

Host range, morphology and sequence analysis of ten temperate phages isolated from pathogenic *Yersinia enterocolitica* strains

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Supplemental Material Figures

Figure S1. Transmission electron micrographs of temperate *Y. enterocolitica* phages. The bar represents 50 nm.

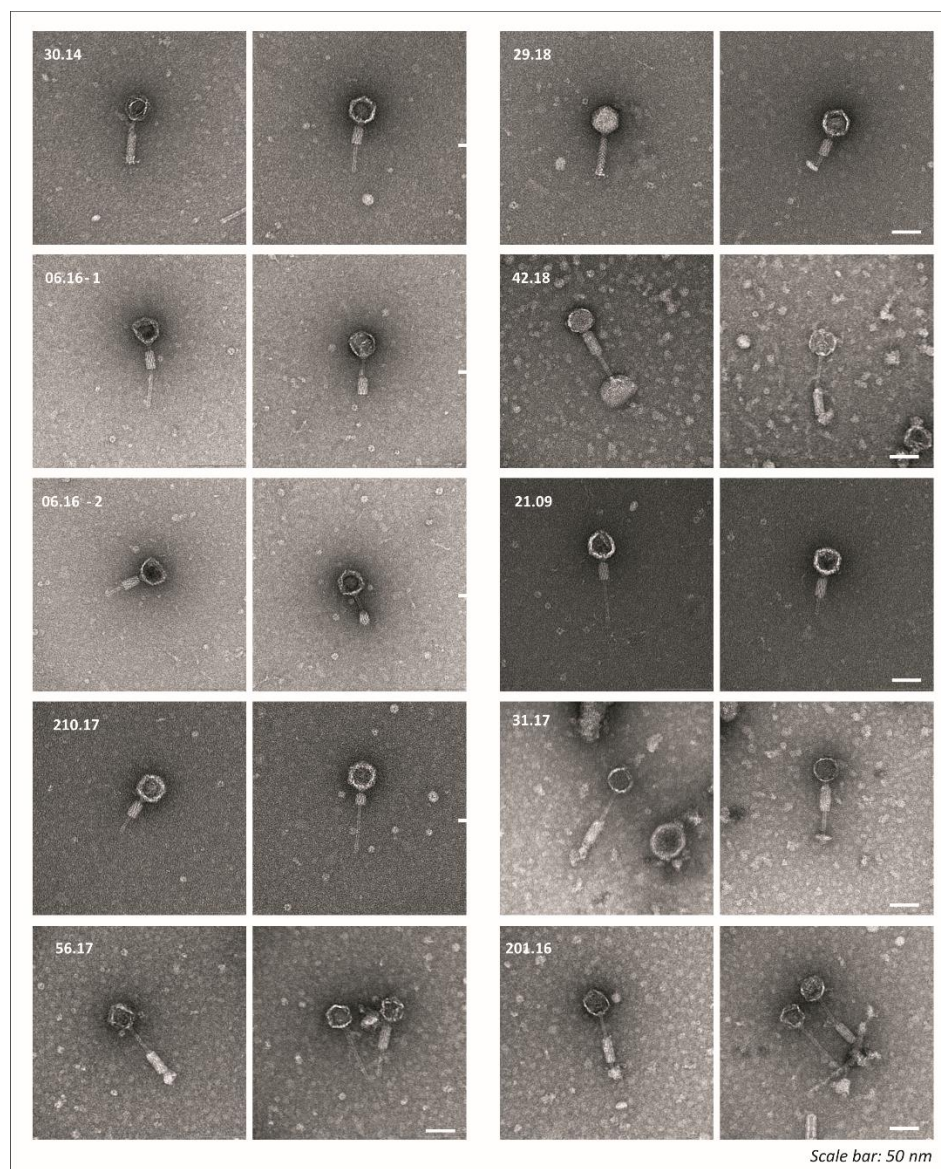


Figure S2. Comparison of the tail fiber protein sequences of *Y. enterocolitica* group 1 phages. (A) Amino acid alignment of the protein sequences, (B) phylogenetic relationship of the sequences using CSIfylogeny (default parameters) and (C) percentage of relationship between the individual protein sequences.

