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Sustainability Statement:

The review altogether describes a new approach to look towards the sustainability of plant proteins as an alternative to animal based protein systems. Plant proteins, being nature friendly are being studied extensively to replace animal based protein wholly or in part, to align with the sustainable UN-SDG's.

On Behalf of all the authors,

Sincerely,

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Review

Protein Complexations and Amyloid Fibrilization as Novel Approaches to Improve Techno-Functionality of Plant-Based proteins

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Abstract: Proteins play a critical role in human diet and nutrition. Plant proteins hold immense potential in the development of sustainable, ethical, and low-cost future foods to achieve food security. Designing novel high-protein foods with plant proteins that mimic the attributes of animal proteins requires plant protein modification to enhance their functionality, quality, and utilization. The review highlights the salient aspects of protein complexation and fibrillization as emerging modulation techniques that can create bioparticles with superior functionality, without forming any chemical conjugates, and thus can be regarded as GRAS (generally recognized as safe) substances. In complexation, the ability of proteins to readily interact with other protein molecules, polysaccharides, surfactants, and polyphenols through van der Waals, hydrophobic, and electrostatic interactions to form binary/ternary complexes is exploited. Fibrils have uniquely ordered structures with superior stability, emulsification, and gelling properties, making them efficient emulsifiers, stabilizers, texturizing agents, and carriers in drug delivery systems.

Keywords: proteins; polysaccharides; phenols; complexation; amyloid fibrilization; techno-functional properties

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1. Introduction

Proteins serve as an important nutritional, as well as structural, component of foods. Not only do they provide an array of amino acids necessary for maintaining human health but also act as thickening, stabilizing, emulsifying, foaming, gelling, and binding agents. The ability of a protein to possess and demonstrate such unique functional properties depends largely on its inherent structure, configuration, and how it interacts with other food constituents, like polysaccharides, lipids, and polyphenolic compounds. Proteins from animal sources have superior functionality, higher digestibility, and lower anti-nutrient components than plant proteins. However, consumer preferences are evolving worldwide for ethically and sustainably sourced, clean, cruelty-free, vegan, or vegetarian plant-based food products [1–5]. The market for meat products has expanded at an incredible rate as a result of the world population's rapid growth as well as the economic expansion of developing countries. Over the past 20 years, there has been a 58% growth in the global demand for meat [6]. But the production and consumption of meat are limited by a number of factors, including excessive resource consumption, pollution, antibiotic residue from animals, and zoonotic illnesses [7]. Concerns about animal welfare, water and land shortages, and climate change are among the issues affecting the production of meat. A high carbon footprint, inefficient production techniques, a potential lack of nutritional balance, and lifestyle illnesses like type 2 diabetes, cardiovascular disease, and cancer have all been criticised for the animal protein-based diet [8].

Unlike proteins from animal sources, plant proteins are more versatile and religiously and culturally acceptable among vegetarian and vegan consumers and associated with lower food-processing waste, water, and soil requirements [1,4,9]. Thus, both the processing and utilization of plant proteins have gained worldwide attention, and, as such, numerous scientific studies are focusing on enhancing the utilization of plant proteins in food and pharmaceutical products through various processing and modification techniques to improve their techno-functional properties, bioactivity, bioavailability, and digestibility [10]. The difficulty in successful utilization and application of plant proteins in food formulations lies in their poor solubility in the aqueous phase, complex structure, and inability to withstand small changes in pH, temperature, and ionic strength [11,12].

The techno-functional properties of plant proteins can be enhanced through controlled alterations in the native structure and configuration of proteins through different modification mechanisms that enable selective and controlled unfolding of protein molecular structures and formation of complexes and aggregates. Since plant proteins are composed of numerous fractions of proteins and polypeptide residues, they do not have a single precise isotonic point; instead, the isotonic point exists over a wide range, like in the case of soy [13], pea protein [14], and flaxseed [15]. Another limitation in the application of plant proteins is the presence of residual antinutrient components, which can otherwise affect the digestibility and bioavailability of proteins, as well as several other associated ingredients, in food formulations, particularly vitamins and minerals. Also, plant proteins are often associated with an undesirable taste that impacts their application in food formulations [16]. The flavour and texture of the first generation of plant protein based food products, such as those derived from mycoproteins, were not well received. Because of this, consumers of meat are less likely to view these products

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as true meat substitutes [17]. Due to the large percentage of legume protein in PPBF products, it can be difficult to retain the flavour of animal meat while avoiding unwanted flavours (such as burned, bitter, earthy, green, or mushroomy) [18].

As a result of these critical challenges, certain modulations are required to improve plant protein characteristics, i.e., physicochemical properties, functionality, digestibility, taste, bioavailability, etc., for successful utilization in the food and pharmaceutical sectors. Thus, plant proteins need to be engineered to bring about certain specific molecular changes to broaden the usability and application of plant proteins in various sectors [10].

The process of utilizing different mechanisms, such as physical, chemical, and biological mechanisms, to alter the structure or configuration or some chemical groups of a protein molecule to enhance its techno-functional properties is referred to as the modification of proteins. Since plant proteins are complex macromolecules that vary widely in structure, configuration, and composition, they require specific modification techniques to achieve a desired change in protein functionality [19]. For instance, to enhance the solubility of plant proteins, modification methods based upon protein molecular unfolding, changes in electrostatic repulsion, net charge on protein, isoelectric point, and increase in protein hydrophobicity are required, and such alterations can be achieved using different approaches, like acylation, glycosylation, esterification, change in pH, ultrasonication, and homogenization [20].

Physical modification methods aim at utilizing a combination of heat, pressure, or force to alter the structure of a protein, wherein either the protein undergoes partial denaturation, unfolding, size reduction, aggregation, disaggregation, or permanent denaturation. Such conformational changes in the protein that lead to the enhancement of protein quality and techno-functionality without the use of enzymes or chemicals can be categorized as physical modification techniques [21]. Table 1 highlights the various physical modification methods employed to bring about desired modulations in protein characteristics.

Table 1. Physical modification techniques for plant protein modulation.

Modification Techniques	Modification Mechanism	Protein Type	Modulation in Protein Characteristics	Reference
Thermal Treatment				
Conventional heating	Mild heat treatment promotes denaturation and controlled unfolding of protein secondary, tertiary, and quaternary structures, which, in turn, exposes internal reactive hydrophobic sites and sulfhydryl groups that can enhance protein characteristics [22].	*Chenopodium album*; cowpea; pulses (lentil, faba bean, and pea)	Increased protein hydrophobicity and sulfhydryl groups.	[23-25]
		Quinoa	Improved emulsifying and foaming properties.	[22]
		Chenopodium album; pulses (lentil, faba bean, and pea)	Enhanced gelling and rheological properties.	[23,25]
		Soybean	Reduced antinutrients like trypsin inhibitors.	[26,27]
		Chenopodium album	Improved digestibility.	[23]
Microwave heating	The method results in the unfolding of protein secondary and tertiary structures without impacting protein quality in terms of EAA. Volumetric and uniform heating makes it an ideal pretreatment given before chemical or biological	Soybean	Improved gelling properties.	[28]
		Lotus seed	Enhanced emulsification.	[29]
		Soybean	Microwave treatment at 600 W (10 min) reduced allergenicity	[13]

	modification methods [28].		by 24.7%.	
Ohmic heating	Heat is generated by passing an alternating electric current through protein material, which offers resistance to the flow of current and thus gets heated up uniformly and rapidly. Ohmic heating results in the production of uniform protein aggregates, which retain much of their original protein quality [30].	Soybean milk	Improved emulsifying properties. Decline in protein solubility and foaming properties	[31]
Extrusion	Extrusion utilizes mechanical shearing under pressure (1.5–30 MPa) to generate heat (90–200 °C) and cause denaturation, conformational changes, realignment, and aggregation of plant proteins. The method involves the use of a high heating temperature and pressure that causes changes in secondary protein structure without altering peptide bonds, thus resulting in protein aggregates with increased molecular weight [32].	Pea	Decreased water-holding capacity but increased protein hydrophobicity nitrogen solubility and oil-holding capacity.	[33]
		Oats	Extrusion in conjunction with enzymatic conditioning, improved protein solubility and textural properties, and particularly induced the formation of a strong fibrous protein structure with high tensile strength.	[34]
Radio frequency treatment	Volumetric heating using radio frequencies, which have a higher wavelength than microwaves. Dielectric properties of protein material, depth of penetration, pH, concentration of proteins, and temperature influence the performance of this heating method [35].	Rice bran	Decrease in α-helix, β-sheet, and β-turn structures; reduced tryptophan florescence; and enhanced surface hydrophobicity.	[35]
		Maize and rice bran	Enhanced oil absorption capacity and emulsifying properties.	[35,36]
	Non-Thermal Treatments			
Gamma irradiation	Gamma irradiation leads to the formation of superoxide anionic and hydroxyl radicles, causing changes in chemical composition (reaction between tryptophan and tyrosine), pH, structural conformation, crosslinking, and aggregation of proteins [37].	Sunflower seed	Changes in secondary and tertiary protein structures, resulting in enhanced thermal stability.	[38]
		Sesame	Improved emulsifying ability and digestibility.	[39]
		Sunflower seed	Reduction in water binding capacity.	[38]
Ultraviolet (UV) radiation	UV treatment induces chemical changes in plant proteins. UV light is absorbed readily by aromatic amino acids (tyrosine, tryptophan, and phenylalanine) and induces protein crosslinking [40]. It triggers	Sesame	Improved mechanical properties of formed film.	[42]
		Wheat flour	Increased sulfhydryl content and enhanced solubility.	[43]

