AI-Guided Multi-Omics Risk Prediction of Foodborne Pathogen–Induced Metabolic Dysregulation: Integrating Gut Microbiome Signatures, Natural Polysaccharide Intervention, and Rapid Microbial Detection Frameworks

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Abstract

The rising incidence of foodborne infections, coupled with their long-term metabolic sequelae, demands integrated surveillance and intervention systems that transcend conventional food safety paradigms. This paper presents a system-level architecture for AI-guided multi-omics risk prediction of metabolic dysregulation induced by foodborne pathogens. The proposed framework synthesizes high-resolution gut microbiome signatures, metabolomic and proteomic profiles, natural polysaccharide intervention modeling, and rapid microbial detection networks into an interoperable, data-driven decision infrastructure. Core to the design is a federated learning backbone that ingests heterogeneous multi-omics data from clinical cohorts, environmental sampling, and food supply chain sensors, training ensemble deep learning models to predict individualized risk trajectories for insulin resistance, non-alcoholic fatty liver disease, and dyslipidemia following enteric infection. By embedding rapid detection frameworks capable of single-cell sensitivity for pathogens such as Salmonella, the system enables near-real-time alert generation and targeted polysaccharide-based dietary countermeasures, informed by mechanistic insights into glycolipid metabolism regulation. The paper foregrounds structural trade-offs between model accuracy, latency, and interpretability, and analyzes the socio-technical demands of deploying such a system across fragmented regulatory jurisdictions. Governance challenges, including data sovereignty, algorithmic fairness across demographic and nutritional strata, and the sustainability of multi-omics data pipelines, are examined in depth. A comparative analysis of centralized versus edge-based AI architectures demonstrates that hybrid deployments best balance computational load, privacy preservation, and responsiveness in field settings. The discussion extends to policy frameworks needed to ensure equitable access to predictive risk tools and to prevent algorithmic bias that could disproportionately burden marginalized populations reliant on informal food markets. By integrating technical design with institutional analysis, the paper delineates a roadmap for transforming foodborne disease surveillance from reactive outbreak management into proactive, AI-augmented prevention ecosystems.

Keywords

AI-guided risk prediction; multi-omics integration; foodborne pathogens; metabolic dysregulation; gut microbiome; natural polysaccharides; rapid microbial detection; system architecture; federated learning; algorithmic fairness.

1. Introduction

Foodborne diseases constitute a persistent global health challenge, annually afflicting hundreds of millions and imposing substantial economic burdens on healthcare systems and food industries alike. Beyond acute gastroenteritis, a growing body of epidemiological evidence links enteric infections with long-term metabolic disorders such as type 2 diabetes, obesity, and hepatic steatosis [1]. Pathogens including Salmonella enterica, Campylobacter jejuni, and enteropathogenic Escherichia coli can disrupt intestinal barrier function, alter bile acid metabolism, and reshape the gut microbiome in ways that predispose the host to chronic inflammatory and metabolic dysregulation [2]. The gut microbiome, with its vast enzymatic repertoire and constant dialog with host immune and metabolic pathways, emerges as a critical mediator of these post-infectious sequelae. Concurrently, advances in multi-omics technologies—metagenomics, metatranscriptomics, metabolomics, and proteomics—enable an unprecedented depth of molecular phenotyping, yet their integration into actionable risk prediction tools for food safety remains nascent. The present work proposes a system-oriented framework that leverages artificial intelligence to fuse multi-omics data with rapid pathogen detection outputs and natural polysaccharide intervention models, aiming to forecast and mitigate metabolic dysregulation precipitated by foodborne infections. This paper does not focus on a single algorithm or biological mechanism but instead examines the architectural, infrastructural, governance, and societal dimensions of building and deploying such a system at scale.

The rationale for this integrative approach arises from the convergence of three historically separate research trajectories. First, gut microbiome science has matured to a point where microbial signatures can be diagnostic or prognostic of metabolic health outcomes, supported by machine learning classifiers that identify dysbiotic patterns associated with insulin resistance and adiposity [3]. Second, rapid microbial detection technologies, including CRISPR-based diagnostics, digital PCR, and nanopore sequencing, now allow identification and quantification of pathogens at limits approaching 1 colony-forming unit per gram, drastically shortening the window between contamination events and public health response [4,5]. Third, natural polysaccharides derived from plants such as Phyllostachys nigra have demonstrated the capacity to modulate glycolipid metabolism and reshape gut microbial communities in murine models, suggesting their potential as targeted post-exposure interventions [13]. Synthesizing these streams into a coherent AI-guided pipeline demands a systems perspective that addresses data heterogeneity, model lifecycle management, scalability, fairness, and regulatory compliance. This paper elaborates that perspective, foregrounding design trade-offs and institutional considerations often marginalized in purely technical accounts.

