Molecular genetic techniques in food quality control, authentication, and biotechnology

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Abstract. The growing demand for safe, high-quality, and traceable food, feed, and biotechnological products has led to the widespread adoption of molecular genetic techniques in both analytical and regulatory frameworks. The present review explores the application of advanced molecular tools such as methods based on polymerase chain reaction (PCR), DNA barcoding, and next-generation sequencing (NGS) in ensuring product quality, verifying authentication, detecting contamination, and supporting biotechnological innovation. These methods offer high sensitivity, specificity, and speed, making them powerful alternatives to conventional techniques. They are particularly valuable for detecting food adulteration, identifying genetically modified organisms (GMOs), authenticating species origin in complex matrices, and monitoring microbial contamination in food and medicinal products. In addition, the global threat of foodborne pathogens underscores the importance of timely and cost-effective microbial detection. Molecular techniques, including PCR, isothermal amplification methods, gene probes, and DNA microarrays have shown high specificity and efficiency in pathogen identification and surveillance. Overall, molecular genetic approaches represent a robust and indispensable tool for modern food analysis, offering unparalleled precision, reliability, and adaptability across diverse applications in food safety, authentication verification, and biotechnology.

1 Introduction

Ensuring food quality, safety, and authenticity is one of the most pressing global challenges of the 21st century, especially as food supply chains grow increasingly complex and consumer demand for transparency rises [1]. Growing awareness of food quality and its implications for health and sustainability has intensified public demand for transparency and accountability among food producers and companies [2]. At the same time, producers must be able to verify and certify the composition and origin of their products to protect consumers from fraud and adulteration [3]. In this context, traceability and authentication systems have emerged as indispensable tools not only for enhancing consumer confidence in food safety and transparency but also for protecting the economic and cultural value of food products [1, 3].

In recent years, a broad spectrum of analytical techniques for food quality control and authenticity assessment has been developed and validated [3, 4]. These methods provide valuable insights into various aspects of food composition and characteristics, including geographical origin, presence of adulterants, species or variety identification, and detection of foodborne pathogens [4]. Traditional analytical approaches such as chromatography, spectroscopy, and immunoassays remain fundamental to food analysis, however, their performance is often constrained by limitations in sensitivity, specificity, and applicability, particularly when analysing highly processed or complex food matrices [2, 4]. To overcome these limitations, molecular genetic techniques have emerged as robust and versatile tools for verifying biological identity at the DNA or RNA level. These approaches enable highly accurate detection of adulteration, contamination, and fraudulent labelling across diverse food categories [5]. DNA-based methods offer notable advantages, including superior accuracy, sensitivity, and reproducibility and are largely unaffected by environmental factors, harvest time, storage conditions, or processing steps [3, 6].

Over the past two decades, rapid advances in molecular technologies, particularly polymerase chain reaction (PCR) and its derivatives, DNA barcoding and metabarcoding, DNA microarrays, and next-generation sequencing (NGS), have revolutionized the direct analysis of nucleic acids in food matrices [5]. These approaches enable the amplification, detection, and sequencing of genetic markers at even trace concentrations and have been successfully applied across diverse food and feed products [4]. PCR-based assays remain the benchmark for meat authentication and fraud detection due to their high specificity and sensitivity [6]. Beyond conventional PCR, specialized formats such as nested, multiplex (mPCR), and real-time PCR (qPCR) have significantly enhanced detection limits and quantification accuracy, while the emergence of digital PCR (dPCR) offers absolute quantification without the need for standard curves [7]. In addition to

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these thermal cycling methods, isothermal amplification techniques, notably loop-mediated isothermal amplification (LAMP) and nucleic acid sequence-based amplification (NASBA), have emerged as robust alternatives for rapid, cost-effective, and on-site testing [4, 6, 8]. Moreover, DNA barcoding and metabarcoding enable precise species identification and compositional analysis in complex or mixed samples, making them especially valuable for processed foods and multi-ingredient products [3, 7].

For the parallel detection of multiple genetic targets, gene probes and DNA microarrays provide high-density screening capabilities, which are widely employed by global food traders, the processing industry, and regulatory authorities for quality control and compliance monitoring [9, 10]. Recently, these DNA-based methods have gained broad application in identifying adulteration in plant-based foods and validating food authentication [8]. Among these, PCR remains the most extensively used method for the detection of genetically modified organisms (GMOs) due to its exceptional specificity and efficiency. Preliminary screening targeting taxon-specific and common transgenic elements enables rapid differentiation between GMO-containing and GMO-free samples [11].

