

Figure S1: ϕ Lmd1 titers before (light grey) and after (dark grey) growth on *L. mesenteroides* A1 or commercial mixed DL starter cultures A, B, C and D. *Leuconostocs* normally constitute between 1 and 10 % of mixed DL cultures. ϕ Lmd1 was suspended in MRS-C and inoculated with approximately 1×10^7 cells/ml and incubated for at least 16 hours. Starter cultures A and C were from one supplier, and B and D from another. ϕ Lmd1 titers are given in plaque forming units (pfu) / ml.

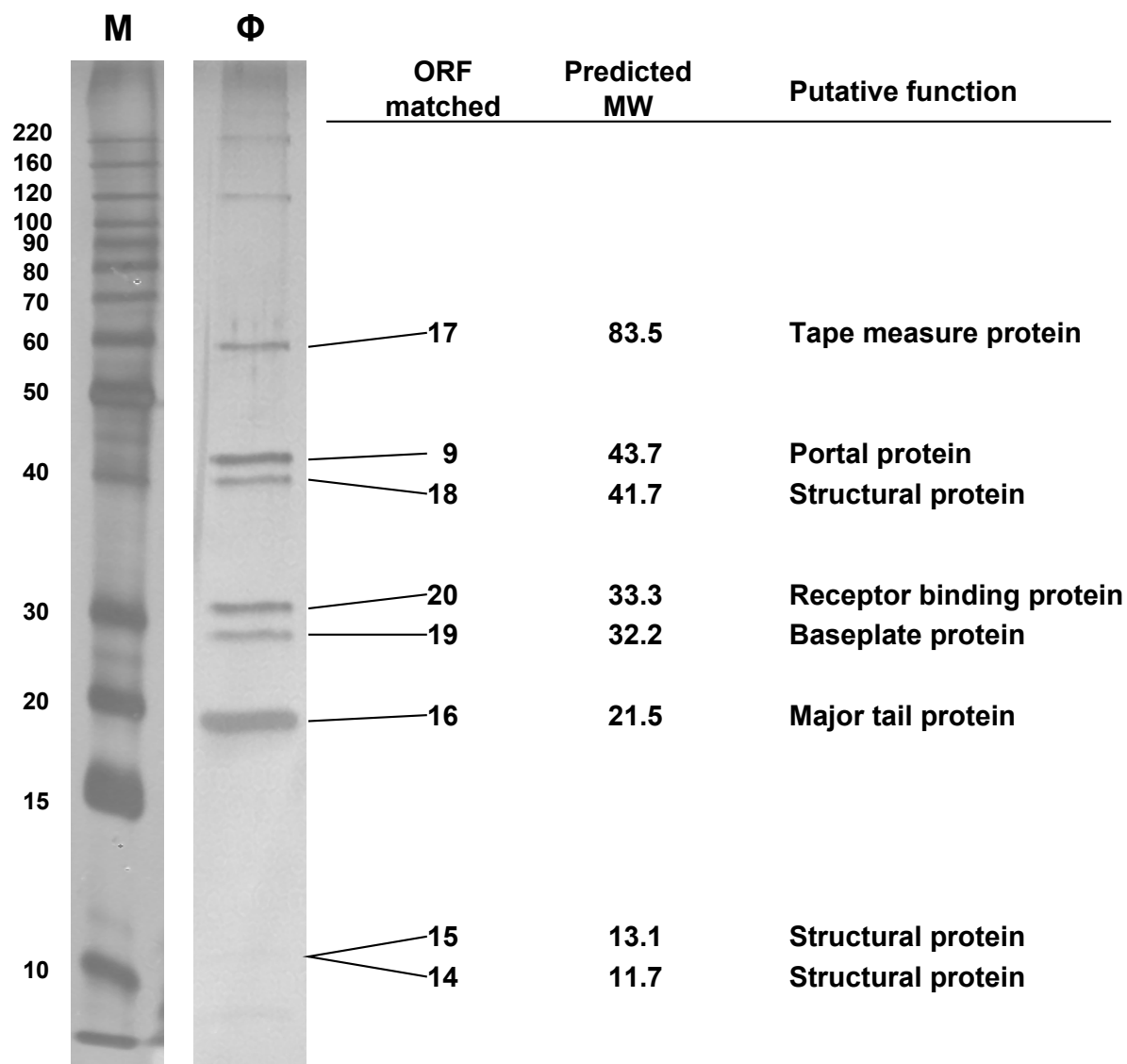


Figure S2: SDS-PAGE analysis and identification of Φ Lmd1 structural proteins. Lane M shows the protein ladder with molecular masses in kilodaltons (kDa) marked on the right. Lane Φ contains purified phage particles. Protein identities determined by MS, calculated molecular masses in kDa and putative functions are shown on the left. Phage particles were precipitated with polyethylene glycol and purified on CsCl gradients as described elsewhere (1). In-gel digestion, MALDI-TOF analysis and protein identification was performed essentially as described by Mehmeti et al. (2), except that database searches were done against the NCBI "nr" database and a local database containing all ORFs of Φ Lmd1 larger than 50 amino acids.

