

E/S/R
Science for Communities



Genom**ESR**

Combining state-of-the-art genome sequencing with advanced scientific expertise to help solve complex problems.

The presence of an unwanted microorganism could lead to damaging and expensive recalls, and erosion of trust in your product and brand.

Our scientists will ensure the best possible results for your business by providing information you can use to identify food safety and quality issues that could otherwise prove potentially serious.

GenomESR can give you surety in obtaining confidential results to identify and characterise isolates (microorganisms) from food, health, water and environmental samples.

What is GenomESR?

GenomESR uses next-generation sequencing technology to determine the entire DNA make-up of a microorganism – commonly referred to as the **genome sequence**. By analysing the genome sequence, we can accurately identify the microorganism and we can also compare the genome sequence of the microorganism with similar microorganisms of interest (known as 'sub-typing').

Genome sequencing provides a significantly greater resolution and precision than other conventional methods and can be used to gain further insight into the microorganism.

What questions can ESR's genome sequencing service help answer?

- Is the pathogen in my processing plant the same as in my food product?
- Did the pathogen in my food product arise from processing water, raw ingredients or the delivery company?
- Is the pathogen in my processing plant the same as the one we found two years ago? If so, where is it hiding, and where should we put more resources into cleaning and sanitation?
- Does the isolate we've found harbour antimicrobial resistance genes?
- Our productivity is down. Is the bacteria in my fermenter the same as our proprietary strain?

How does GenomESR work?

Step 1

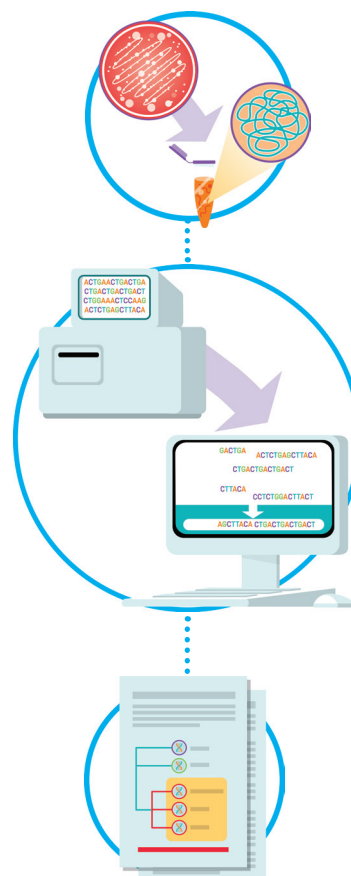
ESR cultures the isolate from your company, and extracts the DNA ready for sequencing.

Step 2

Our scientists sequence the genome of the isolate which is used initially to provide an identification of the microorganism. The genome sequence can also be used to investigate the genetic relationship between bacterial isolates obtained from different sources. We use tools such as the classical seven-gene Multilocus Sequence Typing (MLST), and whole or core MLST which is based on 1,000's of genes to identify isolates that are closely related. Depending on the species and questions asked we can also use single nucleotide polymorphism (SNP) analysis, which can determine the genetic relationship using a reference genome. The analysis process can be performed on multiple genome sequences at a time.

Step 3

ESR provides you with a confidential report explaining the methods, quality controls and analysis used to generate and analyse the genome sequence of the isolate(s) sent.



