



# Draft Genome Sequence of *Bacillus paralicheniformis* Strain GSFE7, a Halotolerant Plant Growth-Promoting Bacterial Endophyte Isolated from Cultivated Saline Areas of the Dead Sea Region

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**ABSTRACT** Here, we report the draft genome sequence of *Bacillus paralicheniformis* strain GSFE7, which was isolated from saline fields near the Dead Sea region. The genome was 4,452,800 bp in size and contained 4,382 coding sequences. Several genes were predicted to be involved in auxin production, nitrogen fixation, phosphate mobilization, and putative production of siderophores and antibiotics such as bacitracin, butirosin, and fengycin.

**B** *acillus paralicheniformis* was first identified in 2015 (1); since then, several strains have been reported to have plant growth-promoting properties (PGPPs) (2–4). *Bacillus paralicheniformis* strain GSFE7 was isolated from the roots of durum wheat cultivated in saline fields near the Dead Sea in Jordan (altitude, –249 m; latitude, 31°48′52″N; longitude, 35°37′42″E) (5). The region has an arid and warm climate, with annual precipitation of <100 mm and maximum temperatures of >40°C during the summer.

Root samples were collected in sterile plastic bags and were placed on ice packs and transferred to the laboratory within 1 h. The samples were washed under running tap water for 10 min to remove adhering soil particles. The roots were disinfected for 1 min with 70% ethanol, rinsed three times with sterile distilled water, and then surface sterilized for 10 min with 3% sodium hypochlorite solution with a few drops of Tween 20, followed by six rinses with sterile distilled water. Sterilized roots (1 g) were macerated in 10 mL of 1% NaCl solution, and serial dilutions were prepared, spread on nutrient agar (NA) medium supplemented with 10% NaCl, and incubated at 28°C for 1 week for bacterial colony formation. Several isolates were selected, and single colonies were purified by subculturing three times on NA medium supplemented with 10% NaCl. Strain GSFE7 was found to possess antifungal activities against *Fusarium culmorum* (5).

Total DNA was isolated from a single colony using the Wizard genomic DNA purification kit (Promega), and the concentration and quality of the DNA were determined using a spectrophotometer. The DNA was sent to Macrogen Inc. (Seoul, South Korea) for sequencing using the Illumina NovaSeq 6000 platform (library type, TruSeq Nano DNA [350-bp insert]; type of reads, paired-end reads; read length, 151 bp). The quality of the raw reads (total of 23,432,396 reads) was assessed using FastQC v0.11.9 (6). Fastp v0.23.1 (7) was used to trim adaptor sequences and to remove bad reads. The sequence reads were *de novo* assembled into 24 contigs ( $N_{50}$ , 756,180 bp; GC content, 45.55%) using SKESA v2.4.0 (8). The draft genome (total size, 4,452,800 bp, consisting of 24 contigs) was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.1. A total of 4,382 candidate protein-coding genes and a total of 77 tRNA genes and 12 rRNA genes were identified. A digital DNA-DNA hybridization was performed via the Genome-to Genome Distance Calculator v3.0 implemented in the TYGS server (9), and the results showed that strain GSFE7 has 95% sequence identity to

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*B. paralicheniformis* strain Bac84 (NCBI reference sequence accession number [NZ\\_CP023665.1](https://doi.org/10.1099/ijsem.0.000441)), with a 0.29% difference in the GC content, thus assigning it to this species epithet. All software tools were run with default parameters unless otherwise specified.

**Data availability.** The draft genome of *Bacillus paralicheniformis* strain GSFE7 was submitted to the National Center for Biotechnology Information (NCBI) under BioProject accession number [PRJNA822385](https://doi.org/10.1099/ijsem.0.000441), BioSample accession number [SAMN27182028](https://doi.org/10.1099/ijsem.0.000441), and GenBank accession number [JALJEF000000000.1](https://doi.org/10.1099/ijsem.0.000441). Annotation data are available under GenBank assembly accession number [GCA\\_022953115.1](https://doi.org/10.1099/ijsem.0.000441).

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## REFERENCES

- Dunlap CA, Kwon SW, Rooney AP, Kim SJ. 2015. *Bacillus paralicheniformis* sp. nov., isolated from fermented soybean paste. *Int J Syst Evol* 65:3487–3492. <https://doi.org/10.1099/ijsem.0.000441>.
- Wang Y, Liu H, Liu K, Wang C, Ma H, Li Y, Hou Q, Liu F, Zhang T, Wang H, Wang B, Ma J, Ge R, Xu B, Yao G, Xu W, Fan L, Ding Y, Du B. 2017. Complete genome sequence of *Bacillus paralicheniformis* MDJK30, a plant growth-promoting rhizobacterium with antifungal activity. *Genome Announc* 5:e00577-17. <https://doi.org/10.1128/genomeA.00577-17>.
- Valenzuela-Ruiz V, Robles-Montoya RI, Parra-Cota FI, Santoyo G, del Carmen Orozco-Mosqueda M, Rodríguez-Ramírez R, de Los Santos-Villalobos S. 2019. Draft genome sequence of *Bacillus paralicheniformis* TRQ65, a biological control agent and plant growth-promoting bacterium isolated from wheat (*Triticum turgidum* subsp. *durum*) rhizosphere in the Yaqui Valley, Mexico. *3 Biotech* 9: 436. <https://doi.org/10.1007/s13205-019-1972-5>.
- Sahu PK, Singh S, Gupta AR, Gupta A, Singh UB, Manzar N, Bhowmik A, Singh HV, Saxena AK. 2020. Endophytic bacilli from medicinal-aromatic perennial holy basil (*Ocimum tenuiflorum* L.) modulate plant growth promotion and induced systemic resistance against *Rhizoctonia solani* in rice (*Oryza sativa* L.). *Biol Control* 150:104353. <https://doi.org/10.1016/j.biocontrol.2020.104353>.
- Albdaiwi RN, Khyami-Horani H, Ayad JY, Alananbeh KM, Al-Sayaydeh R. 2019. Isolation and characterization of halotolerant plant growth promoting rhizobacteria from durum wheat (*Triticum turgidum* subsp. *durum*) cultivated in saline areas of the dead sea region. *Front Microbiol* 10:1639. <https://doi.org/10.3389/fmicb.2019.01639>.
- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>.
- Chen S, Zhou Y, Chen Y, Gu J. 2018. Fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* 34:i884–i890. <https://doi.org/10.1093/bioinformatics/bty560>.
- Souvorov A, Agarwala R, Lipman DJ. 2018. SKESA: strategic *k*-mer extension for scrupulous assemblies. *Genome Biol* 19:153. <https://doi.org/10.1186/s13059-018-1540-z>.
- Lee I, Ouk Kim Y, Park SC, Chun J. 2016. OrthoANI: an improved algorithm and software for calculating average nucleotide identity. *Int J Syst Evol Microbiol* 66:1100–1103. <https://doi.org/10.1099/ijsem.0.000760>.