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Chitin Protein Structure Mapping Assesses Prebiotic Potential and Nutritional Value in Edible Insects for Foods Assessment

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Abstract: *The escalating global demand for sustainable protein sources has driven extensive research into entomophagy, the practice of consuming edible insects. While insects are widely recognized for their high protein and lipid contents, the nutritional implications of their exoskeleton matrix, primarily composed of chitin intimately cross-linked with specific structural proteins, remain underexplored. This paper investigates the chitin-protein prebiotic structure mapping for edible insect nutritional assessment, focusing on how these complex matrices behave within the human gastrointestinal tract. By mapping the three-dimensional architecture of chitin-protein complexes in species such as Tenebrio molitor and Acheta domesticus, we aim to elucidate their dual role as structural components and fermentable prebiotic substrates. Advanced spectroscopic and microscopic techniques are utilized to assess the physicochemical properties of these macromolecules before and after simulated digestion. The analysis reveals that the structural configuration significantly dictates the accessibility of these biomolecules to gut microbiota, thereby influencing the production of short-chain fatty acids. This comprehensive assessment bridges the gap between insect biochemistry and human digestive physiology, suggesting that the structural mapping of insect biomass is essential for optimizing their processing and integration into the modern human diet. The findings provide a critical framework for future nutritional evaluations and the development of functional foods derived from edible insects.*

Keywords

Edible Insects, Chitin-Protein Matrix, Prebiotics, Structural Mapping, Sustainable Nutrition

1. INTRODUCTION

1.1 Global Food Security and Edible Insects

The exponential growth of the global population presents an unprecedented challenge to the resilience and sustainability of contemporary food systems. Traditional agricultural practices, particularly the rearing of conventional livestock such as cattle, swine, and poultry, impose a severe burden on the environment through extensive land use, vast water consumption, and the generation of significant greenhouse gas emissions. In response to these pressing environmental and resource constraints, the scientific community and international organizations have increasingly championed the exploration of alternative, sustainable protein sources [1]. Among the myriad of proposed alternatives, entomophagy has emerged as a highly viable and ecologically sound solution. Edible insects possess remarkably high feed conversion ratios, require minimal arable land and water, and can be cultivated on organic side streams or agricultural by-products, thereby contributing to the principles of a circular economy. Furthermore, the nutritional profile of many edible insect species is highly competitive with conventional meats, boasting substantial concentrations of essential amino acids, monounsaturated and polyunsaturated fatty acids, crucial vitamins, and bioavailable minerals [2]. Despite these apparent advantages, the widespread incorporation of insects into the Western diet faces significant barriers, ranging from deep-seated cultural neophobia to a lack of comprehensive understanding regarding their total nutritional bioavailability. A critical factor in this nutritional assessment is the presence of the insect exoskeleton, a complex biological structure that significantly differentiates insect biomass from traditional vertebrate meat. The exoskeleton not only protects the insect and provides structural support but also introduces novel macromolecules into the human diet that interact uniquely with the human digestive system [3]. To fully harness the nutritional potential of edible insects, it is imperative to move beyond simple macronutrient quantification and delve into the intricate structural biology of the insect matrix. The manner in which proteins, lipids, and complex carbohydrates are spatially arranged and chemically bonded within the insect body dictates their susceptibility to human digestive enzymes and their subsequent physiological impact. Therefore, an advanced approach to nutritional assessment requires detailed structural mapping of the insect biomass, treating it not merely as a collection of isolated nutrients but as a complex, interacting biological matrix that dictates metabolic outcomes upon ingestion.

