# Certificate of Analysis for NR-52276

## Genomic DNA from *Paenibacillus polymyxa*, Strain NCIB 8158

## Catalog No. NR-52276

## Product Description:

Genomic DNA was extracted from a preparation of *Paenibacillus polymyxa (P. polymyxa)*, strain NCIB 8158. The bacterial preparation used for extraction of genomic DNA was produced by culture of BEI Resources NR-52263 lot 70033112. Genomic DNA was extracted using proprietary technology and is provided in TE buffer (10 mM Tris-HCl and 1 mM EDTA, pH 8).

**Lot: 70033338** **Manufacturing Date: 24MAR2020**

| TEST | SPECIFICATIONS | RESULTS |
|---|---|---|
| **Genotypic Analysis**<br>Digital DNA-DNA hybridization (dDDH)[1] | ≥ 70% for species identification | *P. polymyxa* (99.6%)[2,3]<br>*P. jamilae* (86.9%)[2,3] |
| Sequencing of 16S ribosomal RNA gene (~ 1440 base pairs) | ≥ 99% sequence identity to *P. polymyxa*, strain NCIB 8158 (GenBank: AFOX01000032.1) | 99.4% sequence identity to *P. polymyxa*, strain NCIB 8158 (GenBank: AFOX01000032.1) |
| **Agarose Gel Electrophoresis** | High molecular weight chromosomal DNA | High molecular weight chromosomal DNA (Figure 1) |
| **Concentration by PicoGreen® Measurement** | 0.7 to 1.5 µg in 25 to 100 µL per vial | 1.2 µg in 33 µL per vial (37.5 µg per mL) |
| **Amount per Vial** | 0.7 to 1.5 µg | 1.2 µg |
| **Functional Activity by PCR Amplification**<br>16S ribosomal RNA gene | ~ 1500 base pair amplicon | ~ 1500 base pair amplicon |
| **$OD_{260}/OD_{280}$ Ratio** | 1.7 to 2.1 | 1.9 |
| **Bacterial Inactivation**<br>10% of total yield plated on agar for 14 days[4,5] | No viable bacteria detected | No viable bacteria detected |

[1]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684. dDDH analysis was performed using the Type (Strain) Genome Server.
[2]The whole genome of *P. polymyxa*, strain NCIB 8158 was sequenced using the Illumina® MiSeq® system. *De novo* contig sequences were generated using Unicycler v0.4.8-beta.
[3]dDDH analysis of the type strains of *P. polymyxa* and *P. jamilae* shows an 86.9% sequence similarity, suggesting that *P. polymyxa* and *P. jamilae* are genomically the same species.
[4]14 days under propagation conditions
[5]An extraction procedure was used that has been shown to consistently inactivate 100% of Gram-negative and Gram-positive bacteria.

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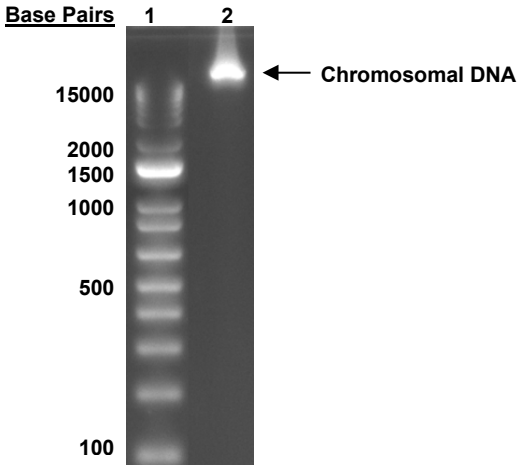
**Figure 1: Agarose Gel Electrophoresis**




**Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder**
**Lane 2: ~ 200 ng of NR-52276**

/Heather Couch/
Heather Couch 21 JUL 2021
Program Manager or designee, ATCC Federal Solutions

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