

Escherichia coli, Strain H001

Catalog No. NR-15821

Product Description:

Escherichia coli (*E. coli*), strain H001 was isolated in 1999 from a human blood stream sample in Canberra, Australian Capital Territory, Australia. The deposited material was used to inoculate a Tryptic Soy agar plate and grown for 1 day at 37°C in an aerobic atmosphere, and the resulting subculture was vialled and frozen. NR-15821 was produced by inoculation of the frozen subculture into Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70001202

Manufacturing Date: 22MAR2017

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis Cellular morphology Colony morphology Motility (wet mount) VITEK® MS (MALDI-TOF)	Gram-negative rods Report results Report results <i>E. coli</i>	Gram-negative rods Circular, convex, entire, smooth and cream (Figure 1) Motile <i>E. coli</i> (99.9%)
Genotypic Analysis Digital DNA-DNA hybridization (dDDH) ¹ Whole-Genome Sequencing (WGS) analysis Virulence gene prediction ⁴ Antimicrobial resistance (AMR) gene prediction ⁵ Serotype prediction by gene analysis ⁶ <i>fliC</i> <i>wzm</i> <i>wzt</i>	≥ 70% for species identification Report results Report results Report results Report results Report results	<i>E. coli</i> (90.2%) ^{2,3} <i>Shigella sonnei</i> (74.8%) <i>Shigella flexneri</i> (74.2%) <i>Shigella boydii</i> (74.0%) <i>Shigella dysenteriae</i> (74.0%) Virulence genes present: <i>pic</i> , <i>vat</i> No acquired AMR genes identified Point mutations identified: <i>parE</i> p.D475E (Appendix I) H10 O8 O8
Purity (post-freeze) 7 days at 37°C in an aerobic atmosphere with and without 5% CO ₂ on Tryptic Soy agar	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)	Growth	Growth

¹Relatedness 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.

²Reclassification of *Shigella sonnei*, *Shigella boydii*, *Shigella flexneri* and *Shigella dysenteriae* as subspecies of *E. coli* (*E. coli* subsp. *shigella* subsp. nov.) has been proposed [Dif, G., et al. "In-Depth Genome-Based Analysis of *Shigella* spp. and *Escherichia* spp.: Resolving Ambiguities and Unveiling Phylogenetic Relationships." *Curr. Microbiol.* 82 (2025): 170. PubMed: 40045049.].

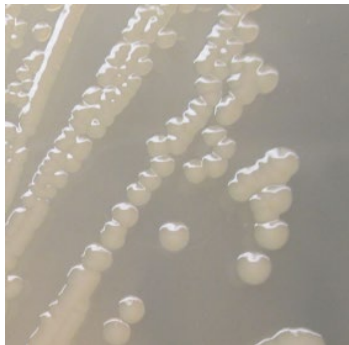
³The whole genome of *E. coli*, strain H001 (Total Contig Length ~ 5.0 megabase pairs) was sequenced using the Illumina® MiSeq™ platform using a v2 2x250 cycle Nano flow cell. *De novo* contig sequences were generated using CLC Genomics Workbench software.

⁴*In silico* analysis of WGS data for virulence-associated genes was performed using the Center for Genomic Epidemiology (CGE) VirulenceFinder 1.5 genome analysis tool. [Joensen, K. G., et al. "Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic *Escherichia coli*." *J. Clin. Microbiol.* 52 (2014): 1501-1510. PubMed: 24574290.]

⁵*In silico* analysis of WGS data for identification of genes or known point mutations associated with antimicrobial resistance was performed using the Center for Genomic Epidemiology (CGE) ResFinder 3.0 genome analysis tool. [Zankari, E., et al. "Identification of Acquired Antimicrobial Resistance Genes." *J. Antimicrob. Chemother.* 67 (2012): 2640-2644. PubMed: 22782487.]

⁶*In silico* analysis of WGS data for serotype prediction based on flagellin and O-antigen processing system genes was performed using the [Center for Genomic Epidemiology \(CGE\)](#) SerotypeFinder 1.1 genome analysis tool. [Joensen, K. G., et al. "Rapid and Easy *in silico* Serotyping of *Escherichia coli* Isolates by Use of Whole-Genome Sequencing Data." *J. Clin. Microbiol.* 53 (2015): 2410-2426. PubMed: 25972421.]

Figure 1: Colony Morphology



APPENDIX I: POINT MUTATIONS

Mutation	Nucleotide Change	Amino Acid Change	Associated Resistance
<i>parE</i> p.D475E	GAC → GAA	D → E	Quinolones and fluoroquinolones ¹

¹Cavaco, L. M., et al. "Prevalence of Quinolone Resistance Mechanisms and Associations to Minimum Inhibitory Concentrations in Quinolone-Resistant *Escherichia coli* Isolated from Humans and Swine in Denmark." *Microb. Drug. Resist.* 14 (2008): 163-169. PubMed: 18500921.

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