

Draft Genome Sequence of Rice Endophyte-Associated Isolate *Kosakonia oryzae* KO348

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***Kosakonia oryzae* KO348 is an endophytic and plant growth-promoting strain isolated from the roots of rice in Italy. Here, we report the draft genome sequence of *Kosakonia oryzae* KO348.**

Received 1 May 2015 Accepted 4 May 2015 Published 4 June 2015

Citation Meng X, Bertani I, Abbruscato P, Piffanelli P, Licastro D, Wang C, Venturi V. 2015. Draft genome sequence of rice endophyte-associated isolate *Kosakonia oryzae* KO348. *Genome Announc* 3(3):e00594-15. doi:10.1128/genomeA.00594-15.

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Created in 1960, the genus *Enterobacter* is one of the largest genera within the family *Enterobacteriaceae* (1). Recently, taxonomic studies have resulted in rearrangement of the *Enterobacter* genera (2). As a result, a new genus designated *Kosakonia*, which includes the species *Kosakonia cowanii*, *Kosakonia radicincitans*, *Kosakonia oryzae*, and *Kosakonia arachidis* (2), was proposed, and in 2014, the nitrogen-fixing bacterium *Enterobacter sacchari* was reclassified as *Kosakonia sacchari* (3). *Kosakonia oryzae* has been associated with rice and has been shown to possess plant growth-promoting properties, including the ability to fix atmospheric nitrogen (4).

Kosakonia oryzae KO348 was isolated from surface-sterilized roots of the Italian rice cultivar Vialone Nano. Phylogenetic analyses using 16s rRNA and multilocus sequence analysis based on *gyrB*, *rpoB*, *infB*, and *atpD* indicate that this novel isolate belongs to genus *Kosakonia*, and here we announce its draft genome sequence. Genomic DNA of *K. oryzae* KO348 was purified following the protocol of the Nextera XT DNA library preparation kit (Illumina) and then used to prepare a sequencing-ready library. Sequencing was performed on Illumina MiSeq platform using 150-bp paired-end reads. Total number of pairs of reads was 5,010,628, representing approximately 10-fold coverage of the genome. We performed the *de novo* assembly using SPAdes v3.0 (5), generating 68 contigs with a maximum length of 462 kbp. The total length of the contig assembly was 5.0 Mbp, and the N_{50} length was 172 kbp, assuming a genome size of 5.0 Mbp. The G+C content was 53.9%, similar to that of other *Kosakonia* sequenced genomes. Automated annotation of the *K. oryzae* KO348 draft genome sequence was performed using RAST (6) assigning a total of 4,763 candidate protein-coding genes with 1,045 (21.94%) annotated as hypothetical proteins. A total of 86 RNA coding sequences were also identified. The *K. oryzae* KO348 genome presents several genes related to plant colonization and plant growth promotion, including genes for exopolysaccharide production, flagellar motility, siderophore production, auxin biosynthesis, and the *nif* gene cluster. Furthermore, it contains genes involved in the biosynthesis of type II, IV, V, VI, VII, and VIII secretion systems.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JZLI100000000](https://www.ncbi.nlm.nih.gov/nuccore/JZLI100000000). The version described in this paper is version JZLI100000000.

ACKNOWLEDGMENTS

This work was supported by Progetto AGER, grant 2010-2369. The Ph.D. program of Xianfa Meng was funded by a grant from CSC (China).

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