

***Escherichia coli* bacteriophages as
candidates for phage therapy and their
involvement in membrane vesicle
biogenesis**

Pappu Kumar Mandal
M. Sc. Medical Microbiology

A thesis submitted in fulfilment of the
requirements for the degree of
Doctor of Philosophy

ithree Institute
University of Technology Sydney
January 2020

Certificate of Authorship/Originality

I, Pappu Kumar Mandal declare that this thesis, is submitted in fulfilment of the requirements for the award of Doctor of Philosophy, in the ithree institute at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise reference or acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

I also certify that the thesis has been written by me and all the associated experimental work with it, has been carried out by me. Any help that I have received in my research work and the preparation of the thesis itself has been acknowledged. In addition, I certify that all information sources and literature used are acknowledged in the text.

This document has not been submitted for qualifications at any other academic institution.

This research is supported by the Australian Government Research Training Program.

Pappu Kumar Mandal

Production Note:

Signature: Signature removed prior to publication.

Date: 14.01.2020

Acknowledgement

The journey of my PhD has been quite challenging due to various changes in supervisory panel throughout the project. However, I am grateful to all of those with whom I have had the pleasure to work during this PhD project. I would like to express my appreciation to all who in one way or another contributed in the completion of this thesis. First and foremost, I wish to thank Dr Nico Petty who gave me an opportunity to begin my PhD project and Prof Cynthia Whitchurch who helped me to finish the project in the absence of Nico. Both of them has provided me extensive personal and professional guidance during different stages of my PhD and taught me a great deal about both scientific research and life in general. I would also like to acknowledge Dr Mohammad Hamidian, who helped me to finalise this thesis and A/Prof Garry Myer and Dr James Lazenby for reading the thesis chapters.

I would like to express my special appreciation and thanks to Dr Eby Sim and Dr Giulia Ballerin for their valuable support and guidance at different stages of this project, which not only helped me in learning different research tools and techniques but also strengthened me to complete this thesis. Thank you both of you for all your help, advice, and patience and it has been a privilege to learn from you and work with you.

I would like to acknowledge all past members of the Petty lab and Whitchurch lab, who have made this journey an amazing and productive one: Dylan, Leanne, Laura, Robarto, David, Joyce, Greg, and Rebecca. A thank of appreciation also goes to Dr Katie, Mark B and Dr Mark L for teaching and assisting me in the TEM at Microstructural Analysis Unit (MAU); Dr Christian, and Dr Louise for helping in the Microbial Imaging Facility (MIF) at UTS; and Sarah and Mercedes for taking care and support in the laboratory.

Very special gratitude goes out to my family: my mom, dad, and brother, thank you all for your support, care, praise and for helping me realise my potential and ambitions throughout my studies.

Last but by no means least, to my life partner Suji, without whose unconditional love, support, patience, and encouragement I would never make it this far. This thesis is especially dedicated to our son “Daksh” who born during this project.

Content page

Certificate of Authorship/Originality	i
Acknowledgement	ii
Content page	iii
List of Figures	vii
List of Tables	ix
Abbreviations	x
Research outputs	xii
Publications	xii
Conference proceedings	xii
Abstract	xiii
Chapter overview	xv
1 Introduction	1
1.1 <i>Escherichia coli</i> : a critical bacterial pathogen	1
1.2 <i>Escherichia coli</i> ST131: a multi drug resistant clonal complex	3
1.3 Alternative approaches to combat multi drug resistant bacterial infections	6
1.4 Bacteriophages	7
1.4.1 Morphology and classification of bacteriophages.....	8
1.4.2 <i>Caudovirales</i> : the tailed phages	9
1.4.3 Genomes of bacteriophages	11
1.4.4 Bacteriophage lifecycles	11
1.4.5 Co-evolution of bacteriophages and bacteria	16
1.4.6 Cultivation and purification of bacteriophages	19
1.4.7 Membrane vesicles in bacteriophage preparations	21
1.4.8 Endotoxin in bacteriophage preparation	22
1.5 Phage therapy: a potential therapeutic approach against multidrug resistant bacteria	24
1.5.1 Introduction to phage therapy	24
1.5.2 The history of phage therapy.....	24
1.5.3 Significance of phage therapy	26
1.5.4 Quality of phages for therapy.....	27
1.5.5 Patenting and regulation of phage therapy	27
1.6 Scope and objective of this study	28
2 Materials and Methods	29
2.1 Media supplements and solutions	29

