Phage Therapy of *Pseudomonas aeruginosa* Infections

V. Krylov, E. Pleteneva, O. Shaburova, M. Bourkaltseva, S. Krylov, E. Chesnokova, O. Polygach

Mechnikov Research Institute for Vaccines & Sera, RAMS, Moscow, Russia
Email: krylov.mech.inst@mail.ru

Received 26 June 2014; revised 26 July 2014; accepted 12 August 2014

Copyright © 2014 by authors and Scientific Research Publishing Inc.
This work is licensed under the Creative Commons Attribution International License (CC BY).
<http://creativecommons.org/licenses/by/4.0/>



Open Access

Abstract

One of the approaches to the treatment of infections caused by multiply-(MDR) or extra drug-resistant (XDR) pathogenic strains may be application of bacterial viruses (bacteriophages)—phage therapy. Results of a long, but quite limited use of phage therapy in several Eastern European countries, as well as experiments on animal models in Western countries support the possibility to use phage therapy. However, given the role of phages in the evolution of bacterial pathogens, it is necessary to discuss and evaluate negative consequences of mass introduction of phage therapy, as the measures necessary for its safe use. We discuss some actions in case of transiting to world-wide use of phage therapy with purpose to prolong the active life of phage therapy and to diminish possible complications.

Keywords

Phage Therapy, Safety Measures, *Pseudomonas aeruginosa*

1. Introduction

Bacteria of *Pseudomonas aeruginosa* species have very high capability for adaptation and survival in different conditions [1] [2]. They belong to the most frequent opportunistic pathogens causing different hospital infections in people with weakened immune systems, infections of open wounds of different origins and are the inevitable component of the lung microbiota in cystic fibrosis (CF, frequent hereditary disease Caucasians) patients. Prolonged use of a variety of antibiotics to eradicate *P. aeruginosa* has been the reason for arising of MDR (multiple drug resistant) and XDR (extra drug resistant) strains *P. aeruginosa* which put serious problems

for practical medicine.

Transition of *P. aeruginosa* infection into chronic state in CF patients greatly worsens the prognosis. As a possible approach, a return to the use of bacterial viruses is offered, bacteriophages—phage therapy (PT). There is no doubt of possibility to use specific phages proved by long time use of PT in Russia and Georgia from the 30-es of last age in treatment of infected wounds or hospital infections. There are plenty of fresh publications on bacteriophages, the history of phage therapy and its possible use in practice, in the case of MDR or XDR-strains [3]-[12].

2. *P. aeruginosa* Virulent (“Lytic”) Bacteriophages

It is generally accepted that one of the most important advantages of phage therapy is relative simplicity in isolation of new natural or mutant phages for substitution of those ones which have lost their activity after arising of phage resistant bacterial variants. Abundance of different phage species active on *P. aeruginosa* [13] with more than 80 different phages with sequenced genomes available in NCBI database [14] confirms the possibility for choosing the active phages.

But it is necessary to take into attention that phage therapy in countries of Eastern Europe has really a limited application. Thus, there is deep concern that the global introduction of phage therapy in real hospital practice could contribute to the emergence of new, more dangerous diseases because bacteriophages are natural motors in the evolution of bacteria. Development of new approaches in studies of bacterial and phage genomes has revealed close interactions of them in evolutionary process, sometimes with unfavorable final result for humankind. Virulent (“lytic”) and temperate phages are capable to transfer separate bacterial genes or pathogenic islands, between different bacterial strains (horizontal gene transfer—HGT), thus creating new highly dangerous pathogens [15]-[18].

Thus, the earlier statements that phage therapy is a simple, cheap procedure, absolutely safe for patient and harmless to the environment and natural microflora can not be more an argument taken without careful considerations. It is evident that the phage therapy can not be complete alternative of antibiotics. Its use is restricted mainly to pyogenic surface infections (infected wounds, urological and gynecological infections, infections of the ear, throat and nose, intestinal infections and abscesses-after their opening and emptying), and, possibly, lung infections in CF patients.

Apparently, right now, before the widespread introduction of phage therapy into medical practice it is necessary to discuss two problems and to look for their solutions.

Firstly, whether PT could be used for a long time, and secondly, how to prevent in course of its use the arising of bacterial strains with features of the so-called “emerging diseases”? Results of practical application in clinical and ambulatory conditions in several countries of Eastern Europe and new experiments with use of animal models support the necessity for its further development and adaptation to new more strict medical standards [19]-[24].

