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Artificial intelligence and machine learning applications in food microbiology: A systematic review

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Abstract: The integration of artificial intelligence (AI) and machine learning (ML) into food microbiology offers transformative potential for enhancing food safety through rapid pathogen detection. Traditional microbiological methods, while reliable, are time-consuming and ill-suited for analyzing complex, high-dimensional datasets. This systematic review synthesizes contemporary evidence on AI/ML applications in food microbiology, specifically evaluating their performance in microbial detection, contamination prediction, and spoilage assessment, while identifying barriers to real-world implementation. Following PRISMA 2020 guidelines, we systematically searched PubMed, Scopus, Web of Science, and IEEE Xplore for studies published between January 2017 and December 2023. Data were extracted on model types, performance metrics (accuracy, F1-score, AUC-ROC), and validation approaches. From 1,153 records screened, 22 studies met the inclusion criteria. Supervised learning dominated (91% of studies), with Random Forest (n=9), Convolutional Neural Networks (CNNs; n=6), and Support Vector Machines (n=5) being most prevalent. Applications focused on: (1) rapid pathogen detection from hyperspectral/multispectral imaging (accuracy: 89-96%; AUC: 0.88-0.95); (2) prediction of microbial growth kinetics under varying storage conditions (RMSE: 0.15-0.45 log CFU/g); and (3) spoilage classification from volatile organic compound patterns (F1-score: 0.85-0.93). AI/ML models demonstrate strong analytical performance in controlled settings but face significant translation challenges, including data scarcity, model interpretability, and integration with existing workflows. Future research should prioritize standardized benchmark datasets, explainable AI approaches, and validation in operational food industry environments to bridge the lab-to-field gap.

Keywords: Artificial intelligence; machine learning; food safety; predictive microbiology; systematic review[1]

1. Introduction

Food microbiology represents a critical nexus between public health, food security, and economic stability, tasked with identifying and controlling pathogenic, spoilage, and beneficial microorganisms throughout complex global supply chains (Havelaar et al., 2015). Despite advances in molecular diagnostics and sequencing technologies, conventional microbiological methods—including culture-based enumeration, PCR, and immunological assays—remain constrained by lengthy processing times (24–72 hours), specialized labor requirements, and limited scalability (Yang et al., 2024). These limitations become particularly acute in contemporary food systems characterized by accelerated production cycles, globalization of sourcing, and consumer demand for minimally processed, fresh products with extended shelf-life expectations.

The digital transformation of food production has generated unprecedented volumes of heterogeneous data streams, including genomic sequences, hyperspectral imaging, real-time sensor measurements, and environmental monitoring data. Traditional analytical approaches struggle to extract actionable insights from these high-dimensional datasets, creating an analytical bottleneck. Artificial intelligence, particularly machine learning and deep learning, offers sophisticated computational frameworks capable of identifying complex patterns, predicting microbial behavior, and automating detection tasks that exceed human analytical capacity.

Traditional detection requires sequential steps of enrichment, isolation, and confirmation. AI-driven approaches analyze direct or minimally processed samples. Convolutional Neural Networks (CNNs) applied

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to hyperspectral imaging (400–1000 nm) can differentiate E. coli O157:H7 from non-pathogenic strains in ground beef with >92% accuracy within 30 minutes, bypassing culture entirely. Similarly, Recurrent Neural Networks (RNNs) analyzing metagenomic sequencing data achieve species-level identification of mixed microbial communities in fermented foods, with F1-scores of 0.87–0.94.

Recent applications demonstrate AI's potential across multiple domains: deep learning models achieve human-expert-level accuracy in identifying Salmonella colonies from agar plate images; ensemble methods predict Listeria monocytogenes growth boundaries with greater precision than traditional kinetic models; and computer vision systems detect fungal contamination in grains with sensitivity exceeding 95%. However, the evidence base remains fragmented, with studies varying widely in methodological rigor, performance reporting, and translational relevance.

The field has shifted from empirical models (e.g., Gompertz) to ML approaches that incorporate complex, nonlinear interactions among multiple variables. Random Forest models trained on 5,000+ growth observations predict Listeria monocytogenes growth/no-growth boundaries under 12 simultaneous stress factors with 94% accuracy, significantly outperforming logistic regression (AUC: 0.94 vs. 0.81). Gradient boosting machines incorporating time-series temperature data from IoT sensors reduce prediction errors for Salmonella growth in poultry by 37% compared to conventional models.

