Supplementary Materials

Details of 16S rRNA gene copy numbers in the genomes used in the analysis are represented in Table S1. The genomes were obtained from the NCBI database while the 16S rRNA gene sequence was downloaded from the individual genome. Some genomes had more than one copy of the 16S rRNA gene. The copies were analyzed and found to be the same. Thus, only one copy was used in drawing the phylogenetic tree.

Table S1: 16S rRNA gene copy number in the related genomes.

Isolate	**Copies**	**Region**	**Genome (Accession number)**
Bdellovibrio sp. LBG001^T	2	953588..955101 1759940..1761453	NZ_CP093442.1
B. bacteriovorus 109J	1	1036899..1038412	NZ_CP007656.1
B. bacteriovorus strain SSB218315	1	2952287-2950774	NZ_CP020946.1
B. bacteriovorus HD100^T	2	819576..821089 1687640..1689153	NC_005363.1
B. bacteriovorus W	2	608416-609941 1360268-1361793	CP002190.1
B. bacteriovorus Tiberius	2	842390..843894 1837658..1839162	NC_019567.1
B. bacteriovorus RO	1	171..1684	NZ_LUKE01000007.1
Bdellovibrio sp. KM01	2	1825819..1827332 3112760..3114273	NZ_CP058348.1
Bdellovibrio sp. NC01	2	858146..859659 1722252..1723765	NZ_CP030034.1
Bdellovibrio sp. ZAP7	2	1960532..1962045 3284792..3286305	NZ_CP030082.1
Bdellovibrio sp. qaytius	1	663487..664991	CP025734.1
Pseudobdellovibrio exovorus JSS	1	751703..753216	NC_020813.1
Halobacteriovorax marinus SJ^T	2	233651…235207 1891950…1893506	NC_016620.1
Halobacteriovorax sp. BALOs_7	2	246974…248526 1293221..1294773	NZ_CP027772.1
Bacteriovorax stolpii DSM 12778^T	2	262357..263907 2166394..2167944	NZ_CP025704.1
Fluviispira sanaruensis RF1110005^T	5	396712..398248 485340..486876 2375456..2376992 2866755..2868291 3332162..3333698	NZ_AP019368.1
Silvanigrella aquatica MWH-Nonnen-W8red^T	5	388357..389887 527078..528608 2286305..2287835 2741060..2742590 3157553..3159083	NZ_CP017834.1

Table S2: A 16S rRNA pairwise alignment of *Bdellovibrio* sp LBG001^{T}with other members of the *Bdellovibrio* genus

Bacteria*	Alignment identity (%)
B. bacteriovorus HD100^{T}	97.2
B. bacteriovorus 109J	97.2
B. bacteriovorus SSB218315	97.2
B. bacteriovorus R0	97.8
B. bacteriovorus Tiberius	97.2
B. bacteriovorus W	95.5
Bdellovibrio sp NC01	96.5
Bdellovibrio zap7	96.8
Bdellovibrio sp KM01	96.8
Bdellovibrio sp. qaytius^{T}	92.2
Bdellovibrio exovorus JSS^{T}	92.7

