List of supplementary files

Supplementary file 1 (this file): Supplementary Figures 1-4.

Supplementary file 2: Table S1. List of isolated bacterial strains.

Supplementary file 3: Table S2. Genome annotation of phage cluster representatives.

Supplementary file 4: Table S3. Phage representation in the obtained metaviromes.

Supplementary file 5: Table S4. Identification of contigs >20 kbp in the obtained metaviral samples.

Supplementary file 6: vConTACT2 analysis .cys file that can be opened using Cytoscape.

Supplementary file 7: Nucleotide sequences of isolated phage genomes.



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Strain isolation source (donor-time point):

D2-S1 D2-S2

D1-S1

D1-S2

0.0020

C

b

	B. ovatus MB20-130	MB20-130	MB20-137	MB20-138	MB20-15	MB20-163	MB20-19	MB20-195	MB20-198	MB20-212	MB20-234	<mark>MB20-40</mark>	MB20-46	MB20-48	MB20-51	MB20-57	MB20-59	MB20-63	MB20-66
	B. ovatus MB20-137	596	15																
	B. ovatus MB20-15	596	15	2															
	B. ovatus MB20-163	11	614	601	601														No. of core
	B. ovatus MB20-19	5	608	595	595	10													genes:
	<i>B. ovatus</i> MB20-195	605	24	11	11	594	604												4996
	<i>B. ovatus</i> MB20-198	12	615	602	602	1	11	595											
	B. ovatus MB20-212	601	20	11	11	610	604	20	609										
	<i>B. ovatus</i> MB20-234	3	606	597	595	12	6	606	13	602									
	B. ovatus MB20-40	599	18	5	5	604	598	14	603	12	600								
	B. ovatus MB20-46	4	607	598	598	13	7	607	14	603	5	601							
	B. ovatus MB20-48	596	15	2	0	601	595	11	602	11	595	5	598						
	B. ovatus MB20-51	594	13	4	4	603	597	13	602	7	595	5	596	4					
	B. ovatus MB20-57	596	15	2	2	601	595	11	602	11	597	5	598	2	4				
	B. ovatus MB20-59	13	616	603	603	18	12	612	19	612	14	606	15	603	605	603			
	<i>B. ovatus</i> MB20-63	593	12	3	3	602	596	12	603	8	594	6	595	3	1	3	604		
	B. ovatus MB20-66	605	0	15	15	614	608	24	615	20	606	18	607	15	13	15	616	12	
	B. ovatus CL03T12C1	8																	
	B. ovatus AM30-13																		
	= B outputs 2725 D1 in																		
	B. Ovalus 3725 D1 IV																		
	B. ovatus AF	14 13AC																	
	B	. ovatus MB18-6	51 MB18-61	MB18 -78	MB20-110	MB20-74													
	В	. ovatus MB18-7	78 376			No. of													
	В	. ovatus MB20-1	10 385	17		core													
	В	. ovatus MB20-7	74 349	153	136	genes: 4863													
	B	. ovatus SD CMC	3f																
	B. ovatus ATCC 8483																		
	B. ovatus V975																		
	B. ovatus CL09T03C03																		
	B. kribbi JCM 31391																		
	B. koreensis JCM 31393																		
L																			
0.01	I																		

Supplementary Figure 1. Phylogenetic trees based on core-genome alignment of *B. uniformis* (a), *B. thetaiotaomicron* (b) and *B. ovatus* (c) strains. The genomic differences between strains clustered in one developmental line are given as number of SNP sites in the adjacent tables.

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Transmission electron microscopy (TEM) revealed siphoviruses in the isolated and purified cultures of phages C1 (A), C2 (B) and C3 (C). Podovirus morphology was observed in TEM micrographs of D2-FW2 (D).

Transmission electron microscopy of cluster C1 representative, C1-85S2P, showed siphovirus morphology with a long, non-contractile tail and capsid diameter around 52 nm (A). The tail length (160 nm) is longer than in typical siphoviruses and ends in an arrow shaped tip. TEM of reference C2 phage, C2-80S2P, also exhibited siphovirus morphology with a 119 nm long tail and a capsid diameter around 51 nm (B). C3 reference phage C3-41T2LP again had siphovirus morphology with 57.5 nm capsid diameter and unusually long, bent tail, which together with a tail fibril measures 325 nm (C). Cluster C7 is Bacuni phage and the siphovirus morphology was described before¹⁹. TEM was additionally performed on fecal water sample D2-FW2, that was the isolation source of C4 phages (Crassphages). Phages of podovirus morphology (67 nm capsid diameter and 22 nm fibril length) were highly abundant (D).

E: Genetic and isolation differences within clusters

Phage cluster	Nucleotide identity within cluster	No. of SNP sites	SNP locations in putative proteins	Isolation method; phage purification and plaque formation*	Lysogeny associated genes**	Detected as a prophage in isolated <i>Bacteroides</i> genomes	
C1	99%	3-9	Tail tape-measure protein, major capsid protein, portal protein; major tropism determinant	DAL; pure and mixed phage lysates; polymorphic plaques	No	no	
C2	97-99%	4-255	Condensed SNPs sites in tail, capsid, coat, fimbrial, membrane domain proteins, putative packaging genes	DAL; pure and mixed phage lysates; polymorphic plaques	No	no	
C3	99%	2-10, genom e inversi ons	Major outer capsid, tail, membrane adhesion protein, envelope glycoprotein	DAL + enrichment; pure and mixed phage lysates, pure and mixed filtrates; slightly turbid 5 mm plaques	Yes	no	
C4	99%	20	Portal protein, lysis regulatory protein, stabilization protein, peptidoglycan hydrolases	Enrichment culturing; mixed phage filtrates	No	no	
C5	99%	n.a.	n.a.	Enrichment culturing; mixed phage filtrates	Yes	Yes; 7 in P. vulgatus, 1 in B. uniformis	
C6	99%	n.a	n.a	DAL; mixed phage lysates;	Yes	Yes, strains from NCBI nr-database	
C7	99%	9-27	Condensed in diversity generating element genes (DGR) especially in target protein DUF1566 (fimbrial tip protein)	DAL + enrichment; pure and mixed phage lysates; 3-0,5 mm plaques	Yes	Yes, 5 in P. vulgatus	

*: DAL double agar layer methods; ** Putative integrase, repressor and excision genes.

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Supplementary Figure 2. Detailed characterization of isolated phages. A-D:Transmission electron microscopy. E: Genetic and isolation differences within clusters. F: Visualization of genome organization modules. ORF: open reading frame. There is little or zero protein homology between isolated bacteriophage clusters.



Supplementary Figure 3. Phylogenetic tree based on core genome alignment and isolation process of C3 phages. The phages with letter P in their names have all been purified by three rounds of plaque assay.



Supplementary figure 4. a-c: plaques of phages on bacterial lawns. Bacteriophage C1_85FV1PM on MB20-85 (a), C2_1880S2P on MB18-80 (b) and C3_41T2LP on MB20-41 (c). d: lysis-like zones on spot assay using strain MB20-185. Phages C1_85FV1PM and C2_1880S2P in middle and bottom rows as indicated. e: lysis-like zones and clearings on MB18-33. The clearings are caused by C7_F1 (bottom) and C1_85FV1PM (right).