Up to recent time the therapeutic phage mixtures were estimated only on the basis of their lytic spectrum. But now their detailed study, including not only the genome sequencing and annotation, but careful studies of phage-bacterium interactions should be considered as the necessary and sufficient condition for choice of phages for therapy. Phage genomes studies would exclude the use of the phages whose genomes encode such undesirable products as toxins, transposases, repressor proteins, etc. But, unfortunately, it still does not guarantee the safety of phages. Genomes of all newly isolated natural phages contain plenty of genes coding gene products with functions which can not be predicted as result of comparison with existing databases. These genes can control some yet unknown pathogenicity factors. Thus, each phage offered for therapy must be studied in interaction with different strains of sensitive bacteria under different conditions.

Uncontrolled use of multicomponent mixtures of unstudied phages may lead to arising of new pathogenic strains. The resulting strains may be similar to epidemic variants of *P. aeruginosa* which have arisen in CF departments as result of possible interactions of numerous different phages and bacterial strains in the lungs of CF patients [18]. Unlike conventional opportunistic strains of *P. aeruginosa*, such epidemic strains exhibit aggression, displacing the usual strains of *P. aeruginosa*, and at the same time, are highly pathogenic and virulent, what can be cause of pneumonia and death of healthy (non CF) people. As it turned out, the reason for this is the activity of genes in new prophage pathogenic islands, which absent in the *P. aeruginosa* PAO1 laboratory strain (which, although is also a clinical isolate of 60-es, does not cause infections in healthy humans).

In **Table 1** are mentioned 10 species of virulent phages active on *P. aeruginosa* (presented in NCBI, June 2014) for which are available some results of phenogenetic studies.

There are several phage species which are almost compulsory components of real therapeutic mixtures (our unpublished results). The most of the currently used phage mixtures include different phiKZ-like phages [25]-[30]. Bacteria in biofilms of *P. aeruginosa* after multiple infection with phiKZ-like phages enter pseudo lysogenic state and produce large amounts of mucous material obstructing access of phage particles to the bacteria in the wound [29]. Such unusual behavior could not be predicted after the sequencing and annotation phage genomes [27] [28] (**Figure 1**). We have isolated specific mutants of phiKZ-like phages where this feature has been lost [30]. Such mutants should replace wild-type phiKZ-like phages in therapeutic mixtures.

KMV-like phages [31] [32] are the other permanent components of different phage mixtures. Their valuable features are short latent period, good yields and in addition the capability to infect and produce phage in culture of old bacteria in biofilm (which are usually resistant to phages of other species).

Among the other well-studied and perspective phages active on *P. aeruginosa* which usually can be found in commercial mixtures are PB1-like phages [33] [34].

In search for new *P. aeruginosa* therapeutic phages there were isolated several phages with good natural lytic activity, inability to stably lysogenize bacterial cells, but exhibiting unusual features. Thus, genome of phage Luz24 is more than 70% identical to the phage genome of temperate phage PaP3 [35] [36]. Despite of the first

Table 1. Representatives for species of *P. aeruginosa* virulent phages with sequenced genomes (presented in NCBI, June 2014).

№	Species	Family	Number of phages	Genome sizes min - max	№	Species	Family	Number of phages	Genome sizes min-max
1	phiKMV	Podoviridae	14	42,954 - 43,548	6	N4	Podoviridae	2	72,544 - 74,901
2	PB1	Myoviridae	10	64,427 - 66,616	7	119x	Podoviridae	2	43,365 - 43,783
3	PaP1	Myoviridae	6	91,175 - 93,198	8	YuA	Syphoviridae	2	58,663 - 61,167
4	KPP10	Myoviridae	4	88,097 - 88,322	9	phiKZ	Myoviridae	1	280,334
5	Luz 24/PaP3	Podoviridae	4	45,503 - 45,625	10	EL	Myoviridae	1	211,215

