Certificate of Analysis for NR-56808

Yersinia pestis, Strain NCTC 5923

Catalog No. NR-56808

Product Description:

Yersinia pestis (Y. pestis), strain NCTC 5923 is derived from *Y. pestis* Type strain ATCC® 19428™. Whole genome sequencing of *Y. pestis strain* NCTC 5923 was carried out using the Illumina MiSeq system. The assembled genome analysis indicated the presence of pCD1, pPCP1 and pMT1 plasmids and absence of the 102-kb *pgm* locus. NR-56808 was produced by inoculation of the deposited material into Tryptic Soy broth and incubated for 2 days at 37°C in an aerobic with 5% CO_2 atmosphere. Broth inoculum was added to Tryptic Soy agar kolles, which were grown for 2 days at 37°C in an aerobic atmosphere with 5% CO_2 to produce this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70053521 **Manufacturing Date: 24JUN2022**

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphologies[1]	Report results	Colony type 1: Large, irregular, slightly peaked, undulate, opaque, and cream (Figure 1) Colony type 2: Small, circular, convex, entire, smooth, and cream (Figure 1)
Motility BBL™ Motility Test Medium w/TTC Indicator for 1 day at 37°C in an aerobic atmosphere	Report results	Non-motile
Biochemical Analyses		
Analytical profile index (API 20 E®)	*Y. pestis*	*Y. pestis* (99.4%)
Oxidase	Negative	Negative
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2,3]	≥ 70% for species identification	*Y. pestis* (99.9%)
Presence of virulence-associated locus and plasmids[3]		
pCD1 (70.3 kb)	Detected	Detected
pMT1 (96.2 kb)	Detected	Detected
pPCP1 (9.6 kb)	Detected	Detected
pgm Locus (102 kb)	Not detected	Not detected
Purity 7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)	Growth	Growth

[1]Two colony types were observed. Plating of the individual colony types showed that they did not revert to the mixed colony type. The 16S ribosomal RNA gene of each colony type was sequenced and found to be consistent with the other colony type and *Y. pestis*, strain NCTC 5923 (GenBank: UAVH00000000).

[2]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.

[3]Testing was performed using source material.

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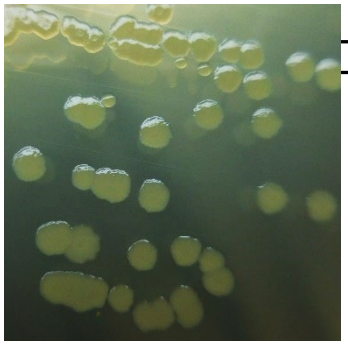
Figure 1: Colony Morphology



/Sonia Bjorum Brower/
Sonia Bjorum Brower 11 JAN 2023
Technical Manager or designee, ATCC Federal Solutions

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