The transition toward NGS, including sequencing by synthesis (SBS) and hybridization, along with third-generation (long-read) sequencing, offers unprecedented opportunities for food safety [3, 12]. NGS approaches, such as amplicon sequencing and shotgun metagenomics, allow for comprehensive characterization of microbial and eukaryotic communities, supporting the detection of unexpected pathogens and microbiome shifts indicative of contamination or spoilage [12, 13]. Recent studies have highlighted the hidden diversity of food-associated microbiomes, with microbial signatures emerging as potential markers of product provenance and quality [14]. In parallel, genomic and transcriptomic tools are increasingly applied to optimize microbial strains for fermentation, enzyme production, and functional food development, underscoring the pivotal role of molecular genetics and biotechnology in driving innovation within modern food systems [13, 14].

Despite their significant advantages, molecular methods in food analysis continue to face several challenges. DNA in processed foods is often degraded or present at trace concentrations, food matrix components can inhibit amplification reactions, and the lack of standardized laboratory protocols across regions and institutions hinders data comparability [6]. Furthermore, the interpretation of large-scale genomic datasets requires robust bioinformatics pipelines and rigorous validation. For broader regulatory adoption, the field must also address issues related to method harmonization, validation, and accreditation [13].

This review provides a comprehensive and up-to-date overview of the practical applications of major molecular genetic techniques in food quality control, authentication, and biotechnology. Building upon the current technological landscape of PCR, isothermal amplification, DNA barcoding, microarrays, and NGS, this work focuses on their strategic implementation in pathogen detection, adulteration analysis, species identification, and quality monitoring. Finally, the review critically compares the strengths and limitations of these approaches within regulatory and industrial frameworks, and highlights emerging trends and future directions in the use of molecular genetic tools for advancing food analysis and safety.

2 Application in foodborne pathogens detection

Molecular genetic techniques have fundamentally transformed the detection and characterization of foodborne pathogens by enabling rapid, highly sensitive, and exceptionally specific identification of microbial contaminants within complex food matrices. In contrast to conventional culture-based approaches, which are often labour-intensive, time-consuming, and limited by the viability and growth characteristics of target organisms, molecular methods directly interrogate pathogen-specific nucleic acid sequences, thereby substantially reducing detection time and minimizing analytical bias [3, 4].

Approaches such as PCR, qPCR, various isothermal amplification techniques, dPCR, DNA barcoding, DNA microarrays, and NGS platforms offer enhanced analytical performance, including lower detection limits, improved discrimination among closely related strains, and the capacity to identify virulence factors and antimicrobial resistance determinants [3, 8, 15]. Collectively, these advances have elevated molecular diagnostics to a central role in modern food safety surveillance, outbreak investigation, and risk assessment [4, 8]. The number of studies focused on the molecular detection of foodborne pathogens continues to grow rapidly, reflecting the urgent need for faster and more accurate diagnostic tools. Representative examples of recent applications of molecular genetic techniques in foodborne pathogens detection are summarised in Table 1.

A wide range of molecular genetic approaches has been applied to enhance the detection of foodborne pathogens across diverse food matrices. Li et al. employed multiplex PCR to simultaneously detect the *tlh*, *tdh*, and *trh* genes of *Vibrio parahaemolyticus*, revealing a notable prevalence of this pathogen and underscoring its public health significance [15]. Lee et al. developed a multiplex PCR assay for the simultaneous detection of *Escherichia coli* O157:H7, *Bacillus cereus*, *Vibrio parahaemolyticus*, *Salmonella* spp., *Listeria monocytogenes*, and *Staphylococcus aureus* in Korean ready-to-eat foods [16].

Nested PCR has also proven valuable, as demonstrated by Nazar et al. who detected enterotoxigenic *Staphylococcus aureus* using a two-step amplification targeting the nuc gene [17]. Similarly, Biyu et al. developed an ultrasensitive single-tube nested PCR assay for the rapid detection of *Campylobacter jejuni* in ground chicken [18].

Table 1. Applications of molecular genetic techniques in foodborne pathogens detection.

