

Modification of Proteins for Improved Functional Properties

Kalli Vasanthi^{1*} and Kinnera Tejaswini²

¹Department of Fish Processing Technology, ICAR-CIFE, Mumbai

²Department of Fish Nutrition and Feed Technology, ICAR-CIFE, Mumbai

*Corresponding author

Email address: Vasanthi.phtpb104@cife.edu.in

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Abstract

Proteins represent a fundamental and structural component of a food system. They play a role in determining the functionality and overall sensory quality of any food. In meat, especially seafood, myofibrillar proteins play a pivotal role in determining the value and functionality. Proteins, being amphipathic, are involved in several interfacial interactions, making them versatile ingredients in animal and plant-based formulations. However, native proteins often exhibit limitations in solubility, stability, or processing performance, which could be improved through modification. This article provides a brief overview of protein modification types, their uses, and significant advantages they offer in improving functionality. A detailed discussion of all the types of modifications currently used in the food processing industry was mentioned. Strategic modification of proteins will help in the optimization of food quality, functionality and innovation of new products. Modification also plays a key role in the formation of restructured meats, especially in the development of plant-based meats. Growing consumer demand for plant-based meats has been driving the search for promising alternatives to convert valuable plant proteins into products that mimic the meat texture while maintaining product integrity.

Keywords: Protein, Amphipathic, Modification, Restructured

Introduction

Food structure is an essential sensory attribute that affects food stability and consumer choices. Proteins, owing to their amphipathic nature, serve as versatile ingredients. They act as dynamic surface-active agents for interfacial protein-to-carbohydrate, protein-to-lipid, protein-to-air, and protein-to-water interactions. Interactions play a pivotal role in determining the functionality and surface activity of a protein (Kinsella & Melachouris, 1976; Foegeding, 2015). Among proteins, myofibrillar proteins play an important role in determining the functional properties of meat. These properties facilitate their use as ingredients in food formulation to confer appearance, flavor, color, odor, texture, and even structure to food products (Akharume et al., 2021).

Table 1. Functional properties of protein, along with the general terminologies used

General property	Functional terminology
Organoleptic	Colour, flavour, odour, mouthfeel, smoothness, grittiness, turbidity
Hydration	Solubility, dispersibility, wettability, thickening, gelling, water holding capacity, water absorption capacity, viscosity
Surface active property	Emulsion, foaming, whipping, flavour binding, stabilization
Structural/rheological property	Elasticity, gelation, stickiness, cohesion, adhesion, chewiness, viscosity, aggregation
Others	Compatibility with additives, enzymatic, inertness, modification properties

Mechanism of Protein Modification

It depends on the functionality of interest, which may further depend on the nature, structural properties, and mechanism of protein modification. A thorough knowledge of the relationship between the structure and function of proteins will help in understanding the modifications, that influence the performance of a food (Mehta et al., 2025; Yadav et al., 2025). For example, an increase in the solubility of a protein may require mechanisms that can provide a reduction in size, electrostatic repulsion, an increase in hydrophilicity or the manipulation of the isoelectric point and net charge. Surface- active properties can be enhanced by balancing the hydrophilic and hydrophobic properties of protein (Phillips, 2013).

