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## **Foodborne disease surveillance using next-generation sequencing**

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The 2017-2018 South African listeriosis epidemic was the world's worst outbreak of *Listeria monocytogenes* food poisoning with more than a 1,000 confirmed cases and an estimated 200 deaths. This outbreak highlighted the vulnerability of the South African population with regards to foodborne diseases and the critical role foodborne disease surveillance plays in public health.

Recently, the World Health Organization encouraged countries to incorporate next-generation sequencing, in particular whole genome sequencing, in their foodborne disease surveillance and response systems. Management of foodborne disease threats requires the swift and correct identification of foodborne pathogens. Whole genome sequencing currently provides the highest possible resolution and strain discrimination for foodborne pathogens with a rapid turnaround time. The data generated by whole genome sequencing enables in silico determination of numerous critical aspects in foodborne disease surveillance such as strain typing, resistance profiling, virulence characterisation and phylogenetic analysis. This negates the often cumbersome and time-consuming traditional typing methods as whole genome sequencing is proving to be an all-encompassing method of foodborne disease surveillance.

Prevention of high-burden foodborne disease outbreaks such as listeriosis and salmonellosis requires surveillance across the entire "farm to fork" value chain. This enables the detection of possible epidemiological hotspots and entry points of foodborne pathogens within the value chain.

Located on the Agricultural Research Council's Onderstepoort Veterinary Institute campus, the Biotechnology Platform (ARC-BTP) was established in 2010 as a major strategic priority of the ARC. The role of the ARC-BTP is to create the high-throughput resources and technologies required for applications in genomics, quantitative genetics, marker assisted breeding and bioinformatics within the agricultural sector. The ARC-BTP is currently involved in various foodborne pathogen and disease surveillance research projects and houses the required technologies and capacity to provide whole genome sequencing and bioinformatic analysis for these research projects.

Foodborne disease surveillance research projects requires the collection of numerous samples from various points within the "farm to fork" value chain which leads to the generation of copious amounts of data. Each sample produces roughly 500 MB of raw sequencing data which is then analysed with published and established workflows. Robust foodborne disease surveillance research projects requires the collection and sequencing of a large cohort of samples which produces a wealth of raw sequencing data. Typical workflows for foodborne disease research therefore require access to high-performance computing environments due to the extensive datasets used and the computational and memory intensive applications used in these research endeavours. The CHPC has proved to be a critical partner in foodborne disease surveillance research projects.

In foodborne disease surveillance the adage "Prevention is better than cure" holds true. The prevention of foodborne disease outbreaks is paramount in public health. The COVID-19 pandemic has demonstrated the critical importance of wide-spread and continuous testing. The same applies to foodborne disease surveillance. The prevention of epidemics such as the South African listeriosis outbreak requires large foodborne disease surveillance and foodborne pathogen testing projects to protect public health and ensure that no lives are lost due to contaminated food.

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