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	unfolding of protein monomers through reduction in disulfide bonds and partially depolymerizes proteins [41].	Wheat gluten	Reduced allergenicity.	[41]
Electron beam irradiation (EBI)	EBI consists of exposing plant proteins to electron beam of high energy that causes molecular and chemical changes in protein structure, thus triggering unfolding and denaturation of proteins [42].	Wheat germ	Reduced molecular weight and surface hydrophobicity, enhanced foaming properties, and increased antioxidant capacity.	[42]
		Walnut	Reduced α-helix structure and increased thermal stability.	[43]
		Soybean	Improved digestibility as a result of decrease in trypsin inhibitor content.	[44]
High hydrostatic pressure processing (HPP)	HPP uses high pressures (100–800 MPa) to unravel protein structures and enhance hydrophobicity to form aggregates. Pressures greater than 400 MPa reduce protein solubility due to aggregate formation, while lower pressures improve protein solubility without the formation of aggregates. HPP is used as a pretreatment to aid glycation and complexation [45].	Legumes	Modulate and improve digestibility and rheological properties.	[46]
		Kidney bean	Assist enzymatic proteolysis of protein isolates to form hydrolysates possessing improved antioxidant and functional properties.	[45]
High pressure homogenization or dynamic high-pressure fluidization (DHP) technology	DHP utilizes pressures of 250–300 MPa to force a fluid at high velocity through a small narrow orifice. This creates extreme shearing action and rapid reduction in pressure as the fluid leaves the orifice, resulting in cavitation and size reduction of protein molecule which favors inter- and intra-particle interactions leading to the formation of stable colloidal dispersions and nano-emulsions [47].	Lentil	Enhanced solubility, foaming, and emulsifying	[48]
		Soy	Improved digestibility and emulsion stability.	[49]
Pulsed electric field (PEF)	Protein modification with PEF involves the generation of electrical pulses at high power between two electrodes. The energy generated by electric pulses causes unravelling of protein structure, which, in turn, enhances the ability of the protein to better interact with water and oil and improve protein functionality [50].	Canola seed	Enhanced the solubility, foaming capacity, and emulsifying properties.	[50]
		Soybean	Enhanced protein surface hydrophobicity, flexibility, and free sulfhydryl content, resulting in improved emulsification and foaming.	[51]

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Cold atmospheric plasma (CAP)	CAP technology is environmentally friendly and involves the use of cold plasma (fourth state of matter), which largely comprises positively charged ions of a gas generated by the excitation of a carrier gas through electrical discharge at a certain temperature and pressure. Reactive species such as NO_3^-, O_3, H_2O_2, OH^-, and O_2^- are generated that alter the protein structure [52].	Gluten	Improved rheological properties. Biodegradable film and containers prepared with modified gluten had smoother surface and did not cling or stick too much to food or impurities.	[53]
		Pea	Enhanced formation of soluble aggregates, surface hydrophobicity, and β-sheet protein structures, resulting in improved gelling and emulsification properties.	[54]

Unlike physical modification, chemical modification involves an irreversible reaction between chemical agents and reactive protein sidechains to alter the physicochemical and techno-functional properties of proteins. These reactive side chains are usually made up of functional groups, namely carboxyl, indole, amino, thioester, imidazole, disulfide/sulfhydryl, and phenolic groups. Chemical modification relies either on the addition or removal of functional moieties to bring about a desired change in the net charge on protein molecules. For example, acetylation, succinylation, deamination, and phosphorylation are commonly used chemical modification techniques that rely on a chemical reaction to increase the net negative charge on protein molecules. However, the chemicals used during modification often result in the production of chemical by-products [55]. Moreover, the commercialization and scale-up of these methods are often associated with high costs and regulatory concerns [56]. On the other hand, glycation is another chemical modification technique that relies on the Maillard reaction to form a covalent conjugate between a protein body and reducing sugar in the presence of mild heating conditions [57] to enhance the solubility, emulsifying ability, and thermal stability of the resulting protein [58]. Since no external chemical is required to modify proteins, glycation is considered a less evasive and clean chemical modification method. Although owning to the need for expensive pretreatment instrumentation like HPP, freeze drying, ultrasonic treatment, etc., this method is still not commercially feasible [59]. Table 2 highlights chemical methods for the modification of proteins.

Table 2. Chemical modification approaches for plant-based proteins.

Methods	**Protein Type**	**Techno-Functional Properties**	**Reference**
Glycation	Whey protein isolate	- ↗ Foaming properties - ↗Protein functionality	[60]
Glycation (electrospun fiber assisted dry)	Pea protein hydrolysate	- ↗ Emulsion stability - ↗ Solubility	[61]
Glycation	Oat protein	- ↗ Emulsification ability - ↗ Solubility	[62]
Glycosylation (microwave-assisted wet)	Rice dreg protein	- ↗ Solubility - With Maillard reaction, ↗ emulsifying capacity - Powerful immunomodulatory properties.	[63]
Glycosylation (wet)	Canola protein isolate	- ↗ Higher viscosity - ↗ Physical structure	[64]

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Glycosylation (ultrasound-assisted dry)	Buckwheat protein isolate	- ↗ Surfactant capacity - Ultrasonication enhanced efficacy of functional properties - ↗ Emulsion stability - ↗ Solubility	[65]
Phosphorylation with sodium trimetaphosphate (STMP)	Potato protein isolate (PP-PPI)	- Phosphorylation is pH dependent: (i) at pH 5.2: ↗ content of all amino acids of PP-PPI; (ii) at pH 10.5 ↘ contents - At pH 8, ↗ oil absorption capacity, ↗emulsion activity, and ↗ foam capacity -At pH 10.5: ↗ water absorption capacity	[66]
STMP phosphorylation	Soybean and peanut proteins	- ↗ Emulsifying activity - ↗ *In vitro* protein digestibility > 1%	[67]
STMP phosphorylation	Soy protein isolate	- ↗ Functional properties relating to aqueous solubility, WAC, emulsifiability and whip-ability.	[68]
STMP phosphorylation	Rice glutelin	- ↗ Turbidity of phosphorylated rice glutelin (PPRG) - ↗ Viscoelasticity. - Phosphorylation ↗ thermal aggregation of RG	[69]
Acylation and additional transglutaminase catalysis	Rapeseed protein isolate (RPI)	- ↗ Gelation properties (viz. thermal stability, gel strength, apparent viscosity, and surface roughness)	[70]
Acylation and glycation	RPI	- ↗ Gelation and gelation properties - ↗ WAC and textural properties were improved	[71]
Deamidation—Proteax/glutaminase SD-C100S	Wheat gluten hydrolysates	- Bitterness-masking property	[72]
Deamidation	Rice bran protein	- ↗ Water solubility (=90%) at pH 12 and 120 °C for 15–30 min - Thermal property was preserved	[73]
Deamidation—alcalase hydrolysis	Wheat gluten	- Bitterness-masking property	[74]
Deamidation—alkaline	Protein from evening primrose (*Oenothera biennis* L.), PG	- ↗ Functional characteristics - Production of edible EPSC protein	[75]
Deamidation—glutaminase	Pea protein isolate, PPI	- ↗ Solubility and techno-functionality features of PPI - ↘ Beany flavor, grittiness, and lumpiness	[76]

↗ = increasing and ↘ = decreasing.

Biological or enzymatic modification is an alternative to using chemicals for the effective modification of proteins under mild reaction conditions (Table 3). Moreover, unlike chemical modification, enzymatic modification preserves the composition of the native protein. Enzymatic modification involves the use of both proteolytic and non-proteolytic enzymes; the former enzyme group (pepsin, alcalase, papain, and trypsin) modifies protein structure and functionality by hydrolyzing peptide bonds in the protein [77], and the latter (transglutaminases and laccase) induces crosslinking between proteins or peptide chains to build up a unique protein structure with improved textural and gelling properties [78]. Fermentation is another biological method of protein modification that utilizes starter cultures from different strains of bacteria, yeast, and mold to improve the solubility [79], oil- and water-holding capacity, foaming properties [80], antioxidant potential [81], digestibility, and taste of modified proteins [79].

However, the major disadvantage of biological modification is the cost associated with producing and procuring desirable microbial cultures and large-scale commercialization of the process.

Table 3. Biological modification approaches for plant-based proteins.

