

Article

Genomic Characterisation of UFJF_PfDIW6: A Novel Lytic *Pseudomonas fluorescens*-Phage with Potential for Biocontrol in the Dairy Industry

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Supplementary Material: Figures S1 and S2

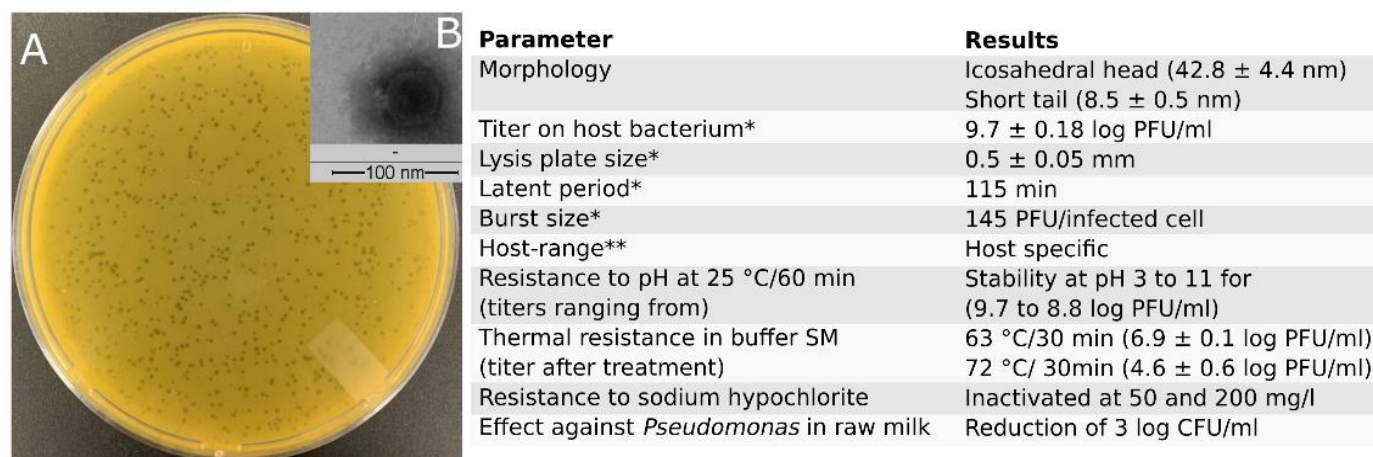


Figure S1. Phenotypic features of *Pseudomonas* phage UFJF_PfDIW6. (A) Lysis plaques formed by UFJF_PfDIW6 on the lawn of *P. fluorescens* UFV 041. Incubation conditions: BHI agar at 30 °C for 24 h. (B) Virion morphology. Transmission electron micrograph (TEM) negatively stained with 2% uranyl acetate. Bar magnification: 140,000X. *Tests performed in TSB medium at 30 °C; **Test performed against 23 bacterial strains belonging to nine genera. The methodology used for phenotypic characterization of UFJF_PfDIW6 was described in detail by Nascimento et. [27].

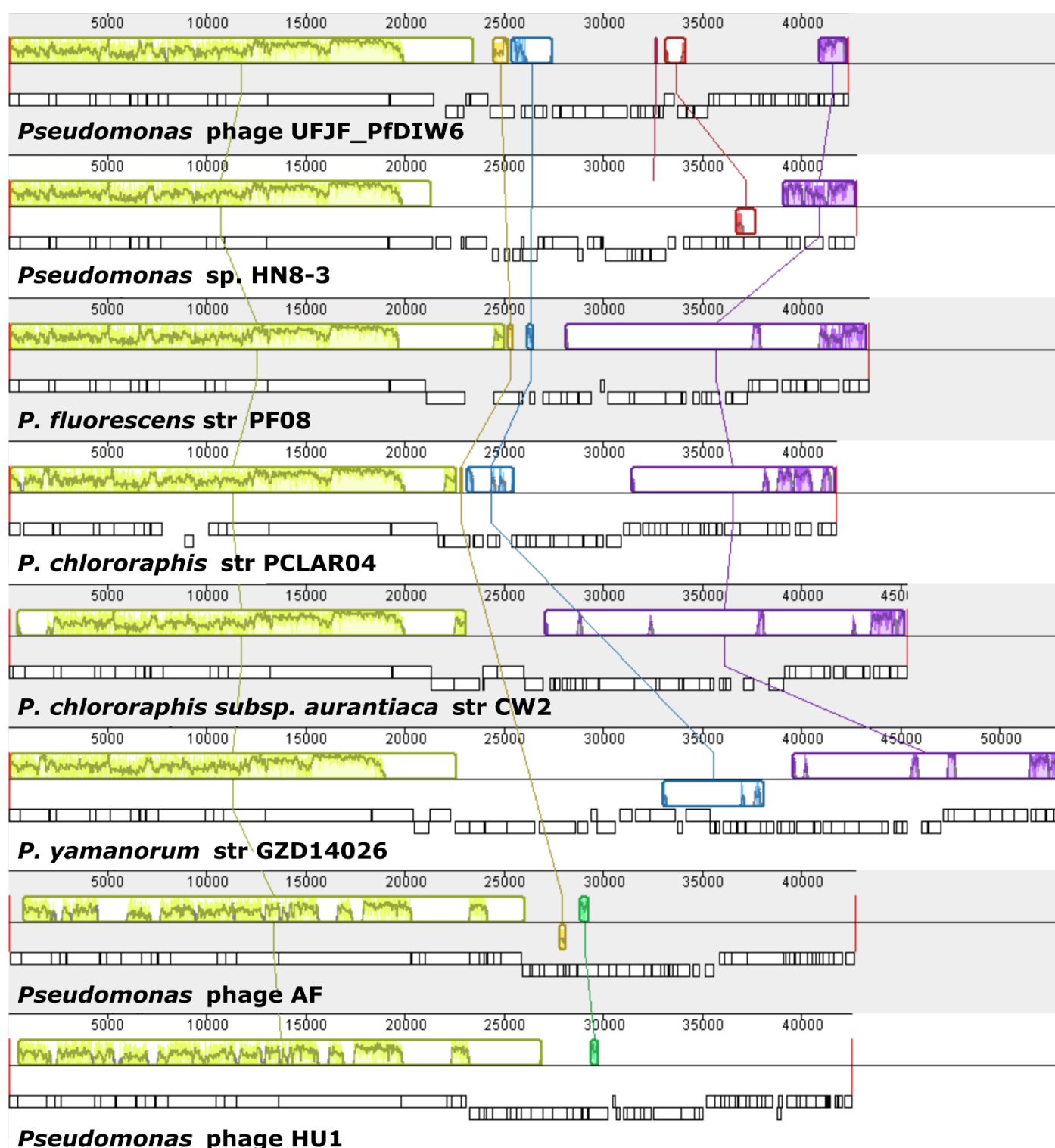


Figure S2. Conserved locally collinear blocks (LCBs) shared among *Pseudomonas* UFJF_PfDIW6 phage, *Pseudomonas* sp. HN8-3 prophage, *P. fluorescens* str PF08 prophage, *P. chlororaphis* str PCLAR04 prophage, *P. chlororaphis* subsp. *aurantiaca* str CW2 prophage, *P. yamanorum* str GZD14026 prophage, *Pseudomonas* phage AF, and *Pseudomonas* phage HU1 genomes. The alignment was performed using progressiveMauve with default parameters. The colored blocks correspond to the LCBs predicted by Mauve. Horizontal white bars correspond to the Coding DNA sequences (CDSs) annotated in each genome.