

# CASE STUDY

## Issue

A ready-to-eat meat producer has isolated a suspected *Listeria* from their final product. Extensive testing of the processing environment has isolated suspected *Listeria* from the meat slicer and packer as well as a floor drain. *Listeria* was also found in a raw ingredient that was supplied from a different company but used during manufacture.

The processor has sent the isolates as pure cultures to ESR to undergo genome sequencing and analysis. They have asked a series of questions:

- Are these microbial contaminants pathogenic *Listeria monocytogenes* or other *Listeria* species?
- Has a cross-contamination event occurred from the factory environment to the product?
- Did the *Listeria* found in the final product come from the raw ingredients used?

## Species identification and evaluation of the similarity of isolates

Genome sequencing enables the accurate identification of the microorganism of interest (see diagram to the right).

## Outcome

The information provided by GenomESR helped the producer identify that a cross-contamination event likely occurred from the meat slicer or packer to the food product during manufacture (slicing or packing). The company can now undertake the necessary interventions to eliminate and resolve the contamination in their processing chain, including non-food contact surfaces such as floor drains. Environmental and food testing procedures should be continued to ensure *L. monocytogenes* does not re-appear.

If the processor encounters *L. monocytogenes* again at a later point in time, genetic comparisons can be made to historical sequence data to establish whether the same *L. monocytogenes* strain is persisting in the processing environment. Greater intervention strategies may be required to eliminate the *L. monocytogenes* permanently.

While genome sequencing can implicate a source, it can also exonerate a potential source, which can be equally valuable.