Methods	Protein Type	Techno-Functional Properties	Reference
Enzymatic (complex proteases)	Walnut gluten	- ↗ Solubility - ↗ Water-holding capacity - ↗ Emulsifiability - ↗ Emulsion stability - ↘ Oiliness - No change in foaming characteristics	[82]
Enzymatic: Tween 20 and Transglutaminase (TGase)	Peanut proteins	- Tween 20: ↗ higher EAI and ESI - Tgase: ↗ gelation and oil-binding properties and ↘ reduced the protein solubility and ESI	[29]
Enzymatic: Tgase	Coconut protein	- ↗ Mechanical and barrier properties of films based on modified coconut protein	[83]
Enzymatic glycosylation black soybean protein isolate catalyzed by Tgase (EGBSPI)	Black soybean protein isolate—BSPI	- ↗ Solubility and rheological properties - ↗ Emulsification	[84]
Enzymatic: proteolytic enzymes	Pea protein isolates	- ↗ Protein solubility at pH 4.5 at all times of hydrolysis - ↗ Foaming with trypsin hydrolysates and emulsifying capacities	[85]
Enzymatic bromelain, chymotrypsin, and protease	Quinoa (QPH) and amaranth (APH) protein hydrolysates	- ↗Antioxidant, antimicrobial, and antihemolytic properties	[86]
Enzymatic: papain and pepsin treatments	Pea protein-enriched flour	- ↗ WHC and OHC - ↘ Foaming properties and emulsifying properties	[87]
Enzymatic: pectin methyl esterase	Pea protein isolate	- ↗ Degree of esterification - ↗ Solubility	[88]
Fermentation: *Lactobacilli* strains and *Staphylococcus xylosus*	Lupin protein isolate	- ↗ Foaming properties and emulsifying properties - At pH 4, no change in solubility; at pH 7, ↘ solubility - ↘ Bitterness	[79]
Fermentation: *Lactobacillus helveticus*	Soy protein isolate	- ↘ Beany and bitter off-flavors	[89]
Fermentation: *Pediococcus pentosaceus* KTU05-9	Lupine protein	- At pH 8, ↗ solubility and functional properties - ↘ Bread hardness, chewiness, and resilience - ↗ Bread springiness	[90]
Fermentation: *Bacillus licheniformis*	Peanut meal	- ↗ Nutritional properties - ↗ Antioxidant potential	[81]
Fermentation: *Pediococcus pentosaceus* and *Pediococcus acidilactici* strains	Chickpea protein	- In sourdoughs, ↗ smell, texture, and color - ↗ WHC	[91]
Fermentation: *Lactobacillus plantarum* strains	Soy protein	- ↗ Surface hydrophobicity - Emergence of β-strand structure	[92]

↗ = increasing and ↘ = decreasing.

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Apart from these commonly known aforementioned modification techniques, fibrillization and complexation are emerging as potential modulation methods for engineering proteins with superior functionalities. Since proteins are highly diverse macromolecules, they can interact and form complexes through molecular interactions like van der Waals, electrostatic, disulfide linkages, hydrophobic, hydrogen bonding, steric repulsion, etc., with different biocompatible macro- and micromolecules to yield bioparticles with specific, desirable techno-functional characteristics. Protein complexation with several micro- and macromolecule-like surfactants (phospholipids, rhamnolipids, ethyl lauroyl arginate hydrochloride, saponins, etc.) [93], polysaccharides [94], and polyphenols [95] have been found to enhance the functionality and utility of native proteins, such as emulsifiers, encapsulating agents, edible coating films, stabilizers, hydrogels, bioactive peptides, and adhesives. Proteins can interact with either one or two of these substances to produce binary and ternary complexes, respectively.

The advantage of complexation as a protein modification technique lies in the fact that complexes are formed as a consequence of some physical interactions rather than covalent bond formation between molecules. Since such complexes are free from any chemical conjugates or chemical ingredients, they can be used for food preparation without extensive legislation and are readily identified as GRAS (generally recognized as safe) substances [96].

Also, complexation has been found to successfully produce emulsion-based bioactive compound delivery systems, without the use of chemicals, which were otherwise used to enhance the stability of these emulsions [97]. Protein-based binary and ternary complexes have been known to produce ultra-stable high internal phase (HIPE) emulsions that can withstand external stresses, prevent coalescence, and protect bioactive substances [97–99]. Novel ternary complexes based on polysaccharides, proteins, and polyphenols have been particularly identified as effective carriers for bioactive materials with a high loading capacity. Moreover, in comparison to binary complexes, ternary complexes are soft substances that deform easily and adapt well as emulsifiers at water–oil interfaces and can be used in high-biosafety applications, like tissue engineering, pharmaceutical, and cosmetic products [97]. In addition to enhanced techno-functionality, protein-based complexes or conjugates (without chemical surfactants) exhibit numerous healthful properties such as strong antioxidant, antitussive, antifungal, antibacterial, and anticoagulant activities [100].

Protein fibrillization is another contemporary modification technique of recent origin that relies on the formation of insoluble protein aggregates from soluble proteins through controlled denaturation. These protein aggregates or fibrils have been found to possess a uniquely ordered structure, high stiffness, superior stability, rheological, and gelling properties, making them efficient emulsifiers, stabilizers, and carriers in drug delivery systems [12]. Protein fibrils, also termed amyloid fibrils, are made up of rod-shaped denatured protein aggregates possessing linear structures, with a high aspect ratio and a diameter usually less than 100 nm and are extremely stable under certain environmental stresses [101,102]. Owing to their biocompatibility, non-toxic nature, antioxidant and antimicrobial bioactivities, and highly improved functional properties (emulsification, gelling, foaming, and rheological properties), these protein fibrils have the potential to be used for formulating a wide variety of foods and nutraceutical products [103]. Thus, amyloid fibrillization and complexation are emerging as highly effective, clean, biologically safe, non-toxic, and efficient means of protein modification, which can allow for the use of plant proteins in designing and engineering novel food and pharmaceutical products. As known, protein functioning may be compromised because heat treatment under OH is limiting the production of amyloid fibrillization. This may be relevant, for example, when it's preferable to have lower gel strengths (for making foods suitable for the elderly, for example) or less foaming during the production process. In addition, OH can be used as a heating

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technique that maintains a greater number of native protein structures, especially when reducing the effect on protein denaturation is a top concern [104]. Over the past few decades, food science has become more interested in fibril protein structures, such as amyloid fibrils, because they have been demonstrated to improve protein activity and can be utilised to modify a variety of food qualities. Amyloid fibrils can produce more durable and aspect-ratio-higher viscoelastic interfaces between phases than native proteins, it can also increase the stability of emulsions or foams [105]. These protein structures have shown promise as building blocks for food gels, with good effects on gel strength, gel structure, or viscosity because AF also has a high mechanical strength and chemical resistance [106, 107].

Both protein complexes and amyloid fibrils have been found to exhibit promising rheological, chemical, and emulsifying properties, without compromising nutritional and sensory properties [97, 103].

This review highlights the recent advancements in protein modification through various complexations of protein molecules with protein, polysaccharide, polyphenol, and their combinations and fibrillogenesis, and it fills the research gap regarding the understanding of their mechanisms for modifying plant proteins in a commercially significant manner. Numerous researchers have performed the review on different aspects of protein modification and recent advancements in the conventional, i.e., physical [4,22,23,29,31,33,36], chemical [61,63,65,67,70,76], and biological [29,79,82,86,91,92], modification of plant proteins. However, a balanced combination of protein modification, protein complexations, and amyloid fibrillogenesis from conventional research to the recent trends has not yet been compiled. This review helps the researchers and scientific community in understanding the protein modification and complexations and forms the basis for new research. This review also provides a glimpse of factors affecting the amyloid fibril formation, which had not been studied extensively till now [108]. This review gives a detailed insight for designing novel food and nutraceutical systems based on these interactions and complexations and by understanding their mechanisms.

2. Complexations

2.1. Protein–Polysaccharide Complexations

The protein–polysaccharide complexations perform an important role in monitoring the structure/construction, texture, and stability of food products. These complexations depend on the polymer, as well as the solvent utilized, and can cause inherently distinct phases [109]. Several studies have revealed that different kinds of intermolecular forces add to these polysaccharide–protein complexations, such as pH, covalent strength, ionic strength, electrostatics, hydrogen bonding, volume exclusion, hydrophobicity, and van der Waals forces [110]. As the developed complex enhances the colloidal stability, the consequence is a volume of the two distinct phases. Numerous pieces of research have explained the polysaccharide compounds that can relate to proteins and absorb greater than one colloidal particle, thus creating bridges, aggregate structures, or polymer-depleted regions and reintroducing protein particles closer together, owing to incompatibility [111, 112].

The application of polysaccharide–protein mixtures enhances the chance of diversifying the gel structure design. Conversely, by blending the specific benefits of polysaccharides (e.g., advanced rheological activity) with proteins (e.g., nutritional properties), a mixed gel with multi-structure and higher nutritional quotient should be obtained, thus presenting a favorable solution to make functional gel-based foods [113,114].

2.1.1. Principle Affecting Plant-Protein–Polysaccharide Interactions

Amphiphilic macromolecules or natural biopolymers are primarily dependent on the interaction between proteins and polysaccharide compounds. Generally, attraction and repulsion are the two main forms of interactions that appear among proteins and polysaccharide compounds in a solution and also can lead to the formation of complexes or the immiscibility of the two biopolymers (thermodynamically incompatible) [115]. Because of the polyelectrolyte interactions in the solution mixture, these interactions, as well as their outcomes for the mixture, will be greatly affected by the pH, ionic strength, structure, charge density, and concentration of the biopolymers [116].

2.1.2. Types of Interactions

The interaction among polysaccharide compounds (also known as hydrocolloids or polyanions), as well as proteins, was initially noticed when it was revealed that numerous sulfated polysaccharides stimulated the *in vivo* appearance of serum lipemia clearing factor, as well as lipoprotein lipase triggered by heparin *in vitro.* Likewise, Cornwell and Kruger [117] revealed the situations that cause the development of complexes amongst sulfated polysaccharides and plasma lipoproteins. There are two major types of interactions among polysaccharides and proteins, i.e., covalent and non-covalent interactions. A covalent type of interaction is achieved by a Maillard-type reaction, where reducing sugars and amino acids interact with each other by the impact of heat to produce aroma, flavors, and brown appearance. This formation of new flavor compounds may result in protein–polysaccharide conjugates with improved thermal stability [118].

