Certificate of Analysis for NR-15844

Escherichia coli, Strain H494

Catalog No. NR-15844

Product Description:

Escherichia coli (E. coli), strain H494 was isolated in 2001 from a human feces sample collected in Canberra, Australian Capital Territory, Australia. NR-15844 was produced by inoculation of the deposited material 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: 70003350 **Manufacturing Date: 10MAR2017**

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TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream (Figure 1)
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*E. coli*	*E. coli* (99.9%)
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[1]	≥ 70% for species identification	*Shigella sonnei* (87.9%)[2,3] *Shigella boydii* (87.7%) *Shigella flexneri* (85.6%) *Shigella dysenteriae* (81.8%) *E. coli* (75.1%)
Purity (post-freeze) 7 days at 37°C in an aerobic atmosphere with 5% CO_2 on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)	Growth	Growth

[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.

[2]Reclassification of *Shigella sonnei, Shigella boydii, Shigella flexnerei 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.].

[3]The whole genome of *E. coli*, strain H494 (Total Contig Length ~ 5.0 megabase pairs) was sequenced using the Illumina® MiSeq™ platform and was analyzed and assembled using CLC Genomics Workbench software.

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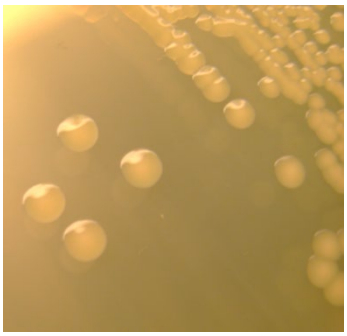
Figure 1: Colony Morphology



/Sonia Bjorum Brower/
Sonia Bjorum Brower 28 AUG 2026
Technical Manager or designee, ATCC Federal Solutions

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