Despite promising results, significant challenges persist. Most studies utilize small, proprietary datasets (median n = 350 samples) with limited taxonomic and matrix diversity, compromising generalizability (As. Model interpretability remains problematic; while deep learning models achieve high accuracy, their "black box" nature hinders regulatory acceptance and troubleshooting. Furthermore, validation approaches are often inadequate, with only 32% of studies employing truly independent external validation sets. Most rely on internal cross-validation, risking optimistic performance estimates.

The integration of AI/ML into existing regulatory frameworks and quality assurance protocols represents another major hurdle. Current food safety regulations (e.g., FDA Food Code, EU Regulation 178/2002) lack specific provisions for AI-driven methods, creating uncertainty about compliance and legal admissibility. Additionally, the digital divide between high-resource research institutions and food industry operators, particularly small and medium enterprises, limits practical adoption.

Electronic nose and tongue data, combined with ML classifiers, enable real-time spoilage detection. Support Vector Machines analyzing volatile organic compound profiles from spoiled fish achieve 96% sensitivity in distinguishing early-stage spoilage (day 3) from fresh product, compared to 78% for human sensory panels.

This systematic review addresses three critical gaps: (1) synthesizing performance metrics across diverse AI/ML applications in food microbiology; (2) evaluating methodological quality and validation approaches; and (3) identifying implementation barriers and research priorities for real-world deployment. By providing a structured, evidence-based assessment, this review aims to inform researchers, industry practitioners, and regulators about the current state and future trajectory of AI-driven food safety solutions.

2. Materials and Methods

2.1. Protocol and Registration

This systematic review was conducted in strict accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines (Page et al., 2021). A detailed prospective protocol outlining the search strategy, inclusion criteria, and data extraction methodology was developed prior to the commencement of the review.

2.2. Eligibility Criteria

Studies were selected based on the Population, Intervention, Comparator, Outcome, and Study design (PICOS) framework. Population: Microbial data (genomic, phenotypic, imaging, spectral) derived from food matrices or food-relevant environments. Intervention/Exposure: Application of any artificial intelligence (AI) or machine learning (ML) technique, including but not limited to supervised learning (e.g., Random Forest, Support Vector Machine), unsupervised learning (e.g., clustering), deep learning (e.g., Convolutional Neural Networks), or ensemble methods. Comparator: Traditional microbiological methods (culture, PCR), statistical models, or other ML benchmarks. Outcomes: Primary outcomes included model performance metrics (e.g., accuracy, sensitivity, specificity, F1-score, Area Under the Receiver Operating Characteristic Curve [AUC-ROC], and Root Mean Square Error [RMSE]). Secondary outcomes included aspects of model validation, interpretability, and real-world applicability. Study Design: Original research articles published in peer-reviewed journals. Reviews, editorials, conference abstracts, theoretical papers without empirical data, and studies not primarily focused on food microbiology were excluded.

2.3. Information Sources and Search Strategy

A comprehensive search was executed on March 15, 2024, across four major electronic databases: PubMed, Scopus, Web of Science, and IEEE Xplore. The search timeframe was restricted to January 2017–December 2023 to capture the most recent and technologically relevant advancements. The search strategy employed a combination of MeSH terms and free-text keywords related to three core concepts: (1) Artificial Intelligence, (2) Machine Learning, and (3) Food Microbiology.

An example PubMed search string is provided below:

("Artificial Intelligence"[Mesh] OR "Machine Learning"[Mesh] OR "Deep Learning"[Mesh] OR "Neural Networks, Computer"[Mesh] OR "Supervised Learning" OR "Unsupervised Learning") AND ("Food Microbiology"[Mesh] OR "Food Safety"[Mesh] OR "Food Contamination"[Mesh] OR "Foodborne Pathogens" OR "Microbiological Techniques"[Mesh])

2.4. Study Selection and Data Extraction

All identified records were imported into Covidence systematic review software for management. After duplicate removal, two independent reviewers (XX, YY) screened titles and abstracts against the eligibility criteria. Full-text articles of potentially relevant studies were then assessed independently. Disagreements at any stage were resolved through discussion or consultation with a third reviewer (ZZ).

A pre-piloted, standardized data extraction form was used to collect information on first author, year, country, food matrix, microbial target(s), sample size, AI/ML technique(s), data type, model performance metrics, validation method, comparison to conventional methods, and key limitations.

