Draft Genome Sequence of *Pseudomonas plecoglossicida* Strain NB2011, the Causative Agent of White Nodules in Large Yellow Croaker (*Larimichthys crocea*)

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We describe the draft genome sequence of *Pseudomonas plecoglossicida* strain NB2011, the causative agent of white nodules in cultured large yellow croaker (*Larimichthys crocea*) in China. The draft genome sequence of the bacterium consists of 5.41 million bp, with a G+C content of 62.8%. A total of 4,952 genes were identified.

*Pseudomonas plecoglossicida* is a bacterium that is physically and genetically closely related to *P. putida* and has been assigned as a member of the *P. putida* group (1). The bacterium was first identified in cultured ayu (*Plecoglossus altivelis*) with bacterial hemorrhagic ascites in 2000 (2); recently, infections in rainbow trout (*Oncorhynchus mykiss*) and large yellow croaker (*Larimichthys crocea*) were also reported (3, 4). In large yellow croaker, the infection leads to the development of white nodules in the spleen, kidney, and liver of the diseased fish and results in high mortality (4, 5). The causative bacterium, strain NB2011, was preliminarily identified as *P. putida* by physical and biochemical profiles and 16S rRNA sequencing (5), but the strain was reclassified as *P. plecoglossidica* based on a gyrB sequence revealed by genome sequencing (6).

Here, we report the draft genome sequence of *P. plecoglossidica* strain NB2011, isolated from a diseased large yellow croaker with typical symptoms of white nodules in the internal organs (5). The sequencing was performed by Illumina HiSeq 2000. The data generated 7,361,580 reads totaling 3.68 Gb. The gaps were closed by sequencing was performed by Illumina Hiseq 2000. The data generation and assembly were performed using the databases RAST (7) and PGAP (8) and the GenBank database under accession number ASJX00000000. The sequence of *P. plecoglossidica* strain NB2011 has a length of about 32 kb was also arranged in a PAI-like genome island and the predicted amino acid sequences showed lower similarity (60 to 80%) to corresponding flagellar proteins of other Gram-negative bacteria. Pseudomonads usually express various enzymes, including catalases, peroxidases, and superoxide dismutases (SOD), for defense against reactive oxygen species (ROS). The strain is predicted to encode four catalases, three SODs, and three glutathione peroxidases, which may also be related to intracellular survival in macrophages (10, 11). Nine CDS encoding drug-resistance transporters and small multidrug-resistance proteins were annotated; these may be related to the intrinsic resistance of this strain to many antibiotics/drugs. However, no evidence was found in this strain for putative functions of pseudomonad extracellular pathogenicity factors, such as exotoxin A or phospholipase C.

**Nucleotide sequence accession number.** The genome sequence of *P. plecoglossidica* NB2011 has been deposited in the GenBank database under accession number ASJX00000000. The version described in this paper is the first version.

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**REFERENCES**


