S1 File. Phages in C. phytofermentans

In order to determine whether the genome of C. phytofermentans contained evidence of phage infection, the sequences of all viruses (including phages) sequenced as of October 10, 2011, were downloaded from NCBI (ftp://ftp.ncbi.nih.gov/genomes/Viruses/) and used to search the predicted ORFs of C. phytofermentans for phage proteins using BLASTP. Two putative prophage-encoding clusters were identified, Cphy 0782-0798 and Cphy 2944-2997 (described in Table A). Both clusters contain genes for phage head and tail structural components, the majority of which, are homologous to those of *Clostridium difficile* phage Φ C2 (Goh et al. 2007). We were unable to identify homologs of many phage genes required for the completion of the phage lifecycle (genes involved in DNA packaging, tail assembly, cell lysis, and lysogeny control as well as DNA replication, recombination, and modification). This result suggests that these phages may no longer actively infect C. phytofermentans. Examination of the microarray data revealed differential transcription of the Cphy 0782-0798 cluster. It was upregulated during growth on cellulose, pectin and *Brachypodium distachyon* (relative to growth on glucose). In summary, the genome of *C. phytofermentans* encodes two clusters enriched in phage proteins, but it is not known whether these encoded phages are still active or affect the growth of the organism.

Table A. Prophage-like genes of C. phytofermentans.

Protein ID	Annotation	Homolog (Phage, e-value) ^a
Cphy_0782	XRE family transcriptional regulator	putative S24-like peptidase (<i>Geobacillus</i> virus E2, 1e-14)
Cphy_0783	hypothetical protein Cphy_0783	Gp2.21 (Bacillus phage SPO1, 0.019)
Cphy_0784	hypothetical protein Cphy_0784	hypothetical protein phiC2p12 (<i>Clostridium</i> phage phiC2, 3e-06)
Cphy_0785	phage protein	putative sheath tail protein (<i>Clostridium</i> phage phiC2, 4e-118)
Cphy_0786	phage protein	putative core tail (<i>Clostridium</i> phage phiC2, 7e-42)
Cphy_0787	XkdN-like protein	XkdN-like protein (<i>Clostridium</i> phage phiC2, 3e-21)
Cphy_0788	phage tape measure protein	putative tail tape measure protein (<i>Clostridium</i> phage phiC2, 7e-79)
Cphy_0789	peptidoglycan-binding LysM	putative LysM (Clostridium phage phiC2, 2e-27)
Cphy_0790	putative phage cell wall hydrolase	putative hydrolase (<i>Clostridium</i> phage phiC2, 1e-66)
Cphy_0791	hypothetical protein Cphy_0791	hypothetical protein phiC2p23 (<i>Clostridium</i> phage phiC2, 3e-09)
Cphy_0792	phage protein	hypothetical protein EJ-1p60 (<i>Streptococcus</i> phage EJ-1, 7e-19)
Cphy_0793	putative phage tail protein	hypothetical protein phiC2p25 (<i>Clostridium</i> phage phiC2, 1e-89)
Cphy_0794	hypothetical protein Cphy_0794	hypothetical protein phiC2p26 (<i>Clostridium</i> phage phiC2, 6e-18)
Cphy_0795	hypothetical protein Cphy_0795	hypothetical protein BC2598 (<i>Bacillus</i> phage phBC6A52, 0.086)
Cphy_0796	hypothetical protein Cphy_0796	nd
Cphy_0797	hypothetical protein Cphy_0797	nd
Cphy_0798	toxin secretion/phage lysis holin	Putative lysis protein (Bacillus virus 1, 9e-11)
Cphy_2944	hypothetical protein Cphy_2944	NLP/P60 family protein, enterotoxin (Clostridium perfringens SM101 phage, 6e-07)
Cphy_2945	toxin secretion/phage lysis holin	holin (Bacillus phage Fah, 9e-24)