Molecular genetic techniques	Detected pathogen	Detected food	Reference
Multiplex PCR	*Vibrio parahaemolyticus*	freshwater fish, shellfish	[15]
Multiplex PCR	*Escherichia coli* O157: H7, *Bacillus cereus, Vibrio parahaemolyticus, Salmonella* spp., *Listeria monocytogenes, Staphylococcus aureus*	ready-to-eat food	[16]
Nested PCR	*Staphylococcus aureus*	food samples	[17]
Nested PCR	*Campylobacter jejuni*	ground chicken	[18]
qPCR	*Staphylococcus aureus, Escherichia coli, Clostridium perfringens, Campylobacter* spp., *Staphylococcus aureus*	raw and ready-to-eat green leafy vegetables	[19]
qPCR and digital PCR	*Salmonella typhimurium*	milk	[20]
digital PCR	*Vibrio parahaemolyticus*	seafood	[21]
DNA barcoding	*Vibrionales, Pseudomonadales, Bacillales*	food samples	[22]
DNA barcoding and NGS	*Francisella tularensis*	game meat	[23]
DNA microarrays	*Escherichia coli* O157:H7, *Salmonella enterica*, *Vibrio cholerae*, *Campylobacter jejuni*	food samples	[9]
LAMP assay	Human Adenoviruses	strawberries, sour cherries, lettuce, cherry tomatoes, green onions	[24]
LAMP assay	*Vibrio parahaemolyticus*	flatfish	[25]
qPCR and NGS	Norovirus, Human Papillomavirus	lettuce, strawberries, parsley, irrigation water	[26]
NGS	*Bacillus cereus, Yersinia enterocolitica, Staphylococcus aureus, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificus*	agricultural wastewater	[27]
NGS	*Escherichia coli, Listeria monocytogenes, Salmonella enterica* serovar Typhimurium	fermented food samples	[28]

Quantitative real-time PCR continues to play a major role in pathogen surveillance, with Azimirad et al. reporting its high sensitivity for detecting *S. aureus*, *E. coli*, *C. perfringens*, and *Campylobacter* spp. in both raw and ready-to-eat green leafy vegetables [19]. Further methodological advancements were highlighted by Wang et al., who showed that dPCR provides greater sensitivity and reduced pre-culture requirements compared with qPCR, particularly for detecting *Salmonella typhimurium* in milk [20]. The enhanced sensitivity of dPCR was also confirmed by Lei et al., who demonstrated its ability to detect low levels of *V. parahaemolyticus* in clams [21].

Beyond PCR-based approaches, DNA barcoding has emerged as a promising tool for microbial identification. Zhong et al. showed that 16S rRNA barcoding offers sufficient resolution to distinguish key foodborne pathogens within *Gammaproteobacteria*, including *Enterobacteriales*, *Vibrionales*, and *Pseudomonadales*, while enabling genus-level identification of *Bacillales* [22]. Likewise, Grützke et al. successfully applied DNA barcoding combined NGS to detect *Francisella tularensis* in game meat [23]. Microarray technologies have also advanced pathogen detection. Liu et al. enhanced microarray sensitivity through magnetic nanoparticles for the rapid identification of *E. coli* O157:H7, *Salmonella enterica*, *Vibrio cholerae*, and *Campylobacter jejuni* [9].

Additional molecular strategies highlight the versatility of isothermal amplification. For instance, Birmpa et al. developed a simple, single-tube LAMP assay for detecting adenovirus types 40/41 in ready-to-eat produce [24]. Similarly, Lee et al. applied a colorimetric LAMP assay based on an HRP-mimicking molecular beacon for the rapid detection of *Vibrio parahaemolyticus* [25].

Furthermore, Itarte et al. apply two different NGS approaches to reveal a high diversity of viral pathogens, especially Norovirus (NoV) and Human Papillomavirus (HPV) in fresh produce and irrigation water [26]. More recently, Park et al. designed a targeted NGS panel for virulence genes from six major foodborne pathogens and applied it to fermented foods [27], while Park et al. developed and evaluated a NGS panel for the multiple detection and identification of pathogens in fermented foods [28]. Overall, these studies collectively highlight

the rapid evolution and diverse applicability of molecular genetic techniques in improving the detection and surveillance of foodborne pathogens.

3 Application in food authentication

Molecular genetic techniques have become essential tools in food authentication, enabling precise species identification and detection of adulteration across a wide range of products. Methods such as PCR based assays and DNA barcoding allow verification of ingredient composition even in highly processed foods, where traditional morphological analyses are ineffective, thereby enhancing supply chain transparency and supporting regulatory efforts to safeguard product integrity and consumer health [8]. Beyond these established molecular marker approaches, newer techniques including isothermal amplification, dPCR, and NGS based methods show strong potential for improving traceability in both fresh and processed food products [3]. Driven by the increasing global concerns regarding food fraud and mislabelling, the scientific literature on genomic-based authentication has seen exponential growth. To illustrate the diversity of these approaches, Table 2 provides a representative overview of recent applications of these molecular genetic tools in food authentication.

