



December 5, 2022

To All OSPHL Clients,

This message serves to notify you of methodology changes for bacterial identification testing for *Campylobacter* spp. and *Listeria monocytogenes* at 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 January 1, 2023, OSPHL will transition from traditional biochemical and PCR-based identification methods to whole genome sequencing (WGS)-based average nucleotide identity (ANI) calculation for *Campylobacter* spp. identification and *Listeria monocytogenes* identification. More information about this method is provided below.

OSPHL biochemical methods currently identify *Campylobacter jejuni*. Non-*C. jejuni* samples are forwarded to CDC for further characterization. The WGS ANI method will identify five *Campylobacter* species: *C. coli*, *C. fetus*, *C. jejuni*, *C. lari*, and *C. upsaliensis*.

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 platform in use and performance specifications closer to the implementation date.

What is not changing?

There are no changes to specimen acceptance criteria or substantive operational changes you need to implement for these tests. Please continue to collect, store, and transport specimens as you currently do. Continue to choose the same orders on the Test Request Form.

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 submitted to the lab 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@dhsoha.state.or.us. For operational questions, please contact Sarah Humphrey King, Client Services Coordinator, at 971-217-3522 or sarah.m.humphrey@dhsoha.state.or.us.

Sincerely,

Melissa Powell
OSPHL Business Director

Marisa Frieder, PhD
Manager, OSPHL General Microbiology

* Konstantinidis, 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