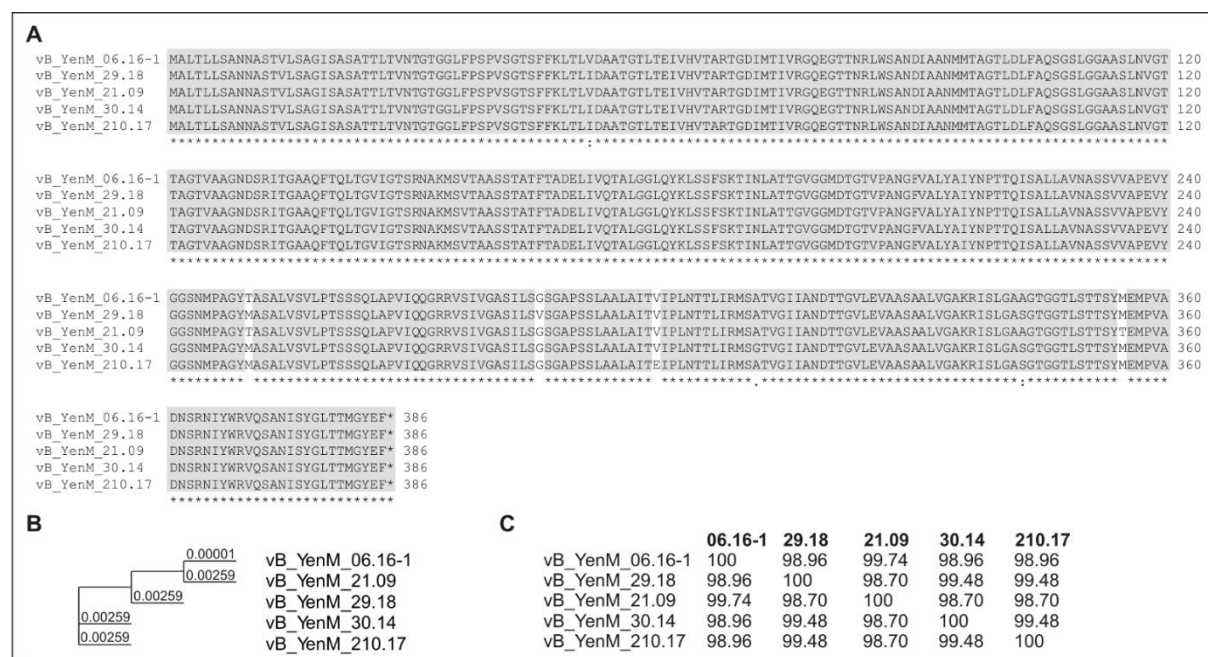


Figure S4. Amino acid alignment of the tail fiber protein sequences of *Y. enterocolitica* group 3 phage vB_YenM_42.18 and YeP4.

[illegible]

Supplemental Material Tables

Table S1. Phage and prophage prediction using PHASTER

<i>Y. enterocolitica</i> phage/isolate	PHASTER result (size, status, score, related phage, accession number, G+C content)	Position
vB_YenM_30.14	28.1 kb, incomplete, 60, <i>Salmonella</i> 118970_sal3, NC_031940, 46.88%	49-28,246 (C1)
14-YE00030	41.1 kb, intact, 150, <i>Salmonella</i> 118970_sal3, NC_031940, 46.43%	40,333-81,441 (C18)
	24.9 kb, intact, 130, <i>Erwinia</i> ENT90, NC_019932, 48.35%	1-24,937 (C50)
	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	143,495-174,510 (C4)
	56.6 kb, questionable, 70, <i>Salmonella</i> 118970_sal3, NC_031940, 47.84%	12,699-69,397 (C6)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	121-26,826 (C28)
	12 kb, incomplete, 50, <i>Aeromonas</i> phiO18P, NC_009542, 42.76%	74,291-86,291 (C7)
	15.1 kb, incomplete, 40, <i>Escherichia</i> 500465_1, NC_049342, 46.56%	2-15,132 (C15)
	9.8 kb, incomplete, 40, <i>Salmonella</i> SEN34, NC_028699, 41.26%	32-9,875 (C40)
vB_YenM_06.16-1	28.3 kb, questionable, 80, <i>Enterobacteria</i> ST104, NC_005841, 47.76%	49-28,422 (C1)
vB_YenM_06.16-2	28.9 kb, intact, 150, <i>Erwinia</i> ENT90, NC_019932, 50.81%	539-29,475 (C1)
16-YE00006	40.8 kb, intact, 150, <i>Salmonella</i> 118970_sal3, NC_031940, 46.44%	40,333-81,195 (C20)
	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	37,061-68,076 (C1)
	45.3 kb, questionable, 90, <i>Enterobacteria</i> ST104, NC_005841, 48.43%	19,265-64,644 (C7)
	38.6 kb, questionable, 70, <i>Erwinia</i> ENT90, NC_019932, 50.84%	882-39,511 (C40)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	242,995-269,700 (C1)
	12 kb, incomplete, 50, <i>Aeromonas</i> phiO18P, NC_009542, 42.77%	74,405-86,404 (C17)
	9.8 kb, incomplete, 50, <i>Enterobacteria</i> mEp237, NC_019704, 41.28%	24,183-34,018 (C41)
	15.1 kb, incomplete, 40, <i>Escherichia</i> 500465_1, NC_049342, 46.56%	2-15,132 (C16)
	14.9 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 41.97%	269-15,258 (C22)
vB_YenM_201.16	29.6 kb, incomplete, 60, <i>Erwinia</i> ENT90, NC_019932, 51.51%	519-30,211 (C1)
16-YE00201	7.9 kb, questionable, 90, <i>Enterobacteria</i> phiP27, NC_003356, 45.01%	4,278-12,189 (C56)
	35.6 kb, questionable, 80, <i>Erwinia</i> ENT90, NC_019932, 47.84%	778-36,424 (C43)
	36 kb, questionable, 70, <i>Erwinia</i> ENT90, NC_019932, 50.92%	116,217-152,217 (C3)
	7.7 kb, questionable, 70, <i>Escherichia</i> 500465_1, NC_049342, 47.62%	45,787-53,530 (C28)
	11.9 kb, incomplete, 40, <i>Enterobacteria</i> P4, NC_001609, 43.44%	46-12,013 (C47)
	24.8 kb, incomplete, 30, <i>Escherichia</i> 500465_1, NC_049342, 38.22%	10,034-34,912 (C47)

