
**Microbiology of the food chain —
Whole genome sequencing for typing
and genomic characterization of
bacteria — General requirements and
guidance**

*Microbiologie de la chaîne alimentaire — Séquençage de génome
entier pour le typage et la caractérisation génomique des bactéries —
Exigences générales et recommandations*





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Published in Switzerland

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Foreword

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This document was prepared by Technical Committee ISO/TC 34, *Food products*, Subcommittee SC 9, *Microbiology*, in collaboration with the European Committee for Standardization (CEN) Technical Committee CEN/TC 463, *Microbiology of the food chain*, in accordance with the Agreement on technical cooperation between ISO and CEN (Vienna Agreement).

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Introduction

Next generation sequencing (NGS) provides rapid, economical and high-throughput access to microbial whole genome sequences and is being applied to an expanding number of problems in food microbiology. Whole genome sequences are representations of the biological potential of the sequenced organism at single base resolution. Whole genome sequencing (WGS) offers significant advantages over existing technologies (e.g. serotyping, pulsed field gel electrophoresis, antibiotic resistance phenotype) for many applications. WGS-based analyses are used by public health laboratories to detect outbreaks, and to detect mutations, genes and other genetic features to characterize virulence and survival potential. Within the food industry, there is interest in using whole genome sequences to characterize bacterial isolates from ingredients and environmental surfaces, to better understand their origin and ecology, and to update procedures to reduce risk. Some companies have developed, or are developing, the capacity to collect and analyse whole genome sequence data. Others are turning to third-party laboratories to perform these services, as they have done for other microbiological analyses.

This document provides guidance for both the laboratory and bioinformatic components of whole genome sequences and associated metadata for bacterial foodborne microorganisms sampled along the food chain (e.g. ingredients, food, feed, production environment). Although microbiology of the food chain includes viruses and fungi, this document is only intended for bacteria. This document is intended to be applicable to all currently available next generation DNA sequencing technologies. It may be applied to analysis of whole genome sequence data with proprietary, open-source or custom software. It is not intended to specify sequencing chemistries, analytical methods or software. This document defines laboratory, data and metadata stewardship practices to ensure that analyses are clearly reported, transparent and open to inquiry. This document is for use by laboratories to develop their management systems for quality and technical operations. Laboratory customers and regulatory authorities can also use it in confirming or recognizing the competence of laboratories. This document can also be applied in other domains (e.g. environment, human health, animal health).