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CO-PROTEIN EFFECTS IN WHEAT-BASED SYSTEMS: MOLECULAR INTERACTIONS, NETWORK FORMATION, AND IMPLICATIONS FOR NOODLE QUALITY

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| Keywords | Abstract |
|---|---|
| <p><i>Gluten Network, Co-Protein Effects, Sulfhydryl–Disulfide Exchange, Globular Proteins, Hydrophobic Interactions, Noodle Texture.</i></p> | <p>Protein network formation is the primary determinant of structure, texture, and cooking quality in wheat-based foods. While gluten proteins provide the structural backbone of dough systems, globular proteins from egg, soy, and whey are frequently incorporated into formulations, giving rise to complex co-protein interactions. These interactions influence thermal denaturation, sulfhydryl–disulfide exchange reactions, hydrophobic aggregation, and phase behaviour. The extent and kinetics of protein polymerization determine whether composite systems exhibit synergistic reinforcement or structural weakening. In noodle systems, optimal protein network formation must accommodate starch gelatinization while maintaining structural integrity during cooking. This review synthesizes current understanding of gluten architecture, globular protein reactivity, intermolecular bonding mechanisms, and their collective impact on noodle texture and cooking stability. Emphasis is placed on balancing covalent and non-covalent interactions to achieve superior product quality. Insights into molecular compatibility and redox control provide opportunities for ingredient substitution, texture optimization, and development of sustainable wheat-based foods.</p> |



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1. INTRODUCTION

The structural performance of wheat-based foods such as bread, pasta, and noodles depends largely on the formation and stabilization of protein networks. Gluten proteins, comprising gliadins and glutenins, are responsible for the unique viscoelastic properties of wheat dough. However, many commercial formulations incorporate additional protein sources, including egg, soy, and whey proteins, to modify texture, nutritional value, or cost efficiency. The coexistence of structurally distinct protein classes results in complex interaction phenomena that influence network formation, thermal behavior, and final product quality.

Unlike gluten, which behaves as an entangled polymeric system, globular proteins possess compact tertiary structures that unfold upon heating. Their denaturation exposes reactive functional groups capable of forming new interactions with gluten proteins. These molecular events can enhance or disrupt the native gluten network depending on compatibility and processing conditions. Understanding the mechanisms governing these co-protein interactions is critical for optimizing noodle quality and designing next-generation cereal-based foods.

2. GLUTEN NETWORK ARCHITECTURE AND FUNCTIONAL BEHAVIOR

Gluten is a dynamic polymeric network formed when wheat flour is hydrated and mechanically mixed. It consists of monomeric gliadins, which contribute extensibility, and polymeric glutenins, which provide elasticity through intermolecular disulfide cross linking (Wieser, 2007; Shewry & Halford, 2002). The viscoelasticity of dough arises from the balance between viscous flow of gliadins and elastic recoil of glutenin macro polymers. Mechanical mixing induces partial unfolding and alignment of gluten proteins, promoting thiol–disulfide interchange reactions that increase polymer size and network connectivity.

Upon heating, further cross linking occurs, stabilizing the protein matrix and fixing structure in thermally processed products (Belton, 1999). Unlike globular proteins, gluten does not exhibit a sharp denaturation transition but instead undergoes gradual conformational rearrangements. Its polymeric architecture allows substantial deformation without rupture, explaining its irreplaceable role in wheat-based systems. However, gluten functionality is highly sensitive to redox conditions, hydration levels, and the presence of other proteins. The introduction of globular proteins modifies molecular mobility and cross linking pathways, thereby altering network topology and rheological performance.

3. THERMAL DENATURATION AND REACTIVITY OF GLOBULAR PROTEINS

Globular proteins from egg, soy, and whey possess well-defined tertiary structures stabilized by hydrogen bonding, hydrophobic interactions, and disulfide bridges. Thermal treatment induces cooperative unfolding, exposing buried hydrophobic residues and sulfhydryl groups (Damodaran, 1996). This structural transition significantly enhances their reactivity within composite protein systems. For example, β -lactoglobulin unfolds near 70–75°C, exposing a free thiol group capable of participating in thiol–disulfide exchange reactions (Havea et al., 2001). Similarly, soy glycinin



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dissociates and unfolds during heating, increasing surface hydrophobicity and aggregation tendency (Renkema & van Vliet, 2002). In wheat-based matrices, these unfolded proteins may either integrate into the gluten network via covalent bonding or form independent aggregates depending on thermodynamic compatibility. Controlled integration can strengthen structure, whereas excessive aggregation may disrupt gluten continuity. Therefore, thermal denaturation represents a pivotal event that governs the balance between reinforcement and destabilization in mixed protein systems.