2.2	Bacterial strains and bacteriophages	30
2.3	Bacteriophage methods	32
2.3.1	Isolation of bacteriophages	32
2.3.2	Propagation and harvesting of bacteriophages.....	33
2.3.3	Concentration and purification of bacteriophages	33
2.3.4	Bacteriophage quantification	35
2.3.5	Bacteriophage host range test.....	36
2.3.6	Bacteriophage Efficiency of Plating (EOP).....	37
2.3.7	Isolation of spontaneous bacteriophage resistant bacterial mutants	37
2.4	Genome sequencing and bioinformatics analysis	38
2.4.1	Bacteriophage DNA extraction	38
2.4.2	Bacteriophage DNA sequencing.....	39
2.4.3	Bacteriophage genome assembly and verification.....	39
2.4.4	Bacteriophage genome annotation and curation	39
2.4.5	Comparative genomic analysis	40
2.5	Microscopy methods	42
2.5.1	Bacterial lysis assay	42
2.5.2	Phase contrast and Super-resolution microscopy.....	43
2.5.3	Electron microscopy.....	43
2.5.4	Image analysis.....	44
2.6	Statistical analysis	44
3	Characterisation of three distinct bacteriophages infecting <i>E. coli</i> ST131.....	45
3.1	Introduction	45
3.2	Results	45
3.2.1	Verification of bacteriophage assembly revealed that each of the bacteriophage assembled in a single contig	45
3.2.2	Comparative nucleotide analysis revealed three types of bacteriophage.....	50
3.2.3	Bacteriophage Syd1, Syd6 and Syd8 each produce different types of plaque morphology.....	54
3.2.4	Bacteriophage Syd1, Syd6 and Syd8 are tailed bacteriophages with distinct morphologies	54
3.2.5	The three bacteriophage genomes are distinct from each other and from other <i>E. coli</i> ST131 infecting bacteriophages.	56
3.2.6	Genomic properties of Syd1, Syd6 and Syd8	57
3.2.7	Bacteriophage Syd1 is genetically similar to members of “Jerseyvirinae”	60
3.2.8	Bacteriophage Syd6 is genetically similar to phiEco32-like bacteriophages.....	65
3.2.9	Bacteriophage Syd8 is genetically similar to SP6-like bacteriophages.	69
3.2.10	The three representative bacteriophages each possess distinct host recognition proteins.....	74
3.2.11	Different patterns of host range infectivity in <i>E. coli</i> ST131 strains	76
3.2.12	Bacteriophage resistant host mutants to each of the three representative bacteriophages and their cross infectivity	82
3.3	Discussion	83
3.4	Conclusion.....	86

4	Membrane vesicle biogenesis in <i>E. coli</i> through virulent bacteriophage infection.....	88
4.1	Introduction	88
4.2	Results	88
4.2.1	Live cell imaging of bacterial lysis during bacteriophage infection	88
4.2.2	Bacteriophage mediated explosive cell lysis in <i>E. coli</i>	92
4.2.3	Bacteriophage mediated explosive cell lysis resulted MV biogenesis in <i>E. coli</i>	94
4.2.4	Membrane blebbing in <i>E. coli</i> under bacteriophage infection	96
4.2.5	Membrane vesicles within phage lysates	97
4.3	Discussion	100
4.4	Conclusion.....	102
5	Development of an optimized bacteriophage purification method.....	104
5.1	Introduction	104
5.2	Results	105
5.2.1	Total retention of bacteriophage through 100 KDa ultrafiltration	105
5.2.2	Adaptation of bacteriophage cultivation process to minimize buffer and media constituents in bacteriophage lysate	106
5.2.3	Optimization of Triton X-114 treatment for maximal removal of endotoxins from phage lysate.....	110
5.2.4	Residual Triton could be removed through ultrafiltration	112
5.2.5	Residual endotoxin removal through ultrafiltration	113
5.2.6	Designing an optimized protocol for bacteriophage purification	114
5.2.7	Validation that the optimized bacteriophage purification protocol reduces levels of Triton, endotoxin and membrane vesicles.....	115
5.3	Discussion	118
5.4	Conclusion.....	120
6	General discussion.....	121
6.1	Overview	121
6.2	New bacteriophages Syd1, Syd6 and Syd8 are potential candidates for phage therapy against <i>E. coli</i> ST131	122
6.3	Generation of MVs during bacteriophage cultivation is problematic for bacteriophage preparation	126
6.4	Use of Triton X-114 and ultrafiltration can remove endotoxin and MVs from bacteriophage preparation	129
6.5	Conclusions and Final remarks	130
	References	133
	Appendices	154
	Appendix 1: Promoters and terminator sequences in bacteriophage Syd1 genome .	154
	Appendix 2: Promoters and terminator sequences in bacteriophage Syd6 genome .	154

