Draft Genome Sequence of Bacillus Species from the Rhizosphere of the Desert Plant Rhazya stricta


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In order to better understand the ecology and diversity of microbes in the rhizosphere of desert plants, we undertook a survey of Bacillus species isolated from soil around Rhazya stricta plants from the area around Jeddah, in The Kingdom, Saudi Arabia. We have sequenced the genomes of 8 Bacillus isolates representing four different species.

Bacillus is the most frequently isolated genus from soil. Several Bacillus species are ubiquitous and broadly adapted to grow in diverse settings within the biosphere. Bacillus species can be isolated in greater numbers than most other spore forming bacteria from the rhizosphere of a variety of plants, and there is evidence that through these associations they can promote plant growth (1–3). Desert soils are known to have heterogeneous microbial biodiversity heavily influenced by local areas of water availability (4). It has been shown that areas of vegetation have a greater microbial species diversity (5).

As part of a wider study to study the ecology of the rhizobiome associated with the desert plant Rhazya stricta growing near Jed- dah in Saudi Arabia, we generated draft genome sequencing of 12 Bacillus isolates collected from soil samples. One gram of soil from each collected sample was transferred into a 10 mL tube containing saline solution (NaCl 0.1 w/v) and left for 30 min at room temperature until the soil particles settled. Sample solutions were diluted 10-fold, spread onto LB agar plates, and incubated overnight at 37°C. Bacilli like colonies were isolated according to their morphological characters. Individual colonies from each site can be picked up and purified by re-streaking. They were then grown in 10 mL liquid Luria broth (LB), and DNA was extracted using QiAamp minikits (Qiagen).

Genomic DNA was fragmented to approximately 500 bp using Covaris sonicator and TruSeq adapters (Illumina) ligated to the DNA fragments using the supplied protocol. Each sample was barcoded with sequence-specific adapters, and the fragments sequenced on a single MiSeq run using forward and reverse 150 bp reads. The sequences were processed to remove low-quality bases using cutadapt (6) and Sickle (https://github.com/najoshi/sickle). Reads were assembled using Velvet (7) using a k-mer length of 71 and annotated using Prokka (8). Whole-genome phylogenies using kSNP were used to assign species (9).

The assembly sizes and number of reads generated are as follows: Bacillus subtilis JRS2 (4,060,709 bp, 1,468,268 reads), Bacillus pumilus JRS3 (3,758,903 bp, 1,258,270 reads), Bacillus amylolyphaquefaciens JRS5 (4,031,481 bp, 1,526,086 reads), Bacillus subtilis JRS6 (3,993,757 bp, 1,716,674 reads), Bacillus subtilis JRS7 (4,116,767 bp, 1,647,846 reads), Bacillus amylolyphaquefaciens JRS8 (4,090,896 bp, 1,491,538 reads), Bacillus subtilis JRS9 (4,044,356 bp, 1,296,858 reads), Bacillus subtilis JRS11 (3,962,286 bp, 1,678,670 reads).

We studied demonstrate that there is a diverse group of Bacillus species present in the rhizosphere of the desert plant R. stricta. The genomes were highly conserved with other previously sequenced species with small differences in accessory genes associated with processes such as iron uptake, nutrient transport and nitrate metabolism.

Nucleotide sequence accession numbers. The complete genome sequences and annotations are deposited at EMBL, EBI under the study accession no. PRJEB9876 and the following assembly accession numbers: Bacillus subtilis JRS2, CYHJ01000001 to CYHJ0100014; Bacillus pumilus JRS3, CYHK01000010 to CYHK01000108; Bacillus amylolyphaquefaciens JRS5, CYHL01000001 to CYHL01000128; Bacillus subtilis JRS6, CYHN01000001 to CYHN01000080; Bacillus subtilis JRS7, CYHO01000011 to CYHO01000211; Bacillus amylolyphaquefaciens JRS8, CYHP01000001 to CYHP01000167; Bacillus subtilis JRS9, CYHS01000001 to CYHS01000125; Bacillus subtilis JRS11, CYHQ01000001 to CYHQ01000076.

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REFERENCES