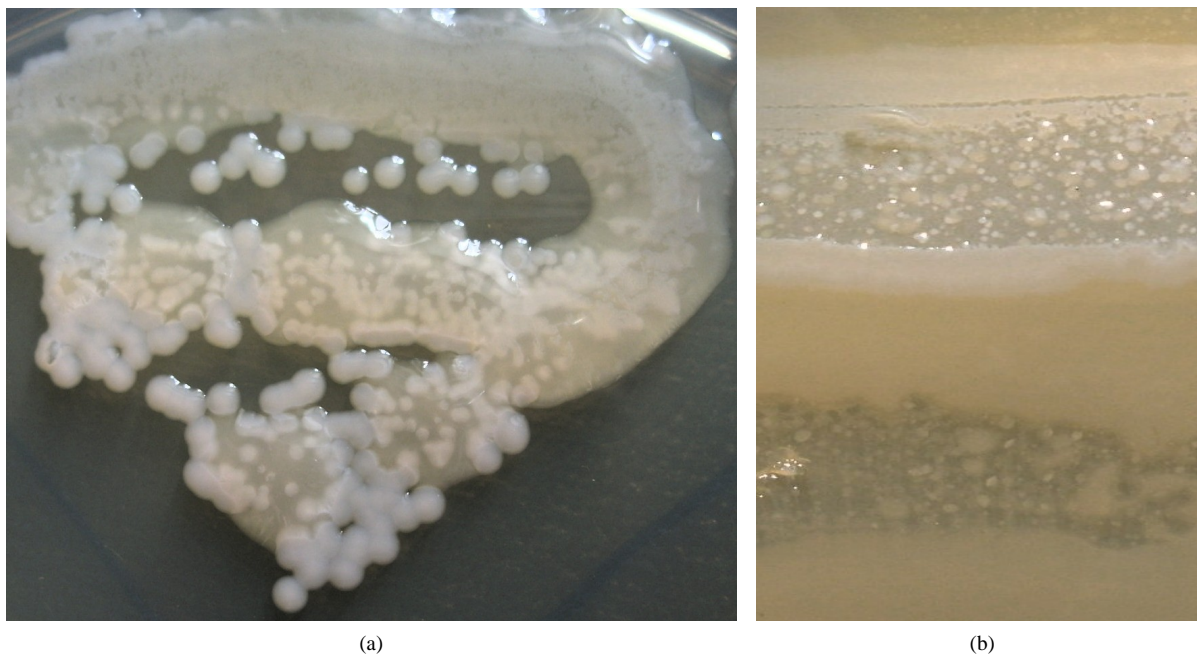


Figure 1. (a) Appearance of *P. aeruginosa* colonies in pseudolysogenic state after phiKZ phage multiple infection; (b) The different growth of phiKZ-like phage EL of wild type (top) and its virulent mutant (bottom).

opinion that PaP3 is a temperate one, repressor genes were not found in genomes of both mentioned phages. Thus such phages are regarded as acceptable and good for phage therapy. Nevertheless the phages TL and CHU, closely related with Luz24, reveal a genetic instability being grown on some clinical isolates (**Figure 2**) or specific mutants of standard host strain PAO1 (not shown). The possible reason for the instability is not evident yet.

The phages of other species also reveal some specific features, which may be important in therapeutic use. For example, lytic phage phiPMG1 (closely related with temperate phage D3) [37] [38], is capable to lyse some KMV-resistant mutants. Thus, phiPMG1 could be considered as a component for inclusion in the lytic mixture but however, a comparison of the phiPMG1 phage genome with existing database shows sequences identical to the sequences in D3-like pathogenic island of epidemic strain *P. aeruginosa* LESB58 (**Figure 3**). Obviously, the procedure used now to extend phage lytic activity will select phages which are similar with phiPMG1 with unpredictable final results. Likewise, the same is true for a lytic phage YMC01/01/P52 PAE BP (GenBank: JX403939.1) [39] which is closely related with temperate phage phi297 (GenBank: HQ711984) [40] [41] and has been selected by its ability to lyse a specific antibiotic resistant clinical strain.

Thus, it seems that the the best approach is use of multivalent phage mixtures, because it is not burdensome in the clinic (does not require a preliminary study on the phage sensitivity of pathogenic strain). But their use being acceptable for example, in the treatment of infected wounds, nevertheless can not be considered as universal or safe enough in other cases.

3. Possible Consequences in Use of Phage Therapy

Wide introduction of phage therapy in everyday medical practice (what may be expected in the near future even in case of CF) will increase the extent of HGT, will accelerate bacterial evolution and can lead to arising of *P.*

