

3D Printing of Starch-Based Foods with Controllable Digestive Kinetics: Multi-Scale Structural Design for Personalized Glycemic Management

Jirui Hu

*Wuhan Britain-China School, Wuhan, China
leonacademic@163.com*

Abstract. Precision nutrition demands customized postprandial glycemic control, but conventional food processing methods lack the capability to precisely modulate starch digestion kinetics through internal structural design. Objective: This study systematically investigates how 3D printing filling rates (40%-100%) and multi-layer configurations influence in vitro digestion kinetics and predicted glycemic index (eGI) of starch-based foods. A thematic synthesis of peer-reviewed literature from Web of Science, PubMed, and Scopus (2018-2026) was conducted. Structural characterization data and corresponding digestive outcomes were extracted to construct a "structure-digestion" correlation framework. Intermediate filling rates (40%-70%) generate dense gel networks that restrict enzyme diffusion via spatial tortuosity, whereas low filling rates (<40%) accelerate hydrolysis due to elevated specific surface area. Double-layer and gradient structures introduce interface barriers that program "fast-slow" glucose release profiles. Retention of 60%-85% B-type and V-type starch crystals positively correlates with sustained slow digestion. 3D printing enables programmable digestive kinetics through multi-scale structural design. The current reliance on static in vitro models and the absence of standardized predictive frameworks remain critical limitations. Future development of multi-variable predictive algorithms and clinical validations is essential for achieving automated personalized glycemic management.

Keywords: 3D food printing, starch digestion, glycemic index, infill density, crystalline structure

1. Introduction

Postprandial glycemic management constitutes a central pillar of precision nutrition, especially given the rising prevalence of type 2 diabetes and obesity [1, 2]. The rate of enzymatic starch hydrolysis in the gastrointestinal tract directly determines blood glucose excursions, establishing a mechanistic link between food microstructure and metabolic response [3]. Designing foods with a low glycemic index (GI) represents a clinically relevant strategy [2, 4]. However, conventional thermal and mechanical processing techniques provide limited ability to tailor the internal pore distribution, density gradients, and crystalline arrangements that govern enzyme accessibility [5].

Extrusion-based three-dimensional (3D) food printing has emerged as a transformative digital manufacturing platform capable of depositing starch-based materials with high spatial resolution [6, 7]. By adjusting parameters such as infill density and layer configuration, the internal architecture and resulting mass transfer properties of printed constructs can be programmatically controlled [8]. Despite these advances, quantitative relationships between multi-scale printed structures—from macroscopic infill patterns to molecular crystalline domains—and starch digestion kinetics remain insufficiently characterized.

This study aims to systematically examine how 3D printing filling rates (40%-100%) and multi-layer structural configurations affect *in vitro* starch digestibility and predicted glycemic index (eGI). A systematic thematic synthesis of literature published between 2018 and 2026 across three major databases was performed to construct a comprehensive "structure-digestion" correlation framework. The significance of this work lies in establishing engineering design principles that bridge digital food fabrication with metabolic nutrition, thereby laying the foundation for automated, personalized glycemic control.

2. Methodology

2.1. Database search strategy

A systematic literature search was executed in Web of Science, PubMed, and Scopus for articles published between January 2018 and March 2026. The search combined the following terms using Boolean operators: "3D food printing," "starch digestion," "in vitro digestion models," "glycemic index," "infill density," and "starch-based gels." Additional descriptors, including "multi-layer structure," "crystalline structure," and "slowly digestible starch", were incorporated to ensure comprehensive retrieval. Only English-language peer-reviewed primary research and review articles were considered.

2.2. Screening and selection criteria

Studies were included if they met three criteria: (i) employed extrusion-based 3D printing of pure starch or multi-component starch systems; (ii) reported at least one quantitative structural parameter (e.g., infill percentage, porosity, crystallinity); and (iii) provided corresponding digestive outcomes such as hydrolysis curves, kinetic rate constants, or eGI values. Articles focusing exclusively on non-extrusion printing modalities, studies lacking digestion-related data, and opinion pieces without empirical evidence were excluded. After duplicate removal, titles and abstracts were screened, and full texts of potentially eligible records were assessed against the inclusion criteria.

2.3. Thematic synthesis and framework construction

Data extraction captured key technical inputs (nozzle diameter, printing speed, fill ratio, and material formulation) and corresponding outputs (pore morphology, crystallinity index, hydrolysis kinetic parameters k and C_{∞} , and eGI). Recurrent patterns linking structural descriptors to digestion outcomes were iteratively identified, grouped, and refined. The synthesized relationships were organized into four thematic domains that collectively constitute the regulatory framework: infill rate and pore architecture, spatial heterogeneity through multi-layer design, crystalline structure transformations, and synergistic multi-component interactions.