Yet, reaction conditions, for example, pH and temperature, must be adjusted appropriately to achieve the desired reaction. Non-covalent driving forces are electrostatic, hydrophobic, hydrogen bonding, and van der Waals interactions. Such forces can create coacervates that are helpful implements for altering the textural properties of foods and encapsulating active compounds [119] (Figure 1a). A mixture of two distinct biopolymers in an aqueous solution works mainly in three mechanisms, namely co-solubility, incompatibility (segregative phase separation), and complex coacervation [116].

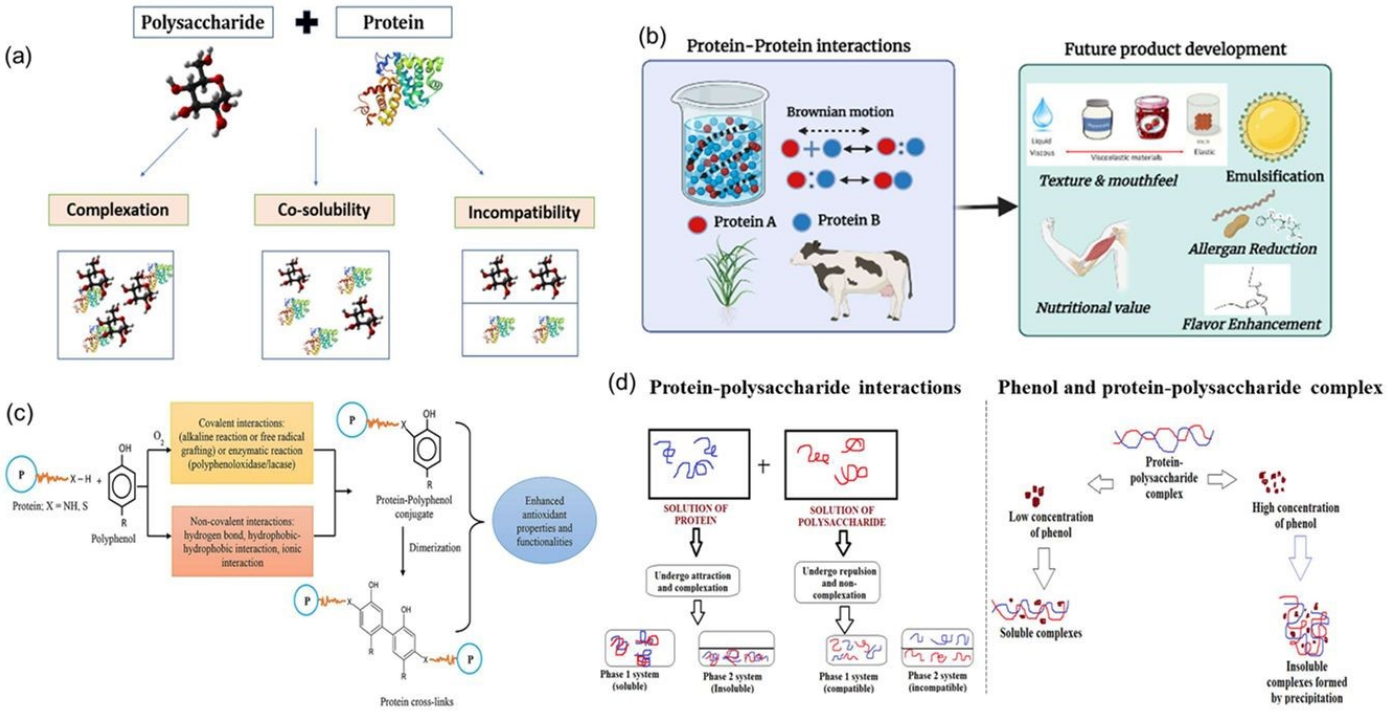

Figure 1. Interactions and complexations in (**a**) protein–polysaccharide, (**b**) protein–protein, (**c**) protein–phenol (*adapted with permission from quan et al. [120]*, and (**d**) protein–polysaccharide–phenol.

In the aqueous solution, complex coacervation occurs among two oppositely charged polymers due to electrostatic interactions. In accordance, the complexation among proteins as well as anionic polysaccharides takes place below the isoelectric point of the protein and at low ionic strength [121, 122]. The factors affecting compatibility and complex formation are the protein/polysaccharide ratio, pH, ionic strength, and nature of the polymer (molecular mass, net charge, ternary structure, and chain flexibility). The polymer solution pretreatment also enhanced the formation of complexes. The treatment of high pressure (dynamic or hydrostatic), as well as temperature, has been described to influence the stability of newly formed complexes.

2.1.3. Compatibility

The thermodynamic compatibility of proteins with polysaccharides declines as the pH reaches the isoelectric point of the protein and similarly as the molecular weight of the polysaccharide increases. For anionic polysaccharide molecules, there is a region near the isoelectric point of the protein that corresponds to perfect thermodynamic compatibility and a region where the system splits into two phases. Significant variations were also observed in the compatibility of several protein compounds with the same polysaccharide, indicating the role of the structure of protein affecting its compatibility with polysaccharide molecules. As per the previous research, the compatibility of protein compounds with anionic polysaccharides decreases in the order of pectin > CMC > sodium alginate > gum arabic > dextran sulfate [123,124].

2.1.4. Effect on Functional Properties of Plant Proteins

Plant protein complexes with polysaccharides lead to the formation of new food biopolymers with new functional properties. Different consequences of protein–polysaccharide interactions (complex or incompatible) can occur simultaneously in different phases of the food system. Protein–polysaccharide interactions play an essential function in the structure, as well as firmness, of processed foods by acting as thickeners, stabilizers, gels, and emulsifiers and are therefore used in food processing [125]. The addition of polysaccharides is of great interest in the development of new foods because it can stimulate intermolecular protein relationships and provide an opportunity to diversify protein functions [126].

The adding of polysaccharides to protein-stabilized oil-in-water emulsions either increases or decreases the stability of the emulsion and is dependent on the type, concentration, kind of polysaccharide utilized for complexation, and solvent requirements (pH and ratio of biopolymers) and degree of complexation with proteins adsorbed at the interface [127]. A crucial attribute of protein–polysaccharide conjugation is the increased solubility of the protein at its isoelectric point. This can be attained through the creation of mixing complexes achieved by blending biomacromolecules at a pH away from the isoelectric point of protein to promote electrostatic interactions. The insoluble complex is then solubilized by titration with acid. In recent research, the solubility of pea protein isolate was observed to improve from 41 to 73%, owing to the addition of high-methoxy pectin (P90) at pH 6.0 and moderated by P90 and low-methoxy pectin (P29) at pH 4.0 and pH 5.0, respectively [127].

The hydration properties of protein–polysaccharide conjugates are associated with the interaction of the conjugate with a solvent (usually water). These properties are commonly assessed according to their effect on solubility and viscosity, especially for their industrial use in food formulations. Generally, a high charge density as well as low average hydrophobicity contributes to the solubility of biomacromolecules.

A study performed by Jarpa-Parra et al. [128] described that there was no enhancement in the foaming ability of lentil proteins when xanthan gum, guar gum, or low methoxy pectin was included at varying pH ranges (3.0, 5.0, and 7.0); nevertheless, the foam stability of plant protein was enhanced at pH 3.0, as well as 5.0, with the addition of pectin at pH 5.0 providing the uppermost stability.

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2.1.5. Applications

Interactions between plant proteins and polysaccharides offer several prospects for improving biological functions and improving existing technologies. In the food industry, protein–polysaccharide complexes exhibit remarkable physicochemical properties as food stabilizers, emulsifiers, and texture modifiers. Additionally, they may be the optimal nutrient delivery system. It is also used in tissue regeneration, food stabilizers, food colloids, nanofibers, edible packaging materials, mixed gels, and nanomedicine. The combination of protein and polysaccharide is particularly interesting because it can change the shelf life of a product by altering the texture of the food, i.e., the rheological properties of the food colloid [125]. The interaction between proteins and polysaccharides allows for the design of amphipathic conjugates that are sturdily fixed to the oil–water interface through the hydrophobic regions of the protein, resulting in a viscoelastic and sterically oriented layer of the non-adsorbed polysaccharides (copolymerization) that can improve the structure and improve gelling properties [125]. For instance, proteins and polysaccharides, due to their ability to form films can both be used as wound dressings for medicinal purposes or as biodegradable films for use in food packaging. Protein films are not an efficient barrier to carbon dioxide, but they do have strong mechanical and oxygen barrier qualities. In contrast, polysaccharide films have better gas barrier properties. Both polymers are weak water vapour barriers because they are hydrophilic. Cross-linking agents are therefore typically used in chemical, enzymatic, or physical processes in order to get around such restrictions and accomplish the desired functionality [129].

2.2. Protein–Protein Complexations

The development of protein-based healthy foods requires the understanding of interactions and complexations of conjugating proteins. Protein complexation occurs when two or more different proteins bind together to form a larger, more complex structure. This can occur between proteins from the same source or between proteins from different sources. Products are made by combining plant proteins, such as soy or pea protein, with animal-based proteins, such as egg white protein or milk protein, to mimic the texture and flavor. The attributes attained after protein–protein association could be permanent or transient changes.

