

# Characterization of fHyAci03, a novel lytic bacteriophage that infects clinical *Acinetobacter* strains

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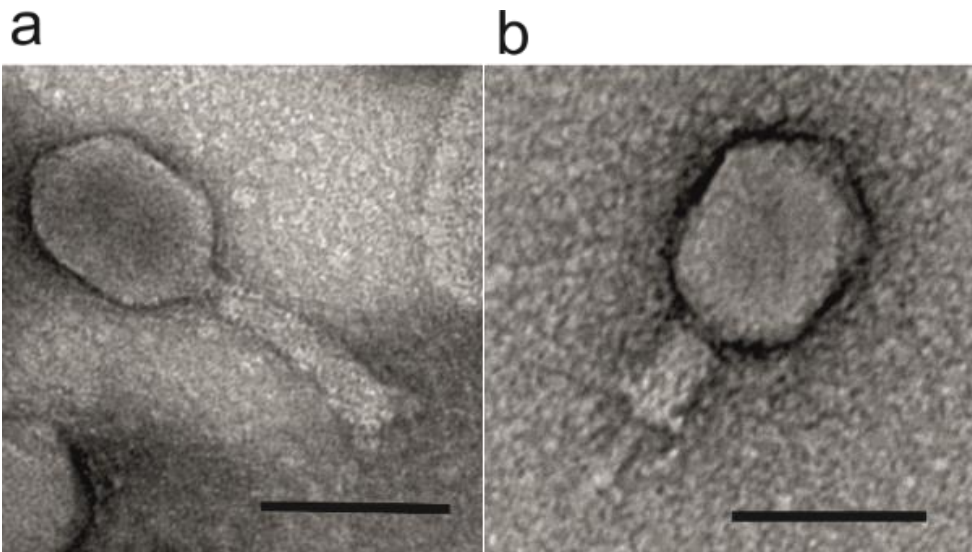
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**Supplementary Fig. 1** Electron micrographs of negatively stained vB\_ApiM\_fHyAci03 (fHyAci03) particles. Phage particles with non-contracted (a) and contracted (b) tails are shown. Samples were examined at the Electron Microscopy Unit (Institute of Biotechnology, University of Helsinki, Helsinki, Finland) with a JEOL JEM-1400 transmission electron microscope JEOL Ltd., Tokyo, Japan. Bars represent 100 nm

**Supplementary Table 1** Host range of fHyAci03

<i>Acinetobacter</i> species (n)	fHyAci03 sensitivity	
	Sensitive	Resistant
<i>A. baumannii</i> (17)	0	17
<i>A. calcoaceticus</i> (1)	0	1
<i>A. junii</i> (1)	0	1
<i>A. lwoffii</i> (3)	0	3
<i>A. nosocomialis</i> (3)	2	1
<i>A. pittii</i> (18)	6	12
<i>A. radioresistens</i> (2)	0	2
<i>A. ursingii</i> (3)	0	3

Sensitive (EOP>10<sup>-3</sup>), resistant (EOP<10<sup>-6</sup>). An EOP of 1 was equivalent to 5.3x10<sup>8</sup> PFU/ml with *Acinetobacter pittii* strain #5565 as the host

**Supplementary Table S2** tRNAs, their positions in fHyAci03 genome, products, and anticodons

<b>tRNA #</b>	<b>Start position</b>	<b>End position</b>	<b>Amino acid</b>	<b>Anticodon</b>
1	77217	77148	Met	CAT
2	77140	77065	Cys	GCA
3	76985	76908	Leu	TAG
4	75353	75283	Thr	TGT
5	74994	74904	Ser	TGA
6	74898	74822	Pro	TGG
7	74812	74737	Phe	GAA
8	74354	74280	Trp	CCA

**Supplementary Table S3** Whole genome BLASTn comparison with related *Acinetobacter* phages

<b>Related <i>Acinetobacter</i> phages</b>	<b>#genes</b>	<b>Query coverage (%)</b>	<b>Identity-%</b>	<b>Accession-no</b>
KARL-1	253	94	98	MH713599.1
ZZ1	256	55	75	HQ698922.4
Acj9	253	52	71	HM004124.1
Acj61	241	46	72	GU911519.1
Ac42	255	29	69	HM032710.1
133	257	18	74	HM114315.1

**Supplementary Table S4** Comparisons of conserved gene product content using CoreGenes3.5

Accession-no	Name	fHyAci03	
		#homologs	%in common
MH713599.1	KARL-1	239	96.76
HQ698922.4	ZZ1	190	76.92
HM004124.1	Acj9	192	77.73
GU911519.1	Acj61	178	72.06
HM032710.1	Ac42	154	62.35
HM114315.1	133	152	61.54
NC_000866.4	T4	113	45.75
NC_005066.1	RB49	99	40.08