3. Regulation of 3D printing structure parameters on starch digestion

3.1. Infill rate and internal pore structure

The infill density directly dictates the size, distribution, and interconnectivity of internal pores within printed starch constructs. Pre-processing treatments such as dry heating improve the rheological properties and structural stability of starch-based inks, facilitating the maintenance of defined infill patterns during extrusion [9]. Once a stable ink is formulated, intermediate filling rates (40%-70%) produce a network of discrete, small-diameter pores that create pronounced spatial tortuosity. This dense gel network physically impedes α -amylase diffusion, resulting in a sustained-release hydrolysis profile [10, 11]. In contrast, filling rates below 40% generate extensive macrovoids and highly interconnected pores. The markedly increased specific surface area accelerates enzyme accessibility, leading to rapid starch hydrolysis during the initial digestive phase [11]. These findings confirm that matrix permeability and the temporal glucose release profile can be digitally programmed through infill percentage alone.

3.2. Multi-layer structure and spatial heterogeneity design

Extrusion-based 3D printing further enables the fabrication of spatially heterogeneous architectures via multi-nozzle systems or variable-parameter deposition strategies. Double-layer and gradient infill structures introduce localized interfacial regions where distinct physical properties create zones of impeded mass transfer [7, 12]. A typical design comprises an outer layer with lower infill density, providing initial moderate glucose release, and an inner dense core acting as a digestion-resistant barrier. The sequential erosion of these layers by enzymatic action prolongs total digestion time and generates a programmable "fast-slow" glucose release profile [12]. This spatiotemporal control over digestive kinetics represents a capability beyond the reach of conventional processing technologies.

3.3. Crystal structure changes and formation of resistant starch

At the molecular scale, starch susceptibility to enzymatic hydrolysis is governed by its crystalline architecture. The hot-extrusion process inherent in many 3D printing workflows subjects amylose and amylopectin to simultaneous thermal and shear forces, disrupting native crystalline domains while promoting recrystallization during cooling [13]. Characterization by X-ray diffraction and scanning electron microscopy reveals that B-type crystallites and V-type inclusion complexes exhibit enhanced resistance to enzymatic degradation. Retention of 60%-85% of these ordered polymorphs during printing positively correlates with slower digestion kinetics and higher resistant starch content [13]. The steric hindrance and hydrogen-bonding networks within these crystalline arrangements serve as a fundamental protective mechanism against rapid glucose release.

3.4. Synergistic effects of multi-component interactions

The digestive fate of printed starch matrices can be further modulated through synergistic interactions with co-extruded components. Starch-lipid inclusion complexes, starch-polyphenol adducts, and pectin-calcium hydrogel matrices physically shield glycosidic bonds from rapid enzymatic cleavage [12, 14]. These interactions shift the balance from rapidly digestible starch toward slowly digestible and resistant fractions, demonstrating the potential of multi-material 3D printing to orchestrate nutritional outcomes through controlled co-localization of interacting components.

3.5. Post-processing effects on structural stability and digestion kinetics

The structural integrity and digestive performance of 3D-printed starch-based constructs are profoundly shaped by post-extrusion processing steps, including drying, steaming, and baking. The drying technique applied after printing determines the final moisture content, porosity, and degree of starch retrogradation, all of which directly impact enzymatic susceptibility. Freeze-drying, for instance, preserves the open porous network generated during printing, maintaining a high specific surface area that facilitates rapid enzyme penetration. In contrast, hot-air drying or oven-baking induces partial collapse of the pore structure and promotes further starch chain reassociation, thereby increasing crystallinity and reducing the hydrolysis rate [11]. Steaming or boiling, commonly applied to starch-based gels, can cause substantial swelling and leaching of amylose, which upon cooling forms a dense outer layer that retards subsequent enzyme diffusion [10]. These post-processing operations can either amplify or counteract the structural features programmed during the printing stage, highlighting the need to consider the entire manufacturing chain when designing foods for targeted glycemic responses. Integrating post-processing parameters into predictive digestion models is therefore essential for achieving consistent and reproducible digestive kinetics in practical applications.

4. Assessment methods for in vitro digestion kinetics and eGI

4.1. In vitro gastrointestinal digestion models

The INFOGEST standardized static in vitro digestion protocol has become the primary evaluative method for 3D-printed starch matrices [15]. This consensus method sequentially simulates oral, gastric, and small intestinal phases using relevant digestive enzymes and physiological pH conditions, with adaptations for solid and semi-solid gel samples. Its widespread adoption facilitates meaningful inter-study comparisons of digestion kinetic parameters across different laboratories and printing setups.

4.2. Digestion kinetic parameters

Starch hydrolysis time-course data are commonly fitted using a first-order kinetic model that describes the accumulation of hydrolysis products over time:

$$C_t = C_{\infty} \cdot (1 - e^{-kt}) \quad (1)$$

where C_t is the cumulative percentage of starch hydrolyzed at time t , C_{∞} is the equilibrium hydrolysis percentage representing the maximum digestible fraction, and k is the first-order digestion rate constant [3]. This model is mathematically equivalent to the exponential decay of the remaining digestible substrate ($C = C_0 \cdot e^{-kt}$), where $C_0 = C_{\infty}$. A lower k value signifies slower overall digestion, while a reduced C_{∞} indicates a larger fraction of starch that remains resistant to enzymatic hydrolysis. Together with the area under the hydrolysis curve (AUC), these parameters provide a robust quantitative system for comparing printed foods with varying structural designs.