Appendix 3: Promoters and terminator sequences in bacteriophage Syd8 genome .	155
Appendix 4: Functional annotation of bacteriophage Syd1	156
Appendix 5: Functional annotation of bacteriophage Syd6.....	159
Appendix 6: Functional annotation of bacteriophage Syd8.....	164
Appendix 7: Nucleotide identity of bacteriophages that genomically resemble with Syd1.....	166
Appendix 8: Nucleotide identity of bacteriophages that genomically resemble with Syd6.....	168
Appendix 9: Identity of Syd6 encoded proteins with reference bacteriophage PhiEco32 proteins.	168
Appendix 10: Nucleotide identity of bacteriophages that genomically resemble with Syd8.....	175
Appendix 11: Identity of Syd8 encoded proteins with reference bacteriophage SP6 proteins.....	176
Appendix 12: List of movies.....	178
Appendix 13: Optimized bacteriophage propagation and purification protocol.....	181

List of Figures

Figure 1. 1: Evolutionary development of multi-drug resistant <i>E. coli</i> ST131.....	5
Figure 1. 2: Diversity of bacteriophage morphology.....	8
Figure 1. 3: Tailed phages structure.....	9
Figure 1. 4 : Life cycle of bacteriophages.....	14
Figure 1. 5: Core steps for bacteriophage and MVs preparation.....	21
Figure 1. 6: Historical milestones in phage therapy.....	25
Figure 2. 1: Endotoxin removal by Triton X-114 phase separation method.....	34
Figure 2. 2: Arrangement of log-fold dilutions of bacteriophage upon spot plate assays.	36
Figure 2. 3: A representative visual assessment of spot tests.....	37
Figure 3. 1: Read coverage over assembly.....	48
Figure 3. 2: Pairwise BLASTn comparison of PhiX-174 genome with bacteriophage assembly.....	49
Figure 3. 3: BLASTn comparison between all the assemblies.....	51
Figure 3. 4 A mapping profile over pseudomolecule.....	52
Figure 3. 5: Plaque morphologies of bacteriophages. (A) Syd1, (B) Syd6, and (C) Syd8 as grown on <i>E. coli</i> ST131 strain EC958.....	54
Figure 3. 6: Representative transmission electron micrographs of bacteriophages (A) Syd1, (B) Syd6 and (C) Syd8.....	55
Figure 3. 7: BLASTn comparison of a concatenated genome sequence of Syd1, Syd6 and Syd8 against each other and other bacteriophages which infect <i>E. coli</i> ST131 strains	57
Figure 3. 8: Linear representation of (A) Syd1, (B)Syd6, and (C) Syd8 genome.....	59
Figure 3. 9: BLASTn comparison of Syd1 against the Jerseyvirinae subfamily.....	62
Figure 3. 10: Pairwise BLASTn comparison of Syd6 with reference bacteriophage phiEco32.....	66
Figure 3. 11: BLASTn comparison of vB_EcoS_Syd6 against the genomes of PhiEco32-like bacteriophages.....	67
Figure 3. 12: Pairwise BLASTn comparison of Syd8 with reference bacteriophage SP6 and K1E.....	70
Figure 3. 13: BLASTn comparison of Syd8 against all the closely related bacteriophages.....	71
Figure 3. 14: Pairwise BLASTn comparison of genomic region from tail adaptor to the end of Syd8 with SP6-like bacteriophages.....	72
Figure 3. 15: A mapping profile over Syd8 terminase region.....	74
Figure 3. 16: Pairwise BLASTn comparison of Syd1 with LM33_P1.....	75
Figure 3. 17: Plaque morphologies of bacteriophage Syd1 (A) and Syd6 (B) on Syd8 resistant <i>E. coli</i> EC958 mutant.....	83
Figure 4. 1: Time lapse image sequence of <i>E. coli</i> MG1655 treated with (A) bacteriophage T4 (B) bacteriophage T7, and (C) lambda diluent.....	90
Figure 4. 2: Time lapse image sequence of <i>E. coli</i> ST131 strain EC958 treated with (A) bacteriophage Syd1, (B) bacteriophage Syd8, and (C) lambda diluent.....	91
Figure 4. 3: Cumulative percentage of bacterial lysis under bacteriophage treatments..	92
Figure 4. 4: Different patterns of explosive cell lysis in <i>E. coli</i>	93
Figure 4. 5: Cell lysis results in MVs formation.....	94
Figure 4. 6: MVs formation through explosive cell lysis in <i>E. coli</i>	96
Figure 4. 7: Membrane blebbing in <i>E. coli</i> under bacteriophage infectionmmersion.....	97

