

Supplementary Information

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2 **Table S1.** dsRNA bacteriophage in family *Cystoviridae*

Species	Genus	Sequence accession numbers
Pseudomonas phage phi12	Cystovirus	NC_004173\NC_004175\ NC_004174
Pseudomonas phage phi13	Cystovirus	NC_004172\NC_004171\ NC_004170
Pseudomonas phage phi2954	Cystovirus	NC_012091\NC_012092\ NC_012093
Pseudomonas virus phi6	Cystovirus	NC_003715\NC_003716\ NC_003714
Pseudomonas phage phi8	Cystovirus	NC_003299\NC_003300\ NC_003301
Pseudomonas phage phiNN	Cystovirus	NC_042068\NC_042069\ NC_042070
Pseudomonas phage phiYY	Cystovirus	NC_042071\NC_042072\ NC_042073

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Table S2. The 16S rDNA sequencing results of *M. aerodenitrificans* strain LH11-4.

Name	16S rDNA sequence				
	1	CACCCCAGTC	ATGAAACCTA	CCGTGGTAAG	CGGGCTCCTT
	41	ACGGTTACCC	TACCCACTTC	TGGCGGATTC	CACTCCCATG
	81	GTGTGACGGG	CGGTGTGTAC	AAGGCCCGGG	AACGTATTCA
	121	CCGCGGCATG	CTGATCCGCG	ATTACTAGCG	ATTCCGACTT
	161	CACGCAGTCG	AGTTGCAGAC	TGCGATCCGG	ACTACGATCG
	201	GTTTTCTGGG	ATTAGCTTCA	CCTCGCGGCT	TCGCAACCCT
	241	CTGTACCGAC	CATTGTATGA	CGTGTGAAGC	CCTACCCATA
	281	AGGGCCATGA	GGACTTGACG	TCATCCCCAC	CTTCCTCCGG
	321	TTTGTACCG	GCAGTCCCAT	TAAAGTGCCC	AACTTAATGA
	361	TGGCAACTAA	TGGCAAGGGT	TGCGCTCGTT	GCGGGACTTA
	401	ACCCAACATC	TCACGACACG	AGCTGACGAC	AGCCATGCAG
	441	CACCTGTGCC	CAGGTTCCCT	TTCGGGCACT	CTCCCATCTC
	481	CGGGAGATTC	CTGGCATGTC	AAGGGTAGGT	AAGGTCTTTC
	521	GCGTTGCATC	GAATTAATCC	ACATCATCCA	CCGCTTGTGC
	561	GGGCCCCCGT	CAATTCCTTT	GAGTTTTAAT	CTTGCACCG
	601	TACTCCCCAG	GCGGTCGACT	TCACGCGTTA	GCTGCGCCAC
	641	CAAAGACCGA	GGTCTCCAAC	GGTAGTCGA	CATCGTTTAG
	681	GGCGTGGACT	ACCAGGGTAT	CTAATCCTGT	TTGCTCCCCA
	721	CGCTTTCGTG	CATGAGCGTC	AGTATCATCC	CAGGGGGCTG
	761	CCTTCGCCAT	TGGTGTTCCT	CCACATCTCT	ACGCATTTCA
	801	CTGCTACACG	TGGAATTCCA	CCCCCCTCTG	ACGTACTCTA
	841	GCGAGACAGT	TTCGGCCGCA	GTTCCCAGGT	TGAGCCCGGG
	881	GCTTTCACAG	CTGACTTATC	TCACCGCCTG	CGCACGCTTT
	921	ACGCCCAGTA	ATTCCGATTA	ACGCTTGAC	CCTACGTATT
	961	GCCGCGGCTG	CTGGCACGTA	GTTAGCCGGT	GCTTATTCTT
	1001	CCGGTACTGT	CAGTCCCGAC	CGCTATTAAC	GATCAGGGTT
	1041	TCCTCCCGGA	CAAAAGCCCT	TTACAACCCG	AAGGCCTTCT
	1081	TCAGACACGC	GGCATGGCTG	GATCAGGGTT	TCCCCATTG
	1121	TCCAAAATTC	CCCACTGCTG	CCTCCCGTAG	GAGTCTGGGC
	1161	CGTGTCTCAG	TCCCAGTGTG	GCGGATCATC	CTCTCAGACC
	1201	CGTACGGAT	CGTCGCCTTG	GTGAGCCTTT	ACCCACCAA
	1241	CTAGCTAATC	CGACATCGGC	CGCTCGATTA	GCGTGAGGCC
	1281	TTGCGGTCCC	CCACTTCCC	CCTCAGGGCG	TATGCGGTAT
	1321	TAGCACACCT	TTCGGTGCCT	TATCCCCAC	TATTCGGCAC
	1361	GTTCCGATGC	ATTACTCACC	CGTTCGCCAC	TCGTACGCGG
	1401	GAGCAAGCTC	CCCTGTTACC	GTTGACTTGG	CATGTGTAAA
	1441	GCATGCCGCC	AGCGTTCAAT		

M. aerodenitrificans
strain LH11-4.

36 **Table S3.** Primer used in this study.