vB_YenM_31.17	32.7 kb, intact, 150, <i>Erwinia</i> ENT90, NC_019932, 48.95%	
17-YE00031	23.4 kb, intact, 150, <i>Erwinia</i> ENT90, NC_019932, 52.07%	42,366-65,853 (C26)
	17.8 kb, intact, 150, <i>Erwinia</i> ENT90, NC_019932, 51.35%	450-18,249 (C54)
	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	01,887-232,902 (C3)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	252-26,957 (C3)
	9.8 kb, incomplete, 50, <i>Enterobacteria</i> mEp237, NC_019704, 41.26%	24,202-34,053 (C40)
	12 kb, incomplete, 50, <i>Aeromonas</i> phiO18P, NC_009542, 42.76%	74,390-86,390 (C5)
	22.2 kb, incomplete, 40, <i>Escherichia</i> 500465_1, NC_049342, 46.07%	74,715-96,966 (C14)
	14 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 41.55%	65,769-79,814 (C19)
vB_YenM_56.17	31.1 kb, incomplete, 60, <i>Erwinia</i> ENT90, NC_019932, 50.72%	32-32,750 (C1)
17-YE00056	40.2 kb, intact, 150, <i>Salmonella</i> 118970_sal3, NC_031940, 46.45%	16,476-56,750 (C30)
	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	37,077-68,092 (C4)
	24 kb, intact, 120, <i>Erwinia</i> ENT90, NC_019932, 48.14%	2-24,069 (C49)
	26.8 kb, questionable, 70, <i>Enterobacteria</i> PsP3, NC_005340, 45.47%	1-26,883 (C29)
	33.2 kb, incomplete, 60, <i>Erwinia</i> ENT90, NC_019932, 49.71%	360-33,605 (C16)
	12 kb, incomplete, 50, <i>Cronobacter</i> ESSI_2, NC_047854, 42.79%	71,938-83,968 (C6)
	9.9 kb, incomplete, 50, <i>Enterobacteria</i> mEp237, NC_019704, 41.16%	24,202-34,117 (C39)
	22.2 kb, incomplete, 40, <i>Escherichia</i> 500465_1, NC_049342, 46.07%	74,685-96,888 (C18)
vB_YenM_210.17	27.3 kb, incomplete, 60, <i>Enterobacteria</i> 933W, NC_000924, 47.73%	49-27,368 (C1)
17-YE00210	40.2 kb, intact, 150, <i>Salmonella</i> 118970_sal3, NC_031940, 46.44%	40,349-80,596 (C20)
	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	20,887-232,902 (C2)
	31 kb, questionable, 70, <i>Enterobacteria</i> 933W, NC_000924, 48.02%	100,198-131,209 (C6)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	252-26,957 (C2)
	12 kb, incomplete, 50, <i>Aeromonas</i> phiO18P, NC_009542, 42.79%	71,938-83,968 (C5)
	9.8 kb, incomplete, 50, <i>Enterobacteria</i> mEp237, NC_019704, 41.28%	24,202-34,037 (C38)
	22.2 kb, incomplete, 40, <i>Escherichia</i> 500465_1, NC_049342, 46.07%	74,703-96,906 (C16)
	15.2 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 42.22%	1-15,274 (C21)
vB_YenM_29.18	27.3 kb, incomplete, 60, <i>Enterobacteria</i> 933W, NC_000924, 47.73%	49-27,368 (C1)
18-YE00029	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	117,722-148,737 (C4)
	36.6 kb, intact, 100, <i>Vibrio</i> VBM1, NC_020850, 47.01%	138,390-175,167 (C5)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	101-26,806 (C28)
	12 kb, incomplete, 50, <i>Cronobacter</i> ESSI_2, NC_047854, 42.79%	71,902-83,932 (C7)
	9.8 kb, incomplete, 50, <i>Salmonella</i> SEN34, NC_028699, 41.25%	24,163-34,039 (C40)

