

"Studying the genetic drivers of risk in *Listeria monocytogenes*".

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Listeriosis is a food illness caused by germs (the bacteria *Listeria monocytogenes*). The bacteria exist and grow throughout the food chain. When humans eat foods containing *L. monocytogenes*, they become ill. They might have an upset tummy or feel like they have the flu. In some cases, people can become extremely ill and can even die. Patients who are most likely to be very sick are:

- pregnant women
 - their born and and newly delivered babies
- people with poor health
- people over the age of 60 (1).

Listeriosis can be life-threatening. Health organisations reported an average of 160 cases each year, for England and Wales. 1 out of 4 diagnosed cases die and 1 out of 3 pregnant women with listeriosis lose their baby before birth (2–5).

We are looking at the different types of *Listeria* that are making people ill most often in England. We are also trying to find what foods are more likely to contain *Listeria* and if they get people sick. We aim to apply population and community significance on the genomic features of the disease.

Bacteria grow by creating copies of themselves. Some of these copies will carry differences in their DNA. Some DNA differences allow them to survive better in the environment they are living in. Some other DNA differences make humans very sick. There are also DNA differences that can do both. Whole genome sequencing (WGS) is a technique that allows us to 'read' the DNA of all organisms. The UK Health Security Agency (UKHSA) applies WGS, on the bacteria copies taken from infected humans, or environments containing *Listeria*.

The UKHSA holds the largest collection of information on WGS of *L. monocytogenes* copies. We used information from 4073 *L. monocytogenes* copies. These were collected and sequenced between January 2015 and December 2020.

The samples were from Scotland, Wales, England and Northern Ireland from:

- food (n=2449)
- humans (n=928)
- environmental sources (n=618)
- undetermined sources (n=73)
- animals (n=5)

We use computers to process this information, and this allows an insight into the structure of the disease population. We can also investigate the key genetic properties that allow the bacteria to survive in our food chain and cause disease.

Studying the genomic makeup of all *L. monocytogenes* copies, identifies the most common copies in the population. It also shows us that some bacteria copies are more common in human disease. Unlike others, which are more common in the environment.

We aim to understand the population and community significance of the disease. Additionally, studying the genetic makeup of the bacteria. Combining these, we can make better predictions to detect outbreaks. These tools allow the UKHSA to protect and inform the public against listeriosis.

References:

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