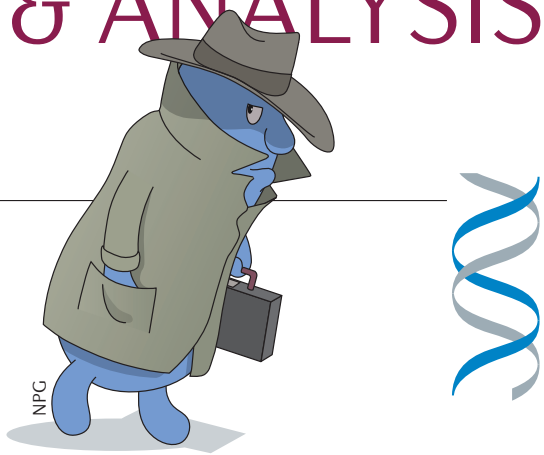

GENOME WATCH

The food-borne identity

Susannah J. Salter

This month's Genome Watch discusses how whole-genome sequencing of bacterial pathogens complements existing techniques for analysing food-borne outbreaks.

Bacterial infections from contaminated food are a major public health issue. Three recent studies[1–3] illustrate how the control of food-borne outbreaks can benefit from the use of whole-genome sequencing (WGS) to differentiate between outbreak isolates, examine potential sources of contamination and enable surveillance in real time. The WHO recognizes food-borne infections as a significant health threat, and global statistics on the burden of disease are needed to drive prevention, intervention and control measures[4]. For example, the US Centers for Disease Control and Prevention operates an active surveillance network that confirmed more than 11,000 food-borne infections in 2013, which were caused by seven bacterial genera, primarily by *Salmonella* spp.[5]. As the cost and time requirements of WGS have reduced considerably in recent years, researchers are starting to apply this powerful tool to analyse bacterial outbreaks that originate from contaminated food.

In 2011, the United States experienced a 34-state outbreak of *Salmonella enterica* subsp. *enterica* serovar Heidelberg, which caused 136 confirmed cases and at least one death[1]. This serovar is usually associated with eggs and poultry and causes gastroenteritis as well as more invasive disease. Turkey mince was implicated as the source of the outbreak, which resulted in a recall of 16 million Kg of meat. In a retrospective study, Hoffmann *et al.*[1] sequenced nine isolates from the outbreak and compared them with 35 strains that were collected between 1982 and 2011, most of which were indistinguishable by traditional techniques, such as PFGE (pulsed-field gel electrophoresis) typing. Based on SNP analysis, the outbreak samples reproducibly grouped together within seemingly clonal groups of strains. Whole-genome analysis showed substantial genetic diversity and the acquisition of virulence determinants associated with phage-driven exchange, and the antibiotic resistance profile of each sample could be correctly predicted from the chromosome and plasmid sequences.

WGS can also aid the control of food-borne outbreaks by including isolates from suspected sources of food contamination. Schmid *et al.* analysed a *Listeria monocytogenes* serovar 1/2b outbreak in Austria and Germany between 2011 and 2013, in which seven invasive cases resulted in two deaths[2]. Routine sampling of cheese and ready-to-eat meat from producers in Germany, Austria and Romania uncovered *L. monocytogenes* strains that matched the type of the patient samples. Blind sequencing of seven patient isolates alongside ten samples from food producers, followed by allelic profiling of about 2,300 genes, placed the most recent outbreak isolates nearest to the meat samples of one producer and the cheese samples of a second producer, and shopping receipts from the patients confirmed that they had purchased the implicated products. As a result of control measures that were implemented by both producers, no further *L. monocytogenes* 1/2b isolates were found.

Another common food-borne pathogen is *Escherichia coli*, with particularly serious disease caused by Shiga toxin-producing *E. coli* (STEC). These infections cause bloody diarrhoea and can lead to haemolytic uraemic syndrome — a condition that is characterized by kidney failure. In Denmark, routine surveillance involves the submission of suspected STEC samples to a central laboratory for confirmation and characterization. Grimstrup Joensen *et al.* evaluated the potential for WGS to improve this process[3]. In addition to routine typing, every isolate that was received was sequenced to determine the presence of virulence genes, toxin subtype and phylogenetic relationships. Good concordance was established between the sequencing results and the routine typing, although poor-quality assemblies prevented some samples from being accurately analysed. Overall, the hands-on time for the genetic analysis, including DNA extraction and sequencing time, was less than one-half of that for the routine methods.

Together, these studies highlight the usefulness of WGS to aid the investigation of food-borne outbreaks, both retrospectively — by examining circulating strains or potential sources of contamination in comparison with patient isolates — and in real time — to provide accurate typing results in less time and with reduced costs. Furthermore, although the initial aim of real-time WGS may be to monitor outbreaks, the richness of generated data will also be of great use for further analysis and can be easily incorporated into larger global data sets for future use.

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Competing interests statement
The author declares no competing interests.