Figure 4. 8: MVs within phage lysates	98
Figure 4. 9: Sizes of MVs observed within different phage lysates.....	99
Figure 4. 10: MVs morphotypes.	100
Figure 5. 1: Bacteriophage harvesting buffer and bacteriophage concentration time on 100 KDa ultrafiltration.....	107
Figure 5. 2: Stability of T4 in phage buffer and lambda diluent.....	108
Figure 5. 3: Bacteriophage harvesting method and bacteriophage concentration time on 100 KDa ultrafiltration.	109
Figure 5. 4: Residual Triton X-114 in bacteriophage sample	113
Figure 5. 5: A schematic representation of the optimized bacteriophage propagation and purification method.	114
Figure 5. 6: Endotoxin level and bacteriophage quantity pre and post purification.	116
Figure 5. 7: Normalized endotoxin level within purified bacteriophage preparation ...	117
Figure 5. 8: Electron micrograph of crude and purified bacteriophages.....	118

List of Tables

Table 1. 1: Pathotypes of <i>E. coli</i> and associated human diseases.....	2
Table 1. 2: Development stages of alternative to antibiotic treatments for MDR Infections.....	7
Table 3. 1: Assembly statistics of bacteriophage genomes.....	46
Table 3. 2: Mapping profiles of the 125 bp repeat sequence in representative pseudomolecules	53
Table 3. 3: General features of the Syd1, Syd6 and Syd8 genomes.	58
Table 3. 4: Host range infectivity pattern of Syd1, Syd6 and Syd8 and Efficiency of Plating (EOP).	79
Table 3. 5: Host range infectivity and EOP of Syd1, Syd6 and Syd8 on bacteriophage resistant host mutants.	82
Table 5. 1: Bacteriophage quantity in pre and post 100 KDa ultrafiltration.....	106
Table 5. 2: Residual endotoxin level and rate of endotoxin removal from successive rounds of 1% Triton X-114 treatment of T4 lysate.....	110
Table 5. 3: Residual endotoxin levels and bacteriophage titres from successive rounds of endotoxin removal from a phage lysate with varying concentration of Triton X-114..	111

Abbreviations

Abbreviation	Meaning
3D-SIM	Three-dimensional structured illumination microscopy
°C	Degree Celsius
aa	Amino acid/s
Abi	Abortive infection
ATP	Adenosine triphosphate
<i>att</i>	Attachment site
BLAST	Basic Local Alignment Search Tool
bp	Base pair/s
CDS	Coding sequence
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
CsCl	Caesium chloride
DNA	Deoxyribonucleic acid
DNase	Deoxyribonuclease
EOP	Efficiency of plating
ESBL	Extended spectrum β -lactamase
ESCs	Extended spectrum cephalosporins
EU	Endotoxin unit
ExPEC	Extra intestinal pathogenic <i>E. coli</i>
FQR	Fluoroquinolone-resistance
g	Relative centrifugal force
G+C	Guanine + Cytosine
h	Hour/hours
ICTV	International Committee on Taxonomy of Viruses
Kb	Kilo base
Kda	Kilo dalton
Kv	Kilo volt
L	Litre
LAL	Limulus amebocyte lysate
LB	Lysogeny broth
LPS	Lipopolysaccharide
M	Molar
Mb	Mega base
MDR	Multi drug resistant
Min	Minute/minutes
μ l	Microlitre
mL	Mililitre
MLST	Multi locus sequence typing
mM	Miliomolar
mRNA	Messenger Ribonucleic acid
MVs	Membrane vesicles
MWCO	Molecular weight cut-off value
NCBI	National Centre for Biotechnology information
ng	Nanogram
nm	Nanometer
nr	Non-reductant nucleotide
nt	Nucleotides

Abbreviation	Meaning
NTP	Nucleotide triphosphate
PB	Phage buffer
pfu	Plaque forming unit
R-M	Restriction modification
RNA	Ribonucleic acid
rpm	Revolutions per minute
SAR	Sequence anchored release
SDS	Sodium dodecyl sulphate
Sec	Second/s
ST	Sequence type
Syd1	vB_EcoS_Syd1
Syd6	vB_EcoP_Syd6
Syd8	vB_EcoP_Syd8
T4	Bacteriophage T4
T7	Bacteriophage T7
TA	Toxin-antitoxin
TEM	Transmission electron microscopy
tRNA	Transfer ribonucleic acid
US FDA	The United States Food and Drug Administration
UV	Ultraviolet
v	Version

Research outputs

Publications

Mandal P. K., Sim E. M., Mansfield D., Haggerty L., Venturini C., Iredell J. R., Whitchurch C. B., & Petty N. K., (2020) Three virulent bacteriophages to combat the multidrug resistant *Escherichia coli* clone ST131 (Manuscript in preparation).