2.2.1. Principle and Mechanism

Protein–protein interaction is subjected to various factors, like protein source, protein type, and amino acid profile. The association of proteins is triggered by a random search of the two protein molecules for each other in a solution, as described by Brownian motion (Figure 1b). This random collision may or may not ensure a complex formation, as their relative orientation is the controlling factor for the rate of reaction [130]. Electrostatic forces can enhance the reaction rate substantially [131]. Brownian dynamic simulations have demonstrated the contribution of electrostatic attraction to form protein complexes. The pair protein molecules that make up the pair associate with each other in a two-step reaction are as follows:

$$A + B \leftrightarrow A:B$$

$$A:B \leftrightarrow AB$$

In these equations, A and B represent proteins; A:B represents encounter complex, and AB denotes the final complex. An encounter complex forms when two proteins diffuse randomly to reach a zone, called the steering region, where they enter into the

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areas of mutual electrostatic attraction. This point of complex formation has been considered important from a research point of view. Larger electrostatic attraction between the proteins leads to a larger volume of the steering region. The encounter complex comprises weakly associated conformations in which proteins rotate freely and reorient themselves, increasing the number of contacts, until optimal binding geometry is achieved and the complex proceeds to an active state which is tightly bound [131]. The encounter complex is stabilized by a combination of long-range electrostatic forces and desolvation and is destabilized by unfavorable entropy. Further, the formation of the final complex from the encounter complex needs desolvation and structural rearrangement of the side chains. To attain the final complex, it is mandatory to have a single orientation with a much lower free energy as compared to other similar orientations. It is usually achieved by multiple short-range interactions, including van der Waals, H-bonding, hydrophobic contacts, and specific salt bridges.

2.2.2. Types of Interactions

In protein systems, there are two major categories of interactions based on covalent and non-covalent bonds that lead to the development of insoluble material. Inter- and intra-molecular disulfide bonds created by sulfhydryl–disulfide interchange or sulfhydryl oxidation processes make up the majority of the former [132]. The latter are non-covalent interactions that also help proteins become insoluble, such as hydrophobic, hydrogen-bonding, ionic, and other weak interactions [133]. Disulfide bonds are covalent bonds between two sulfur atoms in cysteine residues within a protein. They are important for the stability and proper folding of many proteins. Disulfide bonds can form within a single protein molecule (intramolecular) or between different protein molecules (intermolecular), resulting in the formation of protein aggregates or gels. The formation of disulfide bonds can also contribute to the thermal stability of proteins, allowing them to withstand higher temperatures before denaturation occurs. In addition, disulfide bonds are involved in protein–protein interactions, enzymatic activity, and signal transduction pathways. Disulfide bonds play important roles in protein structure and function, and their understanding is crucial for advancing our knowledge of many biological processes [134].

2.2.3. Compatibility

Protein–protein compatibility refers to the ability of different proteins to interact and form complexes with each other. Proteins with similar structures and charges may be more likely to interact and form protein complexes with each other. Additionally, the pH and ionic strength of the surrounding environment can also affect protein–protein compatibility [135]. Compatible proteins can create a food product with the desired texture or stability. During the interaction of proteins, their technological compatibility needs to be seen in different food matrices, along with protein gastrointestinal stability and food safety. Oxidative stress and inflammation caused due to the non-compatibility of food components are generally related to chronicle diseases [136]. With an improved functional and structural understating, it is possible to get health-promoting benefits from the interaction of proteins from different sources. Globally, food scientists and technologists are validating protein–protein compatibility so that functional foods with positive impact can be developed.

2.2.4. Effect on Functional Properties of Proteins

Protein–protein complexations play a crucial role in the functionality and sensory properties of plant-based proteins in food systems. Understanding protein interactions can help to develop new plant-based protein products with desirable texture, emulsifying and foaming properties, and gelation properties. Additionally, due to different molecular structures of different protein fractions present a distinctive attribute that could be beneficial to develop new products [137]. Crosslinking in proteins is attributed to a profound impact on the functional attributes of plant proteins. Different

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protein complexes perform various functions, and the same complex has the potential to perform several functions. Protein–protein complexations lead to changes in solubility [56,138], water-holding capacity [4], gelling capacity [139,140], emulsifying and foaming properties [139,141,142], textural and rheological properties [143], and moisture retention. Processes involving high temperature, alkaline pH, and oxidizing conditions induce protein crosslinks by introducing extensive structure variations, and therefore the functional and nutritional characteristics of the food product.

The major drawback associated with the plant proteins from legumes, oilseeds, or cereals is their low solubility [137]. Contrary to plant proteins, casein micelles are highly hydrated and have the potential to form stable colloidal structures, such as aggregates, gels, foams, and emulsions, when mixed with plant protein bodies. An improvement in the solubility (from ~58% to over 86%) and protein quality was found in lentil–casein protein complexation [138]. Gels have been prepared from soy or pea proteins, wheat, canola, sunflower, or hemp as plant protein fractions, along with milk proteins [140,144,145]. Gel formation is the heat-induced denaturation of globular proteins, followed by the formation of primary aggregates through thiol/disulfide exchanges. Further heating leads to extending these aggregates or making them insoluble by acidification or salt addition. Heating resulted in the denaturation of the globular proteins and the formation of mixed aggregates based on their initial protein mix and the presence of free sulfhydryl groups and disulfide bonds [146].

2.2.5. Applications

Protein–protein interactions are an essential aspect of many food products, particularly those made with plant-based proteins. In recent years, there has been a growing interest in developing new plant-based food products to meet the increasing demand for sustainable and healthy food. Protein–protein interactions play a significant role in texture and mouthfeel. By manipulating protein–protein interactions, it is possible to create products with a range of textures, from smooth and creamy to firm and chewy. Protein–protein interactions are also important for emulsification, or the ability of two liquids to mix [141]. Plant-based proteins are often lower in certain amino acids than animal-based proteins, which can limit their nutritional value. However, by combining different plant-based proteins with complementary amino acid profiles, it is possible to create a product with a more balanced nutritional profile. Many people are allergic to specific proteins, such as those found in soy, wheat, or peanuts [141]. By using plant-based proteins with different protein structures, it may be possible to reduce the allergenic potential of a food product. Protein–protein interactions can also create unique flavor profiles. Overall, protein–protein interactions are a critical aspect of new food product development and, it is possible to create products with a range of textures, nutritional profiles, and flavors, opening up new opportunities for innovative food products. The solubility [56,138], water-holding capacity [4], gelling capacity [139, 140], emulsifying and foaming capabilities [139, 141, 142], textural and rheological properties [143], and moisture retention are all altered by protein–protein complexations. Protein crosslinks are created by processes that introduce significant structural differences, which in turn affect the functional and nutritional characteristics of the food product. These conditions include high temperatures, alkaline pH, and oxidising agents [138-143].

2.3. Protein–Phenol Complexations

Plant protein–phenolic complexations play a significant role in the nutritional and functional properties of plant-based foods. The functionalization of proteins using phenolic compounds has drawn more interest over the last ten years [40]. It is generally known that structural modifications can dramatically enhance the functional characteristics of proteins [147]. Research has shown that phenolics engage in protein interaction via the formation of hydrogen bonds and hydrophobic association [148]. These interactions can lead to changes in the protein structure, such as unfolding or aggregation, which can impact the functional properties of the protein. Several studies found that the interaction between phenolics and proteins improves the techno-functional properties of functions which are important in food industry for creating different food products with varied applications. Therefore, modified plant-based proteins provide the chance to become multifunctional constituents for food systems. Overall, plant-protein–phenolic interactions are complex and have both positive and negative effects on the functional and nutritional properties of plant-based foods. Further research is needed to better understand these interactions and how they can be manipulated to improve the quality of plant-based products.

2.3.1. Principle and Mechanism

Protein–phenolic interactions refer to the complexation of polyphenolic compounds with proteins. Biochemical properties of protein–phenolic conjugate depend on the amino acid composition, protein conformation, hydrophobic nature of the protein, etc., and the presence and position of the hydroxyl group in the conjugated structure of its counterpart [120]. Polypeptides of amino acids and proteins are positively or negatively charged depending on the pH of the environment. Phenolic acids are typically negatively charged due to the presence of hydroxyl groups [149]. The mechanism of protein–phenolic interaction involves several steps (Figure 1c). To begin, polyphenols molecules attach with the protein via forming various chemical bonding like van der Waals interaction (interactions between atoms influenced by their surroundings), electrostatic interaction (between ε-amino groups on Lys and –OH groups on phenolics), hydrogen bond (between oxygen or nitrogen in protein and hydroxyl groups of phenolic compounds), and hydrophobic association (hydrophobic proteins binding with nonpolar phenolic aromatic rings). This interaction can cause changes in the protein structure, such as denaturation or aggregation. Second, the phenolic compounds can bind to specific amino acid residues in the protein, such as tyrosine, tryptophan, or cysteine, via covalent or non-covalent interactions. This can lead to changes in the protein's conformation or function. Liu et al. [40] beautifully outlined the four ways to synthesize protein–phenol complexes: (i) alkaline synthesis is a common method for synthesizing phenolic–protein conjugates (for example, epigallocatechin-3-gallate–protein), which is simple and effective; (ii) ascorbic acid and hydrogen peroxide is widely used to produce phenolic–protein conjugates via grafting method; (iii) enzymatic method—limited use; and (iv) chemical coupling method for synthesizing EGCG–collagen conjugates through glutaraldehyde crosslinking.[120, 149]

In summary, the principle of complexation based on protein–phenolic interaction is driven by the physicochemical characteristics of both macromolecules, and the mechanism involves electrostatic interactions, hydrogen bonding, or hydrophobic interactions, as well as covalent (irreversible) or non-covalent (reversible) binding to specific amino acid residues in the protein.

