

Submit to

ENGINEERING Environment

First practice on bacteriophage-mediated disinfection of tailwater: Targeted removal of multidrug-resistant *vibrio parahaemolyticus* and associated antibiotic resistance genes

Yanxi Liu^{1,2}, Jian Lu^{1,2,*}, Jun Wu³, Jianhua Wang¹, Brian J. Boman⁴

¹ Shandong Key Laboratory of Coastal Zone Environmental Processes and Ecological Security, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Shandong 264003, China.

² University of Chinese Academy of Sciences, Beijing 100049, China

³ College of Materials and Chemical Engineering, Harbin Engineering University, Harbin, Heilongjiang 150001, P.R. China

⁴ Indian River Research and Education Center, University of Florida, Fort Pierce, FL34945-3138, USA

*Corresponding author. Email: jlu@yic.ac.cn (J.L.)

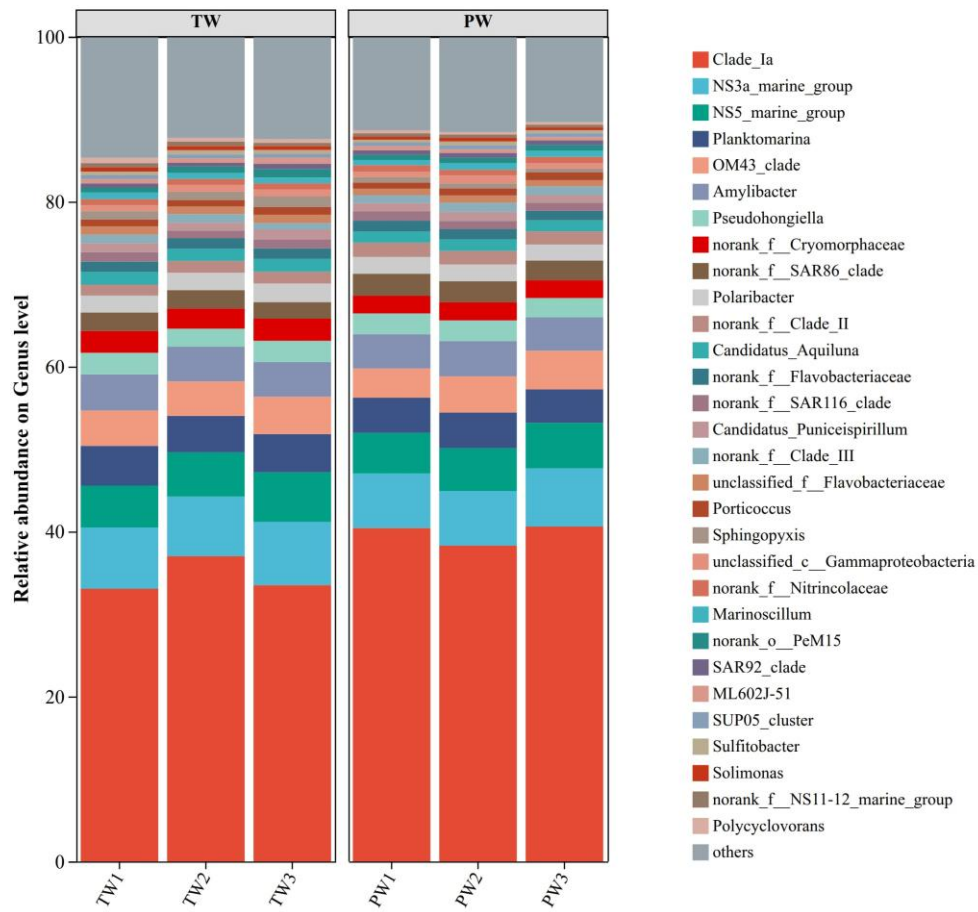


Fig. S1 Changes in the microbial ecology of the tailwater before (TW) and after phage treatment (PW).

Table S1 Primers of target ARGs and *intI1* for q-PCR in this investigation.