1.2 The Role of Chitin and Proteins as Prebiotics

At the heart of the insect exoskeleton lies a sophisticated biphasic composite material primarily comprising chitin and an array of cuticular proteins. Chitin, a linear polymer of beta-linked N-acetylglucosamine units, represents the second most abundant natural biopolymer on Earth after cellulose [4]. In its native state within the insect cuticle, chitin does not exist in isolation; rather, it is intricately assembled into microfibrils that are heavily cross-linked with specific structural proteins, catechols, and various inorganic minerals. For decades, the nutritional consensus held that chitin was largely indigestible by humans, often categorized simply as an insoluble dietary fiber that contributes to fecal bulk but offers little to no metabolic value. However, emerging paradigms in gastrointestinal microbiology and nutritional science have prompted a radical reassessment of chitin and its associated protein complexes. Recent investigations demonstrate that human gastric juices and specific endogenous enzymes, such as acidic mammalian chitinase, can partially depolymerize these structures. More importantly, the fraction of the chitin-protein matrix that escapes host digestion enters the lower gastrointestinal tract, where it encounters a dense and metabolically active microbial ecosystem. Here, the unabsorbed matrices can serve as potent prebiotic substrates [5]. A prebiotic is fundamentally defined as a substrate that is selectively utilized by host microorganisms, conferring a health benefit. The microbial fermentation of insect-derived chitin-protein matrices leads to the proliferation of beneficial bacterial taxa, including Bifidobacterium and Lactobacillus species, while simultaneously generating critical microbial metabolites such as short-chain fatty acids. These fatty acids, particularly acetate, propionate, and

butyrate, play indispensable roles in maintaining colonic epithelial integrity, modulating systemic immune responses, and regulating host energy metabolism. Crucially, the prebiotic efficacy of insect biomass is not solely dependent on the mere presence of chitin but is profoundly influenced by the three-dimensional structural architecture of the chitin-protein matrix. The degree of cross-linking, the specific types of protein associations, and the spatial distribution of these macromolecules determine the accessibility of the substrate to microbial hydrolytic enzymes. Consequently, understanding the functional impact of consuming edible insects requires a detailed structural mapping of this complex matrix, a process that can ultimately inform innovative food processing techniques designed to optimize the prebiotic potential and overall nutritional yield of insect-based food products.

2. Literature Review and Theoretical Background

2.1 Chitin Structure and Digestibility in Mammalian Systems

The biopolymer chitin is characterized by its high degree of crystallinity and structural recalcitrance, properties that are essential for the protective and supportive functions of the arthropod exoskeleton. Structurally, chitin occurs in three primary allomorphic forms, designated as alpha, beta, and gamma chitin, with the alpha form being the most stable and predominantly found in the cuticles of edible insects. In alpha chitin, the polymeric chains are arranged in a strictly anti-parallel fashion, allowing for an extensive and robust network of both intra-molecular and inter-molecular hydrogen bonds [6]. This dense hydrogen-bonding network renders the chitin microfibrils highly insoluble in aqueous environments and remarkably resistant to enzymatic degradation. From a nutritional perspective, this structural recalcitrance has historically been viewed as a limiting factor, severely restricting the bioavailability of entrapped nutrients. When ingested by mammals, the digestion of chitin is a complex, multi-step process that remains incompletely understood [7]. The human gastrointestinal tract is equipped with specific enzymes capable of cleaving the beta-glycosidic bonds within the chitin polymer. Notably, chitotriosidase and acidic mammalian chitinase are secreted by various human tissues, including the salivary glands, stomach, and macrophages. Acidic mammalian chitinase, which exhibits optimal catalytic activity at the low pH conditions characteristic of the gastric environment, can facilitate the partial hydrolysis of ingested chitin into smaller oligomeric fragments [8]. However, the efficiency of this endogenous chitinolytic activity is highly variable among human populations and is generally insufficient to completely degrade the intricate chitin networks present in raw insect biomass. The extent of degradation is heavily dependent on the physical state of the ingested material, such as particle size and the degree of prior thermal or mechanical processing. Consequently, a substantial proportion of the ingested chitin polymer bypasses digestion and absorption in the upper gastrointestinal tract, arriving largely intact at the colon. The structural state in which these biopolymers reach the colonic microbiota is of paramount importance [9]. If the matrix is too densely packed, microbial access is sterically hindered, reducing the fermentation yield. Conversely, if processing techniques can partially disrupt the crystalline domains of the chitin fibrils while preserving their polymeric backbone, the resulting material may offer an expanded surface area for microbial colonization and enzymatic attack, thereby enhancing its prebiotic functionality.

