



August 4, 2023

To All OSPHL Clients,

Update: This message is a copy of a message sent on July 17, 2023. This message includes a change to the implementation date. The method change will now be implemented September 1, 2023 to permit sufficient time for staff training.

This message serves to update you regarding a methodology change for bacterial identification testing for *Vibrio* spp. at the Oregon State Public Health Laboratory (OSPHL). Please share this information with your colleagues. If you do not order this testing from OSPHL or interpret the results, you may disregard this message.

What is changing?

Beginning with specimens received **September 1, 2023**, OSPHL will transition from traditional biochemical identification methods to whole genome sequencing (WGS)-based average nucleotide identity (ANI) calculation for *Vibrio* spp. identification. More information about this method is provided below. This method change has already been made in our laboratory for *Campylobacter* spp. identification and *Listeria monocytogenes* identifications.

OSPHL biochemical methods currently identify various *Vibrio* spp. The WGS ANI method will identify the following clinically significant *Vibrio* species: *Vibrio alginolyticus*, *Vibrio cholerae*, *Vibrio cidicii*, *Vibrio cincinnatiensis*, *Vibrio fluvialis*, *Vibrio furnissii*, *Vibrio harveyi*, *Vibrio metoecus*, *Vibrio metschnikovii*, *Vibrio mimicus*, *Vibrio navarrensis*, *Vibrio parahaemolyticus*, and *Vibrio vulnificus*. In addition, this method will identify *Grimontia hollisae*, previously classified as *Vibrio hollisae*.

Result reports will change only in minor ways; therefore, a detail of the change is not provided in this letter. OSPHL's Test Menu (www.healthoregon.org/labtests) will be updated to specify the testing platform in use and the test performance specifications closer to the implementation date.

What is not changing?

There are no changes to specimen acceptance criteria. In addition, no operational changes need to be implemented by your facility. Please continue to collect, store, and transport specimens as you currently do. Continue to choose the same orders on the Test Request Form.

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Why this change?

Changing this testing method will enhance public health surveillance and specificity of laboratory results. Next Generation Sequencing (NGS) technology, also called high-throughput sequencing, has become a powerful tool for detection, identification, and analyses of microbial pathogens.

Whole Genome Sequencing (WGS) is an available NGS method currently used by OSPHL for surveillance and investigation of foodborne diseases. This methodology has many advantages over conventional methods. In particular, sequencing bacterial genomes can be used for more accurate detection and characterization of pathogens and provide new insights into disease transmission, virulence, and antimicrobial resistance.

What is Average Nucleotide Identity (ANI)* †

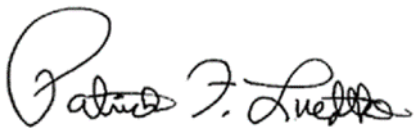
ANI is a method to identify taxonomic groups by comparing the sequences of a bacterial isolate against reference genome strains to identify taxonomic groups. Based on the genetic similarity between the two, the species identification of the bacterial isolate strain can be determined.

For technical questions, please contact Karim Morey, Microbiologist, at 503-693-4100 or karim.e.morey@oha.oregon.gov. For operational questions, please contact Sarah King, Client Services Coordinator, at 971-217-3522 or sarah.m.king@oha.oregon.gov.

Sincerely,

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* Konstantidis, KT, Tiedje JM. 2005. Genomic insights that advance the species definition for prokaryotes. Proc Natl Acad Sci USA 102(7):2567-72.

† Richter R, Rosello-Mora R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci USA 106(45):19126-19131