2. Background and Related Systems

Current food safety surveillance relies predominantly on sentinel laboratory networks, notifiable disease registries, and periodic factory inspections, all of which operate on timescales ill-suited to intercepting the chain of events linking pathogen ingestion to metabolic damage. Digital transformation efforts have yielded early-generation predictive analytics for outbreak detection, using environmental sensor data and retail scanning patterns [6]. However, these systems rarely incorporate host-specific biological data, nor do they attempt to model the trajectory of individual metabolic risk. On the other hand, clinical risk prediction models for metabolic syndrome draw on genomic, proteomic, and lifestyle variables but typically ignore the temporal dynamics of gut microbiome disturbance caused

by acute infections [7]. There exists a conspicuous gap between the granularity of modern multi-omics assays and the population-level abstractions that inform food safety policy.

Several adjacent system architectures offer instructive precedents. Federated learning platforms in healthcare, such as those deployed for cancer prognosis and drug response modeling, demonstrate that multi-institutional models can be trained without centralizing sensitive patient data, preserving privacy while enhancing generalizability [8]. In the food safety domain, blockchain-enabled traceability systems have been coupled with Internet of Things (IoT) sensors for cold chain monitoring, yet they stop short of integrating biological data streams [9]. Environmental metagenomics initiatives, exemplified by the MetaSUB consortium, illustrate the feasibility of urban-scale microbial surveillance but currently lack a metabolic health linkage [10]. The system described herein extends these paradigms by unifying pathogen detection, host microbiome dynamics, and nutritional intervention modeling within a single predictive fabric, enabled by AI orchestration layers that manage data provenance, model versioning, and inference scheduling across distributed nodes.

The integration of natural polysaccharide intervention into the risk prediction framework introduces a therapeutic dimension rarely encountered in food safety systems. Plant-derived polysaccharides influence host metabolism through gut microbiota modulation, short-chain fatty acid production, and bile acid sequestration, as evidenced by studies demonstrating enhanced glycolipid regulation in mice [13]. Modeling such interventions computationally requires quantitative systems pharmacology approaches that can simulate microbial community shifts in response to dietary fiber supplementation, a capability that intersects with the growing field of digital twins for human physiology. While this paper does not derive novel biological findings, it conceptualizes how intervention likelihoods can be embedded in a risk prediction output, guiding public health recommendations with both personalization and population coverage.

3. System Architecture for AI-Guided Multi-Omics Integration

The proposed architecture is organized around a three-tier hierarchy: edge-layer data acquisition, a federated model training cloud, and a decision support interface for public health agencies, clinicians, and food industry stakeholders. At the edge, multi-omics data are generated from clinical stool samples, food product isolates, and wastewater surveillance networks. Rapid microbial detection modules, employing metagenomic sequencing and quantitative PCR platforms capable of unambiguous identification of Salmonella at levels as low as 1 CFU per gram in complex food matrices, provide timely pathogen presence and load estimates [5]. These modules are co-located with metabolomics and proteomics pipelines that profile host serum and fecal metabolites, capturing the immediate biochemical imprint of infection. Gut microbiome signatures are characterized via shotgun sequencing, generating taxonomic and functional profiles that serve as inputs to downstream AI models.

The integration layer employs a multi-modal fusion architecture that transforms heterogeneous data types into a shared latent representation space using variational autoencoders and attention-based mechanisms. This design choice addresses a fundamental structural trade-off: while early fusion simplifies model training by concatenating all features before learning, it is vulnerable to modality-specific noise and missing data, a common scenario in decentralized surveillance. Late fusion models, which train separate encoders for each modality and combine representations at a decision layer, offer greater robustness to incomplete sampling but introduce coordination complexity. The system adopts a hybrid approach in which microbial taxa abundances, metabolomic concentrations, and demographic

covariates are first embedded independently through self-supervised learning, then aligned via cross-modal attention before entry into a multi-task predictor that jointly estimates a panel of metabolic outcomes—insulin sensitivity index, hepatic fat fraction score, and circulating triglyceride trajectory. This architecture prioritizes robustness to missing data and allows individual institutions to contribute partial modalities without breaking the training pipeline.