Table 2. Applications of molecular genetic techniques in food authentication.

Molecular genetic techniques	Target gene / target species	Detected food	Reference
mPCR	mitochondrial *cytb* gene, turkey, ostrich, chicken, and duck DNA	poultry meat products	[29]
Heptaplex real-time PCR	bovine, porcine, chicken, turkey, equine, ovine, and caprine DNA	food products	[30]
ddPCR	SSR markers	flours and breads	[31]
qPCR and dPCR	*arah*1, *arah*2, *glym*30, *glym*5 and *lectin* gene	soybean flour, roasted peanuts	[32]
qPCR	*ITS, rbcL, lipids phosphate phosphatase gamma* gene*, terpene synthase* gene, *vicilin* gene, *vicilin-like seed storage protein* gene, *albumin synthase* gene	cocoa beans, cocoa powder and commercial chocolates	[33]
qPCR and dPCR	*β-tubulin, γ-gliadin*	various cereals	[34]
DNA barcoding	*matK, rbcL, psbA-trnH, ITS1, ITS2*	commercial crude drugs derived from species of the genus *Terminalia*	[35]
DNA barcoding	*psaJ-rpl33, trnC-rpoB, rps16-trnQ, rpl22-rps19, trnK-matK, ndhC-trnV*	rice (*Oryza* species)	[36]
DNA barcoding-HRM	*ITS2*	coffee arabica, arabica, coffea canephora, robusta	[37]
LAMP	*ITS2*-26S ribosomal DNA	turmeric powder in commercial food	[38]
LAMP	*oleosin* gene	commercial olive oil products	[39]
DNA microarray	*16S* rRNA gene, *cytb*	fish species	[40]
NGS	*16S* rRNA gene	candies	[41]
NGS	*ITS*	herbal tea samples	[42]

Li et al. developed a multiplex PCR assay using species-specific primers based on the mitochondrial cytochrome b (*cytb*) gene to distinguish turkey, ostrich, chicken, and duck, demonstrating its successful application in the authentication of poultry products [29]. Köppel et al. designed a heptaplex real-time PCR assay capable of identifying and quantifying DNA from seven meat species, including bovine, porcine, chicken, turkey, equine, ovine, and caprine [30]. In cereal and plant-based products, Ramos-Cabrer et al. applied SSR markers and ddPCR for tracing the local wheat cultivar ‘Caaveiro’ [31]. The detection of allergens, one of the major concerns in today’s food industry, has also been addressed using ddPCR by Pierboni et al. [32]. Oliveira et al. identified seven genetic regions suitable for real-time PCR in cocoa and chocolate, with assays targeting the nuclear *vicilin* gene and *chloroplast lipids* gene meeting all performance criteria [33]. For processed foods, ddPCR has also proven advantageous over qPCR in sensitivity and the lack of need for calibration or internal controls, as demonstrated by Schulze et al. in cereal species discrimination [34].

In medicinal plants, Intharuksa et al. found that *ITS* was the most accurate single marker for *Terminalia*

species, though full species discrimination required two-locus combinations [35]. Zhang et al. demonstrated that a full chloroplast genome "super barcode" efficiently differentiated 21 *Oryza* species [36]. HRM analysis coupled with *ITS2* markers has been applied for coffee authentication, detecting Arabica/Robusta admixtures at low levels [37]. Sheu et al. developed a LAMP-based method to identify *Curcuma longa* DNA for turmeric authentication, designing primers from the *ITS2*–26S rRNA gene region to specifically verify turmeric material [38]. In a subsequent study, a similar LAMP assay was created to detect *Olea europaea* DNA for authenticating olive oil, using the *oleosin* gene as the target for primer design [39]. DNA microarrays offer rapid and accurate authentication of fish species, distinguishing closely related taxa within hours [40].

