



Whole-Genome Sequencing of *Pseudomonas koreensis* Isolated from Diseased *Tor tambroides*

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Abstract

Unlike environmental *P. koreensis* isolated from soil, which has been studied extensively for its role in promoting plant growth, pathogenic *P. koreensis* isolated from fish has been rarely reported. Therefore, we investigated and isolated the possible pathogen that is responsible for the diseased state of *Tor tambroides*. Herein, we reported the morphological and biochemical characteristics, as well as whole-genome sequences of a newly identified *P. koreensis* strain. We assembled a high-quality draft genome of *P. koreensis* CM-01 with a contig N50 value of 233,601 bp and 99.5% BUSCO completeness. The genome assembly of *P. koreensis* CM-01 consists of 6,171,880 bp with a G+C content of 60.5%. Annotation of the genome identified 5538 protein-coding genes, 3 rRNA genes, 54 tRNAs, and no plasmids were found. Besides these, 39 interspersed repeat and 141 tandem repeat sequences, 6 prophages, 51 genomic islands, 94 insertion sequences, 4 clustered regularly interspaced short palindromic repeats, 5 antibiotic-resistant genes, and 150 virulence genes were also predicted in the *P. koreensis* CM-01 genome. Culture-based approach showed that CM-01 strain exhibited resistance against ampicillin, aztreonam, clindamycin, and cefoxitin with a calculated multiple antibiotic resistance (MAR) index value of 0.4. In addition, the assembled CM-01 genome was successfully annotated against the Cluster of Orthologous Groups of proteins database, Gene Ontology database, and Kyoto Encyclopedia of Genes and Genome pathway database. A comparative analysis of CM-01 with three representative strains of *P. koreensis* revealed that 92% of orthologous clusters were conserved among these four genomes, and only the CM-01 strain possesses unique elements related to pathogenicity and virulence. This study provides fundamental phenotypic and genomic information for the newly identified *P. koreensis* strain.

Introduction

Pseudomonas is one of the most diverse genera. At the time of writing, about 300 *Pseudomonas* species have been validly published (excluding subspecies and synonymous species), according to the List of Prokaryotic Names with Standing in Nomenclature (LPSN) [1]. The number of species within this genus is continuously growing, with over 129 new *Pseudomonas* species reported in the last ten years. Genus *Pseudomonas* has undergone a number of taxonomic revisions since its first description [2] due to the advancement of molecular-based methods for species identification. Species within this genus have been designated by biochemical, physiological, and nutritional features [3], DNA–DNA hybridization and rRNA–DNA hybridization [4], and multi-locus sequence analysis (MLSA) of four housekeeping genes (16S rRNA, *gyrB*, *rpoB*, and *rpoD*) [5].

Advances in DNA sequencing technologies have led to a dramatic increase in the number of complete and draft genome assemblies of clinical and environmental isolates

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