Types of Modification

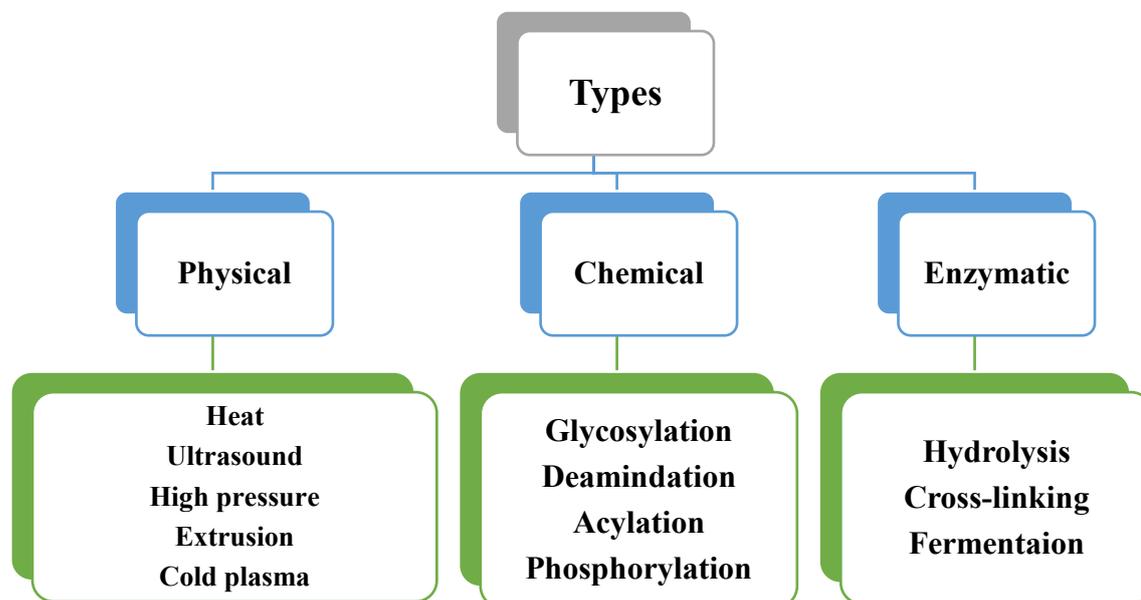


Fig. 1 Types of protein modification

Physical Modification

Heat Treatment

This method is based on the principle that controlled heat could help in modifying the structure of food, thus resulting in an improvement of their functional properties. Rate of modification is dependent on the temperature, heating rate, ionic concentration and solution pH. This can result in improvements in gelation, emulsifying properties and protein digestibility. A decrease in solubility was reported, which facilitated an increase in Fat Binding capacity, Emulsion Activity Index, and Water Holding Capacity (Bubler et al., 2015).

Ultrasound Treatment

Ultrasound treatment involves the use of propagated acoustic waves beyond the threshold of human hearing i.e., 16 kHz. Low-frequency ultrasound (16–100 kHz) at higher power levels (10-1000W/cm²) are applied for structural modification, whereas high-frequency ultrasound (100KHz to 1MHz) and power levels (<1 W/cm²) is applied for physico-chemical evaluation of foods. Modification of proteins is mainly due to localized hydrodynamic shearing, induced as a result of ultrasonic cavitation. This leads to the heating of protein and consequent structural modification (Size and distribution). Ultrasonic cavitation is characterized by rapid build-up

and collapse of gas bubbles, generated by localized pressure differentials in wave propagation over a short period. Enhanced solubility, Emulsion-forming ability, and Foamability have been reported (Hu et al., 2015; Amiri et al., 2018).

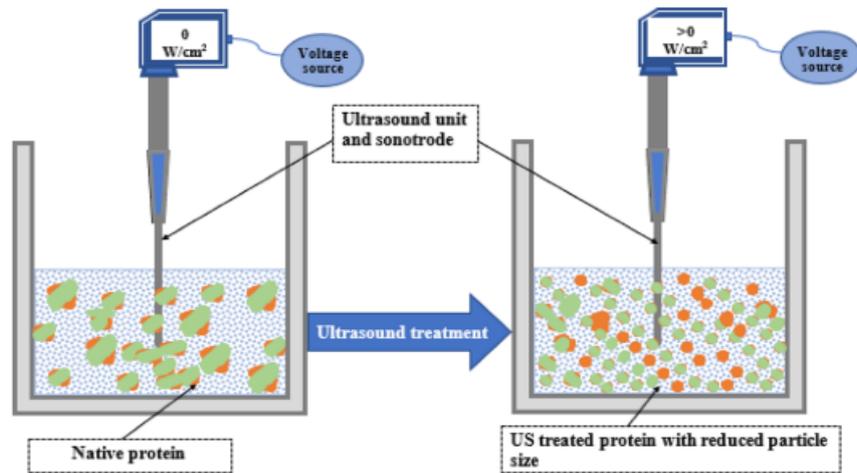


Fig. 2 Ultrasound modification of protein

High-Pressure Processing

This involves a combination of pressure, time and temperature that helps in inducing structural changes in protein, which affects its functionality. Pressures (200-700 MPa) will facilitate the breakage of non-covalent bonds in proteins, resulting in denaturation and aggregation. A change in the volume of protein has been observed, resulting in an alteration of protein structure. Application of high pressure leads to compression of protein cavities, rupture of non-covalent interactions, and formation of new interactions. Hydrogen bonds of protein were found to be stable, and were affected when pressures >1000 MPa were applied. HPP was found to increase surface hydrophobicity, gelation, and rheological properties, whereas a decrease in solubility was observed. Proteins modified at 250 MPa formed a superior gel in comparison to the ones modified at other pressure ranges (Bubler et al., 2015).

Extrusion Process

Extrusion is a HTST process that combines high temperature, pressure, and shear. Short time and intense extrusion conditions impact the functionality of proteins such as solubility, texture, emulsion, and gelation properties. Treatment employing 15% moisture and 130°C resulted in an increase in hydrolysis and solubility of protein. Moisture content plays a role in determining the final protein structure (Chen et al., 2018). Based on this they are divided into:

- **High moisture (50–80%)** – helps in production of structured meats using vegetable proteins stabilized by hydrogen and disulfide bonds
- **Low moisture (<30%)** - results in harder and less soluble proteins stabilized by hydrophobic and disulfide bonds.