Supplementary table 1: Open reading frames of ϕ Lmd1 examined in this study.

ORF	Putative ribosomal binding site and start codon sequence ^A	Position ^B		Size (aa)	Mol. wt. (kDa)	pI	Putative function ^C	Predicted protein		Reference
		Start	End					Closest homolog (Extent, % identities, % positives, % gaps)	Size (aa)	
1	<u>TAAAGGAGGCCTAACATG</u>	2008	3402	464	52.7	5.55	DNA helicase	<i>Lactobacillus plantarum</i> , WCFS1, lp3 protein 8 (442/464, 21, 36, 11)	464	NP_785924
2	<u>ACGGAGGTGCTTTTATG</u>	3392	4162	256	29.8	7.01	DNA primase/polymerase	<i>Leuconostoc</i> phage 1-A4, LM1A4_003 (250/256, 41, 58, 6)	251	ADD71726
3	<u>CCAAGAGGTGATGATG</u>	4215	4694	159	18.4	9.88	HNH endonuclease	<i>Lactobacillus</i> phage A2, ORF57 (139/159, 40, 58, 0)	207	NP_680539
4	<u>CGGGAGGATATACTTTG</u>	4678	6495	605	68.6	6.17	Possible DNA polymerase	<i>Leuconostoc</i> phage 1-A4, LM1A4_005 (605/605, 52, 68, 1)	611	ADD71728
5	<u>CAAGGAAGTGAACAATG</u>	6553	7110	185	21.0	8.53	Cons.	<i>Leuconostoc</i> phage 1-A4, LM1A4_006 (188/185, 46, 68, 4)	190	ADD71729
6	<u>TAAGAGAAGATAATCATG</u>	7180	7803	207	24.2	6.40	Hydrolase (tRNA 3' endonuclease)	<i>Leuconostoc</i> phage 1-A4, LM1A4_007 (209/207, 62, 77, 1)	210	ADD71730
7	<u>GAGGTAATAACCAATG</u>	7822	8172	116	13.4	4.95	Terminase small subunit	<i>Leuconostoc</i> phage 1-A4, LM1A4_008 (98/116, 41, 70, 0)	108	ADD71731
8	<u>TACGGAGAATTGAGTATG</u>	8175	9815	546	62.9	5.50	Terminase large subunit	<i>Leuconostoc</i> phage 1-A4, LM1A4_010 (534/546, 56, 73, 1)	548	ADD71733
9	<u>TTGAAAGGCATGCTATG</u>	9878	11047	389	43.7	5.16	Portal protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_011 (357/389, 52, 70, 4)	373	ADD71734
10	<u>CAGGGAGCACGGCTAATG</u>	10998	11723	241	26.0	4.88	Phage prohead protease	<i>Leuconostoc</i> phage 1-A4, LM1A4_012 (185/241, 57, 72, 4)	239	ADD71735
11	<u>GAGGAAAATTATAATG</u>	11781	12749	322	34.6	5.85	Major capsid protein	<i>Leuconostoc</i> phage 1-A4, LM1A4_013 (303/322, 49, 64, 3)	321	ADD71736
12	<u>AAAGGAACCGACTATTATG</u>	12824	13102	92	11.0	4.49	Cons.	<i>Leuconostoc</i> phage 1-A4, LM1A4_014 (86/92, 34, 65, 0)	90	ADD71737
13	<u>TAGGTGGTGGCAAGATG</u>	13099	14047	315,3	10.5	9.95	Phage tail protein	<i>Leuconostoc</i> phage 1-A4, LM1A4_015 (70/93, 39, 51, 1)	92	ADD71738
14	<u>AGGAGGCAATCGCTAATG</u>	13380	13691	103	11.7	4.83	Structural protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_016 (105/103, 43, 66, 2)	105	ADD71739
15	<u>AAGATGTAGTGGTCTGCTGATG</u>	13691	14047	118	13.1	10.48	Structural protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_017 (114/118, 40, 54, 7)	109	ADD71740
16	<u>ACGTGAGGATAATAAAAAATG</u>	14098	14682	194	21.5	5.10	Major tail protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_018 (189/194, 63, 74, 1)	193	ADD71741
17	<u>AAAAGGAGCTTTTAAATG</u>	14832	17288	818	83.5	10.36	Tape measure protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_019 (859/818, 34, 52, 13)	889	ADD71742
18	<u>TGATATAATCTAGTATG</u>	17332	18447	371	41.7	4.93	Structural protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_020 (404/371, 28, 49, 11)	398	ADD71743
19	<u>ATTTGGAGACTAGAGATG</u>	18450	19319	289	32.2	5.11	Baseplate protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_021 (334/289, 33, 48, 14)	332	ADD71744
20	<u>AAGAAAGGTAATAATATG</u>	19333	20265	310	33.3	8.79	Receptor binding tail protein *	<i>Leuconostoc</i> phage 1-A4, LM1A4_023 (142/310, 39, 61, 5)	255	ADD71746