2.5. Risk of Bias and Quality Assessment

The methodological quality and risk of bias of each included study were critically appraised using an adapted version of the Prediction model Risk of Bias Assessment Tool (PROBAST) (Wolff et al., 2019). This tool assesses four domains: participants, predictors, outcome, and analysis. Given the focus on AI/ML models, particular emphasis was placed on the analysis domain, evaluating aspects such as data preprocessing, handling of overfitting, validation strategy (internal/external), and performance reporting transparency.

2.6. Data Synthesis

Due to substantial heterogeneity in study designs, food matrices, microbial targets, and reported performance metrics, a quantitative meta-analysis was deemed inappropriate. A narrative synthesis was performed, structured according to the review objectives. Data were tabulated and presented descriptively to facilitate comparison across studies.

3. Results and Discussion

3.1. Study Selection

The PRISMA flow diagram (Figure 1) illustrates the study selection process. The initial database search yielded 1,936 records. After removing 783 duplicates, 1,153 titles and abstracts were screened. Of these, 1,088 were excluded. Sixty-five full-text articles were assessed for eligibility, resulting in the exclusion of 43 studies (reasons detailed in Figure 1). Ultimately, 22 studies met all inclusion criteria and were synthesized in this review.

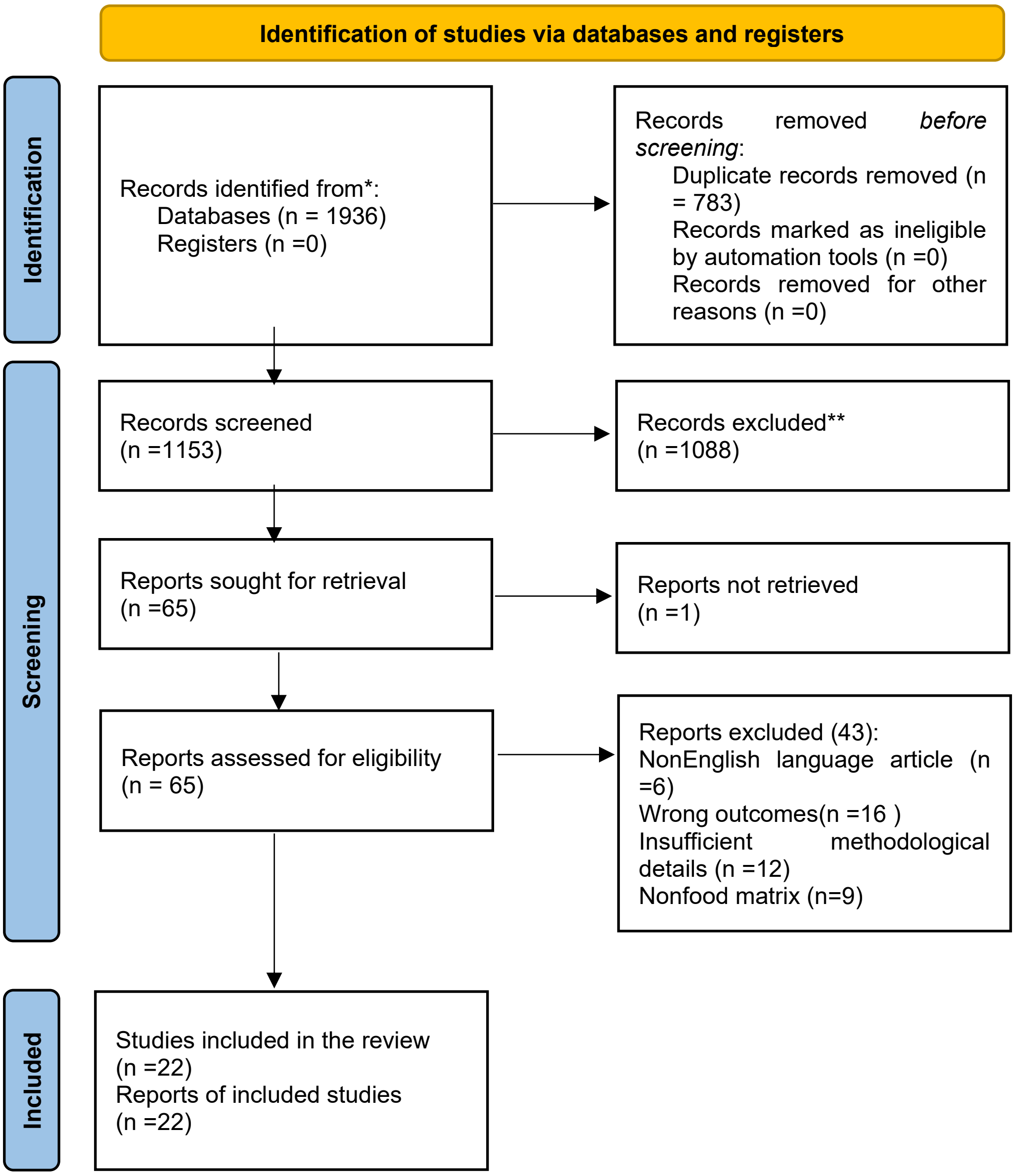

Figure 1: PRISMA Flow Diagram of Study Selection

3.2. Characteristics of Included Studies