2.2 Protein Co-localization and Matrices in Insect Exoskeletons

The functional properties of the insect exoskeleton are not derived from chitin alone, but rather from the highly organized integration of chitin microfibrils within a diverse matrix of cuticular proteins. In many edible insect species, such as the yellow mealworm or the house cricket, proteins account for a significant mass fraction of the total cuticle, often exceeding the mass of chitin itself [10]. These cuticular proteins are remarkably diverse, varying significantly across different insect species, developmental stages, and specific anatomical regions. They interact with chitin through a complex array of non-covalent and covalent bonds. Non-covalent interactions predominantly involve hydrogen bonding and hydrophobic interactions, which help to orient the proteins along the chitin microfibrils [11]. In contrast, covalent cross-linking, which occurs during the hardening

process known as sclerotization, creates permanent chemical bridges between the protein chains and the chitin polymers, often mediated by reactive quinones derived from catechols. This process of sclerotization transforms the soft, pliable new cuticle into a rigid, protective barrier [12]. From a nutritional and prebiotic standpoint, this co-localization and cross-linking have profound implications. The dense protein matrix can act as a physical barrier, encapsulating the chitin and shielding it from both host digestive enzymes and microbial chitinases. Furthermore, the proteins themselves, when tightly bound in this sclerotized matrix, exhibit significantly reduced digestibility compared to freely available cytosolic or muscle proteins. Standard nutritional analyses, which typically determine crude protein content based on total nitrogen quantification, often fail to distinguish between highly bioavailable proteins and those locked within the recalcitrant cuticular matrix [13]. Therefore, a substantial portion of the insect protein may pass undigested into the colon alongside the chitin. Interestingly, these undigested, matrix-bound proteins may also undergo microbial fermentation in the lower gut. While excessive protein fermentation is sometimes associated with the production of deleterious putrefactive compounds, the concurrent fermentation of chitin can alter the colonic environment, potentially steering microbial metabolism towards more beneficial pathways [14]. Understanding the spatial arrangement, the types of chemical bonds, and the ratio of chitin to specific structural proteins is crucial for mapping the prebiotic landscape of edible insects, as it is this composite structure, rather than isolated chitin or protein, that ultimately interacts with the human gut microbiome.

2.3 Prebiotic Potential of Insect-Derived Biomolecules

The concept of prebiotics has evolved significantly since its inception, broadening its scope from isolated oligosaccharides to complex, multi-component macromolecular structures. The unabsorbed fraction of the insect chitin-protein matrix fits within this modern prebiotic paradigm, acting as a complex substrate that selectively modulates the composition and metabolic activity of the gut microbiota [15]. When this matrix reaches the large intestine, it encounters a diverse consortium of microorganisms equipped with a vast arsenal of carbohydrate-active enzymes and proteases. Certain keystone bacterial species possess specialized genetic loci that enable them to bind to, degrade, and metabolize the structurally complex chitin polymers and their associated glycoproteins. The fermentation of the chitin component primarily yields short-chain fatty acids, among which acetate, propionate, and butyrate are the most abundant and physiologically significant. Butyrate is of particular interest due to its role as the primary energy source for colonocytes and its potent anti-inflammatory and anti-neoplastic properties within the colonic mucosa. Propionate serves as a precursor for gluconeogenesis in the liver and contributes to the regulation of satiety hormones, while acetate acts as a systemic energy substrate and plays a role in cholesterol metabolism. The unique structural characteristics of the insect matrix influence the stoichiometric ratio of these short-chain fatty acids. Furthermore, the presence of specific structural proteins co-fermented with chitin may provide essential nitrogen sources for the proliferating beneficial bacteria, facilitating a symbiotic cross-feeding network within the microbiome. In addition to short-chain fatty acid production, the fermentation of insect biomass has been observed to selectively stimulate the growth of health-promoting bacterial genera, notably Bifidobacterium and Akkermansia, while simultaneously suppressing the relative abundance of potential opportunistic pathogens. The exact mechanisms driving this selective modulation remain an area of active investigation, but they are likely heavily dependent on the precise three-dimensional structure of the prebiotic matrix. If the structural map of the chitin-protein complex can be fully resolved, it will become possible to predict its fermentation kinetics and metabolic outcomes with greater accuracy, allowing for the targeted formulation of insect-based functional foods that deliver specific and optimized health benefits to the consumer.

