

Study of a novel *Pseudomonas* phage isolated from soil reveals interesting features against *Pseudomonas aeruginosa*

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Abstract: Bacteriophages or phages, viruses that specifically kill bacteria, have been recently considered to be a promisingly alternative therapy for drug-resistant pathogens, especially *Pseudomonas aeruginosa*, a notoriously opportunistic pathogen and major cause of nosocomial infection. Even though *P. aeruginosa* phages have been extensively isolated, the infection machinery of how the phage takes over and replicates inside the cell is still elusive. Here, we firstly isolated a bacteriophage targeting *P. aeruginosa*, designated as JJ01, from soil in Chulalongkorn university. Lysogeny test and genome analysis indicated that JJ01 is a lytic bacteriophage whose genome size of 66,346 bp with 55.7% of G+C content contains 92 ORFs divided into 67 of hypothetical genes, 7 of DNA replication and transcription, and translation, 2 of DNA metabolism and modification, 9 of virion structural and assembly, 2 of lysis protein and 5 of others without tRNA gene. JJ01 is genetically close to Pbnavirus in GenBank ranging from 88 to 98% identity. Given the fact that hijacking host metabolic pathways by phages can possibly trigger the morphology change of phage-infected cells, we will further elucidate the possible mechanism of pre-killing (MOK) of JJ01 by single cell-leveled infection under fluorescence microscopy in combination with bacterial cytological profile (BCP) principle. This study sheds the light into how phages take control the host through hijacking fundamental cellular machinery providing deep insights into the phage infection machinery at single cell-level.

Keywords: Bacteriophage; *P. aeruginosa*; Mechanism of pre-killing (MOK); Bacterial cytological profile (BCP)



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Acknowledgments: This study was funded by Mid-Career Research Grant through National Research Council of Thailand (NRCT) and the Sci-Super VII grant, Faculty of Science, Chulalongkorn University. W.W. is financially supported by The Second Century Fund (C2F), Chulalongkorn University for Doctoral Scholarship.