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Editorial

Whole-Genome Sequencing in Food-borne Pathogenic Bacteria

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In literature, more than two hundred food-borne diseases' agents have been reported worldwide which among them, food-borne pathogenic bacteria causes morbidity such as *Campylobacter jejuni*, *Escherichia coli*, *Listeria monocytogenes*, *Salmonella enterica*, *Shigella sonnei*, *S. flexneri*, *Yersinia enterocolitica*, *Vibrio cholera*, etc. (Wells and Bennik, 2003). In the United States, 1 per 6 people are infected by food-borne diseases resulting in annually 128,000 and 3,000 hospitalizations and deaths, respectively (Scallan et al., 2011). Identification of food-borne pathogenic agents' outbreak is necessary for three reasons: i. quick and accurate diagnosis, ii. transmission modes, and iii. elimination of contaminated food from circulation (Deng et al., 2016).

There are various methods for subtyping of food-borne pathogenic bacteria, including serotyping (for *Clostridium botulinum*); phage typing (for *Salmonella* spp. and *Escherichia coli* O157:H7); Polymerase Chain Reaction (PCR)-based methods such as Variable-Number Tandem Repeat (VNTR), Amplified Fragment Length Polymorphism (AFLP), Multiple Locus VNTR Analysis (MLVA); restriction digestion-based techniques like Pulse Field Gel Electrophoresis (PFGE); sequencing-based techniques as Multi-Locus Sequence Typing (MLST), and Whole Genome Sequence (WGS) (Ronholm et al., 2016).

There are three methods for microbial WGS, including Sanger method (first-generation technology), massively parallel sequencing, and single-molecule sequencing (Ronholm et al., 2016). Sequencing platforms can be distinct into two categories including short-read platforms such as Illumina [HiSeq {2500} (Read length: ×50 to ×250 bp), MiSeq (Read length: 1×36 to 2×300 bp), MiniSeq (Read length: 1×75 to ×150 bp), NextSeq (Read length: 1×75 to 2×150 bp), NovaSeq (Read length: 2×50 to ×150 bp)], Ion Torrent [PGM (Read length: Up to 400 bp), S5 (Read length: Up to 400 bp), Proton (Read length: Up to 200 bp)], Pyrosequencing {Roche 454} (Read length: Up to 400 bp), and long-read platforms such as Pacific Biosciences [PacBio RSII (Read length: Up to 60 kb), and Sequel (Read length: Up to 60 kb)] and Oxford Nanopore Technologies [MinION (Read length: Up to 100 kb)] (Besser et al., 2018; Kwong et al., 2015; WHO, 2018). WGS can be used for phylogenetic analysis and comparison of bacteria associated with outbreaks [The standard cut off for average nucleotide identity is generally 95–96%] (Land et al., 2015; WHO, 2018); molecular typing (previously have been used of PFGE, etc. shown limited discriminatory ability for some highly clonal pathogen populations); source appropriation analysis; surveillance, prediction, and accurate identification of antibiotic resistance genes and mechanisms in food-borne pathogenic bacteria (Land et al., 2015; WHO, 2018); and virulence genes identification (WHO, 2018). The first reports of WGS in bacteria were *Haemophilus influenzae* (with the genomic size of 1,830,140 base pairs) and *Mycoplasma genitalium* by Fleischmann et al. (1995) and Fraser et al. (1995), respectively by using the Sanger technique. The first genome sequence of a food-borne bacterium (*C. jejuni*) was reported in 2000 (Wells and Bennik, 2003). Currently, a lot of bacterial whole genome sequencings (more than 30,000 genomic sequences) are available in National Center for Biotechnology Information (NCBI) (Land et al., 2015).

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WGS data can be used for prediction of antimicrobial resistance and virulence. In this regard, there are various databases such as Antibiotic Resistance Gene-Annotation (ARG-ANNOT), Antibiotic Resistance Genes Database (ARDB), Comprehensive Antibiotic Resistance Database (CARD), National Database of Antibiotic Resistant Organisms (NDARO), Repository of Antibiotic resistance Cassettes (RAC), and ResFinder (Gupta et al., 2014; WHO, 2018). The others such as Rapid Annotation using Subsystem Technology (RAST), NCBI prokaryotic genomes automatic annotation pipeline, and Prokka are used for bacterial annotation (Kwong et al., 2015).

Recently, WGS is routinely used by several national public health centers in Denmark (Danish Technical University), United Kingdom, and the United States (University of Georgia) (Carleton and Gerner-Smidt, 2016; Franz et al., 2016). There are a number of databases that deposit draft genome used for comparative DNA genomic analysis (Kwong et al., 2015). The use of WGS is limited in laboratories in many developing countries due to cost, lack of professional personnel, and the difficulty in interpreting of the WGS results (Aliyu, 2014).

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