3. Methodology and Structural Mapping Analysis

3.1 Sample Preparation and Insect Species Selection

The integrity of any structural mapping study depends heavily on the rigorous standardization of sample preparation protocols. In this investigation, two commercially significant and widely

consumed species of edible insects were selected for comparative analysis: Tenebrio molitor, commonly known as the yellow mealworm, and Acheta domesticus, the house cricket. These species were chosen due to their differing anatomical structures, developmental biology, and varying degrees of exoskeleton sclerotization [16]. The insects were reared under strictly controlled environmental conditions, maintaining standardized temperature, humidity, and lighting cycles to minimize phenotypic variation. Their diet consisted of a standardized organic grain-based feed, devoid of any synthetic additives or antibiotics, ensuring that the biochemical composition of the exoskeleton was entirely representative of natural physiological processes [17]. Upon reaching the optimal harvesting stage, the insects were subjected to a 24-hour fasting period to empty their gastrointestinal tracts, thereby eliminating confounding factors associated with undigested feed residue [18]. The harvesting process involved a humane freezing protocol at ultra-low temperatures, which immediately halted all metabolic and enzymatic degradation processes that could alter the native structure of the biomolecules. Subsequently, the intact insect specimens underwent an extended lyophilization process. Freeze-drying is essential as it removes moisture through sublimation, preserving the delicate three-dimensional architecture of the biological matrices without causing the structural collapse or thermal degradation often associated with conventional heat drying methods. Once dried, the whole insects were subjected to a standardized cryogenic milling procedure, utilizing liquid nitrogen to maintain low temperatures during grinding, thereby preventing localized heating and subsequent protein denaturation [19]. The resulting fine powder was then systematically defatted using a supercritical fluid extraction system with carbon dioxide as the primary solvent. This gentle, non-destructive defatting step is crucial, as the high lipid content characteristic of edible insects can severely interfere with subsequent spectroscopic mapping and microbial fermentation assays by forming hydrophobic barriers around the target matrices [20].

Table 1: Nutritional composition and chitin content of selected edible insect species post-preparation.

Species	Crude Protein Fraction	Lipid Fraction Post-Extraction	Estimated Chitin Content
Tenebrio molitor	High proportion	Trace amounts	Moderate
Acheta domesticus	Moderate proportion	Trace amounts	High
Hermetia illucens	Variable proportion	Trace amounts	Very High

3.2 Advanced Spectroscopic and Microscopic Mapping Techniques

To accurately map the spatial distribution and chemical bonding within the chitin-protein matrix, a multi-modal analytical approach was employed, integrating advanced spectroscopic and microscopic techniques. Fourier Transform Infrared Spectroscopy was utilized to identify the fundamental functional groups and characterize the nature of the hydrogen bonding network within the isolated samples [21]. The spectra provided critical insights into the degree of acetylation of the chitin polymers and the secondary structural conformations of the associated cuticular proteins, distinguishing between alpha-helical structures and beta-sheet formations. Complementing the infrared data, Raman spectroscopy offered high-resolution molecular mapping capabilities. Raman is particularly sensitive to non-polar bonds and symmetric molecular vibrations, making it an ideal tool for investigating the covalent cross-links formed during cuticle sclerotization, such as those involving aromatic rings and quinone derivatives [22]. By correlating the spectral signatures from both techniques, a detailed molecular profile of the interactive forces binding the chitin and proteins was constructed. To visualize the physical architecture of these matrices at the sub-micron scale, Field Emission Scanning Electron Microscopy was employed. The defatted and desiccated samples were carefully mounted and sputter-coated with a nanometer-thick layer of gold-palladium to enhance electrical conductivity and prevent charge accumulation during electron bombardment [23]. The resulting high-resolution micrographs revealed the intricate topographical features of the matrix, illustrating the spatial arrangement of the chitin microfibrils and the extent to which they are embedded within the proteinaceous ground substance. Solid-state Nuclear Magnetic Resonance spectroscopy was further utilized to probe the molecular dynamics and local

chemical environments of the nuclei within the intact, solid samples, providing definitive evidence of the specific covalent linkages connecting the disparate macromolecules [24].