Genes	Amplification length (bp)	Primer Sequence (F, R: 5'-3')
<i>cat1</i>	550	ACAACAGCAACGGTACTAGC CAACTTTCACCGATGCCAC
<i>tetO</i>	172	GATGGCATAACAGGCACAGACC GCCCAACCTTTTGCTTCACTA
<i>qnrB</i>	175	TCGGCTGTCAGTTCTATGATCG TCCATGAGCAACGATGCCT
<i>sul1</i>	162	CGCACCGGAAACATCGCTGCAC TGAAGTTCCGCCGCAAGGCTCG
<i>intI1</i>	146	GGCTTCGTGATGCCTGCTT CATTCCCTGGCCGTGGTTCT

Table S2 Lytic range of phage VBY by spot testing.

species	strain	isolation source	lysis effect ^a
<i>Vibrio parahaemolyticus</i>	YTLJ74	Seawater	+
<i>Vibrio parahaemolyticus</i>	CICC 24174	Seawater	+
<i>Vibrio parahaemolyticus</i>	CICC 23924	Seawater	+
<i>Aeromonas enteropelogenes</i>	AP027940.1	Seawater	-
<i>Vibrio alginolyticus</i>	CP054700.1	Seawater	-
<i>Vibrio diabolicus</i>	CP014134.1	Seawater	-
<i>Vibrio diabolicus</i>	CP014094.1	Seawater	-
<i>Vibrio alginolyticus</i>	CP054700.1	Seawater	-
<i>Vibrio alginolyticus</i>	CP042449.1	Seawater	-
<i>Vibrio alginolyticus</i>	MK167375.1	Seawater	-
<i>Aeromonas caviae</i>	MK841333.1	Seawater	-
<i>Aeromonas caviae</i>	MK841333.1	Seawater	-
<i>Klebsiella pneumoniae</i>	CP137423.1	Seawater	-
<i>Vibrio alginolyticus</i>	CP054700.1	Seawater	-
<i>Vibrio alginolyticus</i>	MG262457.1	Seawater	-
<i>Escherichia coli</i>	CICC 24106	CICC	-
<i>Nitrospina gracilis</i>	ATCC25379	ATCC	-

^a +, susceptible to phage VBY; -, unsusceptible to phage VBY.

Table S3 Functionally annotated ORFs in the genome of phage VBY.

ORF	E-Value	Score	COG_category	Function
1	2.00E-239	658	S	Phage major capsid protein, P2 family
2	8.37E-171	476	L	Phage small terminase subunit
3	4.67E-65	201	S	Phage head completion protein (GPL)
4	2.43E-99	290	S	P2 phage tail completion protein R (GpR)
6	7.64E-224	622	S	Protein of unknown function (DUF2586)
7	4.47E-87	258	S	Protein of unknown function (DUF2597)
8	5.34E-31	110	T	Prokaryotic dksA/traR C4-type zinc finger
9	1.27E-67	209	M	lytic transglycosylase activity
12	2.16E-23	92	S	Phage tail assembly chaperone
13	1.88E-251	714	S	Phage-related minor tail protein
14	4.78E-52	166	S	Protein of unknown function (DUF2590)
15	3.80E-190	538	S	Baseplate J-like protein
16	1.78E-73	227	S	Phage tail protein (Tail_P2_I)
17	5.51E-123	399	S	Phage tail-collar fibre protein
19	1.44E-137	392	S	Rhs element vgr protein
20	1.87E-134	384	S	Rhs element vgr protein
22	2.93E-221	613	L	Phage integrase family
23	4.63E-06	55.1	L	Protein of unknown function (DUF1524)
24	5.80E-121	347	K	Bacteriophage CI repressor C-terminal domain
27	1.68E-116	334	S	Phage regulatory protein CII (CP76)
32	6.88E-130	368	H	DNA restriction-modification system
34	0	1314	S	Bacteriophage replication gene A protein (GPA)
37	1.79E-11	63.5	K	transcriptional regulator with C-terminal CBS domains
39	4.76E-57	182	S	Ogr/Delta-like zinc finger
40	2.53E-240	661	S	portal protein

41	0	1153	S	Terminase RNaseH-like domain
42	1.93E-175	493	S	Phage capsid scaffolding protein (GPO) serine peptidase
