**Genome Sequence of a Novel Indigo-Producing Strain, *Pseudomonas monteilii* QM**

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*Pseudomonas monteilii* is a versatile bacterium found in various niches. A newly isolated strain, *P. monteilii* QM, can effectively produce indigoids from indoles. Here we present a 5.76-Mb assembly of the *P. monteilii* genome for the first time. It may provide abundant molecular information for the transformation of aromatics.

Pseudomonads demonstrate a deal of metabolic diversity and consequently are able to colonize a wide range of niches. Most *Pseudomonas monteilii* strains are associated with degradation of aromatic and heterocyclic compounds (6). Some *Pseudomonas monteilii* strains were isolated from clinical specimens (2, 3), yet no *P. monteilii* infection has been reported. Recently we isolated a strain (named QM) from soil samples which was deposited in the China General Microbiological Culture Collection Center (accession number 5054). The 16S rRNA gene nucleotide sequence analysis, and physiological and biochemical features identify the strain as *P. monteilii*. Interestingly, strain QM can effectively produce indigo from indole, which could make it a potential candidate for industrial indigo production (8). Besides indigo, some novel indigo-like pigments and colorless products are also produced, indicating that special indole transformation pathways are involved in strain QM (data not shown). This is the first report of the genome sequence of a *P. monteilii* strain. The *P. monteilii* genome sequence may provide fundamental molecular information on the conversion to indole and other aromatics, especially the mechanism of transformation of heterocyclics used by *Pseudomonas* strains.

The draft genome sequence of strain QM was sequenced by Solexa High-Seq 2000 paired-end sequencing (75 bp for each read, ~93-fold) in BGI-Shenzhen. The reads were assembled using SOAPdenovo software version 1.05 to yield 278 large contigs (>200 bp) (5). rRNA and tRNA were predicted using rRNAmer and tRNAscan, respectively (9). Annotation was performed by using the RAST autoannotation server and the NCBI PGAAP pipeline (7). The gene functions and metabolic pathways were predicted with the help of KEGG and Clusters of Orthologous Groups (COG) databases (4).

The draft genome sequence of strain QM is 5,763,138 bp with a G+C content of 61.8% and 5,224 predicted coding sequences (CDSs) (950-bp average length, 86.1% coding density). There are 524 subsystems represented in the sequence, and the metabolic network of QM (determined by RAST server) was reconstructed (1). The three types of protein secretion pathways for virulence factors in the opportunistic human pathogen *Pseudomonas aeruginosa* PAO1 were not found in the sequence of strain QM (11). The genome of strain QM contains about 200 distinct CDSs most encoding hypothetical proteins that are absent from other completely sequenced (E < 10^-5) *Pseudomonas* strains. Strain QM shows versatile aromatic degradation capacities, similar to other *Pseudomonas* strains (10, 12). The gene clusters for degradation or transformation of benzoate (benABCD), catechol (catABC), phenol (dmpK dmpLMNOP), salicylate (nahG), and p-hydroxybenzoate (pobA) were annotated in the sequence. These data indicate that strain QM may possess abundant gene clusters for aromatic degradation or transformation, which may encode multiple mechanism pathways. The genomic information for strain QM will serve as a reference for understanding the metabolic and biological aspects of the genus *Pseudomonas*. Further studies will focus on acquiring and manipulating genes involved in the metabolism of aromatics in order to realize this organism’s versatile transformation capabilities.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AHGZ00000000. The version described in this paper is the first version, AHGZ01000000.

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**REFERENCES**