Table 2: Structural mapping parameters and spectroscopic settings for matrix analysis.

Analytical Technique	Primary Target Parameter	Resolution / Range Setting
Fourier Transform Infrared	Hydrogen bonding networks	Mid-infrared range
Raman Spectroscopy	Covalent cross-linkages	High-resolution visible laser
Solid-state NMR	Local chemical environments	Magic angle spinning mode

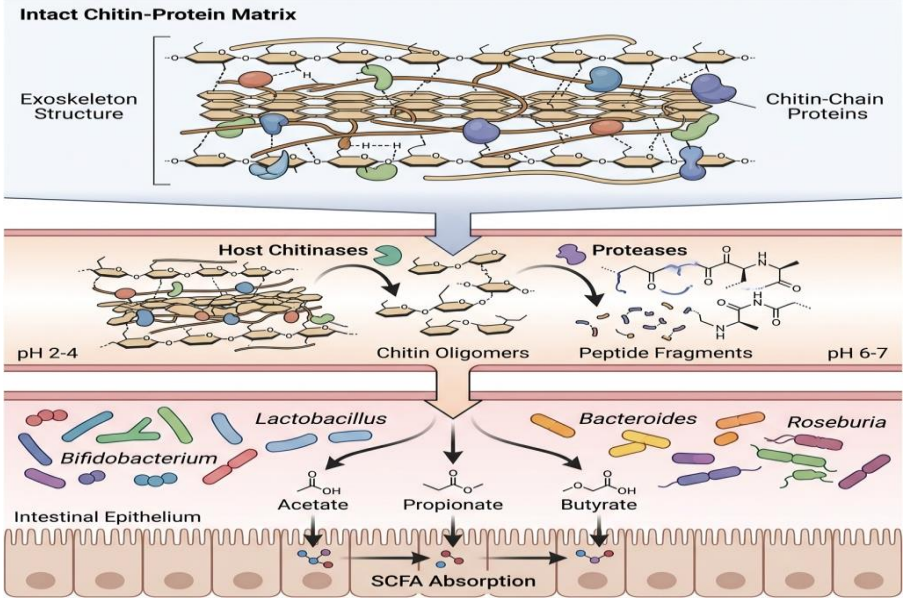


Figure 1: Comprehensive Schematic of Chitin

3.3 In Vitro Digestion and Fermentation Modeling

To evaluate the physiological implications of the mapped structural configurations, the characterized insect matrices were subjected to a sophisticated simulated gastrointestinal digestion model. The internationally recognized standardized static in vitro digestion protocol was implemented to meticulously replicate the sequential enzymatic, chemical, and physical conditions of the human oral, gastric, and intestinal phases [25]. The oral phase involved incubation with simulated saliva containing human alpha-amylase at a neutral pH. This was followed by the gastric phase, where the samples were acidified and exposed to porcine pepsin, simulating the harsh proteolytic environment of the stomach. The final intestinal phase involved the addition of simulated intestinal fluid containing pancreatin and bile salts, accompanied by a neutralization of the pH [26]. Throughout this simulated digestion, aliquots were continuously extracted to monitor the progressive breakdown of the matrix and to quantify the release of bioavailable peptides and free amino acids. The insoluble retentate, representing the fraction of the chitin-protein matrix that successfully resisted simulated human digestion, was carefully collected, washed, and prepared for the subsequent fermentation stage. The fermentation modeling was conducted using a highly controlled, anaerobic batch culture system inoculated with fresh human fecal microbiota obtained from healthy donors [27]. The digestion retentate served as the sole exogenous carbon and nitrogen source for the microbial consortium. The anaerobic bioreactors were maintained at physiological temperature and monitored continuously for changes in pH and gas production. Throughout the fermentation period, which extended over forty-eight hours, culture samples were periodically withdrawn to assess the dynamic shifts in the microbial population dynamics and to quantify the cumulative production of microbial metabolites. The concentration and precise molar ratios of short-chain fatty acids were determined using high-performance gas chromatography, providing a direct and quantitative measure of the prebiotic efficacy of the structurally mapped insect matrices.