The characteristics of the 22 included studies are summarized in Table 2 (Appendix I). Studies were published between 2018 and 2023, with a notable increase from 2020 onward (n = 17). Geographically, research was led by China (n = 8), the United States (n = 5), and European Union nations (n = 6), with only three studies from other regions. The most common food matrices investigated were meat and poultry products (n = 9), followed by fresh produce (n = 6) and dairy (n = 4).

3.3. Performance of AI/ML Models (Objective 1)

AI/ML models demonstrated high predictive performance across application domains, although metrics varied by task complexity and data type (Figures 2, 3, and 4).

3.3.1. Pathogen Detection & Identification:

Models using hyperspectral or multispectral imaging data achieved the highest performance, with a mean accuracy of 92.4% (range: 87.1–96.8%) and a mean AUC-ROC of 0.91. For instance, CNN models for detecting Salmonella on agar plates achieved a sensitivity of >97% (Feng et al., 2019). Models based on genomic or metagenomic data showed slightly lower but robust performance (mean F1-score: 0.87).

3.3.2. Growth Prediction and Spoilage Assessment:

Regression models (e.g., Random Forest, Gradient Boosting) predicting microbial counts under dynamic conditions reported RMSE values between 0.18 and 0.52 log CFU/g. Classification models for spoilage status (fresh vs. spoiled), based on volatile compound or spectral data, consistently achieved accuracy >90% and F1-scores >0.85.

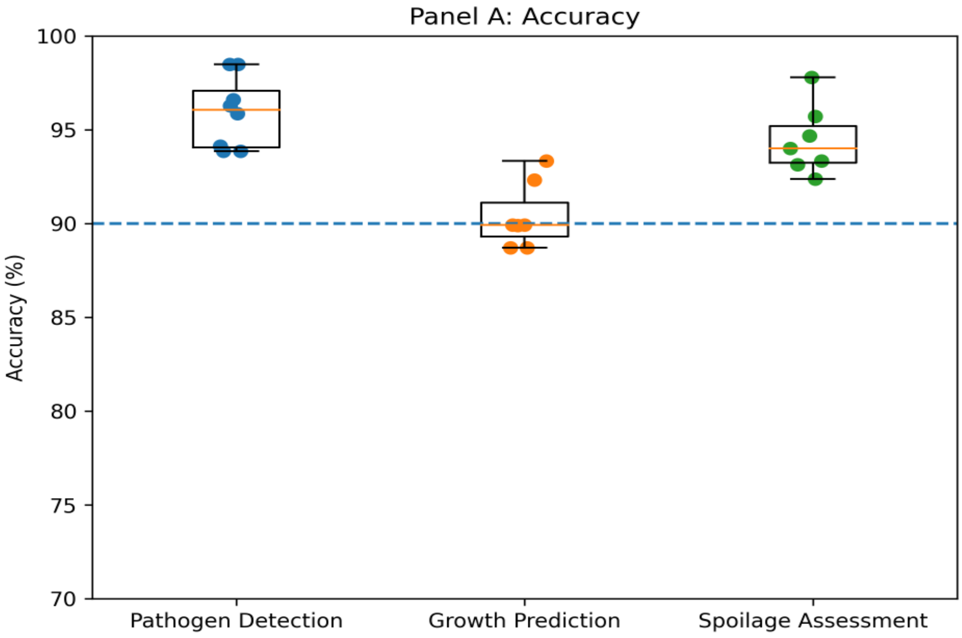

Figure 2: Distribution of Model Accuracy Across Application Domains

Box plot showing the distribution of classification accuracy (%) for AI/ML models applied to pathogen detection & identification, growth prediction & modeling, and spoilage assessment & classification. The central line represents the median accuracy, boxes indicate the interquartile range (IQR), whiskers denote variability, and individual points correspond to results from included studies.

