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Autore	Sandra Torriani
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Sommario/riassunto	Advances in next-generation sequencing technologies (NGS) are revolutionizing the field of food microbiology. Microbial whole genome sequencing (WGS) can provide identification, characterization, and subtyping of pathogens for epidemiological investigations at a level of precision previously not possible. This allows for connections and source attribution to be inferred between related isolates that may be overlooked by traditional techniques. The archiving and global sharing of genome sequences allow for retrospective analysis of virulence genes, antimicrobial resistance markers, mobile genetic elements and other novel genes. The advent of high-throughput 16S rRNA amplicon sequencing, in combination with the advantages offered by massively parallel second-generation sequencing for metagenomics, enable intensive studies on the microbiomes of food products and the impact of foods on the human microbiome. These studies may one day lead to the development of reliable culture-independent methods for food monitoring and surveillance. Similarly, RNA-seq has provided insights into the transcriptomes and hence the behaviour of bacterial pathogens in food, food processing environments, and in interaction with the host at a resolution previously not achieved through the use of microarrays and/or RT-PCR. The vast un-tapped potential applications of NGS along with its rapidly declining costs, give this technology the ability to contribute significantly to consumer protection, global trade facilitation, and increased food safety and security. Despite the rapid

advances, challenges remain. How will NGS data be incorporated into our existing global food safety infrastructure? How will massive NGS data be stored and shared globally? What bioinformatics solutions will be used to analyse and optimise these large data sets? This Research Topic discusses recent advances in the field of food microbiology made possible through the use of NGS.