

Supplement information

Characterization of the first double-stranded RNA bacteriophage infecting *Pseudomonas aeruginosa*

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Supplementary Table S1:List of all the ssRNA phages from GenBank Genomes database.

Genome	Accession	Length
Acinetobacter phage AP205	NC_002700	4268 nt
Caulobacter phage phiCb5	NC_019453	3762 nt
Enterobacteria phage BZ13	NC_001426	3466 nt
Enterobacteria phage C-1 INW-2012	NC_019920	3523 nt
Enterobacteria phage FI	NC_028902	4184 nt
Enterobacteria phage FI sensu lato	NC_004301	4276 nt
Enterobacteria phage Hgal1	NC_019922	3562 nt
Enterobacteria phage M	NC_019707	3405 nt
Enterobacteria phage MS2	NC_001417	3569 nt
Enterobacteria phage Qbeta	NC_001890	4215 nt
Pseudomonas phage PP7	NC_001628	3588 nt
Pseudomonas phage PRR1	NC_008294	3573 nt

Supplementary Table S2:List of all the dsRNA phages from GenBank Genomes

database.

Genome	Isolated from	Accession	Length (nt)
Pseudomonas phage phi 12	U.S.A	NC_004174	2322
		NC_004175	4100
		NC_004173	6751
Pseudomonas phage phi13	U.S.A	NC_004170	2981
		NC_004171	4213
		NC_004172	6458
Pseudomonas phage phi2954	U.S.A	NC_012091	6501
		NC_012093	2578
		NC_012092	3606
Pseudomonas phage phi6	U.S.A	NC_003715	6374
		NC_003716	4063
		NC_003714	2948
Pseudomonas phage phi8	U.S.A	NC_003301	3192
		NC_003299	7051
		NC_003300	4741
Pseudomonas phage phiNN	Finnish	KJ957166	2945
		KJ957165	3814
		KJ957164	6503
Pseudomonas phage phiYY (This study)	China	KX074203	3004
		KX074202	3862
		KX074201	6648

Supplementary Table S3: The detailed phage sensitivity rate for each cluster and hospital. The number after “/” is the total strains in this cluster and the number before “/” is the number of phage sensitive colonies.

Hospital	Southwest Hospital	Xinqiao Hospital	Daping Hospital	West China Hospital	Sichuan Provincial People's Hospital	Xijing Hospital	Henan Provincial People's Hospital
Cluster 1	9/18	0/1	1/2			0/1	7/13
Cluster 2	0/2						4/4
Cluster 3	0/3						
Cluster 4	3/10	3/3	1/1	1/2	1/1	1/1	1/2
Cluster 5	18/26	4/10	2/2	4/11	5/16	6/11	5/22
Cluster 6	1/6						
Cluster 7	3/10			0/3			
Cluster 8			1/1				1/5
Cluster 9	4/15	0/1	5/14	0/1	0/2	1/2	0/1
Cluster 10	0/2						1/1
Cluster 11	1/1						
Cluster 12						1/1	
Cluster 13	1/1						
Cluster 14							1/1
Cluster 15		1/2					
Cluster 16		1/1					

Supplementary Fig. S1: A representative picture of the ERIC-PCR profiles from *P. aeruginosa* strains. M: DNA maker; lanes 1–16, *P. aeruginosa* isolates.

