Chapter 9
Molecular Diagnostics and Genomic Tools for Food Contaminant Detection

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ABSTRACT

Molecular diagnostics and genomic tools have recently been recognised as game-changing resources for contaminant detection in environmental, agricultural, clinical, and industrial settings. These tools use nucleic acid-based detection methods like PCR, qPCR, digital PCR, and next-generation sequencing (NGS) to detect contaminants at minute concentrations, frequently before traditional phenotypic methods can pick them up. Genomic tools such as metagenomics, transcriptomics, and CRISPR-based assays further enable the identification of unculturable organisms and the surveillance of resistance genes, virulence factors, and microbial community dynamics. In industrial contexts, especially in food production, these diagnostics contribute

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to quality control, contamination prevention, and supply chain integrity. As these technologies become more affordable and user-friendly, their adoption is expected to grow, offering robust solutions for real-time, field-deployable contaminant detection.

INTRODUCTION

The dependability and recognition of culture-based microbiological methods as "gold standards" for microbial enumeration and identification have been upheld for more than a century in the analysis of foods and other materials (Bonnet et al., 2020). The imperative for rapid detection tools for the food industry and public health agencies is highlighted by the protracted duration (hours to days) required to attain conclusive results, potentially resulting in substantial economic losses for food producers due to increased holding costs. An optimal method would swiftly ascertain the level of contamination and the presence of pathogens within a few hours (Ogidi et al., 2025a).

Nonetheless, the rapid detection of hazardous bacteria in food samples remains challenging due to the complicated physical and chemical nature of food matrices, as pathogenic germs typically present in contaminated foods exist at low concentrations and sometimes possess compromised cells that are difficult to cultivate. A new epoch in food microbiology has commenced, propelled by molecular techniques that depend on sequencing microbial genomes or genes (Stasiewicz et al., 2015; Walsh et al., 2017). These molecular approaches identify microbial taxa and functional features such as antibiotic resistance or pathogenicity by detecting specific gene sequences. For the detection, characterisation, and molecular typing of foodborne microbial isolates, polymerase chain reaction (PCR) technology has been the backbone of most nucleic acid amplification tests (NAATs) and sequencing approaches. In the last ten years, next-generation sequencing (NGS) and whole-genome sequencing (WGS) have revolutionised the methods used to identify microbes in food, water, and environmental samples. Molecular epidemiology research has also relied on sequencing-based typing methods like cgMLST (core-genome) and wgMLST (whole-genome multi-locus sequence typing) (Allard et al., 2018; Stevens et al., 2022).

WGS-based methodologies are progressively replacing different electrophoretic mobility techniques used for DNA fingerprinting and typing in public health contexts. These techniques include ribotyping, restriction fragment length polymorphism (RFLP), and pulsed-field gel electrophoresis (PFGE). The predominant method for identifying bacteria in clinical and public health laboratories is culture-independent diagnostic tests (CIDTs), encompassing several nucleic acid amplification tests (NAATs). These assays can identify both foodborne and gastrointestinal pathogens (Stevens et al., 2022). Moreover, other domains of functional genomics, such as