MLS Laboratory Update: MDH-PHL 16S Identification Test Method Change

MAY 29, 2024

Purpose of this Message:

To inform clinical laboratory partners that the Minnesota Department of Health - Public Health Laboratory (MDH-PHL) is discontinuing Sanger Sequencing for 16S ribosomal RNA (rRNA) bacterial identification. Next Generation Sequencing (NGS) using the Oxford Nanopore GridION platform will replace Sanger Sequencing.

Action Item:

Please continue to submit isolates to MDH-PHL for reference identification, as needed, using current submission processes. Please forward information regarding this method change for 16S Identification to microbiology laboratory staff.

Background:

One microorganism identification method utilized by the MDH-PHL is sequencing of the ubiquitous 16S rRNA gene from bacterial isolates. This gene is present in all bacteria, but sequence variations allow for a genus and, frequently, a species to be determined. MDH-PHL internally tests isolates by 16S rRNA gene sequencing, as needed, for identification of organisms that do not characterize well with other methods.

Sanger sequencing has been the preferred method of 16S rRNA gene sequencing for many years. However, the ability to cost-effectively sequence the full 16S gene using NGS platforms is now feasible and will replace and improve upon the traditional method. This new platform utilizes DNA extracted from bacterial cells, followed by amplification of the 16S gene and DNA sequencing using the Oxford Nanopore GridION instrument. Downstream analysis involves a bioinformatic pipeline hosted on Linux Operating systems, with an end result of bacterial genus and, often, species.

Additional Information:

There will be no change in how 16S rRNA bacterial identification is reported. This MLS update is for information purposes only.

Questions: If you have any questions, please contact

Sean Wang, Ph.D.

Sequencing and Bioinformatics Supervisor

Phone: 651-201-5050

Sean.wang@state.mn.us

Paula M. (Snippes) Vagnone, MT (ASCP)

Microbiology Supervisor

Phone: 651-201-5581

Paula.snippes@state.mn.us

Public Health Laboratory, Minnesota Department of Health

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Minnesota Laboratory System
Minnesota Department of Health, Public Health Laboratory
601 Robert St. N, St. Paul, MN 55164-0899
651-201-5200
health.mnlabsystem@state.mn.us
www.health.state.mn.us/diseases/idlab/mls/index.html

To obtain this information in a different format, call: 651-201-5200