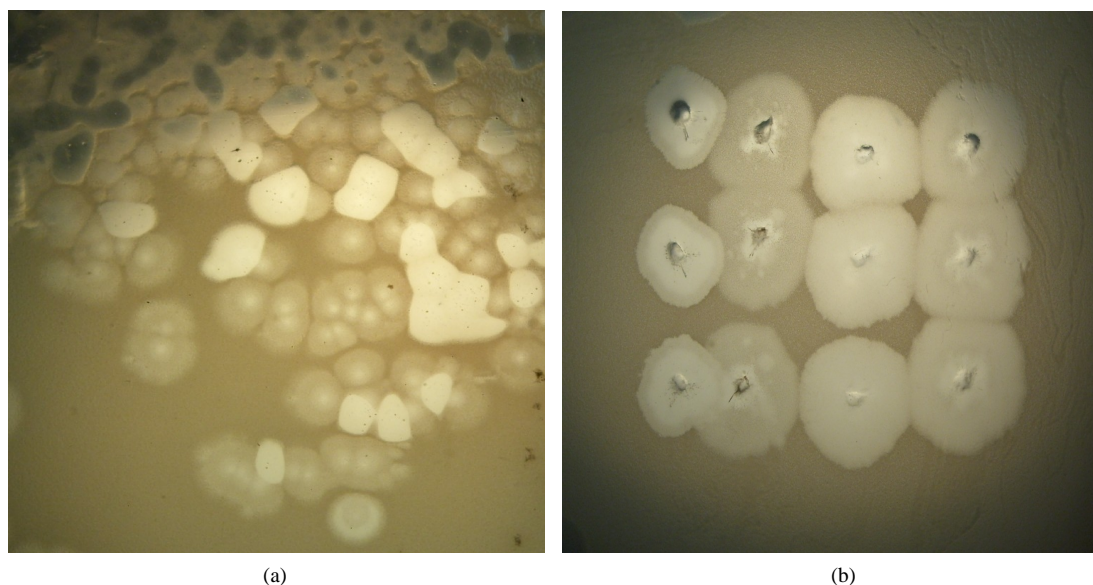


Figure 2. Growth of phage CHU on the lawn *P. aeruginosa* 8 - 20 isolate strain. (a) Plating of a single plaque; (b) Pickup plating from different types of plaques. The bacterial strain 8 - 20 is kindly provided by Prof. C. Pourcel.

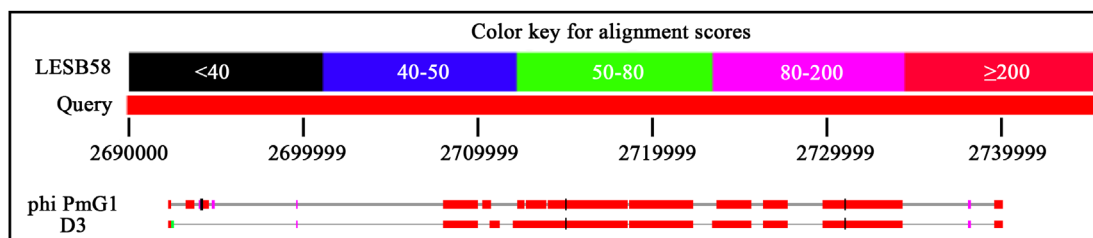


Figure 3. NCBI BLAST alignment of *P. aeruginosa* LESB58 epidemic strain genome fragment (in the region of DNA homology) against phiPMG1 and D3 bacteriophages genome sequences.

aeruginosa epidemic strains in general hospitals. It can be argued that only lytic phages will be used in therapeutic phage mixtures. Yes, of course. However, lytic phages will accomplish general transduction. Moreover, some of the lytic phages have relatedness to temperate phages or carry genes that are functionally similar to the phage repressor genes of temperate phages (see before). Furthermore, phage therapy will be conducted in respect of clinical strains of *P. aeruginosa*, which often contain the same prophages, whose unusual activity was the reason for arising of epidemic variants. Thus, introduction of phage therapy in a real hospital could recreate the same algorithm which led to the emergence of epidemic strains in CF condition. It's hard to say how long it will take.

Interest to phage therapy stimulates search and study of new *P. aeruginosa* phages and some of them increase our knowledge on possible evolutionary events. For example, in [42] has been described a chimeric phage, whose genome have arisen as a result of natural recombination of temperate D3-like phage of *P. aeruginosa* and *Pseudomonas putida* phage AF. Another unusual phage displaying a high level of relationship with transposable phage D3112, as it turned out, can infect *P. aeruginosa* and *Staphylococcus aureus* (!!!) [43]. Naturally, at first glance it seems promising to use such phage in therapy. But it is only at first glance. The use of such phage in complex wound microbiota can lead to unpredictable consequences due to interspecies exchanges between unrelated pathogens. We consider may be it will be better to avoid such actions and accomplish a deep study of such unusual phages.

4. Discussion

What should be taken to prevent such scenario, to avoid *P. aeruginosa* epidemics in hospital conditions and to ensure long and safe use of phage therapy? We propose to discuss the necessity of special organizational preventive and mandatory measures in relation with full introduction of phage therapy into hospital conditions. But one can object-basically such measures already exist as measures to prevent the spread of epidemics. It is right. Their strict application intends to exclude (in principle) the existence of hospital pathogens, however, this is not happening. That means that their compliance is not enough. Indeed, slight air flows or some smallest violations of the existing accepted anti-epidemic measures could lead to undesired phage distribution. And, sure, there is no place for propositions to use phages as antiseptics in hospital conditions [44].

The following measures can be proposed for discussion as obligatory ones in good phage therapy practice (GPTP):

Public relation level

To stop any public promotion of phage therapy preparations as a kind of panacea.

