

Certificate of Analysis for NR-59312

Middle East Respiratory Syndrome Coronavirus, Isolate Hu/Jordan-N3/2012

Catalog No. NR-59312

Product Description:

Middle East Respiratory Syndrome (MERS) Coronavirus, Jordan-N3/2012, was isolated in April 2012 from a bronchial wash and sourced from the National Institutes of Health, with material deposited by the Integrated Research Facility, Fort Detrick, MD. NR-59312 lot 70059827 was produced by infecting Caco-2 cells (ATCC® HTB-37™) with MERS Coronavirus, Jordan-N3/2012 and incubating in Eagle's Minimum Essential Medium (ATCC® 30-2003™) supplemented with 2% fetal bovine serum (ATCC® 30-2020™) for 2 days at 37°C with 5% CO2. The cells and supernatant were spin-clarified at 1500 × g for 10 minutes at 4°C.

Total Passage: 2

Passage History:

V(1)/Ca(1) (IRF/BEI Resources); V = Chlorocebus (formerly Cercopithecus) aethiops kidney cells (Vero); Ca = Caco-2

Lot: 70059827 Manufacturing Date: 16FEB2023

| TEST | SPECIFICATIONS | RESULTS | |
|--|---|--|--|
| Identification by Infectivity in Caco-2 Cells | Syncytia formation and sloughing | Syncytia formation and sloughing | |
| Next-Generation Sequencing (NGS) of Complete Genome Using Illumina® iSeq™ 100 Platform (Refer to Appendix I for NGS information) | ≥ 98% identity with isolate Hu/Jordan-N3/2012 (GenBank: KC776174) | 99.98% identity with isolate Hu/Jordan-N3/2012 (GenBank: KC776174) | |
| Titer by TCID₅₀ Assay in Caco-2 Cells by Cytopathic Effect ^{1,2} (5 days at 37°C and 5% CO₂) | Report results | 1.8 × 10 ⁸ TCID ₅₀ per mL | |
| Endotoxin Content (<i>Limulus</i> Amoebocyte Lysate Assay) | Report results | ≤ 0.03 EU per mL | |
| Sterility (21-day incubation) | | | |
| Harpo's HTYE broth, 37°C and 26°C, aerobic ³ | No growth | No growth | |
| Trypticase Soy broth, 37°C and 26°C, aerobic | No growth | No growth | |
| Sabouraud broth, 37°C and 26°C, aerobic | No growth | No growth | |
| Blood agar, 37°C, aerobic | No growth | No growth | |
| Blood agar, 37°C, anaerobic | No growth | No growth | |
| Thioglycollate broth, 37°C, anaerobic | No growth | No growth | |
| DMEM with 10% FBS, 37°C and 5% CO ₂ | No growth | No growth | |
| Mycoplasma Contamination | | | |
| Agar and broth culture (14-day incubation at 37°C) | None detected | None detected | |
| DNA detection by PCR of extracted Test Article nucleic acid | None detected | None detected | |

¹The Tissue Culture Infectious Dose 50% (TCID₅₀) endpoint is the 50% infectious endpoint in cell culture. The TCID₅₀ is the dilution of virus that under the conditions of the assay can be expected to infect 50% of the culture vessels inoculated, just as a Lethal Dose 50% (LD₅₀) is expected to kill half of the animals exposed. A reciprocal of the dilution required to yield the TCID₅₀ provides a measure of the titer (or infectivity) of a virus preparation. ²Titer was determined by cytopathic effects (CPE) and completed in quadruplicate (1.6 × 10⁸ per mL, 2.8 × 10⁸ per mL, 2.8 × 10⁸ per mL, and 1.6 ×

³Atlas, Ronald M. <u>Handbook of Microbiological Media</u>. 3rd ed. Ed. Lawrence C. Parks. Boca Raton: CRC Press, 2004, p. 798.

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15 FEB 2024

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^{10&}lt;sup>7</sup> per mL). The average of the four values is reported.



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ATCC®, on behalf of BEI Resources, hereby represents and warrants that the material provided under this certificate has been subjected to the tests and procedures specified and that the results described, along with any other data provided in this certificate, are true and accurate to the best of ATCC®'s knowledge.

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APPENDIX I: NGS Information for NR-59312 lot 70059827

Sequence analysis using fastp 0.23.2 and variant caller LoFreq version: 2.1.5 resulted in the discovery of five SNPs when compared to Middle East Respiratory Syndrome virus, isolate Hu/Jordan-N3/2012 (GenBank: KC776174) (see Table I below).

Table I: Variants with different nucleotides between NR-59312 lot 70059827 and KC776174.1 (Human betacoronavirus 2c Jordan-N3/2012, complete genome)

| Variant Type | Variant Position and Identified Alternative Base | Coverage | Length of Variant | Frequency of Variant | Gene (Region) | Amino Acid Mutation |
|-----------------|--|----------|----------------------|-------------------------|----------------|---------------------|
| SNP | T7276G | 794 | 1 | 6.6751% | ORF1ab protein | Silent mutation |
| SNP | T19349A | 1058 | 1 | 7.6560% | ORF1ab protein | L6373Q |
| SNP | T24045C | 1563 | 1 | 34.6129% | S protein | I879T |
| SNP | T26948A | 1245 | 1 | 8.1124% | ORF5 protein | L52Q |
| SNP | T27490C | 1578 | 1 | 7.6046% | Intergenic | Untranslated |

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