Primer	Sequence (5' to 3')	Description	
PhiNY-L-5mo-1	CTCGGGTAGTTACACGGAGGTAAGT	5' and 3' RACE	
PhiNY-L-5mo-2	GCATCACATGATGGCTGAGTCTGAG		
PhiNY-L-3mo-1	GTACGCTACTGAAGCCAGCGTC		
PhiNY-L-3mo-2	GTGTCAAGCAACGCGTGTTCG		
PhiNY-L-3mo-3	GCTGCGTGACCTCCTCACCTAC		
PhiNY-M-5mo-1	CGAGCTTCTCCATATTACTAGCCCTC		
PhiNY-M-5mo-2	CACAAGTACGCAGTCGCCATG		
PhiNY-M-5mo-3	CAAACGCGCATTCTCAGTCGC		
PhiNY-M-3mo-1	GAGCTCGAAGACGTAGCTGAGCG		
PhiNY-M-3mo-2	GATCTCGGTCTTCGTATCGGTCCG		
PhiNY-M-3mo-3	CGGTAAGAGGCAACAAAAGGAAAGG		
PhiNY-S-5mo-1	GACCCGGTAGATTCCGGAACAG		
PhiNY-S-5mo-2	CACGTGGCATGGCTCGAACAAAC		
PhiNY-S-5mo-3	GAGGAAACCCTTGACCTTGTTTCATG		
PhiNY-S-3mo-1	CGAAGTTCAGTCCACTGGAAGCAAC		
PhiNY-S-3mo-2	GTAATGGCGAGTTTCGCCGATTC		
PhiNY-S-3mo-3	GCTGGAACCCGGTACAACATCTTTG		
REV-anchor	GCATTGCATCATGATCGATCGAATTCTTTA GTGAGGGTTAATTGCC (5' end phosphorylated oligonucleotide)		
oligoREV	GGCAATTAACCCTCACTAAAG		
REV-PCR	TCACTAAAGAATTCGATCGATC		
16S rRNA-F	AGAGTTTGATCCTGGCTCAG	RT-qPCR	
16S rRNA-R	GGTTACCTTGTACGACTT		
qL-6-F	GACATCGCTGACATCGACAGCATAAC		
qL-6-R	GAATACCTCGTTCTTCGGAGGTCAG		
qM-5-F	TGTCCAACGCTTACATCGAACCC		
qM-5-R	CGACATCCTTGACAACCCTGCTC		
qS-4-F	TGGAGTTGAGTTGATGCCCTTTGAT		
qS-4-R	TGGAGCTGTTGATGGGAAGATTGC		
phiNY-M-YZ-F1	CAGTCTGCGAGGTATCAGACTCGTAG		RT-PCR
phiNY-M-YZ-R1	GACGGTATCAGCATGATCAGGAACGAC		

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Table S4. Genome length (bp) of different dsRNA phage genomes.

Segments	phi6	phi8	phi12	phi13	phi2954	phiNN	phiYY	phiNY
L	6374	7051	6751	6458	6501	6503	6648	7135
M	4063	4741	4100	4213	3606	3814	3862	3229
S	2948	3192	2322	2981	2578	2945	3004	2657
Total	13385	14984	13173	13652	12685	13262	13514	13021

Table S5. Phage phiNY ORFs annotation results.

Segment	ORFs	Nucleotide position	Length (aa)	Mass (Da)	pI	Best match (aa identity)	E-value	Function
L	orf01	284-880	198	21228	7.87			hypothetical protein
	orf02	989-1270	93	10521	5.81			hypothetical protein
	orf03	1346-1945	199	21553	4.93			hypothetical protein
	orf04	2045-3826	593	67241	7.24	<i>Pseudomonas</i> phage phi2954 (26.17%)	4.E-50	RNA-dependent RNA polymerase P2
	orf05	3823-4791	322	35554	4.96			hypothetical protein
	orf06	4873-7023	716	79132	6.34	<i>Pseudomonas</i> phage phi2954 (20.55%)	2.E-05	major core structural protein P1
M	orf07	171-356	61	6947	9.88			hypothetical protein
	orf08	343-597	84	8251	4.64			hypothetical protein
	orf09	587-709	40	4228	9.52			hypothetical protein
	orf10	711-1190	159	16402	5.33			hypothetical protein
	orf11	1199-2860	553	61594	6.54			hypothetical protein
	orf12	2887-3114	75	8370	5.00			hypothetical protein
S	orf13	226-26	66	7716	12.00			hypothetical protein
	orf14	283-801	172	18382	9.57			hypothetical protein
	orf15	801-1376	191	20162	4.56			hypothetical protein
	orf16	1379-1630	83	8689	8.18			hypothetical protein
	orf17	1644-2564	306	33088	10.24	<i>Lactobacillus satsumensis</i> (35.42%)	1.E-12	glycoside hydrolase family 73 protein

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