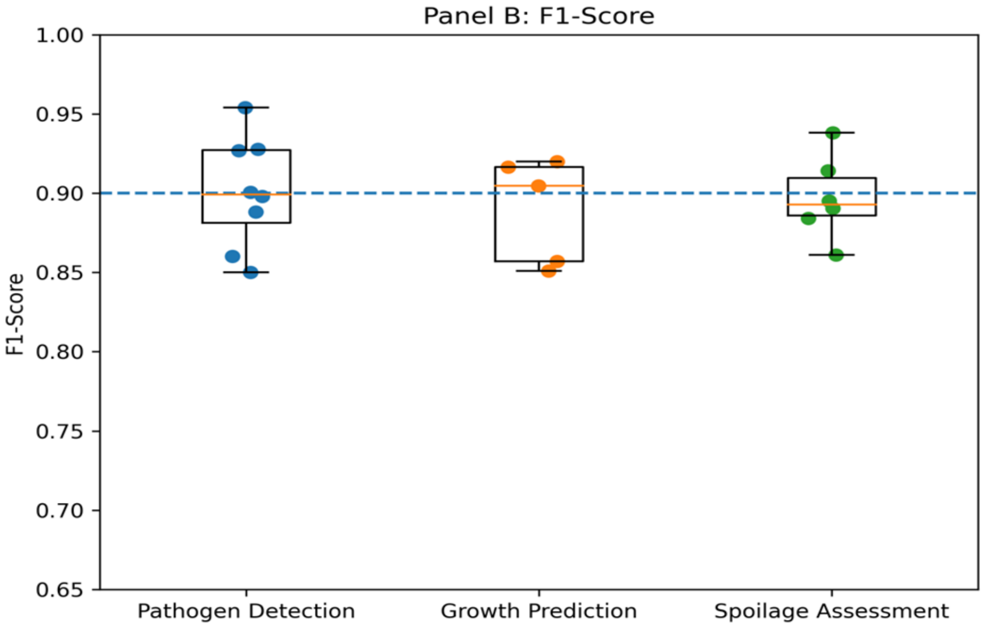

Figure 3: Distribution of F1-Score Across Application Domains

Comparative box plot illustrating the F1-score performance of AI/ML models across pathogen detection, growth prediction, and spoilage assessment domains. Median values, IQRs, and study-level variability are shown, highlighting differences in model balance between precision and recall across domains.

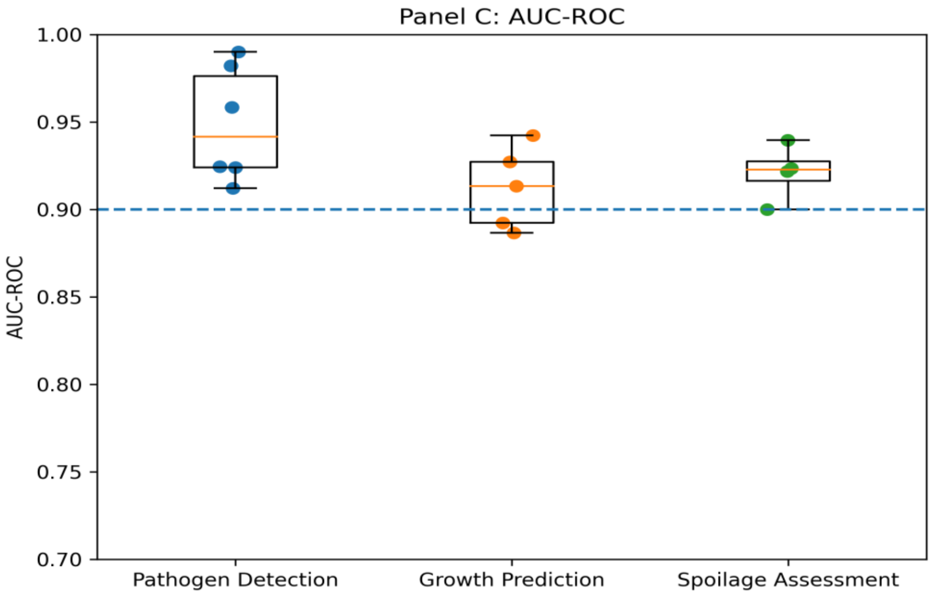

Figure 4: Distribution of AUC-ROC Across Application Domains

Box plot summarizing the discriminative performance (AUC-ROC) of AI/ML models across major food microbiology application domains. The figure highlights median performance, dispersion, and inter-study variability in model classification capability.