Laboratory level

- 1) Search for phages which can be propagated on standard laboratory strains (to avoid HGT).
- 2) Development of *in vitro* in-depth physiological studies of bacteriophages in different conditions simulating real infection (for instance, presence of resident prophages and plasmids, different multiplicity of infection, viscosity, presence of other microbiota components and its phages).
- 3) Genomes of all phages proposed for inclusion in therapeutic mixtures should be sequenced and annotated to exclude phages coding at least known unacceptable products and properties.
- 4) Compare adsorption specificity of phages included into the same mixture to increase time interval before arising of multi-phage resistant bacterial strains.

Production level

To give doctors capability to choose the optimal approaches for phage therapy, depending on the specific conditions that it is necessary to produce different sets of phage preparations, including:

- 1) Sets of individual phages with different spectra of lytic activity for personalized use in clinical settings, including the cases of primary lung infections in CF patients.
- 2) Traditional broad-spectrum mixtures for use in cases of wound and hospital infections.

Distribution level

To stop distribution of phage therapeutic mixtures without medical prescriptions. Introduce direct delivery and sale of phage preparations in hospitals which are using phage therapy.

Hospital level

The use of phage therapy requires specific conditions. Each hospital participating in use of phage therapy should organize special "Phage Hospital Ward" (PHW), which is safely isolated to prevent accidental spread of

bacteriophages to the other parts of hospital. The PHW should be equipped for quick and reliable disinfection with chemicals and UV irradiation. Personnel hospital clothing must be sterilized after a single use in PHW. Permanent monitoring of the possible spread of phages outside of PHW is compulsory condition for use of PT. Any case of nosocomial *P. aeruginosa* pneumonia (in surgery departments, wound or burn centers, blocks for intensive therapy) must be carefully analyzed to exclude the possible arising of epidemic strain as the reason. Patients with non evident origin pneumonia should undergo treatment in conditions of strict isolation to prevent dissemination of possible epidemic strain.

International cooperation

Exchange of phages and mixtures of phages, additional joint studies, elaboration of common standards for phage therapeutics.

Road by walking!

References

- [1] Clarke, P.H. and Richmond M.H. (1975) Genetics and Biochemistry of Pseudomonas. John Wiley and Sons, London.
- [2] Cornelis, P. (Ed.) (2008) Pseudomonas: Genomics and Molecular Biology. Caister Academic Press, Belgium.
- [3] Krylov, V.N. (2001) Phagotherapy in Terms of Bacteriophage Genetics: Hopes, Perspectives, Safety, Limitations. *Russian Journal of Genetics*, **37**, 715-730. <http://dx.doi.org/10.1023/A:1016716606135>
- [4] Kutter, E. and Sulakvelidze, A. (Eds.) (2005) Bacteriophages—Biology and Application. CRC Press, Boca Raton.