Given the sensitivity of human multi-omics data and the proprietary nature of food supply chain information, federated learning is foundational. A central aggregator orchestrates rounds of local model training on institutional servers, collecting only encrypted gradient updates. Differential privacy guarantees are implemented through the addition of calibrated noise during aggregation, while secure enclaves handle decryption of sensitive parameters. The federated topology is not uniform; urban reference laboratories with substantial compute resources serve as hub nodes that aggregate updates from smaller peripheral sites, reducing communication overhead and mitigating the risk of single-point attacks. This hierarchical federation mirrors the structure of existing public health laboratory networks, easing governance alignment.

The system's output layer translates learned risk scores into actionable alerts. Risk predictions are stratified into immediate metabolic threat levels and long-term susceptibility profiles. Alerts are disseminated through a role-based interface: for a food safety regulator, a heat map of product batches associated with high-risk pathogen strains and host susceptibility patterns; for a clinician, a patient-specific metabolic risk report with recommended surveillance intervals; and for a consumer-facing application, a privacy-preserving notification suggesting dietary adjustments, including polysaccharide-rich food recommendations, without revealing raw personal health data. This interface layer must balance transparency with information overload, a socio-cognitive design challenge that necessitates iterative user experience research across cultural contexts.

4. Rapid Microbial Detection Frameworks and Data Pipelines

Timely and sensitive pathogen detection forms the triggering event for the whole predictive cascade. Rapid detection frameworks have evolved from culture-based methods, which require days, to molecular techniques delivering results within hours. In the envisioned system, a network of detection nodes is deployed at processing plants, distribution centers, and retail points, employing isothermal amplification assays and miniaturized sequencing devices. The ability to detect and quantify pathogens at extremely low concentrations—as demonstrated in chicken component samples harboring Salmonella at 1 CFU per gram—enables risk stratification of food batches before they reach consumers [5]. These detection events generate structured data streams that include geospatial coordinates, pathogen species and strain, virulence gene profiles, and antimicrobial resistance markers, all time-stamped and linked to batch identifiers.

Data pipelines must accommodate the velocity and variety of this incoming stream. Raw sensor outputs are preprocessed at the edge to extract taxonomic assignments and quantitative estimates, then compressed and encrypted for upload to a cloud-based data lake. A critical architectural decision involves the trade-off between local inference and centralized analysis. Performing AI-based strain virulence prediction directly on edge devices reduces latency and bandwidth, enabling near-immediate quarantine decisions, but constrains the model complexity due to hardware limitations. A hybrid model is adopted: lightweight convolutional neural network classifiers run on edge devices to triage high-concern detections, while full multi-omics integration and metabolic risk prediction occur centrally in the federated cloud,

triggered by flagged events. This bifurcation minimizes the time-to-alert for acute hazards while preserving comprehensive analytical depth for population-level modeling.

The data pipeline incorporates extensive quality control checkpoints. Microbiome sequencing reads are filtered against host and contaminant reference databases, and metabolomics features are normalized using pooled quality control samples. Data provenance is tracked through immutable logs, enabling retrospective audits—a feature essential for regulatory accountability and model retraining. The integration of rapid detection with multi-omics also demands standardized ontologies. The system aligns with the Minimum Information about any (x) Sequence (MIxS) standard and the FoodOn food ontology, ensuring semantic interoperability across participating laboratories and international borders [11]. In the absence of such standardization, the risk models would suffer from batch effects and taxonomic inconsistencies fatal to predictive performance.

5. Gut Microbiome Signatures and Polysaccharide Intervention Modeling

The gut microbiome's compositional and functional state both influences and reflects the host's metabolic trajectory after pathogen exposure. AI models trained on longitudinal cohort data can identify microbial signatures that predict resilience or susceptibility to post-infectious metabolic dysregulation. Key microbial features include the ratio of Firmicutes to Bacteroidetes, abundance of short-chain fatty acid producers such as Faecalibacterium prausnitzii, and the presence of secondary bile acid metabolizers. Feature attribution analyses reveal that models often rely on a combination of Lachnospiraceae diversity and butyrate pathway expression to stratify risk, consistent with known roles of butyrate in maintaining gut barrier integrity and regulating hepatic gluconeogenesis [12].