* Only members of the *Bdellovibrio* genus

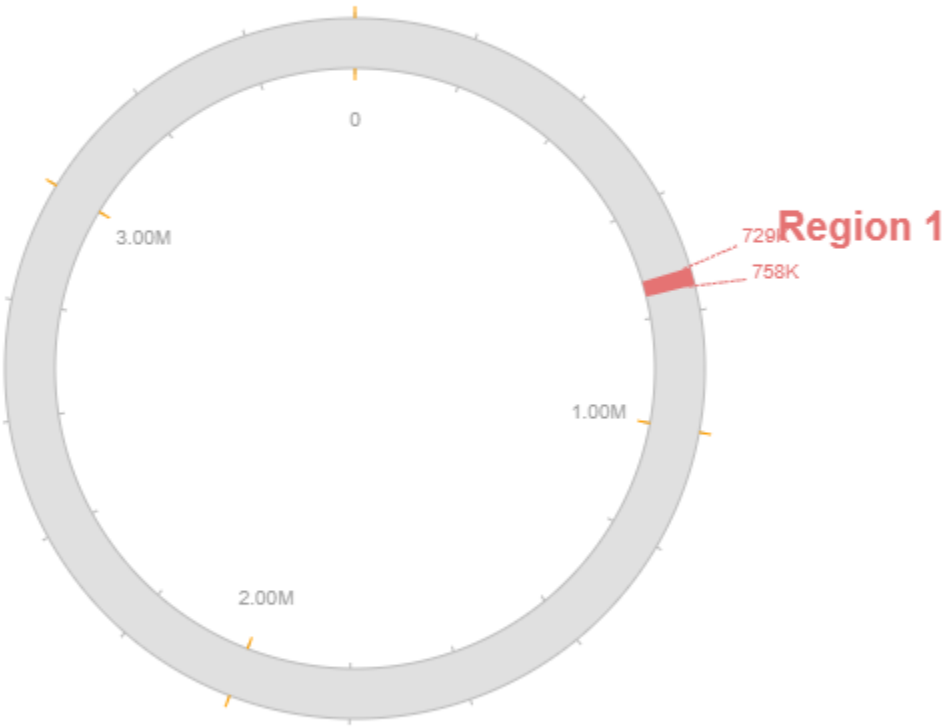

Fig S1: Location of degenerate prophage (Region 1) in LBG001^{T}

The prophage sequence is located at 728,575-758,048 of the LBG001^{T} genome.