- [5] Merabishvili, M., Pirnay, J.P., Verbeken, G., Chanishvili, N., Tediashvili, M., Lashkhi, N., Glonti, T., Krylov, V., Mast, J., Van Parys, L., Lavigne, R., Volckaert, G., Mattheus, W., Verween, G., De Corte, P., Rose, T., Jennes, S., Zizi, M., De Vos, D. and Vaneechoutte, M. (2009) Quality-Controlled Small-Scale Production of a Well-Defined Bacteriophage Cocktail for Use in Human Clinical Trials. *PLoS ONE*, **4**, Article ID: e4944. <http://dx.doi.org/10.1371/journal.pone.0004944>
- [6] Krylov, V., Shaburova, O., Krylov, S. and Pleteneva, E. (2013) A Genetic Approach for Development of New Therapeutic Phages to Fight Pseudomonas Aeruginosa in Wound Infections. *Viruses*, **5**, 15-53. <http://dx.doi.org/10.3390/v5010015>
- [7] Chan, B.K., Abedon, S.T. and Loc-Carrillo, C. (2013) Phage Cocktails and the Future of Phage Therapy. *Future Microbiology*, **8**, 769-783. <http://dx.doi.org/10.2217/fmb.13.47>
- [8] Chanishvili, N. (2012) Phage Therapy—History from Twort and d’Herelle Through Soviet Experience to Current Approaches. *Advances in Virus Research*, **83**, 3-40. <http://dx.doi.org/10.1016/B978-0-12-394438-2.00001-3>
- [9] Krylov, V.N. (2014) Bacteriophages of *Pseudomonas aeruginosa*: Long-Term Prospects for Use in Phage Therapy. *Advances in Virus Research*, **88**, 227-278. <http://dx.doi.org/10.1016/B978-0-12-800098-4.00005-2>
- [10] Skurnik, M. and Strauch, E. (2006) Phage therapy: Facts and Fiction. *International Journal of Medical Microbiology*, **296**, 5-14. <http://dx.doi.org/10.1016/j.ijmm.2005.09.002>
- [11] Brüßow, H. (2012) What Is Needed for Phage Therapy to Become a Reality in Western Medicine? *Virology*, **434**, 138-142. <http://dx.doi.org/10.1016/j.virol.2012.09.015>
- [12] Fortier, L.C. and Sekulovic, O. (2013) Importance of Prophages to Evolution and Virulence of Bacterial Pathogens. *Virulence*, **4**, 354-365. <http://dx.doi.org/10.4161/viru.24498>
- [13] Krylov, V.N., Tolmachova, T.O. and Akhverdian, V.Z. (1993) DNA Homology in Species of Bacteriophages Active on *Pseudomonas aeruginosa*. *Archives of Virology*, **131**, 141-151. <http://dx.doi.org/10.1007/BF01379086>
- [14] NCBI GenBank. <http://www.ncbi.nlm.nih.gov/genbank/>
- [15] McCallum, S.J., Gallagher, M.J., Corkill, J.E., Hart, C.A., Ledson, M.J. and Walshaw, M.J. (2002) Spread of an Epidemic *Pseudomonas aeruginosa* Strain from a Patient with Cystic Fibrosis (CF) to Non-CF Relatives. *Thorax*, **57**, 559-560. <http://dx.doi.org/10.1136/thorax.57.6.559>
- [16] Armstrong, D.S., Nixon, G.M., Carzino, R., Bigham, A., Carlin, J.B., Robins-Browne, R.M. and Grimwood, K. (2002) Detection of a Widespread Clone of *Pseudomonas aeruginosa* in a Pediatric Cystic Fibrosis Clinic. *American Journal of Respiratory and Critical Care Medicine*, **166**, 983-987.
- [17] Panagea, S., Winstanley, C., Walshaw, M.J., Ledson M.J. and Hart C.A. (2005) Environmental Contamination with an Epidemic Strain of *Pseudomonas aeruginosa* in a Liverpool Cystic Fibrosis Centre, and Study of Its Survival on Dry Surfaces. *Journal of Hospital Infection*, **59**, 102-107. <http://dx.doi.org/10.1016/j.jhin.2004.09.018>
- [18] Winstanley, C., Langille, M.G.I., Fothergill, J.L., Kukavica-Ibrulj, I., Paradis-Bleau, C., Sanschagrin, Fo., Thomson, N.R., Winsor, G.L., Quail, M.A. and Lennard, N. (2009) Newly Introduced Genomic Prophage Islands Are Critical Determinants of *in Vivo* Competitiveness in the Liverpool Epidemic Strain of *Pseudomonas aeruginosa*. *Genome Re-*

