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Things are getting hairy: Enterobacteria bacteriophage vB_PcaM_CBB

Colin Buttimer[1], Hanne Hendrix[2], Hugo Oliveria[3], Aidan Casey[4], Horst Neve[5], Olivia McAuliffe[4], R. Paul Ross[4], Colin Hill[6], Jean-Paul Noben[7], Jim O'Mahony[1], Rob Lavigne[2], Aidan Coffey[1,6]

[1]Department of Biological Sciences, Cork Institute of Technology, Bishopstown, Cork, Ireland; [2]Laboratory of Gene Technology, KU Leuven, Leuven, Belgium; [3]CEB – Centre of Biological Engineering, LIBRO – Laboratório de Investigação em Biofilmes Rosário Oliveira, University of Minho, 4710-057, Braga, Portugal; [4]Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland; [5]Department of Microbiology and Biotechnology, Max Rubner-Institut, Kiel, Germany; [6]APC Microbiome Institute and School of Microbiology, University College, Cork, Ireland; [7]Biomedical Research Institute and Transnational University Limburg, Hasselt University, Diepenbeek 3950, Belgium.

The objective of this study was to characterise a 'jumbo' phage isolated from activated sludge obtained from Little island, Co. Cork, Ireland. The phage was characterised in terms of its bacterial host range across a number of genera, bioinformatic analysis of its genome, transmission electron microscopy examination of its morphology and proteomic analysis of its virion. Enterobacteria phage vB_PcaM_CBB is a 'jumbo' phage belonging to the family *Myoviridae.* It possesses highly atypical whisker-like structures along the length of its contractile tail. It has a broad host range with the capability of infecting species of the genera *Erwinia*, *Pectobacterium* and *Cronobacter*. With a genome of 355,922 bp, excluding a predicted terminal repeat of 22,456 bp, phage CBB is the third largest phage sequenced to date (2016). Its genome was predicted to encode 554 ORFs with 33 tRNAs. Based on prediction and proteome analysis of the virions, 29% of its predicted ORFs could be functionally assigned. Protein comparison showed that CBB shares between 33 and 38% of its proteins with *Cronobacter* phage GAP32, coliphages PBECO4 and 121Q as well as *Klebsiella* phage vB_KleM_Rak2. This work presents a detailed and comparative analysis of vB_PcaM_CBB of a highly atypical jumbo myoviridae phage, contributing to a better understanding of phage diversity and biology. CBB is member of a group of phages represented by GAP32 (the first phage of this group to be described) and of which the jumbo phages PBECO4, 121Q, Rak2 and K64-1 are members. These phages share a number of homologous proteins with those found within the *Tevenvirinae* subfamily. However, due to a low number of core T4 universal proteins, the lack of an even distribution of homologs along their own genomes and the possession of their own species-specific proteins, we propose that they should be grouped separately as 'GAP32viruses'.