4.3. Calculation and grading of predicted glycemic index (eGI)

The hydrolysis index (HI) is calculated by expressing the AUC of the test sample as a percentage of the AUC of a reference standard, typically white bread [16]. The eGI is then derived using the empirical equation: $eGI = 39.71 + 0.549 \times HI$. Based on this calculated value, printed starch products can be classified as low-GI (≤ 55), medium-GI (56–69), or high-GI (≥ 70) [2, 4]. This grading system provides actionable design targets for developing products tailored to specific consumer glycemic requirements.

4.4. Limitations of current in vitro frameworks

Static in vitro digestion models cannot replicate dynamic gastric emptying, continuous product removal, peristaltic shear forces, or hormonal feedback mechanisms present in vivo [15]. Consequently, eGI values derived exclusively from static protocols represent approximations that may over- or underestimate true postprandial glycemic responses, particularly for structurally complex printed foods where digestion is a time-dependent, diffusion-limited process.

5. Current research challenges and future trends

5.1. Existing knowledge gaps and technical constraints

A critical limitation in the current literature is the absence of unified, data-driven frameworks that quantitatively link mathematical infill descriptors to metabolic outcomes. Most studies present structural and digestive data in parallel but do not develop validated predictive algorithms. Furthermore, there is a pronounced over-reliance on laboratory static simulations, and well-controlled clinical trials confirming the long-term glycemic benefits of 3D-printed starch foods remain exceedingly scarce [1, 13]. Without in vivo validation, the clinical efficacy of structurally engineered foods remains uncertain.

5.2. Future prospects and engineering trends

Addressing these gaps demands the development of advanced machine learning algorithms and multivariable predictive models trained on integrated datasets encompassing structural descriptors (porosity, tortuosity, and crystallinity), digestion kinetic parameters, and eGI values. Such tools would enable the a priori reverse-engineering of printing parameters required to achieve a target glycemic profile. Concurrently, the field must transition toward dynamic in vitro gastrointestinal simulators and conduct rigorous randomized controlled clinical trials measuring postprandial blood glucose responses in target populations. The convergence of these efforts will enable automated, on-demand 3D printing platforms that fabricate personalized meals with digitally programmed digestive kinetics.

The construction of robust predictive models requires systematic data generation covering a wide range of starch types, infill geometries, and post-processing conditions. Digital twin frameworks that simulate the entire print-to-digestion pipeline in silico could dramatically accelerate the design cycle by reducing the need for extensive in vitro screening [17]. Integrating real-time sensing of ink rheology and print fidelity with downstream digestion models would allow adaptive control during manufacturing, ensuring that the target structural features are faithfully reproduced. Furthermore, linking these engineering datasets with individual metabolic profiles, including gut microbiota composition and hormonal responses, would refine glycemic predictions and enable truly

individualized dietary interventions [13]. The interdisciplinary collaboration among food engineers, data scientists, and clinical nutritionists is indispensable for translating these concepts into practical precision nutrition solutions.

6. Conclusion

This paper systematically elucidates the multi-scale structural mechanisms by which 3D printing parameters govern the digestive kinetics of starch-based foods. Internal infill density directly dictates matrix permeability: intermediate filling rates (40%-70%) restrict enzymatic penetration through spatially tortuous pore networks, while lower rates (<40%) accelerate hydrolysis due to an expanded specific surface area. Advanced spatial configurations, including double-layer and gradient structures, introduce interface blocking and crystalline barriers that successfully execute a programmatic "fast-slow" glucose release profile. At the molecular level, maintaining a 60%-85% retention of ordered B-type and V-type starch crystals during hot-extrusion printing provides a fundamental protective mechanism against rapid enzymatic degradation [13]. Post-processing operations such as drying and steaming further modulate structural integrity and digestibility, underscoring the importance of holistic process control. Multi-component interactions involving lipids, polyphenols, and polysaccharides such as pectin enhance this resistance by forming physical shields around glycosidic bonds.

Despite these advances, significant limitations persist. Current knowledge relies heavily on static *in vitro* gastrointestinal models that cannot replicate dynamic physiological conditions [15], and no standardized, universally applicable mathematical framework exists for predicting real-time glycemic responses from digital printing inputs. The absence of clinical *in vivo* validation studies represents a major translational barrier [1]. To overcome these gaps, future research must prioritize the development of multi-variable predictive algorithms that integrate structural attributes, crystallinity indexes, post-processing parameters, and eGI outputs. Rigorous clinical trials in target populations are essential to confirm the efficacy of structure-engineered foods for glycemic control. The ultimate objective is the realization of automated, reliable precision nutrition platforms capable of fabricating personalized starch-based foods with tailored digestive kinetics, thereby advancing the management of metabolic health through digitally designed diets.

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