## Analysis of the atypical 'hairy' Enterobacteriacea phage vB\_PcaM\_CBB

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In this study the morphological atypical jumbo Myoviridae phage vB\_PcaM\_PBB is characterised. This bacteriophage was isolated from activated sludge from a waste water treatment facility in Co. Cork, Ireland. Transmission electron microscopy analysis of CsCl gradient purified phage particles shows that this phage possesses a large capsid with a short contractile tail which is covered with hair like structures. The phage was found to possess a board host range capable of infecting species of the genera Pectobacterium, Erwinia and Cronobacter. The genome of this phage was found to be 355,922 bp, which ranks it as the third largest phage genome sequence currently known. As well as this, examination of reads obtained from genomic sequencing shows that the genome of the phage possesses terminal repeats with a size of 22,456 bp (total genome size of 378,378 bp). The genome was predicted to have 554 ORFs (excluding ORFs of the predicted terminal repeat) and only 22.5% of these ORFs could be annotated with a predicted function. It was also found to possess 27 tRNA like genes. The proteome of this phage shares strong similarity to that of a number of GAP32 like phages. At a cut off value of 75% identity, this phage shares 86.46% of its proteins with Cronobacter sakazakki phage GAP32, 43.14% with Escherichia coli phage 121Q and 41.52% with Klebsiella phage RAK2. This is the third description of a phage with morphology like that of phage CBB with regard its atypical hair-like capsid structures. The two other examples of this feature were Escherichia coli phage PhAPEC6 (Tsones 2014) and the phage known as X particle, identified in the fluid of crushed silkworm larvae but never propagated (Ackermann et al 1994).

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