Certificate of Analysis for NR-50573

Pseudomonas aeruginosa, Strain PA14

Catalog No. NR-50573

Product Description: *Pseudomonas aeruginosa* (*P. aeruginosa*), strain PA14 was isolated in the early 1970s from the blood of a burn patient at Mercy Hospital in Pittsburgh, Pennsylvania, USA. *P. aeruginosa*, strain PA14 was deposited as resistant to rifampicin and susceptible to meropenem, ofloxacin, ceftazidime, amikacin and tobramycin.

Lot[1]: 70002165 **Manufacturing Date: 02FEB2017**

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology[2]	Report results	Circular, slight peaked, undulate, smooth and green (Figure 1)
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[3]		
VITEK® (AST-GN81 Card)		
Ampicillin	Report results	Resistant (≥ 32 µg/mL)
Amoxicillin/Clavulanic Acid	Report results	Resistant (≥ 32 µg/mL)
Piperacillin/Tazobactam	Report results	Sensitive (= 8 µg/mL)
Cefazolin	Report results	Resistant (≥ 64 µg/mL)
Cefoxitin	Report results	Resistant (≥ 64 µg/mL)
Ceftazidime	Sensitive	Sensitive (= 2 µg/mL)
Ceftriaxone	Report results	Resistant (= 32 µg/mL)
Cefepime	Report results	Sensitive (≤ 1 µg/mL)
Meropenem	Sensitive	Sensitive (≤ 0.25 µg/mL)
Amikacin	Sensitive	Sensitive (≤ 2 µg/mL)
Gentamicin	Report results	Sensitive (≤ 1 µg/mL)
Tobramycin	Sensitive	Sensitive (≤ 1 µg/mL)
Ciprofloxacin	Report results	Sensitive (≤ 0.25 µg/mL)
Levofloxacin	Report results	Sensitive (= 0.25 µg/mL)
Tetracycline	Report results	Resistant (= 8 µg/mL)
Nitrofurantoin	Report results	Resistant (≥ 512 µg/mL)
Trimethoprim/sulfamethoxazole	Report results	Resistant (= 80 µg/mL)
Etest® antibiotic test strips[4]		
Gentamicin[5]	Report results	Sensitive (= 1.5 µg/mL)
Ofloxacin[5]	Sensitive	Sensitive (= 0.75 µg/mL)
Rifampicin[6]	Report results	32 µg/mL
Streptomycin[7]	Report results	1024 µg/mL
Trimethoprim/sulfamethoxazole[8]	Report results	4 µg/mL[9]
Genotypic Analysis		
Sequencing of 16S ribosomal RNA gene (~ 1530 base pairs)	≥ 99% sequence identity to *P. aeruginosa* type strain (GenBank: CP000438)	100% sequence identity to *P. aeruginosa* type strain (GenBank: CP000438)
Digital DNA-DNA hybridization (dDDH)[10]	≥ 70% for species identification	*P. aeruginosa* (87.2%)[11]
Purity (post-freeze)[12]	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)[2]	Growth	Growth

[1]NR-50573 was produced by inoculation of the deposited material into Nutrient broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Nutrient agar kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce this lot.
[2]1 day at 37°C in an aerobic atmosphere on Nutrient agar

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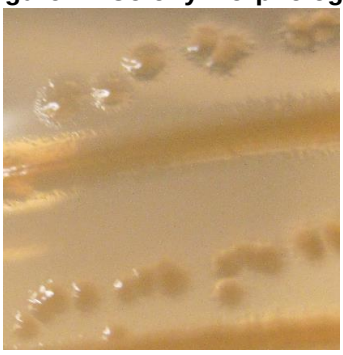
[3]Minimum Inhibitory Concentration (MIC); MIC interpretation was determined using VITEK® 2 software version 07.01 combined with the bioMérieux Advanced Expert System™ (AES) software using the interpretation standard CLSI M100-S22 (2012) and the interpretation guideline "Natural Resistance." For more information, please refer to Sanders, C. C. et al. "Potential Impact of the VITEK 2 System and the Advanced Expert System on the Clinical Laboratory of a University-Based Hospital." J. Clin. Microbiol. 39 (2001): 2379-2385. PubMed: 11427542.
[4]1 day at 37°C in an aerobic atmosphere on Mueller Hinton agar
[5]Minimum Inhibitory Concentration (MIC); MIC interpretation guidelines CLSI M100-S22 (2012)
[6]Rifampicin MIC interpretive standards are not available for *P. aeruginosa*. Strain PA14 was reported by the depositor to be resistant to rifampicin.
[7]Streptomycin MIC interpretive standards are not available for *P. aeruginosa*.
[8]Trimethoprim/sulfamethoxazole MIC interpretive standards are not available for *P. aeruginosa*, however most clinical isolates are resistant to trimethoprim/sulfamethoxazole. For more information, please refer to Köhler, T., et al. "Multidrug Efflux in Intrinsic Resistance to Trimethoprim and Sulfamethoxazole in *Pseudomonas aeruginosa*." Antimicrob. Agents Chemother. 40 (1996): 2288-2290. PubMed: 9036831.
[9]MIC result is based on the trimethoprim component of the test strip.
[10]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, please 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.
[11]The whole genome of *P. aeruginosa*, strain PA14 (Contig Total Length ~ 5.9 megabase pairs) was sequenced using the Illumina® MiSeq® system and was assembled and analyzed with CLC Genomics Workbench Version 7.0.2.
[12]Purity of this lot was assessed for 7 days on Nutrient agar at 37°C in an aerobic atmosphere with 5% CO_2

Figure 1: Colony Morphology



Date: 29 SEP 2017 **Signature:**

BEI Resources Authentication

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