- search, **19**, 12-23. <http://dx.doi.org/10.1101/gr.086082.108>
- [19] Shabalova, L.A., Kapranov, N.I., Krylov, V.N. and Solovieva, T.I. (1993) *Pseudomonas aeruginosa* Bacteriophages in Treatment of *Pseudomonas aeruginosa* Infection in CF. 7th Annual North American Cystic Fibrosis Conference, Dallas, Texas, 13-16 October 1993, 264.
- [20] Golshahi, L., Lynch, K.H., Dennis, J.J. and Finlay, W.H. (2011) *In Vitro* Lung Delivery of Bacteriophages KS4-M and ΦKZ Using Dry Powder Inhalers for Treatment of *Burkholderia cepacia* Complex and *Pseudomonas aeruginosa* Infections in Cystic Fibrosis. *Journal of Applied Microbiology*, **110**, 106-117. <http://dx.doi.org/10.1111/j.1365-2672.2010.04863.x>
- [21] Lynch, K.H. and Dennis, J.J. (2012) Cangene Gold Medal Award Lecture—Genomic Analysis and Modification of *Burkholderia cepacia* Complex Bacteriophages. *Canadian Journal of Microbiology*, **58**, 221-235. <http://dx.doi.org/10.1139/w11-135>
- [22] Vandenhevel, D., Singh, A., Vandersteegen, K., Klumpp, J., Lavigne, R. and Van den Mooter, G. (2013) Feasibility of Spray Drying Bacteriophages into Respirable Powders to Combat Pulmonary Bacterial Infections. *European Journal of Pharmaceutics and Biopharmaceutics*, **84**, 578-582. <http://dx.doi.org/10.1016/j.ejpb.2012.12.022>
- [23] Alemayehu, D., Casey, P.G., McAuliffe, O., Guinane, C.M., Martin, J.G., Shanahan, F., Coffey, A., Ross, R.P. and Hill, C. (2012) Bacteriophages φMR299-2 and φNH-4 Can Eliminate *Pseudomonas aeruginosa* in the Murine Lung and on Cystic Fibrosis Lung Airway Cells. *mBio*, **3**, Article ID: e00029-12. <http://dx.doi.org/10.1128/mBio.00029-12>
- [24] Henry, M., Lavigne, R. and Debarbieux, L. (2013) Predicting *in Vivo* Efficacy of Therapeutic Bacteriophages Used to Treat Pulmonary Infections. *Antimicrobial Agents and Chemotherapy*, **12**, 5961-5968. <http://dx.doi.org/10.1128/AAC.01596-13>
- [25] Krylov, V.N. and Zhazykov, I.Zh. (1978) *Pseudomonas* Bacteriophage phiKZ—Possible Model for Studying the Genetic Control of Morphogenesis. *Genetika*, **14**, 678-685.
- [26] Krylov, V.N., Smirnova, T.A., Minenkova, I.B., Plotnikova, T.G., Zhazikov, I.Z. and Khrenova, E.A. (1984) *Pseudomonas* Bacteriophage phiKZ Contains an Inner Body in its Capsid. *Canadian Journal of Microbiology*, **30**, 758-762. <http://dx.doi.org/10.1139/m84-116>
- [27] Mesyanzhinov, V.V., Robben, J., Grymonprez, B., Kostyuchenko, V.A., Bourkaltseva, M.V., Sykilinda, N.N., Krylov, V.N. and Volckaert, G. (2002) The Genome of Bacteriophage phiKZ of *Pseudomonas aeruginosa*. *Journal of Molecular Biology*, **317**, 1-19. <http://dx.doi.org/10.1006/jmbi.2001.5396>
- [28] Hertveldt, K., Lavigne, R., Pleteneva, E., Sernova, N., Kurochkina, L., Korchevskii, R., Robben, J., Mesyanzhinov, V., Krylov, V.N. and Volckaert, G. (2005) Genome Comparison of *Pseudomonas aeruginosa* Large Phages. *Journal of Molecular Biology*, **354**, 536-545.
- [29] Pleteneva, E.A., Krylov, S.V., Shaburova, O.V., Burkal'tseva, M.V., Miroshnikov, K.A. and Krylov, V.N. (2010) Pseudolysogeny of *Pseudomonas aeruginosa* Bacteria Infected with phiKZ-Like Bacteriophages. *Russian Journal of Genetics*, **46**, 20-25. <http://dx.doi.org/10.1134/S1022795410010047>
- [30] Krylov, S.V., Pleteneva, E.A., Bourkaltseva, M.V., Shaburova, O.V., Miroshnikov, K.A., Lavigne, R., Cornelissen, A. and Krylov, V.N. (2011) Genome Instability of *Pseudomonas aeruginosa* Phages of the EL Species: Examination of Virulent Mutants. *Russian Journal of Genetics*, **47**, 162-167. <http://dx.doi.org/10.1134/S1022795411020116>
- [31] Lavigne, R., Burkal'tseva, M.V., Robben, J., Sykilinda, N.N., Kurochkina, L.P., Grymompres, B., Jonckx, B., Krylov, V.N., Mesyanzhinov, V.V. and Volckaert, G. (2003) The Genome of Bacteriophage phiKMV, a T7-Like Virus Infecting *Pseudomonas aeruginosa*. *Virology*, **312**, 49-59.
- [32] Ceysens, P.J., Glonti, T., Kropinski, N.M., Lavigne, R., Chanishvili, N., Kulakov, L., Lashkhi, N., Tediashvili, M. and Merabishvili, M. (2011) Phenotypic and Genotypic Variations Within a Single Bacteriophage Species. *Virology Journal*, **8**, 134. <http://dx.doi.org/10.1186/1743-422X-8-134>
- [33] Pleteneva, E.A., Shaburova, O.V., Sykilinda, N.N., Miroshnikov, K.A., Krylov, S.V., Mesianzhinov, V.V. and Krylov, V.N. (2008) Study of the Diversity in a Group of Phages of *Pseudomonas aeruginosa* Species PB1 (Myoviridae) and Their Behavior in Adsorption-Resistant Bacterial Mutants. *Russian Journal of Genetics*, **44**, 185-194. <http://dx.doi.org/10.1134/S1022795408020051>
- [34] Ceysens, P.J., Miroshnikov, K., Mattheus, W., Krylov, V., Robben, J., Noben, J.P., Vanderschraeghe, S., Sykilinda, N., Kropinski, A.M., Volckaert, G., Mesyanzhinov, V. and Lavigne, R. (2009) Comparative Analysis of the Widespread and Conserved PB1-Like Viruses Infecting *Pseudomonas aeruginosa*. *Environmental Microbiology*, **11**, 2874-2883. <http://dx.doi.org/10.1111/j.1462-2920.2009.02030.x>
- [35] Tan, Y., Zhang, K., Rao, X., Jin, X., Huang, J., Zhu, J., Chen, Z., Hu, X., Shen, X., Wang, L. and Hu, F. (2007) Whole Genome Sequencing of a Novel Temperate Bacteriophage of *P. aeruginosa*: Evidence of tRNA Gene Mediating Integration of the Phage Genome into the Host Bacterial Chromosome. *Cellular Microbiology*, **9**, 479-491. <http://dx.doi.org/10.1111/j.1462-5822.2006.00804.x>

