



Draft Genome Sequence of *Paenibacillus polymyxa* DSM 292, a Gram-Positive, Spore-Forming Soil Bacterium with High Biotechnological Potential

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ABSTRACT *Paenibacillus polymyxa* DSM 292 was originally isolated from soil in 1947 due to its ability to produce antibiotics. The low proteolytic properties of strain DSM 292 warrant its examination as a host for heterologous protein production. Here, we report the draft genome sequence of DSM 292 as established by Illumina MiSeq paired-end sequencing.

Paenibacillus polymyxa is the type species of the genus *Paenibacillus* (1), a genus of soil bacteria with a multitude of useful properties. Some examples include plant growth promotion (for example, through nitrogen fixation or production of phytohormones), production of antimicrobial compounds, such as polymyxins, and industrially relevant substances, like 2,3-butanediol or exopolysaccharides (2, 3).

In comparison to other strains of the same species, *Paenibacillus polymyxa* DSM 292 shows some distinguishing traits. *P. polymyxa* is readily amenable to genetic modification using the transmuting procedure described by Heinze et al. (4). Most notably, strain DSM 292 did not form halos on milk agar plates, indicating a significantly lower exoprotease activity than strain DSM 365 or the type strain *P. polymyxa* DSM 36. This may lead to higher stability of heterologously expressed, secreted target proteins, making *P. polymyxa* DSM 292 an interesting candidate for production. This is a new application of this organism, meeting the increased demand for highly efficient expression systems to produce industrially relevant enzymes (5). *P. polymyxa* DSM 292 may be a promising alternative to the existing expression strains, which mainly belong to the genus *Bacillus* (5, 6).

As a basis for successfully working with *P. polymyxa* DSM 292, its genome was sequenced. The strain was obtained from DSMZ (Leibniz Institute DSMZ–German Collection of Microorganisms and Cell Cultures) and cultivated for 24 h at 37°C and 180 rpm in liquid LB medium (7). Chromosomal DNA was extracted from a clonal pure, stationary-phase culture, and 1 µg genomic DNA in total was used to prepare a DNA library with the TruSeq DNA PCR-free sample preparation kit (Illumina, Inc., San Diego, USA). A protocol for optimized DNA shearing and fragment size selection was applied to prepare the DNA library (8), which was sequenced using the Illumina MiSeq system in 150-bp paired-end mode according to the manufacturer's instructions. The sequence data were assembled using SPAdes v3.6.1 with the BayesHammer tool for error correction and the MismatchCorrector for postassembly mismatch and indel corrections activated (9), resulting in 23 contigs with an average of 90.4-fold coverage. The assemblies were evaluated using QUAST v3.1 (10). Default parameters were used for all software unless otherwise specified. The combined length of the 23 contigs is 6,030,236 bp, with a G+C content of 45.5 mol% and an N_{50} value of 576,871 bp. Prokka

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v1.11 (11), with default parameters, was used for the prediction and annotation of open reading frames (ORFs). In this way, 5,365 coding sequences and 99 tRNAs were identified.

The genome sequence provided here will enable studies on *P. polymyxa* DSM 292 as a potential host for heterologous enzyme production, for example, by providing the basis for selection of genetic elements or targets for genome editing.

Data availability. This whole-genome shotgun project has been deposited in ENA under the accession number [OXKC00000000](https://ena.ebi.ac.uk/ena/record/OXKC00000000). The version described in this paper is OXKC02000000. The GenBank assembly accession number is [GCA_900406265.2](https://www.ncbi.nlm.nih.gov/GenBank/assembly/GCA_900406265.2). Raw sequencing reads are available at the Sequence Read Archive under accession number [SRR10970105](https://www.ncbi.nlm.nih.gov/SRA/record/SRR10970105).

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