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

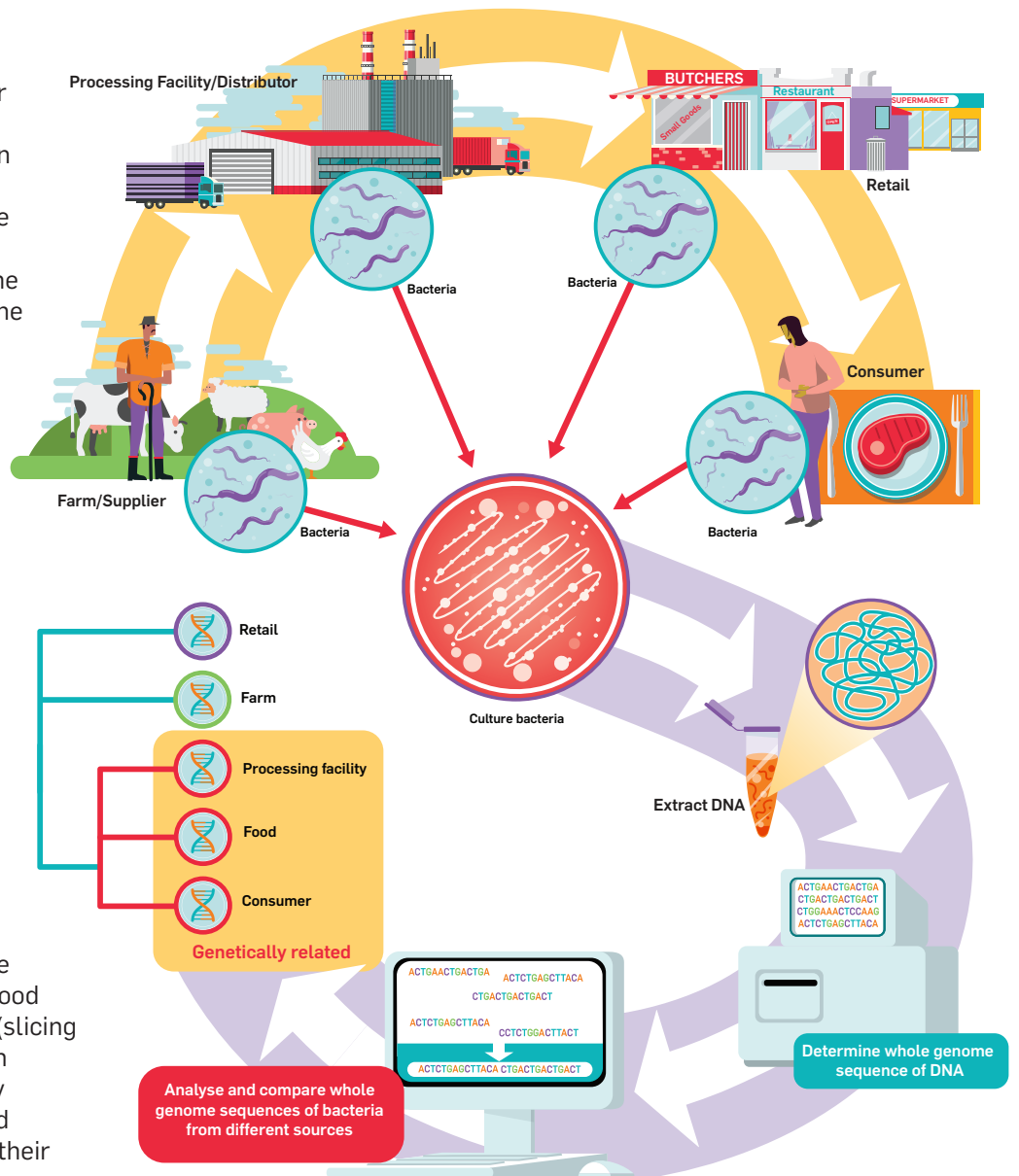
Genome sequencing enables the accurate identification of the microorganism of interest (see diagram to the right).

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.



Pricing and timing

Pricing varies according to the species, number of samples submitted and urgency of your timeframe.

Timing depends on the sample size, and we can work on a case-by-case basis to create faster turnaround times in certain situations. The bioinformatics analysis required to answer your question may also influence the overall cost.

Contact us to discuss options and ensure the best possible results from the GenomESR service.

Data handling and security

The isolates and results remain the property of the client and will be kept confidential. The sequence data outputs will be incorporated into the ESR database for future reference use by the client. ESR will always ask permission before using data for any research or publication purposes.

ESR will store the raw sequence files and they are available for the client if required. An option to upload the files onto the public NCBI Sequence Read Archive with minimal isolation information (species, country, year and 'food' isolate label) is available for long-term storage and does not

incur an ongoing cost. No client or further isolation information is included in this option. Alternatively, long term private storage of data is available and may incur an additional annual cost.

The extracted DNA from client samples will also be stored for one year. The client may request the return of the DNA and remaining sample following completion of the sequencing project.

Additional analyses

We can undertake a wide range of other analyses to fit your requirements. Scientific support is available from our scientists who can provide expert advice as to the best genome sequencing analyses for your purpose and further interpretation of the results obtained. We can look for specific genes of interest, for example, antimicrobial resistance and virulence genes.

We can also provide you with the raw high-throughput sequenced files if desired. Otherwise, the data is stored confidentially on our database for future analyses. For example, we can compare new isolates over time against other historical microbes isolated from your processing environment, or we can ascertain if your commercial strain has undergone mutations.

**Get in touch with our team
at ESR today**

**To find out more or to talk to
someone about how GenomESR
can help you and your business,
please phone 03 351 0077
or email genomesr@esr.cri.nz.**

We are here to help.

E / S / R
Science for Communities

About the Institute of Environmental Science and Research

The Institute of Environmental Science and Research (ESR) is a New Zealand Crown Research Institute specialising science related to communities. We help safeguard people's health, protect food-based economies, improve the safety of freshwater and groundwater resources, and contribute expert forensic science to justice systems.

Using the largest team of forensic, social, radiation, environmental, epidemiology and infectious disease scientists in New Zealand, we deliver solutions for local and central government, the commercial sector and other science organisations. Our expertise, experience and networks are trusted to solve complex problems, collect, collate and annotate huge amounts of data and manage a range of critical science assets and facilities for New Zealand.