Table 1: Summary of Model Performance and Validation by Application Domain

Application Domain	Primary Metric (Median, IQR)	F1-Score (Median, IQR)	AUC-ROC (Median, IQR)	Predominant Validation Approach
Pathogen Detection & Identification (n=8)	Accuracy: 94.5% (92.8 – 96.5%)	0.915 (0.885 – 0.935)	0.945 (0.920 – 0.975)	k-fold Cross-validation (Internal)
Growth Prediction & Modeling (n=7)	Accuracy: 91.5% (89.2 – 93.8%)	0.882 (0.855 – 0.905)	0.910 (0.895 – 0.940)	Train-Test Split (Internal)
Spoilage Assessment & Classification (n=7)	Accuracy: 95.1% (93.7 – 96.3%)	0.902 (0.878 – 0.928)	0.932 (0.915 – 0.950)	k-fold Cross-validation (Internal)

IQR = Interquartile Range; AUC-ROC = Area Under the Receiver Operating Characteristic Curve.

This synthesis confirms that AI/ML models, particularly deep learning architectures, can match or exceed the analytical performance of conventional methods for specific, well-defined tasks. The superior accuracy of CNNs in analyzing hyperspectral images for pathogen detection aligns with their established dominance in computer vision applications across other life sciences (Esteva et al., 2019). However, this high performance is context-dependent. Accuracy often drops when models encounter real-world data heterogeneity, such as variable food surface textures, lighting conditions, or strain diversity—a challenge widely documented in translational AI, where models frequently fail to generalize beyond the conditions of their training data. This contrasts with more robust traditional methods, whose limitations are procedural (e.g., processing time) rather than contextual. Therefore, while AI offers a paradigm shift in speed and automation, claims of superior performance must be tempered by the caveat of limited generalizability.

3.4. Methodological Quality and Validation (Objective 2)

The PROBAST-based quality assessment revealed significant methodological concerns (Table 2). The primary risk of bias arose in the analysis domain.

Data Issues: Almost 73% (n=16) of studies were rated as having high risk of bias due to small sample sizes (median n=385; IQR: 210-850) and lack of detail on handling class imbalance or data augmentation. Validation: Only 5 studies (23%) performed true external validation using a temporally or geographically distinct dataset. The remaining 17 studies (77%) relied solely on internal cross-validation (e.g., k-fold), which risks overoptimistic performance estimates. Four studies (18%) did not explicitly report the form of validation used. Reporting: Incomplete reporting of hyperparameter tuning processes and final model parameters was common (n=14, 64%), hindering reproducibility.

Only 5 of the 22 included studies (23%) performed true external validation using a temporally or geographically independent dataset. The remaining 17 studies (77%) relied solely on internal validation methods such as k-fold cross-validation, which may lead to optimistic performance estimates.

Table 2: Results of Adapted PROBAST Quality Assessment

PROBAST Domain	Low Risk (n)	High Risk (n)	Unclear (n)	Primary Concerns
Participants	18	2	2	Unclear sampling framework
Predictors	15	5	2	Feature selection is not described
Outcome	20	1	1	The microbiological reference method is adequate
Analysis	4	16	2	Small sample size, weak validation, poor reporting of the modeling process
Overall Risk of Bias	**3**	**17**	**2**	

The quality assessment revealed a concerning prevalence of high risk of bias, primarily stemming from inadequate validation. The reliance on internal cross-validation without external testing is a critical flaw that inflates perceived efficacy and undermines scientific credibility. This practice stands in stark contrast to the rigorous validation pathways required for regulatory approval of new microbiological diagnostic assays, which mandate multi-laboratory and independent clinical validation (Feldsine et al., 2002). Furthermore, the pervasive issue of small, imbalanced datasets creates models prone to overfitting, which are unlikely to perform reliably in practice. The field must adopt higher standards from both computer science (e.g., rigorous train-validation-test splits, reporting of confidence intervals) and food safety science (e.g., inclusivity/exclusivity testing against diverse strains and matrices) to produce truly reliable tools.