21	<u>ATTGTTTAATCAATTTCTTG</u> (20286 .. 20537)			83	9.4	9.83	Cons.	<i>Leuconostoc</i> phage 1-A4, position (19145..19360) (41/83, 54, 78, 0)	72	GQ451696
22	<u>AAAGGACGAACCAACATG</u> (20512 .. 20892)			126	14.6	4.78	Cons.	<i>Leuconostoc</i> phage 1-A4, LM1A4_022 (114/126, 49, 67, 2)	133	ADD71745
23	<u>AATGGAACGTAATAATG</u> (20957 .. 21340)			127	14.2	6.09	Holin	<i>Leuconostoc</i> phage 1-A4, LM1A4_024 (109/127, 43, 62, 0)	123	ADD71747
24	<u>TAGGAGATAAAAAATG</u> (21420 .. 21608)			62	7.0	7.09		No significant similarity		
25	<u>AAAGGGTGAATTTAATG</u> (21601 .. 21966)			121	13.2	4.47		No significant similarity		
26	<u>AAAGGAGAACAATAATG</u> (21966 .. 22241)			91	10.7	9.46	Cons.	<i>Paenibacillus lactis</i> 154, predicted protein (87/91, 41, 57, 0)	106	ZP_09002987
27	<u>TAAGGAGCCAGAGAGATG</u> (22241 .. 22768)			175	20.4	5.19	Cons.	<i>Weissella paramesenteroides</i> ATCC33313, predicted protein (68/175, 53, 71, 1)	141	ZP_04782166
28	<u>AGGAGATGATATATTTG</u> (22765 .. 22983)			72	8.1	5.52	Cons.	<i>Leuconostoc</i> sp. C2, LGMK_06970 (60/72, 47, 73, 0)	61	YP_004706067
29	<u>TTAAAGGAAAATAGAATG</u> (23039 .. 23287)			82	9.7	4.66		No significant similarity		
30	<u>TGATGGAGATATATGATG</u> (23303 .. 23626)			107	12.6	4.63	Cons.	<i>Leuconostoc gelidum</i> KCTC 3527, predicted protein (79/107, 41, 59, 11)	112	ZP_08479517
31	<u>GAGAGGATTTTCAAAAAATG</u> (23639 .. 23848)			69	8.2	9.42		No significant similarity		
32	<u>ACGAGGTAAATGGTATG</u> (23845 .. 23991)			48	6.1	11.41		No significant similarity		
33	<u>AAAGCGCAATTATAATG</u> (23988 .. 24257)			89	10.7	9.97		No significant similarity		
34	<u>AAAGGAGGTCACAAAAGATG</u> (24257 .. 24508)			83	9.7	9.47		No significant similarity		
35	<u>AAGAGGCAGAGCGAGTTG</u> (24620 .. 25480)			286	32.1	6.83	Lysin	<i>Leuconostoc</i> sp. C2, LGMK_06825 (180/286, 83, 89, 0)	319	YP_004706038
36	<u>GAAAGGAGGATTAACACATG</u> (25422 .. 25859)			145	15.5	7.19	Cons.	<i>Leuconostoc citreum</i> KM20, LCK_01036 (132/145, 48, 65, 0)	140	YP_001728307
37	<u>AAAGGAACGATAAGACTATG</u> (25863 .. 26009)			48	5.6	5.47	Repressor	<i>Clostridium scindens</i> ATCC 35704, CLOSCI_00042 (45/48, 42, 64, 0)	59	ZP_02429839
38	<u>ATTGTGTTCAAGAAATATG</u> (435 .. 746)			103	12.4	8.88	HNH endonuclease	<i>Leuconostoc</i> phage 1-A4, LM1A4_047 (90/103, 42, 58, 0)	100	ADD71770
39	<u>AAGGGGGCTAAAAACAAAATG</u> (743 .. 1252)			169	18.9	10.08	HNH endonuclease	<i>Enterococcus</i> phage EFRM31, gp11 (166/169, 45, 61, 5)	173	YP_004306639
40	<u>GGAATGAGGTGTCACAAATG</u> (1245 .. 1571)			108	12.7	9.03	Endonuclease	<i>Leuconostoc</i> phage 1-A4, LM1A4_050 (106/108, 69, 80, 1)	124	ADD71773

^A Predicted ribosomal binding site and start codons are underlined.

^B ORF positions on complement strand are shown in parentheses

^C Putative function based on BLASTP and PSI-BLAST results at www.blast.ncbi.nlm.nih.gov (June 2012). Structural proteins identified in this study are indicated with an asterisk. Cons.: Conserved hypothetical protein.

References

- Boulanger, P.** 2009. Purification of bacteriophages and SDS-PAGE analysis of phage structural proteins from ghost particles, p. 227-238. In M.R.J. Clokie and A.M. Kropinski (ed.), *Bacteriophages: Methods and Protocols, Molecular and Applied Aspects*, vol 502. Springer, New York, NY.
- Mehmeti, I., M. Jönsson, E.M. Fergestad, G. Mathisen, I.F. Nes and H. Holo.** 2011. Transcriptome, proteome and metabolite analyses of a lactate dehydrogenase-negative mutant of *Enterococcus faecalis* V583. *Appl Environ Microbiol* **77**:2406-2413