Mandal P. K., Ballerin G., Petty N. K., & Whitchurch C. B., (2020) Membrane Vesicles biogenesis in *Escherichia coli* through Bacteriophage infection (Manuscript in preparation).

Mandal P. K., Sim E. M., Whitchurch C. B., & Petty N. K., (2020) Phage purification and endotoxin removal utilising Triton X-114 and ultrafiltration (Manuscript in preparation).

Conference proceedings

Mandal P. K., Ballerin G., Petty N. K., & Whitchurch C. B., (July 2019) **ORAL PRESENTATION.** Membrane vesicles (MVs) as an outcome of bacteriophage mediated bacterial lysis. *Australian Society of Microbiology Annual Scientific Meeting*, Adelaide, Australia.

Abstract

The emergence of multidrug-resistant (MDR) bacterial pathogens is one of the biggest threats to global health. The WHO has recently prioritized the carbapenem-resistant Gram-negative bacteria, including *Escherichia coli*, as critical pathogens for which new therapeutic treatments are urgently required. However, there have been no new antibiotics approved in the past few decades and there is a trend of rapid development of bacterial resistance against the available antibiotics. Thus, non-conventional approaches are essential to control such MDR bacteria and therapy-utilising bacteriophages currently experiencing revival as an effective strategy. Bacteriophages are bacterial viruses that infect and multiply in bacteria thereby lysing them. Bacteriophages can only be cultivated in a susceptible bacterial host and may contain potential contaminants from bacterial cell. Membrane vesicles (MVs) are spherical nanostructures produced by bacteria and are also observed within bacteriophage preparations. However, there is no direct evidence linking bacteriophage activity and MVs formation. This Thesis established a collection of three new bacteriophages Syd1, Syd6, and Syd8 infecting one of the high risks MDR *Escherichia coli* Sequence Type 131 (ST131) and determined the source of MVs within bacteriophage preparations.

The genomic analysis determined that Syd1, Syd6, and Syd8 each lacked genes encoding for lysogeny, bacterial virulence, or antibiotic resistance. Electron microscopy and comparative genomic analyses revealed that Syd1, Syd6, and Syd8 were both morphologically and genetically distinct from each other and other previously characterized ST131 infecting bacteriophages. These three bacteriophages each possessed a completely distinct host recognition gene from each other and other closely related bacteriophages, indicating that each bacteriophage targeted a different surface receptor. Host range analysis on a panel of *E. coli* strains showed that all three bacteriophages can infect multiple ST131 strains efficiently and had different host range infectivity patterns, suggesting them as appropriate candidates for therapy. Live-cell super-resolution microscopy of *E. coli* infected with bacteriophages T4 and T7 showed that during bacteriophage infection, bacterial cells lyse explosively and MVs were formed from shattered membrane fragments. Electron microscopy revealed the presence of different forms of MVs within phage lysates, consistent with MVs formation through phage mediated bacterial lysis. A bacteriophage purification method utilising

ultrafiltration and Triton X-114 phase separation was optimised to remove endotoxins and MVs from bacteriophage preparations. Validation of the method on a panel of *E. coli* bacteriophages including Syd1, Syd6, and Syd8 showed the possibility of up to 5-log reduction in endotoxin and MVs were not detected from electron microscopy of any of these purified bacteriophages.

Chapter overview

This Thesis is composed of six chapters. Chapter one provides a general introduction to the *Escherichia coli* specifically a high-risk strain *E. coli* ST131, bacteriophage specifically tailed phages, phage therapy and preparation and purification of phages. Chapter two describes the materials and methodologies used to achieve the aims of this thesis. Chapter three details the isolation, morphology, genomic and host range characterization of three distinct bacteriophages Syd1, Syd6 and Syd8, which can infect and kill *E. coli* ST131 strains. Chapter four explores the membrane vesicles (MVs) biogenesis in *E. coli* through virulent bacteriophage infection and demonstrates the source of MVs within phage preparation. Chapter five describes a phage purification method, which is proposed for separating MVs from phages and getting pure phages with minimal endotoxin level. Chapter six discuss the main conclusions of the studies presented in this thesis and outlines recommendations for future work.