Cold Plasma

Cold plasma is a partially ionized gaseous state comprising reactive oxygen species (ROS), reactive nitrogen species (RNS), and UV radiation. These reactive species interact with protein molecules, resulting in high-energy breaks. Covalent bonds were broken, and new functional groups, such as sulfhydryl (–SH) or sulfoxide (–SO) groups, were formed in this modification. Such modifications resulted in altered protein conformation, improved solubility, enhanced water and fat binding, and stabilized emulsions (Bubler et al., 2015).

Chemical Modification of Proteins

Chemical methods of modification use chemical agents that primarily rely on reactive side chains. This process might involve the addition of new functional groups, thus altering the net charge of protein. Although significant improvements in functionality were observed, commercialization is limited by regulatory and safety concerns (Akharume *et al.*, 2021). Chemical modification of proteins includes:

Glycosylation

This method involves the attachment of carbohydrate moieties, primarily to the side chains of lysine residues or to the N-terminus of a protein molecule. This is typically observed during the early stages of the Maillard reaction. Temperature (60-80°C), time, pH (7 to 8.5), Relative humidity, degree of glycosylation, type of protein and protein–polysaccharide ratio (1:1 to 1:4) influence the rate of modification. Improved thermal stability, viscosity, solubility, emulsification, foaming, and water-holding capacity were observed following this modification (Sharif et al., 2018).

Acylation

This is a chemical derivatization method that involves the transfer of acyl groups to the amino or hydroxyl groups of an amino acid. Nomenclature of acylation varied depending on the acylating agent and the side chain to which it is attached. This includes Succinylation (Succinic anhydride attached to Lysine), acetylation (Acetyl group to Protein), and palmitoylation

(Palmitic acid to Cysteine). Reduction in the protein net surface charge, dissociation of the protein spatial structure, and unfolding of the polypeptide chain were observed. Functional properties such as flexibility, surface tension, and foaming were altered (Gruener and Ismond, 1997).

Deamidation

A process in which ammonia is lost due to the reaction between protein and strong acid or alkali at elevated temperatures. This involves the conversion of δ - (asparagine) or γ - (glutamine) amide groups to carboxylic groups (α - and γ -aspartic and glutamic acids) with the release of ammonia. Factors such as temperature, pH, water activity, amino acid sequence, and nonionic catalyst will influence the rate of deamidation. This resulted in an increase in the net negative charge of the protein, and the unfolding of the protein. 72% deamidation showed a significant increase in solubility, foamability, and emulsifying properties of the protein (Akharume et al., 2021).

Phosphorylation

Phosphorylation involves the covalent attachment of phosphoryl groups (PO_3^-) to the protein at specific amino acids. An increase in hydrophilicity and negative surface charge was observed, which led to an enhanced solubility and increased emulsifying properties (Hu et al., 2019).

Enzymatic Modification

Enzymatic approaches are often preferred due to their specificity, speed, and mild reaction conditions. They resulted in altered structural properties. Enzymes used in modification are grouped as

- ✓ **Proteolytic enzymes** (Papain, Pepsin, Trypsin, Alcalase) that cleave peptide bonds.
- ✓ **Non-proteolytic enzymes**, especially Transglutaminase (TGase), which catalyze crosslinking reactions.

Microbial TGase (Ca^{+2} independent) from *Streptoverticillium moboarense* (optimal pH 5–8; temperature 50°C) catalyzes acyl transfer, deamidation and crosslinking between glutamine (acyl donor) and lysine (acyl acceptor) residues. This resulted in enhanced gelation, emulsification, and water-binding capacity without significant change in pH, color, flavor, or nutritional quality. This modification is employed mostly in the preparation of restructured

meat and fish products (Gaspar & de Goes-Favoni, 2015). Examples of protein crosslinkers include tyrosinase (crosslinks quinone to protein), laccase, sulfhydryl oxidase and peroxidase. They contribute significantly in restructuring of meat, surimi setting and improvement of textural properties (Buchert et al., 2010).

Conclusion

Protein modification has emerged as a powerful tool in the field of food technology to tailor food functionality. The main objective of any modification is to improve the functional properties and overall digestibility of protein. Modification can be of any type, whether physical, or chemical, or enzymatic. They directly play a role in influencing solubility, emulsification, gelation, and the stability of proteins. As consumer demand shifts towards sustainable protein systems and value-added formulations, modification techniques offer pathway to optimize performance without compromising on nutritional or sensory quality. They play a role in the preparation of restructured meats and plant-based meats, which are in high demand in the present-day scenario.

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