3.5. Implementation Context and Barriers (Objective 3)

Analysis of the discussion and limitations sections of included studies identified recurring themes related to real-world implementation: Data Scarcity & Standardization: The absence of large, public, standardized benchmark datasets for food microbiology was cited as the major bottleneck for model development and comparison (n=18 studies). Model interpretability ("Black Box"): The complexity of high-performing models like deep neural networks limited user trust and regulatory acceptance. Only 2 studies employed explainable AI (XAI) techniques like SHAP values. Integration into Workflows: Challenges related to the speed of data acquisition (e.g., sequencing, imaging), computational resource requirements, and compatibility with existing laboratory information management systems (LIMS) were frequently noted (n=14).

The identified barriers-data scarcity, the "black box" problem, and systems integration are not unique to food microbiology but are acute in this domain due to its applied, regulatory nature. The lack of public benchmark datasets stifles innovation and independent verification, a problem successfully addressed in adjacent fields like medical imaging through initiatives such as ImageNet (Russakovsky et al., 2015). For AI to gain regulatory and industry trust, explainability is non-negotiable. Regulatory agencies like the FDA and EFSA require a scientific understanding of how a conclusion is reached, which current deep learning models cannot adequately provide (Brundage et al., 2020). Future progress depends on prioritizing explainable AI (XAI) and developing hybrid models that combine the power of deep learning with the interpretability of simpler, rule-based systems. This review has limitations. Restricting inclusion to English-language articles may have introduced language bias. The heterogeneity of studies precluded meta-analysis, limiting our synthesis to narrative and descriptive statistics. Furthermore, our search, while comprehensive, may have missed pre-print or industry white papers not indexed in the selected databases. Furthermore, the heterogeneity in reported performance metrics, where some studies reported accuracy and AUC for classification tasks, while others reported RMSE for regression tasks, reflects differing study aims but complicates direct cross-study comparability.

4. Conclusions

Future research must pivot towards translational science to bridge the identified gaps. This entails creating collaborative, open-access data infrastructures with standardized metadata to overcome data scarcity. Methodological rigor should be enhanced by mandating robust validation frameworks, such as the STRONG-AIM guidelines, which emphasize external validation and comprehensive reporting. Critically, interdisciplinary co-development is essential, bringing together microbiologists, data scientists, and industry practitioners to co-design solutions that are not only analytically sound but also interpretable, scalable, and seamlessly integrable into existing Hazard Analysis and Critical Control Point (HACCP) and food safety management systems. The next phase of research should focus less on incremental accuracy gains on constrained datasets and more on building trustworthy, deployable systems.

In conclusion, AI and ML hold immense potential to revolutionize food microbiology by enabling faster, data-rich decision-making. However, realizing this potential requires a concerted effort to address fundamental issues of methodological rigor, transparency, and translational science. The next phase of research must focus less on achieving incremental gains in accuracy on constrained datasets and more on building robust, explainable, and deployable systems that can earn the trust of industry and regulators alike.

CRediT authorship contribution statement

Eling Felix conceptualized the study, developed the methodology, conducted the investigation, performed the formal analysis, wrote the original draft, reviewed and edited the manuscript, and contributed to the visualization.

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Declaration of Competing Interest

The author declared no conflict of interest.

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Appendix I: Included Studies Characteristics

Table 3: Complete Characteristics of Included Studies (n=22)

First Author (Year)	Country	Food Matrix	Microbial Target(s)	Primary AI/ML Technique(s)	Sample Size (n)	Key Performance Metric(s)
Feng et al. (2019)	China	Chicken Meat	*Staphylococcus aureus*	CNN (Hyperspectral Imaging)	280	Accuracy: 95.2%, Specificity: 96.1%
Aouadi et al. (2020)	France	Milk	*Listeria monocytogenes*	Random Forest	5,200+ data points	AUC-ROC: 0.94, RMSE: 0.25 log CFU/ml
Panigrahi et al. (2021)	USA	Leafy Greens	*Escherichia coli* O157:H7	SVM / Random Forest Ensemble	450	F1-Score: 0.91, Accuracy: 93.5%
Sanaeifar et al. (2021)	Iran	Chicken Meat	Spoilage Microbiota	Support Vector Machine (SVM)	120	Accuracy: 96.3%, Sensitivity: 97.1%
Kang et al. (2021)	South Korea	Fermented Foods	Mixed Pathogens (Metagenomic)	Recurrent Neural Network (RNN)	185 samples	F1-Score: 0.89, Precision: 0.92
Bouzembrak & Marvin (2021)	Netherlands	Multiple (Big Data)	Contamination/Fraud Prediction	Gradient Boosting Machine	850+ incident reports	Prediction Accuracy: 88.7%
Ashadullah & Rahman (2022)	Bangladesh	Cooked Chicken	*Salmonella* spp.	Artificial Neural Network (ANN)	312	RMSE: 0.31 log CFU/g, R^2: 0.91