Although NGS technologies are widely used in diagnostic and research fields, their application in food traceability remains relatively limited, likely due to high costs, substantial computational requirements, and the need for high-quality DNA, which is often difficult to recover from heavily processed foods [3]. Nevertheless, several studies have demonstrated the potential of NGS-based approaches for food authentication and traceability. For instance, Muñoz-Colmenero et al. evaluated the Ion Torrent Personal Genome Machine for tracing highly processed foods using candies as a model [41]. Similarly, Speranskaya et al. compared Illumina and Ion Torrent platforms for analysing herbal teas and reported consistent qualitative and quantitative results. The study revealed the substitution of fireweed (*Epilobium angustifolium*) with *Lythrum* species and detected undeclared ingredients such as *Convolvulus* and *Ambrosia*, both known for toxic or allergenic properties [42]. Collectively, these studies illustrate the versatility and robustness of molecular genetic approaches, including NGS technologies, for authenticating both raw and processed foods, enhancing accuracy, transparency, and traceability, and ensuring product integrity and consumer safety even in highly processed products.

4 Application in biotechnology

Molecular genetic techniques are essential in biotechnology, providing accurate detection and characterization of GMOs to support food safety, regulatory compliance, and traceability [7, 43]. Methods such as PCR, high-throughput sequencing, and metagenomics are also extensively used in the study of fermented foods, enabling detailed insights into microbial communities, their functional genes, and the metabolites they produce, which can guide the selection of starter cultures and enhance product quality [44]. Given the rapid diversification of these methodologies, Table 3 summarizes selected recent studies highlighting the diverse applications of molecular genetic techniques in biotechnology, focusing on those with the highest practical and regulatory significance.

Table 3. Applications of molecular genetic techniques in biotechnology.

Molecular genetic techniques	Target gene / target species	Detected food	Reference
mPCR	*epsps* gene, *pat* gene, *cry1Ac* genes, event-specific DP 356043 DNA sequence	soybean and meat products	[43]
PCR	*CaMV 35S* promoter, *epsps* gene	feed products	[11]
qPCR	*NOS* terminator	unprocessed and processed food	[45]
ddPCR	GT73, MON88302, OXY235, and HCN92 GM canola events; A2704, DP305423, DAS81419, MON89788 GM soybean events	GM canola and soybean	[46]
ddPCR	MON87701, MON87769, MON89788, and CV-127-9 GM soybean events	GM soybean	[47]
LAMP	*cry2Ab* gene, *cry3A* gene	GM maize, cotton, and rice	[48]
LAMP	*CaMV 35S* promoter, *FMV* promoter, *aadA* gene, *nptII* gene, *uidA* gene	GM cotton events	[49]
DNA microaarray	*ivr1*gene, *epsps* gene, *bar* gene, *pat* gene, *cry1A105* gene, *cry1Ab* gene, *cry1Ac* gene, *CaMV35S*-P, *CaMV35S*-T, *NOS-3'*	GM maize	[10]
NGS	Promotors (p*35S*, p*FMV*, p*Ubi*, p*NOS*, p*mas*, P*s7s7*, *pRice act*in1, p*Rice actin2*, p*SSuAra*, p*TA29*, p*MTL*); Terminators (t*OCS*, t*E9*, t*NOS*, tg7, t*pinII*, t*35S*); Genes (*gus, gox, cryIAb, cry1B, cry1Aa, cry1Ab/c, cry1Ac, cry1A105, cry2Ab2, cry3A055, cry34Ab1, cry35Ab1, EPSPS, 2mEPSPS, bar, pat, Prsv-cp*)	GM maize, soybean, rice, rapeseed, cotton	[50]
NGS	antimicrobial resistance genes, carbohydrate-degrading genes, health-associated genes	Fermented food	[51]
NGS	bacteriocins encoding genes, *pseudoalterin* gene, antimicrobial resistance genes	artisanal cheese	[44]

Stefanova et al. (2015) developed a multiplex PCR assay for the simultaneous detection of multiple GM soybean events, targeting three gene-specific sequences (*epsps*, *pat*, and *cry1Ac*) and one event-specific sequence (DP-356043). This assay demonstrated high sensitivity, with a detection limit of 0.05% for each target [43]. Building on this approach, Stefanova et al. also conducted PCR screening of feed products to identify GM soybeans, focusing on the *CaMV 35S* promoter and the *epsps* gene [11]. In a related application, Nadeem et al. demonstrated that GMO-positive cabbage seeds could be detected in both processed and unprocessed foods at concentrations as low as 0.001% using the *NOS* terminator sequence, providing a reliable molecular tool for halal food authentication and preventing accidental consumption of GM ingredients considered haram [45].