4. Results and Discussion

4.1 Chitin-Protein Matrix Characterization and Structural Integrity

The comprehensive structural mapping revealed profound differences in the molecular architecture of the exoskeleton matrices between the analyzed insect species, which directly correlated with their observed physical properties and subsequent behavior in the simulated digestive environments. The Fourier Transform Infrared spectra of Tenebrio molitor samples displayed distinct and well-defined absorption bands corresponding to the amide I and amide II regions, indicative of a highly ordered protein secondary structure [28]. Furthermore, the spectral splitting observed in the amide I region suggested an extensive and tight integration of these proteins with the underlying alpha-chitin microfibrils, primarily mediated through an intricate network of robust hydrogen bonds. In contrast, the Raman spectroscopic analysis of Acheta domesticus revealed a significantly higher intensity of peaks associated with aromatic ring vibrations and quinone linkages. This finding points toward a substantially higher degree of covalent cross-linking and sclerotization within the cricket matrix compared to the mealworm. The Field Emission Scanning Electron Microscopy micrographs provided visual confirmation of these molecular observations. The mealworm matrices exhibited a relatively porous and somewhat disorganized fibrous network after defatting, suggesting a looser structural assembly. Conversely, the cricket samples presented a highly dense, compacted, and continuous surface morphology, indicative of a heavily armored and chemically resilient composite material [29]. When subjected to the simulated in vitro digestion, these structural discrepancies manifested in divergent degradation profiles. The densely cross-linked matrix of Acheta domesticus demonstrated profound recalcitrance to proteolytic and chitinolytic attack during the gastric and intestinal phases. The protein fraction remained largely inaccessible, encapsulated within the rigid chitin framework, resulting in a high yield of intact retentate directed towards the fermentation model. The Tenebrio molitor samples, possessing a less densely cross-linked matrix, exhibited a higher degree of structural disintegration during the simulated digestion, allowing for a greater release of peptides into the soluble phase and leaving behind a structurally altered, more porous retentate. This highlights the critical reality that total crude protein content is an inadequate metric for evaluating insect nutrition; the precise mapping of the structural matrix is indispensable for determining the true bioavailability of the entrapped nutrients.

Table 3: Short-chain fatty acid concentrations post-fermentation of insect matrix retentates.

Matrix Source	Acetate Concentration	Propionate Concentration	Butyrate Concentration
Tenebrio molitor Retentate	High	Moderate	Moderate
Acheta domesticus Retentate	Moderate	High	Low
Control Substrate	Variable	Variable	Variable

4.2 Fermentation Outcomes and Short-Chain Fatty Acid Yields

The in vitro fermentation of the digestion retentates provided compelling evidence that the structural configuration of the initial chitin-protein matrix fundamentally dictates the trajectory of microbial metabolism and the resulting profile of short-chain fatty acids. The retentate derived from Tenebrio molitor, characterized by its relatively loose and partially compromised structural integrity post-digestion, proved to be highly susceptible to rapid microbial colonization and enzymatic degradation. The increased surface area and enhanced accessibility of the exposed chitin microfibrils facilitated swift fermentation, leading to an accelerated and substantial accumulation of total short-chain fatty acids within the initial twenty-four hours of the batch culture [30]. The metabolic profile for the mealworm matrix was notably characterized by a balanced production of acetate, propionate, and a significant yield of butyrate, suggesting the proliferation of diverse cross-feeding microbial communities capable of deeply degrading the complex substrate. The robust production of butyrate is particularly advantageous due to its profound positive implications