- [36] Ceysens, P.J., Hertveldt, K., Ackermann, H.W., Noben, J.P., Demeke, M., Volckaert, G. and Lavigne, R. (2008) The Intron-Containing Genome of the Lytic *Pseudomonas* phage LUZ24 Resembles the Temperate Phage PaP3. *Virology*, **377**, 233-238. <http://dx.doi.org/10.1016/j.virol.2008.04.038>
- [37] Krylov, S.V., Kropinski, A.M., Pleteneva, E.A., Shaburova, O.V., Burkal'tseva, M.V., Miroshnikov, K.A. and Krylov, V.N. (2012) Properties of the New D3-Like *Pseudomonas aeruginosa* Bacteriophage phiPMG1: Genome Structure and Prospects for the Use in Phage Therapy. *Russian Journal of Genetics*, **48**, 902-911. <http://dx.doi.org/10.1134/S1022795412060087>
- [38] Kropinski, A.M. (2000) Sequence of the Genome of the Temperate, Serotype-Converting *Pseudomonas aeruginosa* Bacteriophage D3. *Journal of Bacteriology*, **182**, 6066-6074. <http://dx.doi.org/10.1128/JB.182.21.6066-6074.2000>
- [39] Jeon, J., Kim, J.W., Yong, D., Lee, K. and Chong, Y. (2012) Complete Genome Sequence of the Bacteriophage YMC01/01/P52 PAE BP, Which Causes Lysis of Verona Integron-Encoded Metallo- β -Lactamase-Producing, Carbapenem-Resistant *Pseudomonas aeruginosa*. *Journal of Virology*, **86**, 13876-13877. <http://dx.doi.org/10.1128/JVI.02730-12>
- [40] Burkal'tseva, M.V., Krylov, S.V., Kropinski, A.M., Pletneva, E.A., Shaburova, O.V. and Krylov, V.N. (2011) Bacteriophage phi297—The New Species of Temperate Phages *Pseudomonas aeruginosa* with a Mosaic Genome: Potential Use in Phagotherapy. *Russian Journal of Genetics*, **47**, 794-798. <http://dx.doi.org/10.1134/S102279541106007X>
- [41] Krylov, S.V., Kropinski, A.M., Shaburova, O.V., Miroshnikov, K.A., Chesnokova, E.N. and Krylov, V.N. (2013) New Temperate *Pseudomonas aeruginosa* Phage, phi297: Specific Features of Genome Structure. *Russian Journal of Genetics*, **49**, 806-818. <http://dx.doi.org/10.1134/S1022795413080073>
- [42] Latino, L., Essoh, C., Blouin, Y., Vu Thien, H. and Pourcel, C. (2014) A Novel *Pseudomonas aeruginosa* Bacteriophage, Ab31, a Chimera Formed from Temperate Phage PAJU2 and *P. putida* Lytic Phage AF: Characteristics and Mechanism of Bacterial Resistance. *PLoS ONE*, **9**, Article ID: e93777. <http://dx.doi.org/10.1371/journal.pone.0093777>
- [43] Kim, S., Rahman, M., Seol, S.Y., Yoon, S.S. and Kim, J. (2012) *Pseudomonas aeruginosa* Bacteriophage PA1Ø Requires Type IV Pili for Infection and Shows Broad Bactericidal and Biofilm Removal Activities. *Applied and Environmental Microbiology*, **78**, 6380-6385. <http://dx.doi.org/10.1128/AEM.00648-12>
- [44] Ahiwale, S., Tamboli, N., Thorat, K., Kulkarni, R., Ackermann, H. and Kapadnis, B. (2011) *In Vitro* Management of Hospital *Pseudomonas aeruginosa* Biofilm Using Indigenous T7-Like Lytic Phage. *Current Microbiology*, **62**, 335-340. <http://dx.doi.org/10.1007/s00284-010-9710-6>

Scientific Research Publishing (SCIRP) is one of the largest Open Access journal publishers. It is currently publishing more than 200 open access, online, peer-reviewed journals covering a wide range of academic disciplines. SCIRP serves the worldwide academic communities and contributes to the progress and application of science with its publication.

Other selected journals from SCIRP are listed as below. Submit your manuscript to us via either submit@scirp.org or [Online Submission Portal](#).

