Draft Genome Sequence of the Nitrogen-Fixing Endophyte
*Azoarcus communis* SWub3

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**ABSTRACT** Here we report a draft genome sequence of *Azoarcus communis* SWub3, a nitrogen-fixing bacterium isolated from root tissues of Kallar grass in Pakistan.

Biological nitrogen fixation is a process in which a living organism reduces atmospheric dinitrogen into two NH₃ molecules. This reaction is catalyzed by the nitrogenase complex present exclusively in *Bacteria* and *Archaea* species. Plants can benefit from biological nitrogen fixation when they are in association with these nitrogen-fixing prokaryotes, either free living or as symbionts associated with their roots. *Azoarcus* is a bacterial genus that comprises species isolated from different environments, such as plant roots, sediments, aquifers, and contaminated soil (1–4). All *Azoarcus* species are Gram-negative rods with a strictly aerobic metabolism that can fix nitrogen microaerobically. The interest in this bacterial genus resides in its ability to efficiently infect several crops, including rice, which is a food staple for more than half of the world’s population (5–7). Moreover, one of its strains, *Azoarcus* sp. BH72, has been established as a model for nitrogen-fixing endophytes in grass (8). All plant-associated *Azoarcus* species share several features, like their ability to grow on various organic acids but not on carbohydrates, high optimum growth temperatures (37 to 42°C), and doubling times of 2 h (1).

*Azoarcus communis* SWub3 (=LMG 9095) was isolated from Kallar grass [*Leptochloa fusca* (L.) Kunth] roots in Punjab (Pakistan) in 1988 (1). For genomic sequencing, *A. communis* was grown in 4 ml of liquid ATCC medium 3 at 28°C. After 16 h, cells were harvested, and the DNA was extracted using the Wizard genomic DNA purification kit (Promega). The library was prepared using a KAPA HyperPrep kit (Roche) and run in a MiSeq PE300 cycle at the University of California, Davis, DNA Technologies Core. The run yielded 2,251,695 paired-end reads. Assemblies were done using SPAdes v. 3.12 with the careful option to minimize mismatches and provided an average of 192.3-fold coverage (9), as computed by the SPAdes software. The obtained genome sequence included 231 contigs (>200 bp) with an *N₅₀* value of 217,902 for contigs greater than 200. The calculated genome size was 5,004,685 bp with an average GC content of 62.5%.

This sequence allowed us to identify the nitrogenase operon and other loci involved in bacterium-plant symbiosis. It provides additional data to broaden our knowledge about the interaction of this nitrogen-fixing bacterial species with plants.
Data availability. The sequence data for *Azoarcus communis* SWub3 have been deposited in GenBank under the accession number GCA_003226565.

REFERENCES