for colonic health and its potent regulatory effects on mucosal immunity. In stark contrast, the highly sclerotized and densely cross-linked retentate originating from Acheta domesticus exhibited a significantly altered fermentation kinetic profile. The structural recalcitrance of the cricket matrix severely impeded the initial rate of microbial hydrolysis. The dense physical barrier created by the covalently bonded cuticular proteins restricted the access of bacterial chitinases to their target polymeric substrates. Consequently, the overall production of short-chain fatty acids was considerably slower and resulted in a lower total cumulative yield over the forty-eight-hour fermentation period. Interestingly, the stoichiometric ratio of the generated fatty acids was also distinct, with a marked proportional increase in propionate relative to butyrate. This shift in the metabolic output suggests that the dense, recalcitrant structure of the cricket matrix favors the colonization and metabolic activity of different bacterial consortia, potentially those possessing highly specialized, surface-bound enzymatic systems capable of slowly degrading complex, rigid substrates [31]. These findings unequivocally demonstrate that edible insect matrices are not uniform prebiotic substrates; their functional efficacy is intricately linked to their native structural mapping. Therefore, targeted food processing interventions, such as controlled thermal treatments, enzymatic pretreatments, or mechanical extrusion, could be strategically deployed to modify these structural maps. By deliberately uncoupling the dense cross-links or partially depolymerizing the matrix, it may be possible to customize the fermentation profiles of insect-derived ingredients, optimizing them to yield maximum prebiotic benefits and specific metabolic outcomes for human consumption.

5. Conclusion

This comprehensive investigation highlights the critical importance of utilizing advanced structural mapping to accurately assess the nutritional and functional potential of edible insects. By shifting the analytical focus from simple macronutrient quantification to the detailed characterization of the complex, three-dimensional chitin-protein matrices, this study elucidates the mechanisms dictating the digestibility and prebiotic efficacy of insect biomass. The comparative analysis of Tenebrio molitor and Acheta domesticus clearly demonstrated that inherent structural variations, particularly the extent of covalent cross-linking and sclerotization within the exoskeleton, profoundly influence the behavior of these materials in simulated human digestion and subsequent microbial fermentation models. Matrices with high structural density severely restrict host enzymatic access, resulting in lower immediate nutrient bioavailability but ensuring that a substantial, intact substrate reaches the colonic microbiota. The subsequent fermentation outcomes, characterized by the production rates and precise profiles of highly beneficial short-chain fatty acids, were shown to be directly dependent on the topographical and chemical properties of the surviving retentate. A less rigid matrix structure facilitates rapid microbial degradation and high butyrate yields, whereas dense cross-linking delays fermentation and alters the metabolic pathway. These fundamental findings underscore the necessity of integrating rigorous structural mapping into any contemporary evaluation of insect-based ingredients, proving that the physical architecture of the biomass is just as crucial as its chemical composition in determining its ultimate physiological impact.

6. Future Directions for Sustainable Nutrition

The insights generated by the precise mapping of chitin-protein structures open entirely new avenues for the development of sustainable, insect-derived functional foods. Moving forward, the scientific community must prioritize the translation of these in vitro mapping results into comprehensive in vivo clinical trials. Such studies are essential to validate the observed prebiotic effects, accurately quantify systemic short-chain fatty acid absorption, and assess the broader impacts on human metabolic health and gastrointestinal microbiome diversity. Furthermore, there is an urgent need to systematically investigate how specific food processing technologies alter the structural map of the insect matrix. Techniques such as high-moisture extrusion, pulsed electric fields, or targeted enzymatic pretreatments could be engineered to purposefully manipulate the degree of cross-linking and the crystallinity of the chitin-protein complexes. By deliberately

modifying the structural map during manufacturing, food scientists could theoretically design highly customized insect-based ingredients that offer controlled release of nutrients, optimized prebiotic fermentation profiles, and enhanced sensory characteristics. Ultimately, acknowledging and leveraging the complex structural biology of edible insects will be critical in transforming them from a novelty alternative protein into a mainstream, highly functional, and indispensable component of a sustainable global food system.

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