2.3.2. Compatibility

One interesting aspect of the protein–phenolic matrix interaction is mutual compatibility. It is important for the stability and functionality of food products. In many cases, plant-based proteins serve as carriers for phenolic compounds. Kopjar et al. [151] investigated the complexation of quercetin at varied concentrations with two plant protein matrixes, almond (dry fruit) and brown rice (cereal). Using various instrumental techniques to characterize protein/phenolic complexes, Kopjar and his team concluded

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that quercetin's adsorption on the brown rice caused it to become thermally stable while the thermal stability of quercetin–almond protein was severely compromised. The affinity of brown rice protein matrices increased proportionately with an increase in the quercetin concentration. Hence, the protein matrix of brown rice is a more effective transporter of phenolic substances. A possible explanation for these differences in a protein matrix structure is that brown rice has a greater protein content (85%) than almond (50%). These non-covalent interactions—(i) hydrophobic association and (ii) hydrogen bond are the factors that contribute to the improved thermal stability and binding specificity of protein–phenolic complexes [151]. In an experiment conducted by Kopjar et al. [152], cinnamic acid exhibited a different adsorption trend on pea (legume), almond (dry fruit), and pumpkin (gourd family) protein matrices; pumpkin had the strongest affinity, and almond had the weakest. Cinnamic acid adsorption onto the almond protein matrix increased thermal stability, whereas adsorption of cinnamic acid onto a pumpkin, as well as a pea, protein matrix decreased thermal stability. A conjugate of gallate and zein was more thermally stable than pure zein. Conjugates of maize protein (zein) and chlorogenic acid, on the other hand, had denaturation temperatures comparable to pure protein [72]. Meanwhile, Pham et al. [153] investigated the interfacial and biological activities of protein–phenolic complexes by using phenolic sources of flaxseed polyphenols and hydroxytyrosol for the same protein matrix (flaxseed protein isolate) adsorption. A flaxseed-protein–flaxseed-polyphenol complex provided the maximum storability against oxidation during 21-day storage as compared to a flaxseed-protein–hydroxytyrosol emulsion. Overall, mutual compatibility between proteins and phenolic compounds is a complex and multifaceted phenomenon that is important for the stability and functionality of many food products. Further research in this area is needed to fully understand the factors that influence mutual compatibility and how they can be utilized to develop innovative food products with enhanced health benefits.

2.3.3. Effect of Interaction on Functional Properties

Protein–phenolic interaction leads to changes in various aspects of functional properties, i.e., antioxidant, anti-inflammatory, antibacterial, and antiviral properties, associated with potential benefits for food quality and health. When phenolics form complexes with plant proteins, they are protected from degradation in the digestive system and exert their antioxidant activity more effectively. In the context of plant-protein–phenolic interaction, frequently investigated uses of phenolics include their ability to act as antioxidants [154]. Complexation with phenolic compounds reduced the allergenicity of plant proteins. This is because the complex changes the protein structure in a way that reduces its ability to trigger an allergic response. Most investigations showed a hypoallergenic effect of phenolic binding in vitro, in terms of a reduced IgE-binding capacity and alleviated basophil degranulation through non-covalent and covalent interactions of phenolics to various well-known allergens or allergenic protein fractions [155]. Two significant peanut allergens, Ara h 1 and Ara h 2, were easier for pepsin to digest when green tea catechins were present, but they resisted being broken down by phenolic oxidase [156].

There are negative effects also where complexation led to a reduction in bioavailability. It is unclear how dietary proteins affect the bioaccessibility and bioavailability of interacting phenolics both *in vitro* and *in vivo*. After the fortification with green coffee flour, the bioaccessibility of the constitutive phenolic compounds of the bread was improved; however, their potential bioavailability was decreased [157]. The interaction between soybean protein and grape/wine polyphenol (instant mixing) did not affect the bioavailability [139]. A transportation model for understanding protein bioavailability proposed by Zhang et al. [152] suggests that covalent interactions between

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protein–phenolics (anthocyanins) disrupt water–peptide hydrogen bonds to inhibit passive absorption of peptides. Fu et al. [158] described how proteins improve the stability of co-existing phenolic compounds, preventing their degradation in the gastrointestinal tract as a result of the presence of dietary proteins.

Protein–phenolic complexation affects plant protein digestibility in the human intestine. Some phenolics bind to proteins in a way that makes them less accessible to digestive enzymes, resulting in lower protein digestibility. However, other phenolics may enhance protein digestibility by improving the solubility and stability of the protein. Research has indicated that complexation with phenolics affects protein digestibility dually. Complexation between a phenolic compound and protein reduces the protein digestibility of the conjugate by inhibiting protease activity or inactivation of digestive enzymes. In previous work, Rawel et al. [159] found soybean proteins with reduced lysine, cysteine, and tryptophan content when complexed with selected phenolic compounds, protein–phenolic binding affects the bioavailability of essential amino acid (Lys, Cys, and Trp). In contrast, protein structures were partially unfolded by phenolics, facilitating the accessibility of susceptible peptide bonds. Soymilk added to green coffee enhanced protein digestion [160].

To produce functional foods, a strong understanding of the impact of the plant-protein–phenolics interaction on the conjugate's techno-functionality is essential. The solubility in walnut kernels decreased due to the non-covalent interaction between protein and phenolic compounds [161]. Polyphenolic compounds crosslink with protein during wine and juice production, causing insoluble particles to scatter light. Two processes can explain the precipitation action of phenolics: (1) simultaneous interaction with several proteins, and (2) monolayers covering less hydrophilic proteins [154]. Rheological properties were also affected due to the protein–phenolic interaction. It has been reported that phenolic compounds in polyphenol-fortified wheat flour have an impact on the physicochemical properties of dough and bread-making quality via intramolecular interactions [154]. In their study, Gawlik-Dziki et al. [162] observed that quinoa leaves added to bread decreased loaf volume and increased hardness, cohesiveness, and gumminess. Several investigations have found that interactions between phenolics and proteins improve their heat stability. There have also been several studies that have concluded that enthalpy changes occur as a result of phenolic conjugation during protein unfolding. Phenolics modified the stability of protein tertiary structures by introducing intra- and intermolecular forces in the flaxseed-protein–polyphenol complex [153].

2.3.4. Applications

Plant protein–phenolic interactions have been the subject of extensive research in recent years, and their potential applications are numerous (Table 4). Due to the phenolics and bioactives present in these complexations, they were used in both the food and pharma industries. In the food industry, these are generally used to develop phenolic- and antioxidant-rich emulsions, as well as to improve emulsifying properties and develop phenolic- and antioxidant rich-powder which can be used in beverages. The phenolics or antioxidant compounds can be used as coloring and flavoring agents with good antioxidant potential to increase shelf-life. The protein–phenolic complex has huge potential for the preparation of antioxidant and antimicrobial edible films. Proteins are suitable due to their biodegradable properties but have poor barrier properties due to the free matrices available, which are filled with phenolics, improving barrier properties of protein-based biodegradable films. Zein–gallic acid, for example, has demonstrated enhanced antimicrobial properties and greater tensile strength when phenolic compounds are incorporated into protein-based films [163,167,168].

In addition to showing enormous potential in the food industry, protein–phenolic complexes also showed enormous potential in the pharmaceutical field. By combining plant proteins with phenolic compounds, it may be possible to develop new drugs with enhanced efficacy and fewer side effects. Some studies link their antioxidant capability to

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their anticarcinogenic properties. Gawlik-Dziki et al. [162] found that bread enhanced with broccoli sprout phenolics 2% substitution increases antioxidant potential and consumer acceptance. Nutraceutical encapsulation into nanoparticle delivery systems has received a lot of interest in recent years. Encapsulating bioactives (curcumin and resveratrol) with epigallocatechin-gallate–zein conjugates enhanced thermal stability, UV light stability, and antioxidant activity and provided better bioaccessibility under a variety of physiological conditions [163].

Table 4. A summary of the practical applications of plant-based protein–phenolic complexation.

Plant Protein	Phenolics	Synthetic Methods	Characterization Methods	Effects	Applications	Reference
Chickpea protein isolate	Gallic acid	Alkaline method	FTIR spectroscopy	Emulsification activity, antioxidant activity	Water-in-oil (W/O) emulsion system	[148]
Brown rice protein	Raspberry juice	Magnetic stirrer for 15 min at room temperature	DSC, FTIR, GC/MS	Color parameter, total antioxidant activity, flavor profile	Food colorant and flavoring agent	[164]
Pumpkin, Pea Almond protein matrices	Cinnamic acid	Magnetic stirrer for 15 min for 600 rpm at room temperature	HPLC, DSC, FTIR-ATR		Nanoencapsulating agent	[152]
Pea protein	Grape seed proanthocyanidin	Alkaline method	Isothermal titration calorimetry (ITC), molecular simulations	Storage stability	Oil-in-water emulsifying agent	[165]
Flaxseed protein	Ferulic acid, hydroxytyrosol, flaxseed polyphenols	Alkaline method	SDS-PAGE, MALDI-TOF-MS, FTIR, CD, DSC	Antioxidant activity	Natural antioxidant	[153]
Soy protein isolate	Anthocyanins	Alkaline method	FTIR, fluorescence	Antioxidant activity	Natural antioxidant	[166]
Soy protein isolate	EGCG	Alkaline method	SDS-PAGE, CD, fluorescence, surface hydrophobicity	Antioxidant activity	Emulsifying agent	[167]
Zein	EGCG	Alkaline method			Nanoparticles for co-delivery of curcumin and resveratrol	[161]
Zein	Tannic caid	Alkaline method			Edible film	[168]
Soy protein isolate	Phenolic extract of ogaja (*Acanthopanax sessiliflorus)*		Rheometer, RVA, DSC	Rheological properties, thermal properties	Gluten-free noodle	[13]
Peanut protein	Anthocyanins and proanthocyanidins	At room temperature, 15 min	ATR-FTIR	Reduced IgE-binding, increased digestibility	Oral immunotherapy	[169]
Wheat protein	Quinoa		SEC-HPLC	Antioxidant	Functional food	[170]

gluten, gliadin	(*Chenopodium quinoa*)	potential, rheological parameters	View Article Online DOI: 10.1039/D4FB00193A