4. SULFHYDRYL–DISULFIDE EXCHANGE REACTIONS IN COMPOSITE NETWORKS

Thiol–disulfide interchange reactions are central to protein polymerization in wheat-based systems. These reactions involve nucleophilic attack by a free sulfhydryl group on an existing disulfide bond, resulting in bond rearrangement and polymer growth (Kinsella & Melachouris, 1976). In gluten, such dynamic reshuffling contributes to extensibility and strength during mixing and heating. When globular proteins containing reactive cysteine residues are introduced, additional crosslinking routes emerge. Whey proteins and serum albumin can form mixed disulfide bonds with glutenin subunits, altering network architecture (Croguennec et al., 2004). Reaction kinetics depend on temperature, pH, and redox potential. Oxidative conditions promote crosslink formation, whereas reducing agents weaken the network. Importantly, excessive cross linking may reduce flexibility, impairing the matrix’s ability to accommodate starch swelling during cooking. Thus, optimal noodle quality requires controlled sulfhydryl reactivity to balance structural strength and elasticity.

5. HYDROPHOBIC INTERACTIONS AND PHASE BEHAVIOR

In addition to covalent bonding, hydrophobic interactions significantly influence composite protein structure. Protein unfolding exposes non-polar residues that associate to minimize water contact, driving aggregation (Clark et al., 2001). In mixed systems, differences in molecular size, charge, and solubility may lead to thermodynamic incompatibility and micro phase separation (Tolstoguzov, 1997). Moderate hydrophobic association can densify networks and enhance firmness. However, excessive aggregation creates structural discontinuities that weaken mechanical properties. Environmental factors such as solvent polarity, ionic strength, and water activity modulate hydrophobic interactions. The presence of lipids, particularly in egg yolk, further affects network organization by interacting with hydrophobic gluten domains. Therefore, understanding phase behavior is crucial for predicting structural homogeneity and mechanical stability in wheat–globular protein blends.

6. IMPLICATIONS FOR NOODLE TEXTURE AND COOKING STABILITY

Noodle texture depends on coordinated protein network formation and starch gelatinization. During cooking, starch granules swell and exert mechanical stress on the surrounding protein matrix. A sufficiently crosslinked gluten network restricts excessive swelling and reduces cooking



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loss, thereby enhancing firmness (Hou, 2010). When globular proteins are incorporated, their influence depends on their degree of integration into the gluten matrix. Moderate cross linking may improve tensile strength, whereas insufficient interaction results in weak structure and increased leaching of soluble solids. Conversely, overly rigid networks formed by excessive disulfide bonding reduce elasticity and produce brittle textures. Egg proteins generally enhance firmness due to their gel-forming capacity, while whey proteins may have variable effects depending on processing conditions (Baik et al., 2003). Optimal noodle performance therefore requires precise control over polymerization kinetics and molecular compatibility.

7. CONCLUSIONS AND FUTURE PERSPECTIVES

Co-protein interactions in wheat-based systems involve a complex interplay of covalent and non-covalent forces. Gluten provides the structural backbone, while globular proteins modify network topology through thermal unfolding, sulfhydryl reactivity, and hydrophobic aggregation. The balance between crosslink density and molecular flexibility determines final product quality. Future research should focus on predictive modeling of protein compatibility, real-time monitoring of redox-controlled polymerization, and molecular imaging of composite networks. Such insights will facilitate rational formulation strategies aimed at improving noodle quality, enabling sustainable ingredient substitution, and advancing cereal-based food innovation.

8. AUTHOR(S) CONTRIBUTION

The writers affirm that they have no connections to, or engagement with, any group or body That provides financial or non-financial assistance for the topics or resources covered in this Manuscript.

9. CONFLICTS OF INTEREST

The authors declared no potential conflicts of interest with respect to the research, authorship, And/or publication of this article.

10. PLAGIARISM POLICY

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