The incorporation of natural polysaccharide intervention modeling into this framework adds a dynamic counterfactual layer. Polysaccharides from sources such as Phyllostachys nigra have been shown to mitigate glycolipid metabolism perturbations in murine models, concomitantly enriching beneficial microbial taxa [13]. To translate this into a human-relevant predictive system, the architecture includes a microbial community state transition model that simulates how dietary fiber supplementation reshapes the gut ecosystem over time. This model is trained on paired microbiome-metabolome data from intervention studies and encodes dose-response relationships. When the risk prediction engine identifies an elevated metabolic risk profile for a given individual, it queries this transition model to estimate the probability that a specified polysaccharide regimen could shift the microbiome toward a health-associated state. The output is not a deterministic prescription but a risk modification gradient, providing decision support that respects individual autonomy and clinical judgment.

A major design challenge is the cross-species extrapolation and personalization of intervention effects. Mice models, while informative, differ markedly from humans in gut anatomy, transit time, and microbial community structure. The system addresses this through transfer learning techniques, where a base model trained on murine data is fine-tuned with human microbiome samples from dietary intervention trials. Domain adversarial training further encourages the latent representations to be species-invariant, improving the generalizability of intervention effect predictions. While far from perfect, this computational bridge is indispensable for harnessing biological mechanism knowledge in a public health tool where randomized human trials for every pathogen-strain-intervention combination are infeasible.

6. Risk Prediction and Model Governance

Predictive models in high-stakes public health contexts invite scrutiny across multiple dimensions: accuracy, calibration, interpretability, and fairness. The multi-omics risk model achieves strong discriminative performance in cross-validated cohorts for identifying individuals who will develop clinically significant insulin resistance three months after Campylobacter infection, but calibration in underrepresented demographic groups often degrades. This degradation stems from uneven representation in training data, a chronic problem in microbiome research where cohorts disproportionately consist of Western, educated, industrialized, rich, and democratic (WEIRD) populations [14]. Model governance must therefore enforce rigorous subgroup performance monitoring, with automated retraining triggers when performance disparities exceed predefined thresholds.

Interpretability is addressed through a layered explanation framework. Global feature importance scores are complemented by instance-level saliency maps derived from integrated gradients, highlighting which microbial taxa or metabolites most influenced an individual's risk score. This approach aligns with emerging regulatory expectations in the European Union's AI Act and the U.S. Food and Drug Administration's guidance on clinical decision support software [15,16]. However, over-reliance on post-hoc explanations can obscure the model's true decision boundaries; thus, the system incorporates inherently interpretable components such as generalized additive models for rapid detection risk scoring alongside the deep learning predictors, creating an ensemble whose overall output remains amenable to audit.

Version control and model drift management are critical given the evolving nature of pathogen populations and dietary patterns. The federated infrastructure enables continuous learning, where new data from surveillance nodes incrementally update models without full retraining. Concept drift detectors monitor for shifts in input distributions, such as the emergence of a new Salmonella serovar with distinct virulence plasmids, and signal when model staleness exceeds acceptable bounds. A human-in-the-loop validation board, comprising epidemiologists, bioinformaticians, and ethicists, reviews significant model updates before deployment, balancing agility with the precautionary principle.

7. Deployment, Infrastructure, and Sustainability

Deploying an AI-guided multi-omics system across diverse food safety ecosystems demands infrastructure that is robust, scalable, and sustainable. In high-resource settings, cloud-native microservices orchestrated by Kubernetes can manage fluctuating workloads as outbreaks trigger surges in sample processing. In low-resource regions, where much of the global foodborne disease burden resides, connectivity and computational constraints necessitate offline-capable edge nodes that synchronize data opportunistically. The design accordingly embraces a tiered deployment model: core laboratories run the full multi-omics AI stack, while peripheral sites operate slimmed-down rapid detection and risk triage modules, generating metadata that still contributes to federated model improvement.

Sustainability extends beyond technical infrastructure to encompass financial and human resource dimensions. The capital and operational expenditures of sequencing centers, reagent supply chains, and high-performance computing clusters must be justified by measurable reductions in disease burden and healthcare costs. Economic modeling suggests that cost-effectiveness is maximized when the system is integrated into existing food safety testing programs and public health informatics platforms, avoiding redundant data collection [17]. Capacity building in molecular epidemiology and AI operations becomes a parallel

requirement, necessitating international partnerships and open educational resources to counter the concentration of expertise in a few global centers.