	18.1 kb, incomplete, 30, <i>Salmonella</i> 118970_sal3, NC_031940, 48.06%	29,219-47,393 (C33)
	12 kb, incomplete, 30, <i>Escherichia</i> 500465_1, NC_049342, 46.28%	84,374-96,436 (C16)
	15.2 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 42.20%	64,796-80,045 (C21)
vB_YenM_42.18	11.2 kb, incomplete, 10, <i>Klebsiella</i> 4LV2017, NC_047818, 51.27%	904-12,183 (C1)
	8.7 kb, incomplete, 30, <i>Klebsiella</i> OXA48phi14.1, NC_049454, 50.84%	15,228-23,954 (C1)
	7.1 kb, incomplete, 20, <i>Klebsiella</i> OXA245phi4.2, NC_049449, 46.69%	28,164-35,325 (C1)
18-YE00042	65.1 kb, intact, 150, <i>Enterobacteria</i> mEp390, NC_019721, 45.20%	84,251-149,443 (C5)
	13.6 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 44.34%	11,458-25,093 (C51)
	7.2 kb, incomplete, 50, <i>Salmonella</i> SEN34, NC_028699, 43.65%	38,110-45,358 (C34)
	28.9 kb, incomplete, 30, <i>Salmonella</i> Fels_2, NC_010463, 45.80%	121,090-150,004 (C7)
	7.3 kb, incomplete, 30, <i>Erwinia</i> ENT90, NC_019932, 49.97%	2-7,316 (C71)
	10.6 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 40.67%	12,714-23,363 (C52)
vB_YenM_21.09	28.2 kb, questionable, 80, <i>Salmonella</i> SE1, NC_011802, 47.93%	49-28,303 (C1)
21-YE00009	31 kb, intact, 120, <i>Vibrio</i> 12B12, NC_021070, 47.94%	37,029-68,004 (C2)
	11.6 kb, intact, 110, <i>Salmonella</i> 118970_sal3, NC_031940, 50.99%	533-12,182 (C60)
	28.2 kb, questionable, 90, <i>Salmonella</i> 118970_sal3, NC_031940, 44.52%	305-28,581 (C24)
	31.9 kb, questionable, 90, <i>Salmonella</i> SE1, NC_011802, 48.18%	25,706-57,652 (C25)
	26.7 kb, incomplete, 60, <i>Enterobacteria</i> PsP3, NC_005340, 45.49%	242,963-269,668 (C2)
	12 kb, incomplete, 50, <i>Cronobacter</i> ESSI_2, NC_047854, 42.76%	74,186-86,186 (C6)
	12.1 kb, incomplete, 30, <i>Escherichia</i> 500465_1, NC_049342, 46.30%	311-12,430 (C15)
	15.2 kb, incomplete, 10, <i>Enterobacteria</i> 186, NC_001317, 42.19%	64,784-80,021 (C19)

In grey, predicted prophage matching to the respective phage genomes are indicated. Additionally to the nucleotide positions within the WGS sequences of the bacteria, further information about the respective contig is given in brackets.

Table S2. *Enterobacterales* isolates tested for lytic activity

Phage group	1					2				3
Isolate ID	06.16-1	09.21	29.18	30.14	210.17	06.16-2	31.17	56.17	201.16	42.18
<i>Klebsiella</i> spp. (n=10)										
<i>K. pneumoniae</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>K. oxytoca</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>K. variicola</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>K. michiganensis</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>K. quasipneum.</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Escherichia</i> spp. (n=10)										
<i>E. coli</i> (O157, n=2)	-	-	-	-	-	-	-	-	-	-
<i>E. coli</i> (O104, n=2)	-	-	-	-	-	-	-	-	-	-
<i>E. coli</i> (O26, n=2)	-	-	-	-	-	-	-	-	-	-
<i>E. hermannii</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>E. marmotae</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Salmonella</i> serovar (n=10)										
<i>S. Typhimurium</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>S. Braenderup</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>S. Schwarzengrund</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>S. Enteritidis</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>S. Paratyphi</i> (n=2)	-	-	-	-	-	-	-	-	-	-
Other bacteria (n=10)										
<i>Proteus mirabilis</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Enterobacter cloacae</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Morganella morganii</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Citrobacter freundii</i> (n=2)	-	-	-	-	-	-	-	-	-	-
<i>Raoultella ornitholytica</i> (n=2)	-	-	-	-	-	-	-	-	-	-

Type phages of the respective groups are indicated bold.