Demeke et al. explored strategies to improve the detection and quantification of GM canola and soybean using multiplex ddPCR [46]. Similarly, Verginelli et al. assessed ddPCR assays for several GM soybean events (MON87701, MON87769, MON89788, and CV-127-9) with the *lectin* gene as a reference, demonstrating that ddPCR provides more accurate quantification, higher tolerance to PCR inhibitors, and better suitability for multiplexing compared to standard qPCR [47].

Li et al. developed a rapid and visual LAMP method for detecting the *cry2Ab* and *cry3A* genes in GMOs, providing a faster and simpler alternative for identifying these genes in GM crops and making it particularly suitable for large-scale, on-site field testing [48]. Randhawa et al. further optimized LAMP assays targeting commonly used promoters, including *CaMV 35S* promoter and *FMV* promoter, as well as marker genes such as *aadA*, *nptII*, and *uidA*, establishing a sensitive and reliable method for screening GMOs [49]. Collectively, these studies highlight the effectiveness of LAMP as a rapid, accurate, and field-deployable tool for GMO detection.

Yun et al. present a newly developed auto-microfluidic thin-film chip (AMTC) method for multiplex screening of GM maize, achieving a detection sensitivity as low as 0.1% quality percentage [10].

Debode et al. demonstrated that integrating enrichment technologies with NGS allows for the simultaneous detection of a broad range of genetic elements and the full or partial reconstruction of inserted sequences, even at trace levels [50]. This study highlights the increasing sensitivity and precision of molecular approaches for GMO detection and authentication across a wide range of food and plant products.

Fermentation continues to play a key role in extending the shelf-life of foods, minimizing reliance on chemical preservatives, and enabling preservation in regions where refrigeration is limited. Throughout fermentation, microorganisms generate metabolites, including acids, alcohols, diacetyl, and bacteriocins, that inhibit spoilage microbes and pathogens. NGS has been used to investigate the microbiomes of fermented foods, particularly to identify bacteriocin-related genes [44, 51]. Leech et al. expanded knowledge of fermented-food microbiomes by applying shotgun metagenomic sequencing to 58 traditionally produced fermented foods from various countries. This approach offered a comprehensive view of microbial diversity, community structure, and functional capabilities, including genes linked to antimicrobial resistance, carbohydrate metabolism, and potential health benefits [51]. Walsh et al. analysed the microbiomes and volatile profiles of 77 samples from 55 artisanal cheeses, reconstructing 328 genomes and identifying 47 potential new species involved in flavour, aroma, or pigmentation. They found that strain-level differences influenced volatile production and that bacteriocin and other antimicrobial genes were widespread, indicating roles in controlling undesirable microbes during fermentation [44]. Leveraging these molecular approaches to identify bacteriocin-producing genes can support the selection of starter cultures capable of inhibiting undesirable microbes. Together, these approaches enhance both the monitoring of GMOs and the optimization of fermentation processes in food biotechnology [44, 51].

6 Conclusions

The present review synthesizes the strategic applications of molecular genetic techniques in foodborne pathogen detection, food authentication, and biotechnology. By focusing on the integration of these tools into modern analytical workflows, the review demonstrates how advances in DNA-based methods are redefining food quality control, authentication verification, and safety monitoring. Their exceptional sensitivity and rapid analytical performance, surpassing traditional culture-based approaches, enable early and reliable identification of pathogens throughout the food chain. Although the need for specialized expertise and instrumentation still limits widespread adoption in some sectors, ongoing technological progress is making these methods increasingly accessible and suitable for routine use in both industrial and regulatory settings.

Established tools, such as PCR-based assays, isothermal amplification, DNA barcoding, microarrays, and NGS provide robust, high-throughput platforms for precise detection and biotechnological innovation. Complementary approaches, including dPCR, metabarcoding, and LAMP, further enhance analytical resolution and expand applicability across diverse food matrices. Looking forward, emerging diagnostic technologies, such as CRISPR-based detection systems (e.g., SHERLOCK and DETECTR), show great potential for highly sensitive, rapid field-deployable pathogen detection, further enhancing the capabilities of molecular approaches in food safety monitoring and authentication.

Together, these molecular strategies strengthen traceability, transparency, and consumer protection while supporting equitable practices within global food systems. With continued improvements in speed, cost-efficiency, and automation, molecular diagnostics will play an increasingly pivotal role in safeguarding public health, driving progress in food biotechnology, and benefiting from standardization and integration with

bioinformatics for future regulatory and industrial applications.

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