Protein ID	Annotation	Homolog (Phage, e-value) ^a
Cphy_2946	hypothetical protein Cphy_2946	nd
Cphy_2947	hypothetical protein Cphy_2947	nd
Cphy_2948	hypothetical protein Cphy_2948	gp4 (Mycobacterium phage Bxz2, 0.012)
Cphy_2949	hypothetical protein Cphy_2949	hypothetical protein phiC2p26 (Clostridium phage phiC2, 4e-18)
Cphy_2950	baseplate J family protein	hypothetical protein phiC2p25 (<i>Clostridium</i> phage phiC2, 5e-90)
Cphy_2951	phage protein	hypothetical protein EJ-1p60 (<i>Streptococcus</i> phage EJ-1, 1e-17)
Cphy_2952	hypothetical protein Cphy_2952	hypothetical protein phiC2p23 (Clostridium phage phiC2, 1e-13)
Cphy_2953	putative phage cell wall hydrolase	putative hydrolase (<i>Clostridium</i> phage phiC2, 8e-61)
Cphy_2954	peptidoglycan-binding LysM	putative LysM (Clostridium phage phiC2, 2e-31)
Cphy_2955	hypothetical protein Cphy_2955	putative tail tape measure protein (<i>Clostridium</i> phage phiC2, 8e-43)
Cphy_2956	XkdN-like protein	hypothetical protein phiC2p16 (<i>Clostridium</i> phage phiC2, 1e-24)
Cphy_2957	phage protein	putative core tail (<i>Clostridium</i> phage phiC2, 3e-56)
Cphy_2958	phage protein	putative sheath tail protein (<i>Clostridium</i> phage phiC2, 1E-143)
Cphy_2959	hypothetical protein Cphy_2959	nd
Cphy_2960	phage protein	hypothetical protein phiC2p12 (<i>Clostridium</i> phage phiC2, 5e-28)
Cphy_2961	phage protein	hypothetical protein phiC2p11 (<i>Clostridium</i> phage phiC2, 3e-32)
Cphy_2962	phage protein	hypothetical protein phiC2p10 (<i>Clostridium</i> phage phiC2, 1e-26)
Cphy_2963	hypothetical protein Cphy_2963	hypothetical protein LJ771_034 (<i>Lactobacillus johnsonii</i> prophage Lj771, 8e-04)
Cphy_2964	phage coat protein	coat protein (<i>Enterococcus</i> phage phiFL3A, 1e-90)
Cphy_2965	hypothetical protein Cphy_2965	scaffold protein (<i>Enterococcus</i> phage phiFL3A, 4e-21)
Cphy_2966	hypothetical protein Cphy_2966	hypothetical protein lb338_phage_74 (<i>Lactobacillus</i> phage Lb338-1 ,7e-24)

Protein ID	Annotation	Homolog (Phage, e-value) ^a
Cphy_2967	hypothetical protein Cphy_2967	nd
Cphy_2968	hypothetical protein Cphy_2968	hypothetical protein phiC2p05 (<i>Clostridium</i> phage phiC2, 8e-06)
Cphy_2969	SPP1 family phage head morphogenesis protein	putative head morphogenesis protein (Clostridium phage phiC2, 3e-132)
Cphy_2970	SPP1 family phage portal protein	putative portal protein (<i>Clostridium</i> phage phiC2, 1e-103)
Cphy_2971	phage uncharacterized protein	TerL (Lactococcus phage TP901-1, 9e-151)
Cphy_2972	hypothetical protein Cphy_2972	hypothetical protein Tuc2009_28 (<i>Lactococcus</i> phage Tuc2009, 2e-43)
Cphy_2973	hypothetical protein Cphy_2973	nd
Cphy_2974	hypothetical protein Cphy_2974	hypothetical protein CST121 (<i>Clostridium</i> phage c-st, 5e-05)
Cphy_2975	hypothetical protein Cphy_2975	nd
Cphy_2976	hypothetical protein Cphy_2976	nd
Cphy_2977	hypothetical protein Cphy_2977	77ORF009 (Staphylococcus phage 77, 3e-10)
Cphy_2978	hypothetical protein Cphy_2978	
Cphy_2979	transcriptional regulator, CdaR	putative bacteriophage regulatory protein; Lambda gpCro analog (Phage Gifsy-2, 0.067)
Cphy_2980	hypothetical protein Cphy_2980	polyprotein precursor (GB virus A ,0.099)
Cphy_2981	hypothetical protein Cphy_2981	nd
Cphy_2982	hypothetical protein Cphy_2982	nd
Cphy_2983	hypothetical protein Cphy_2983	nd
Cphy_2984	superfamily II helicase	ORF001 (Staphylococcus phage PT1028, 3e-17)
Cphy_2985	zinc finger CHC2-family protein	primase (Abalone shriveling syndrome-associated virus, 0.008)
Cphy_2986	hypothetical protein Cphy_2986	nd
Cphy_2987	single-strand binding protein	SSB (Lactococcus phage bIL286, 6e-25)

Protein ID	Annotation	Homolog (Phage, e-value) ^a
Cphy_2988	hypothetical protein Cphy_2988	gp70 (Mycobacterium phage 244, 7e-30)
Cphy_2989	hypothetical protein Cphy_2989	hypothetical protein phi105_44 (<i>Bacillus</i> phage phi105, 2e-04)
Cphy_2990	hypothetical protein Cphy_2990	gp53 (Listeria phage P35, 1e-39)
Cphy_2991	metal dependent phosphohydrolase	nd
Cphy_2992	AbrB family transcriptional regulator	Transcription state regulatory protein abrB (<i>Bacillus</i> phage phBC6A51, 4e-14)
Cphy_2993	putative phage-related DNA binding protein	ORF032 (Staphylococcus phage X2, 4e-10)
Cphy_2994	XRE family transcriptional regulator	putative S24-like peptidase (<i>Geobacillus</i> virus E2, 1e-12)
Cphy_2995	hypothetical protein Cphy_2995	hypothetical protein phiETA3_gp05 (Staphylococcus phage phiETA3, 0.004)
Cphy_2996	hypothetical protein Cphy_2996	nd
Cphy_2997	resolvase domain-containing protein	putative phage site-specific recombinase (<i>Clostridium</i> phage phiCD27, 2e-78)

^a nd indicates not detected.

References:

Goh S, Ong P, Song K, Riley T, Chang B. 2007. The complete genome sequence of *Clostridium difficile* phage phiC2 and comparisons to phiCD119 and inducible prophages of CD630. Microbiology (Reading, England). 153:676–685.