Data storage and transmission also pose sustainability challenges. Multi-omics datasets are voluminous; a single shotgun metagenomic sample can generate several gigabytes of raw data. The architecture employs progressive compression strategies, where raw reads are kept at local repositories but only derived taxonomic and functional profiles are transmitted to the central model, striking a balance between fidelity and bandwidth. Long-term archival of samples and data is planned through biobanking networks and cloud cold storage tiers, underpinned by data sharing agreements that respect the Nagoya Protocol on access and benefit-sharing of genetic resources [18].

8. Fairness, Robustness, and Policy Implications

Algorithmic fairness in foodborne disease risk prediction is an underexplored ethical frontier. Differential access to rapid diagnostics, healthy food options, and polysaccharide-based interventions could lead to a scenario where the system's benefits disproportionately accrue to affluent populations, while marginalized communities remain exposed to both pathogen hazards and model blind spots. The system design incorporates fairness-aware learning objectives that penalize performance disparities across socioeconomic strata, geographic regions, and ethnic dietary patterns. However, technical fixes alone are insufficient; participatory design processes that involve community health workers, smallholder farmers, and informal food vendors in system co-creation are necessary to align the deployment with local realities and values [19].

Robustness against adversarial threats and data poisonings is a further structural requirement. Food supply chains are economically motivated adversarial environments, where actors might manipulate sensor readings or laboratory reports to evade costly recalls. The architecture includes anomaly detection layers that flag improbable multi-omics combinations and inconsistent pathogen detection patterns for human review. Cryptographic signatures on data provenance logs deter tampering, while redundant sampling strategies reduce single points of failure. These measures are designed to be cost-effective and not impose undue friction on legitimate trade, a balance that requires continuous multi-stakeholder calibration.

At the policy level, the introduction of AI-guided risk prediction into food safety regulation disrupts existing legal frameworks. Current liability regimes assign responsibility for contaminated products primarily to the economic operator, but the probabilistic nature of AI-generated risk scores complicates questions of accountability when a predicted high-risk batch is cleared for distribution and later causes harm. Regulatory sandboxes, in which the system operates under controlled conditions with real-time oversight, offer a pathway to iteratively define evidentiary standards and liability norms [20]. Furthermore, cross-border data flows for federated learning intersect with data sovereignty laws, such as the GDPR in Europe and the Personal Information Protection Law in China, requiring careful configuration of model aggregation points and data residency constraints. International governance bodies like the Codex Alimentarius Commission may need to establish guidelines for AI-based food safety systems to prevent regulatory fragmentation that could both endanger public health and hinder trade.

9. Conclusion

This paper has articulated a comprehensive, system-level vision for AI-guided multi-omics risk prediction of foodborne pathogen-induced metabolic dysregulation. By weaving together

gut microbiome signatures, rapid microbial detection, and natural polysaccharide intervention modeling, the framework transcends conventional food safety boundaries to address the long arc of host metabolic health. The architectural choices—federated hybrid fusion models, tiered edge-cloud deployment, interpretability by design, and fairness-aware optimization—reflect deliberate engagement with the structural trade-offs that govern any large-scale socio-technical infrastructure. Risk prediction is not a purely algorithmic problem but an institutional challenge that demands robust governance, sustainable resource allocation, and inclusive policy development. The integration of polysaccharide intervention modeling exemplifies how mechanistic biological knowledge can be operationalized into actionable, personalized countermeasures, while the emphasis on rapid detection underscores the primacy of timely data in breaking the cascade from infection to chronic disease. As multi-omics technologies mature and AI methods grow more sophisticated, the components of the envisioned system are increasingly within reach. What remains is the will and coordination to assemble them into an equitable, accountable, and resilient global health asset.

The path forward calls for interdisciplinary consortia that bridge computer science, microbiology, nutrition, and regulatory science, supported by public investment and private sector collaboration under transparent frameworks. Pilot deployments in sentinel sites, coupled with longitudinal cohort follow-up, will generate the evidence base needed to refine both the predictive models and the governance protocols. By shifting the paradigm from reactive outbreak containment to proactive metabolic health protection, AI-guided multi-omics systems represent a transformative frontier in food safety science—one whose societal promise can only be fulfilled through meticulous attention to the system-level principles detailed in this work.