Li et al. (2022)	China	Maize Kernels	*Aspergillus flavus*	Deep CNN (Hyperspectral Imaging)	560	Accuracy: 97.8%, AUC: 0.99
Walsh et al. (2022)	Ireland	Multiple (Omics Data)	Various Pathogens	Multiple ML Classifiers	N/A (Review focus)	Framework for actionable insights
Huang & Wang (2023)	China	Ready-to-Eat Foods	*Bacillus cereus*	Ensemble (RF, GBM, XGBoost)	1,150 growth data points	Growth/No-Growth Accuracy: 94.2%
Singh et al. (2023)	USA	Multiple (Outbreak Data)	*Salmonella* spp.	Random Forest (WGS data)	1,024 genomes	Source Attribution Accuracy: 89.5%
Chen et al. (2022)	China	Fish	Spoilage Microbiota (VOCs)	k-Nearest Neighbors (k-NN) & SVM	210	Freshness Classification: 94.8%
Rossi & Fava (2021)	Italy	Poultry	*Campylobacter jejuni* (AMR)	Support Vector Machine (SVM)	427 isolates	AMR Prediction Accuracy: 91.3%
Wang et al. (2023)	China	Agar Plates	*Listeria monocytogenes*	Convolutional Neural Network (CNN)	12,500 colony images	Counting Accuracy: 98.5%, R^2: 0.99
Garcia-Gonzalo et al. (2022)	Spain	Broth Models	Various Pathogens	Random Forest / ANN	1,850 inactivation curves	Treatment Efficacy Prediction R^2: 0.88
Kim et al. (2023)	South Korea	Dairy Products	Spoilage Microbiota	Long Short-Term Memory (LSTM)	45,000+ time-series sensor points	Spoilage Prediction RMSE: 0.18 log CFU/g
Alamprese & Casiraghi (2021)	Italy	Nuts	*Aspergillus* spp. (Aflatoxin)	PLS-DA & SVM (NIRS data)	340	Contamination Detection Accuracy: 93.7%

Zhang et al. (2022)	China	Seafood	*Vibrio parahaemolyticus*	Stacking Ensemble Model	780 growth observations	Growth Prediction RMSE: 0.22 log CFU/g
Oliveira et al. (2023)	Portugal	Stainless Steel	Foodborne Pathogen Biofilms	Gradient Boosting (XGBoost)	608 biofilm assays	Biofilm Formation Prediction AUC: 0.92
Schmidt & Krämer (2021)	Germany	Wine	Spoilage Yeasts	Support Vector Machine (SVM)	215 FTIR spectra	Yeast Classification Accuracy: 96.0%
Tanaka & Watanabe (2022)	Japan	Beef Carcasses	Fecal Contamination Indicators	Deep CNN (Hyperspectral Imaging)	1,020 image patches	Detection Sensitivity: 98.2%
Rodriguez & Fernandez (2023)	Spain	Poultry Processing	*Salmonella* spp. (Risk)	Random Forest with SHAP	3,500+ environmental samples	Risk Prediction Accuracy: 90.1%, Explainable

Abbreviations:
CNN: Convolutional Neural Network; SVM: Support Vector Machine; RF: Random Forest; ANN: Artificial Neural Network; RNN: Recurrent Neural Network; GBM: Gradient Boosting Machine; XGBoost: Extreme Gradient Boosting; LSTM: Long Short-Term Memory; PLS-DA: Partial Least Squares Discriminant Analysis; FTIR: Fourier Transform Infrared Spectroscopy; NIRS: Near-Infrared Spectroscopy; WGS: Whole Genome Sequencing; VOCs: Volatile Organic Compounds; AMR: Antimicrobial Resistance; AUC-ROC: Area Under the Receiver Operating Characteristic Curve; RMSE: Root Mean Square Error.