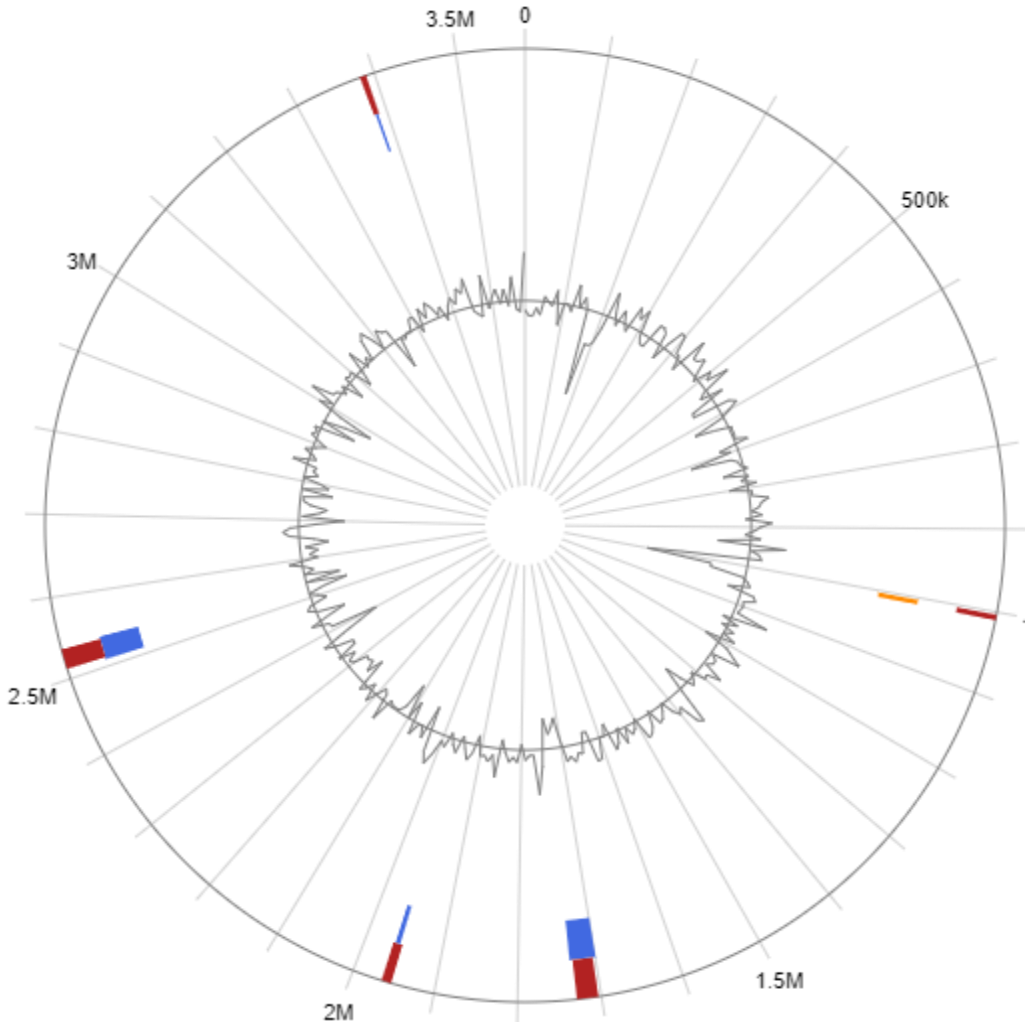

Fig S2: Location of 5 genomic islands within LBG001^{T}

Coordinate numbers of genomic islands within LBG001^{T}

Islands	Start	End	Size
1.	1,003,250	1,009,985	6,735
2.	1,703,472	1,729,408	25,936
3.	1,952,347	1,964,324	11,977
4.	2,512,597	2,536,676	24,079
5.	3,382,539	3,389,809	7,270

Text 1. Housekeeping genes that were used to construct the phylogenetic analysis

The 30 housekeeping genes were extracted from each analyzed genome by using the AMPHORA software. 30 house-keeping genes are: *dnaG, frr, infC, nusA, pgk, pyrG, rpIA, rpIB, rpIC, rpID, rpIE, rpI*F, *rpIK, rpIL, rpIM, rpIN, rpIP, rpIS, rpIT, rpoB, rpsB, rpsC, rpsE, rpsI, rps*J *rpsK, rpsM, rpsS, smpB, tsf*

Text 2. Details of the experimental protocol for a microscopic view of the *Bdellovibrio*

Materials and Methods

Purified cells of wild-type *B. bacteriovorus* 109J and *B. reynosensis* LBG001^T were prepared as follows. Each predator was grown on ~10^{10} CFU of *K. pneumoniae* (ATCC 43816) in 1 mL of (4-(2-hydroxyethyl)-1-piperazineethanesulphonic acid) Complete buffer (HEPES) at 30^{o}C with aeration until >99% of prey cells were lysed, and a high titer of predator was apparent by examination under dark field microscopy (~48 h). HEPES buffer was made by dissolving 3 g of HEPES into 500 mL deionized water, then adding 0.4 ml 10 N NaOH, 1.5 ml 1 M $MgCl_2$, and 1 ml 1 M $CaCl_2$, filtering through a 0.22 µm filter, and stored at 4^{o}C for up to 2 months. The remaining prey cells and debris were removed by differential centrifugation at 1500 RCF for 2 min, and the supernatant was filtered consecutively through 0.45 µm and 0.22 µm PVDF 4 mm syringe filters (Millex^{TM}-HV SLHVR04NL, SLGVR04NL) attached to 1cc syringes to obtain pure cultures of *B. bacteriovorus* and *B. reynosensis*. Note that the 0.22 µm filter units clog after passing ~0.2 mL through, requiring changing of the filter unit several times to achieve filtration of the 1 mL volume. The purified predator cells were labelled briefly with a 1/500 volume of BactoView^{TM} Live Green stain (Biotium, 40102) at 37^{o}C in a microfuge tube for 5 min. Unincorporated dye was

removed by pelleting the cells at 21,000 RCF for 2 min, removing the supernatant, washing the cells once, and resuspending in 0.5 mL of HEPES buffer. Labelled predator was added a multiplicity of infection of ~4 to freshly grown *Klebsiella pneumoniae* (ATCC 43816) resuspended in 1 mL of HEPES buffer and incubated in a 2 mL microfuge tube at 30^{o}C with aeration. After 10 and 80 min, half the volume was removed, and differential centrifugation at 1100 RCF for 2 min was used to remove most of the extracellular, unattached predator cells from the prey cells: The cell pellet, which was very loose, was washed once with HEPES, centrifuged again at 1100 RCF for 2 min, the supernatant removed, and the cell pellet of infected prey cells was resuspended in 0.5 mL HEPES. A 4 µl volume of the infected prey cells was examined on agarose pads on microscope slides by 100x bright field and fluorescence microscopy using the FITC channel on a Revolve microscope (Echo Laboratories, RVL-100-B2).

Reference

Csaba Kerepesi, Dániel Bánky, Vince Grolmusz, *AmphoraNet: The webserver implementation of the AMPHORA2 metagenomic workflow suite,* Gene, Volume 533, Issue 2, 10 January 2014, Pages 538-540, ISSN 0378-1119, http://dx.doi.org/10.1016/j.gene.2013.10.015