Sick through foodborne germs: Genetic makeup reveals source of infection

The investigation of foodborne disease outbreaks is a race against time for the responsible authorities. The sooner the source is found, the fewer the cases of disease, the fewer fatalities and the lower the costs. The use of whole genome sequencing to characterise the pathogen enables the unequivocal identification of infection sources. The BfR also uses this technology as a test method.

Laboratory diagnostic examination methods to characterise the disease pathogen are used to recognise or exclude a food as the source of an infection. The underlying principle is to isolate the causal germ and compare it with isolates of the same pathogen from foods. Specific properties such as the genetic information of the pathogen – DNA or RNA – are used to make the comparison. The relationship of the isolates is established in this way and a common origin determined accordingly. The more comprehensively a method characterises the pathogen, the more reliable the result of the comparison.

The basis of whole genome sequencing is genetic information such as DNA from isolates of pathogenic germs.

Whole genome sequencing shines through cells

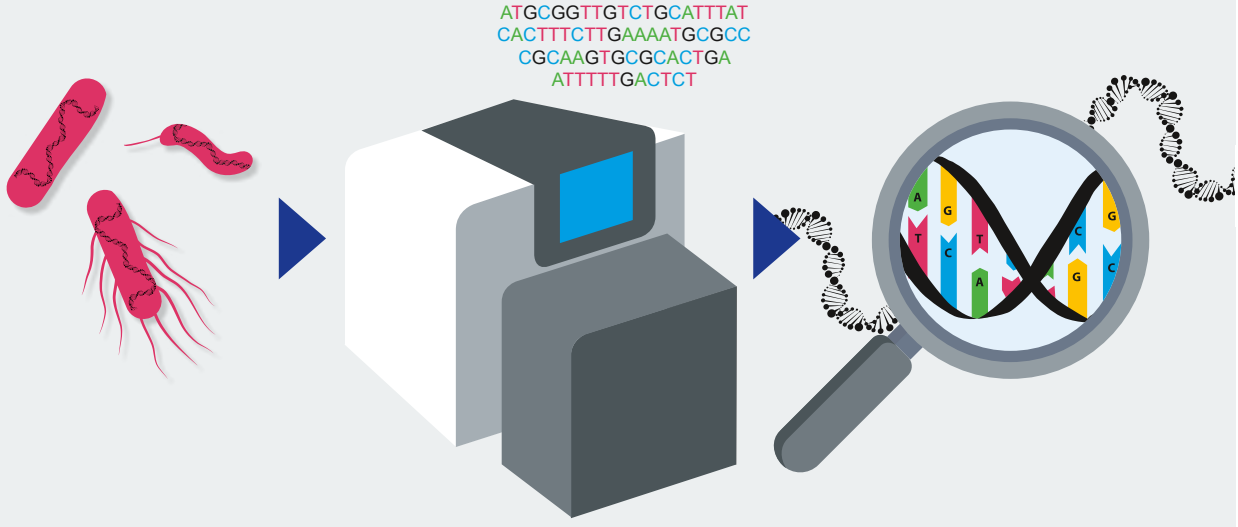
Using conventional methods, such as pulsed-field gel electrophoresis, it has only been possible up to now to determine and compare sections of genetic information. The information acquired in this way was often insufficient to reliably identify a food as the source of infection. In contrast, whole genome sequencing permits the deciphering of the complete genetic information of viruses, bacterial and parasite cells. Whole genome sequencing shines through the genetic information; this is comparable to the notion of switching on a light in a dark room and recognising what is in it. Without the light, the objects could only be recognised vaguely.

Listeriosis outbreak solved

Whole genome sequencing cast some light into some dark places during the investigation of a protracted listeriosis outbreak in southern Germany. Between 2012 and 2016, 78 people took ill with the same strain of the bacterium *Listeria monocytogenes*, eight of whom died. Patient surveys provided only vague indications as to which foods could be the cause of the outbreak. The reason for this is that with listeriosis, several weeks can often expire between the consumption of the contaminated food and the occurrence of symptoms of disease. For those who have contracted the disease, it is not easy to remember in any detail what foods they had eaten after such a long time. The severity of the disease often means that those affected can often only be questioned long afterwards, if at all.

Thereupon, the National Reference Laboratory for *Listeria monocytogenes* at the BfR typed more than 500 isolates of the listeria pathogen from many different foods. Using methods that were standard up to then, several foods of different origin were identified as the

The principle of whole genome sequencing



Pathogenic bacteria
with genetic information
(e.g. from foods or from patients)

Whole genome sequencing
of the bacterial genetic
information

Detailed information
about the pathogenic bacteria, e.g. for
the investigation of disease outbreaks

possible source of infection. The correct allocation was only achieved through the use of whole genome sequencing in March 2016, when an official test laboratory in Bavaria positively tested a pork product for *Listeria monocytogenes*. The sequencing of this isolate at the BfR showed that its genome was identical with the DNA of the *Listeria monocytogenes* isolates found with those who had taken ill. It was also possible to exclude other foods which had previously been suspected as sources of infection due to the methods used.

New challenges

The new world of whole genome sequencing poses a challenge to science: huge quantities of data are produced which have to be evaluated, administered and made accessible to the laboratories. As with every new method, the goal is to develop international standards and establish databases. To this end, the BfR is involved in national and European third party-funded projects to promote the harmonisation of technology, the build-up of genome databases and the exchange of scientific knowledge. The use of whole genome sequencing makes it possible to follow precisely the spread of microbial pathogens through foods and feeds across national frontiers and stop outbreaks of disease or even prevent them in advance. ◘

More information:
Lüth et al. 2018: Whole genome sequencing as a typing tool for foodborne pathogens like Listeria monocytogenes – The way towards global harmonisation and data exchange. Trends Food Sci Technol. 73: 67–75.

Kleta et al. 2017. Molecular tracing to find source of protracted invasive listeriosis outbreak, Southern Germany, 2012–2016. Emerg Infect Dis. 23 (10): 1680–1683.

www.bfr.bund.de/en > Research > Third party projects of the BfR > Exposure estimation and assessment of biological risks

www.engage-europe.eu