2.4. Protein–Polysaccharide–Phenol Complexations

In addition to binary conjugates (protein/polysaccharide and protein/polyphenols), protein–polysaccharide–polyphenol conjugates are obtained to improve techno-functional properties and physicochemical stability [171]. These ternary conjugates are naturally present in edible and medicinal plants [100]. The molecular properties of each component (structure, charge density, and molecular size), the concentrations of them, and environmental factors (temperature, pH, ionic strength, and presence of small molecules) can influence the properties of ternary conjugates [172]. The main principle is based on the fact that phenols interact with protein–polysaccharide complexes either via covalent or non-covalent bonding through a reversible hydrophobic association that may be stabilized by hydrogen bonding [173].

2.4.1. Mechanism

There are different mechanisms for the fabrication of ternary conjugates of protein/polysaccharide/polyphenols for example non-covalent reactions; electrostatic interactions; induction with Ca^{+2}; a combination of a single covalent reaction and electrostatic interaction; and a combination of the Maillard and polyphenol covalent reactions [171].

The protein–polysaccharide–phenol complex is developed in two stages (Figure 1d). Firstly, a protein–polysaccharide complex is formed via different types of interactions, as discussed in Section 2.1.2. After that, the phenols obtained from the plants may either bind covalently or non-covalently with the protein–polysaccharide complex. The binding depends on the ratio of the phenols to the protein–polysaccharide complex. It is executed in two ways. In the first case, multiple phenol compounds may bind to a single complex. This is known as multisite. Another case may occur in which one specific phenol binds to multiple sites of the complex. This type of binding is called multidentate. Thus, phenols strongly bond with these complexes, leading to the alteration of phenolic structure, characterization, and biological availability, and accessibility may also be affected because of this property [163].

2.4.2. Types of Interactions

Irreversible interactions take place between phenol compounds and protein–polysaccharide complexes because of covalent bonding. It usually takes place through carbon–sulfide or carbon–nitrogen linkage. Quinones are formed via the modification of enzymes in alkaline pH or the presence of oxygen. The hydroxylation of monophenols into ortho-diphenols, which easily oxidize into ortho-quinones, can be mediated by polyphenol oxidases. As quinones are potent electrophiles, they can induce severe crosslinking by reacting with the nucleophilic residues of proteins, using the Schiff base and Michael addition reaction [174].

Non-covalent interactions typically involve hydrophobic, hydrogen-bonding, electrostatic, and van der Waals contacts, and they are all reversible. However, the primary mechanisms causing the non-covalent creation of complexes between protein–polysaccharide complex and phenol compounds are hydrogen bonding and hydrophobic interactions. In general, interactions between hydrophobic amino acids and the aromatic ring structure of polyphenols may occur. The studies imply that proteins' open and adaptable structures may make it easier for phenols to enter by enhancing the surface area accessible for hydrophobic interactions and hydrogen bonding [175].

2.4.3. Compatibility

The compatibility of the interaction depends on the length, interactions, and cohesion energy density. The aforementioned parameters control the protein–

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polysaccharide and phenol complex's melting point and their resistance to ionic strength-induced dissociation. The interaction between the protein–polysaccharide complex and phenols occurs because of the denaturation of the molecule. The compatibility of protein–polysaccharide–phenol complexes can be enhanced by the process of denaturation brought about by heat and also by the addition of cations like calcium, iron, and copper. The ability of divalent cations to crosslink the protein–polysaccharide–phenol complex may be the cause of their stabilizing effects. An escalation in the hydrophobic contacts, hydrogen bonds, and ionic bonds within the complex is responsible for the enhancement in stability brought on by thermal denaturation [176]. The functional characteristics of protein–polysaccharide–phenol electrostatic complexes are irreversibly altered by these interactions, in addition to modifications brought on by precipitation. A highly stable emulsion is obtained with improved characteristics because of the encapsulation. The generation of this complex also leads to the escalation of the concentration of protein, polysaccharides, and polyphenols.

2.4.4. Effects on Functional Properties of Protein

Protein–polysaccharide–phenol interactions are widely used to form and stabilize proteins by either forming a polysaccharide–protein–phenol complex or Maillard conjugates. The variation in ionic strength in the protein–polysaccharide–phenol interaction leads to the acceleration of phase separation, causing an enhancement of the crosslinking of proteins, thereby providing stability [177].

The surface hydrophobicity of pea protein isolate/maltodextrin/epigallocatechin-3-gallate ternary conjugates was determined in the study of Chen et al. [171]. The surface hydrophobicity index of a native pea protein isolate and maltodextrin was found to be 2786 and 1101, respectively. It decreased to 338 for ternary conjugates, which can be resulted from the hydrophilic nature of covalently attached saccharide or epigallocatechin gallate molecules [102].

The emulsion activity index and emulsion stability index of the binary conjugates of pea protein isolate/maltodextrin/epigallocatechin-3-gallate were determined to be 89.8 m^2/g and 101.73 min higher than those of pea protein isolate and protein isolate/maltodextrin binary system [171]. The improvement of the emulsion activity and stability indexes may be due to the strong steric hindrance and charge repulsion between droplets that resulted from the combination of glycation and polyphenol covalent binding; in this way, the flocculation of droplets can be prevented, and the stability of emulsions increases [178]. The improvement of emulsion activity and stability index values is very important for the quality of emulsion-based systems such as mayonnaise, salad dressings, etc.

2.4.5. Applications

In addition to exhibiting techno-functional properties, protein–polysaccharide–polyphenol ternary conjugates also exhibit antioxidant, antifungal, antibacterial, and antitussive activities [100].

Natural polyphenolic–protein–polysaccharide ternary complexes extracted from *H. dulcis* showed remarkable antioxidant, antiglycation, and antidiabetic effects [179]. The bioactive characteristics of ternary conjugates are significantly affected by the process applied before and during extraction process. Naturally occurring polyphenolic–protein–polysaccharide ternary conjugates had effective antioxidant and antimicrobial properties against *K. pneumoni*, *S. aureus*, *B. cereus*, *E. faecalis*, and *M. luteus* and antifungal properties against *A. niger*, *F. oxyporum*, *B. cinerea*, and *A. solani*; therefore, this conjugate can be used as a natural biopreservative [180]. Different drying techniques were employed before the extraction of ternary conjugates from *Hovenia dulcis*, and microwave- and vacuum-drying techniques were determined as the most suitable, considering their antioxidant antiglycation activities and inhibitory activities on α-amylase and α-glucosidase [100]. The antioxidant activity of soy protein hydrolysates/glucan/ferulic-acid ternary complex

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without heat and formed with high-pressure homogenization and microwave treatment was compared, and the best treatment was found to be high pressure, followed by microwave treatment [170]. The results of the related studies about the determination of the bioactive properties of protein–polysaccharide–polyphenol conjugates highlighted that ternary conjugates have a great potential for the fabrication of functional foods and medicines.

Protein–carbohydrate–polyphenol conjugates have also been used as encapsulating wall materials for different bioactive compounds, such as curcumin and β-carotene. Zein–carboxymethyl-chitosan–tea-polyphenols conjugate nanoparticles used for encapsulating β-carotene. This ternary complex showed the highest stability when compared with zein and the zein–carboxymethyl-chitosan complex, considering the color stability of β-carotene under ultraviolet light due to the effective antioxidant properties of the conjugate. In addition, color changes at 5, 20, 37, and 60 °C storage temperatures were minimum in the samples encapsulated with ternary complex during 7 days of storage [181]. Ternary conjugates of protein–carbohydrate–polyphenol highly protect the bioactive compounds against environmental factors such as temperature, light, and acid, and this is very important for the production of healthy foods for bioaccessibility of the desired compounds to the target parts of the body. The results of the study indicated that this conjugate can be used for the encapsulation of colorants and antioxidants used in food products to improve their stability.

Curcumin loaded ternary conjugate emulsions were fabricated by pea protein isolate–maltodextrin–epigallocatechin-3-gallate. The loading efficiency of pea protein isolate was found to be about 40% and it increased remarkably to 92.3%. The retention rate of curcumin at different temperatures, i.e., 4, 25, and 55 °C, was determined as the lowest when compared with the protein isolate and binary mixtures. The findings of the present study indicated that such a ternary emulsion system can be used for an effective delivery and release system for bioactive compounds [171].

Protein–carbohydrate–polyphenol conjugates have great bioactive properties, including antioxidant, antimicrobial, and antifungal properties. They are more effective than protein unitary and binary conjugates of protein/polyphenol or protein/carbohydrate. They also have better emulsion activity and emulsion stability index values. The results indicated that ternary conjugates of protein–carbohydrate–polyphenol can be used in food products due to their techno-functional and bioactive properties. More attempts should be achieved to observe their performance in model food systems (Figure 2).