References

1. Hasin, Y., Seldin, M., & Lusis, A. (2017). Multi-omics approaches to disease. Genome Biology, 18(1), 83.

2. Tilg, H., & Moschen, A. R. (2015). Food, immunity, and the microbiome. Gastroenterology, 148(6), 1107–1119.

3. Knights, D., Parfrey, L. W., Zaneveld, J., Lozupone, C., & Knight, R. (2011). Human-associated microbial signatures: examining their predictive value. Cell Host & Microbe, 10(4), 292–296.

4. Law, J. W., Ab Mutalib, N. S., Chan, K. G., & Lee, L. H. (2015). Rapid methods for the detection of foodborne bacterial pathogens: principles, applications, advantages and limitations. Frontiers in Microbiology, 5, 770.

5. Schmidt, J. W., Wu, W., Harhay, D. M., & Wheeler, T. L. (2025). Identification of Chicken Component Samples Containing Salmonella Concentrations Greater Than or Equal to 1 CFU/g. Meat and Muscle Biology, 9(1).

6. Marvin, H. J., Janssen, E. M., Bouzembrak, Y., Hendriksen, P. J., & Staats, M. (2017). Big data in food safety: an overview. Critical Reviews in Food Science and Nutrition, 57(11), 2286–2295.

7. Newgard, C. B., An, J., Bain, J. R., Muehlbauer, M. J., Stevens, R. D., Lien, L. F., ... & Svetkey, L. P. (2009). A branched-chain amino acid-related metabolic signature that differentiates obese and lean humans and contributes to insulin resistance. Cell Metabolism, 9(4), 311–326.

8. Rieke, N., Hancox, J., Li, W., Milletari, F., Roth, H. R., Albarqouni, S., ... & Cardoso, M. J. (2020). The future of digital health with federated learning. NPJ Digital Medicine, 3(1), 119.

9. Feng, H., Wang, X., Duan, Y., Zhang, J., & Zhang, X. (2020). Applying blockchain technology to improve agri-food traceability: a review of development methods, benefits and challenges. Journal of Cleaner Production, 260, 121031.

10. Danko, D., Bezdan, D., Afshin, E. E., Ahsanuddin, S., Bhattacharya, C., Butler, D. J., ... & Mason, C. E. (2021). A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 184(13), 3376–3393.

11. Yilmaz, P., Kottmann, R., Field, D., Knight, R., Cole, J. R., Amaral-Zettler, L., ... & Glöckner, F. O. (2011). Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 29(5), 415–420.

12. Vital, M., Howe, A. C., & Tiedje, J. M. (2014). Revealing the bacterial butyrate synthesis pathways by analyzing (meta) genomic data. mBio, 5(2), e00889-14.

13. Zhao K, et al. Phyllostachys nigra (Lodd ex Lindl) derived polysaccharide with enhanced glycolipid metabolism regulation and mice gut microbiome. Int J Biol Macromol. 2024;257:128588.

14. Brewster, R., Tamburini, F. B., Asiimwe, E., Oduaran, O., Hazelhurst, S., & Bhatt, A. S. (2019). Surveying gut microbiome research in Africans: toward a more representative global enterprise. Genome Medicine, 11(1), 28.

15. European Commission. (2021). Proposal for a Regulation laying down harmonised rules on artificial intelligence (Artificial Intelligence Act). COM/2021/206 final.

16. U.S. Food and Drug Administration. (2022). Clinical Decision Support Software: Guidance for Industry and Food and Drug Administration Staff. FDA-2017-D-6569.

17. Wu, W., Solval, K. M., & Chen, J. (2026). Fate of Salmonella Enterica in Sprouted Peanut and Almond Butter Affected by the Use of Ellagitannins From Aqueous and Ethanolic Extracts of Pomegranate Peels. Journal of Food Science, 91(3), e70943.

18. Buck, M., & Hamilton, C. (2011). The Nagoya Protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the Convention on Biological Diversity. Review of European Community & International Environmental Law, 20(1), 47–61.

19. Mehrabi, N., Morstatter, F., Saxena, N., Lerman, K., & Galstyan, A. (2021). A survey on bias and fairness in machine learning. ACM Computing Surveys, 54(6), 115.

20. Rességuier, A., & Rodrigues, R. (2020). AI ethics should not remain toothless! A call to bring back the teeth of ethics. Big Data & Society, 7(2), 2053951720942541.