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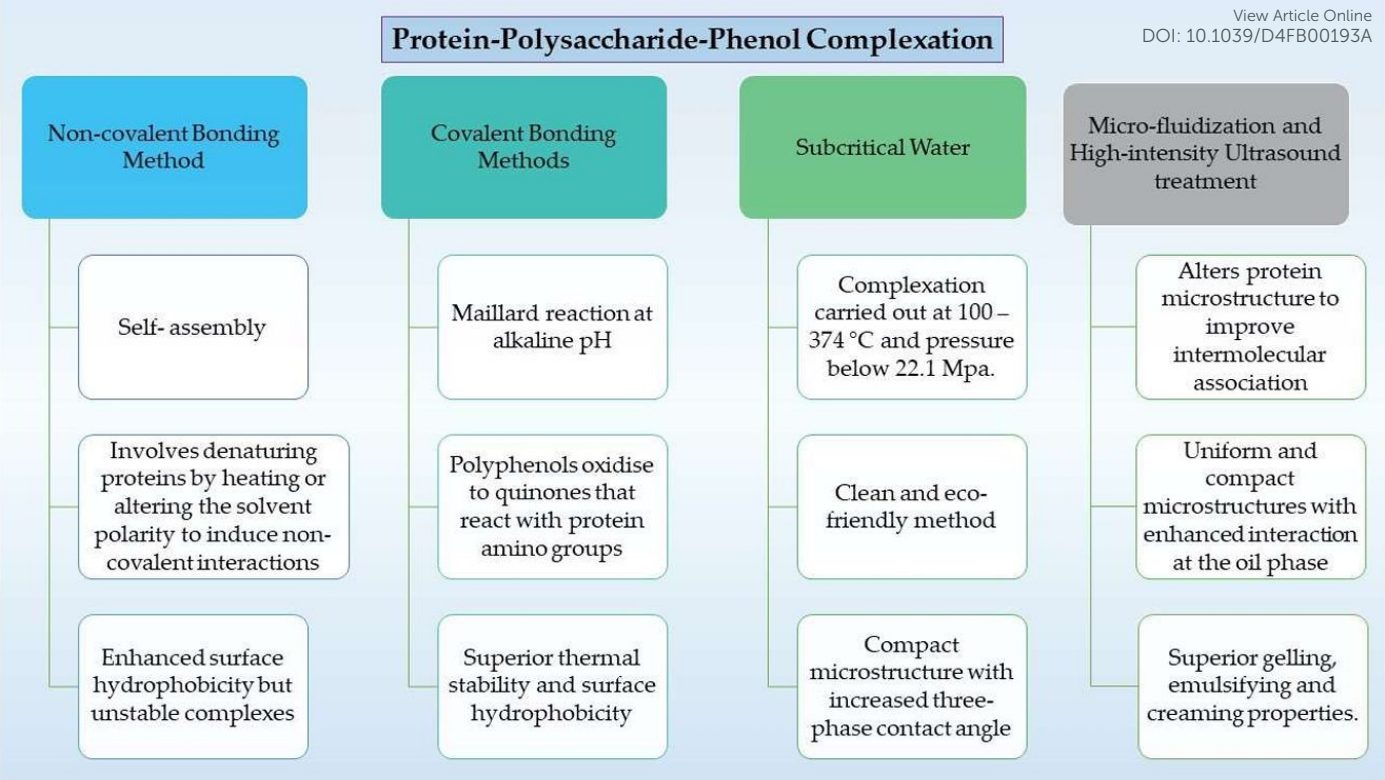

Figure 2. Fabrication of protein–polysaccharide–phenol complexes (*Adapted from Najari et al. [182]*).

3. Amyloid Fibrillization

Amyloid fibrils were earlier linked with neurodegenerative diseases, but with an increase in exposure, it was discovered to be a generic property of protein when treated in a specified conditions [183]. In recent years, the formation of amyloid fibrils in food systems has also become a topic of interest, as the presence of amyloid fibrils in food can affect the quality, safety, and functionality of food products. Under a particular condition, a wide variety of proteins can form amyloid fibrils. When proteins are treated under a specified set of conditions, such as a pH near 2.0 or temperature around 70 to 90 °C, their structure gets unfolded or partially unfolded and forms a β-sheet linear structure. This very low pH (2.0) and high temperature (90 °C) convert the protein monomers into amyloid fibrils [108]. During the process, due to the positive charge of protein or polypeptide, electrostatic repulsion occurred, which facilitates the development of organized fibrils. These fibrils are organized by the formation of linear β-sheet-type structures and stabilized by intermolecular hydrogen bonding [184]. Other than that, van der wall forces and hydrophobic interactions also help in the formation of fibrils.

3.1. Factors Affecting Amyloid Formation

The fibrillization process depends upon various factors, including the source of protein, concentration of protein, nature of protein, amino acid composition, denaturing agents, environmental conditions (temperature, pressure, pH, and ionic strength), surface, agitation, and even time. Protein composition is the base for the development of amyloid fibrils. The sequence of protein and their structures significantly affects the formation of fibrils [195,196,197,198]. The sequences containing higher amounts of β-sheet amino acids (tyrosine, tryptophan, phenylalanine, etc.) are more prone to the formation of fibrils. The most widely used technique for creating amyloid fibrils involves heating in an acidic environment, which unfolds and hydrolyzes proteins before 1D peptide assembly in the distinctive cross-beta pattern that characterizes amyloid aggregation [185]. According to Akkermans et al. [186], a portion of the peptides that were produced during the process of hydrolyzing β-lactoglobulin (BLG) was found in

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the fibrils of BLG that were formed after heating it for 20 h at 85 °C, at pH 2. These peptides were not made of intact BLG. Similar reports were found in amyloid fibrils developed from soy protein [96] and potato protein [187]. The protein composition significant for the growth of amyloid fibrils is β-sheets. These sheets are made up of unbranched, ribbon-like β-strands of the same length that interact with one another through hydrogen bonds (N–H···O—C) between two consecutive peptide backbones [12]. These β-sheets link together to form a β-sheet structure with the help of various interactions which are van der Waal forces, hydrogen bonds between amide groups and sheets, hydrophobic interactions, and the development of bonding side chain ladders on the paired sheet surfaces. The protein source and its amino acid composition highly affect the formation of fibrils. The fibrillization of vicilin from three distinct sources—mung, red, and kidney beans—was compared by Liu and Tang [188] under heating at 85 °C and pH 2.0 for 1–24 h. According to their findings, kidney beans had a better capacity to generate well-ordered fibrils, whereas mung beans had the highest potential for amyloid fibril development. These variations were caused by variations in the makeup of their amino acids and the tendency of their polypeptides to undergo acid hydrolysis. Li et al. [189] investigated three different legume sources, namely cowpea, chickpea, and lentil, to develop amyloid fibrils. The cowpea protein's vicilin has a longer, more flexible shape than lentil and chickpea proteins' semi-flexible and hard fibrils, respectively; it has the highest capacity to create amyloid fibrils with superior rheological characteristics. The concentration of protein is another major factor that affects the rate of fibril formation. High protein concentrations increase the rate, while low protein concentration decreases the rate, of fibril formation [15,188,190]. The environment in which proteins are present also affects the formation of fibrils. High temperature and pressure promote fibril formation by increasing the rate of protein unfolding and aggregation. The change in pH can trigger the formation of amyloid fibrils by destabilizing the protein structure and promoting unfolding. The effects of pH (2–10) on the development of soy protein isolate amyloid fibrils were examined by Wan and Guo [191], and their findings revealed that the assembled component peptides had distinct forms at various pH levels. The β-sheets produced formed amyloid fibrils exclusively at pH 2, among pH levels below 6. A high salt concentration can lead to protein denaturation, and a high sugar concentration increases the viscosity of the solution and slows down protein diffusion, thereby promoting fibril formation [192]. Short, curved, and highly branched fibrils might form when the salt concentration was raised, while simultaneously lowering the necessary protein content. Agitation can speed up fibril formation by promoting protein–protein interactions. The type of surface provides nucleation sites for protein aggregation, thereby increasing the rate of fibril formation. Time is the most important factor in any reaction. The length of time to which protein is exposed to any condition affects the formation of fibrils. The increase in exposure of time to the same condition promotes fibril formation in hemp seed protein [183]. The heating time also affected the formation of amyloid fibrils. Xia et al. [193] demonstrated the formation of short worm-like fibrils and long semi-flexible fibrils, respectively, by heating soy protein isolate and soy protein β-conglycinin hydrolysates at 95 °C and pH 2 for 60 min. In both protein samples, increasing the heating time to 360 min resulted in clusters coexisting with fibrils, while heating for 720 min prevented the formation of fibrils. This suggests that the right heating time can also affect the structural and functional characteristics of the amyloid fibrils that are formed. According to Pang et al. [194], the structural features of rice bran protein fibrils were shown to be influenced by the heating duration. Specifically, an increase in heating time to 420 min resulted in a rise in the number of β-sheets and surface hydrophobicity. On the other hand, there was a declining tendency when the heating duration was increased to 600 min. The heating and manufacturing time also had an impact on the other characteristics of rice bran protein fibrils, such as their molecular flexibility and emulsifying abilities. It has been shown that the best heating period for the best physicochemical and emulsifying qualities is between 420 and 480 min. The specific

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conditions required for the formation of fibrils vary with the food product, especially the type of food and its amino acid composition (Figure 3).

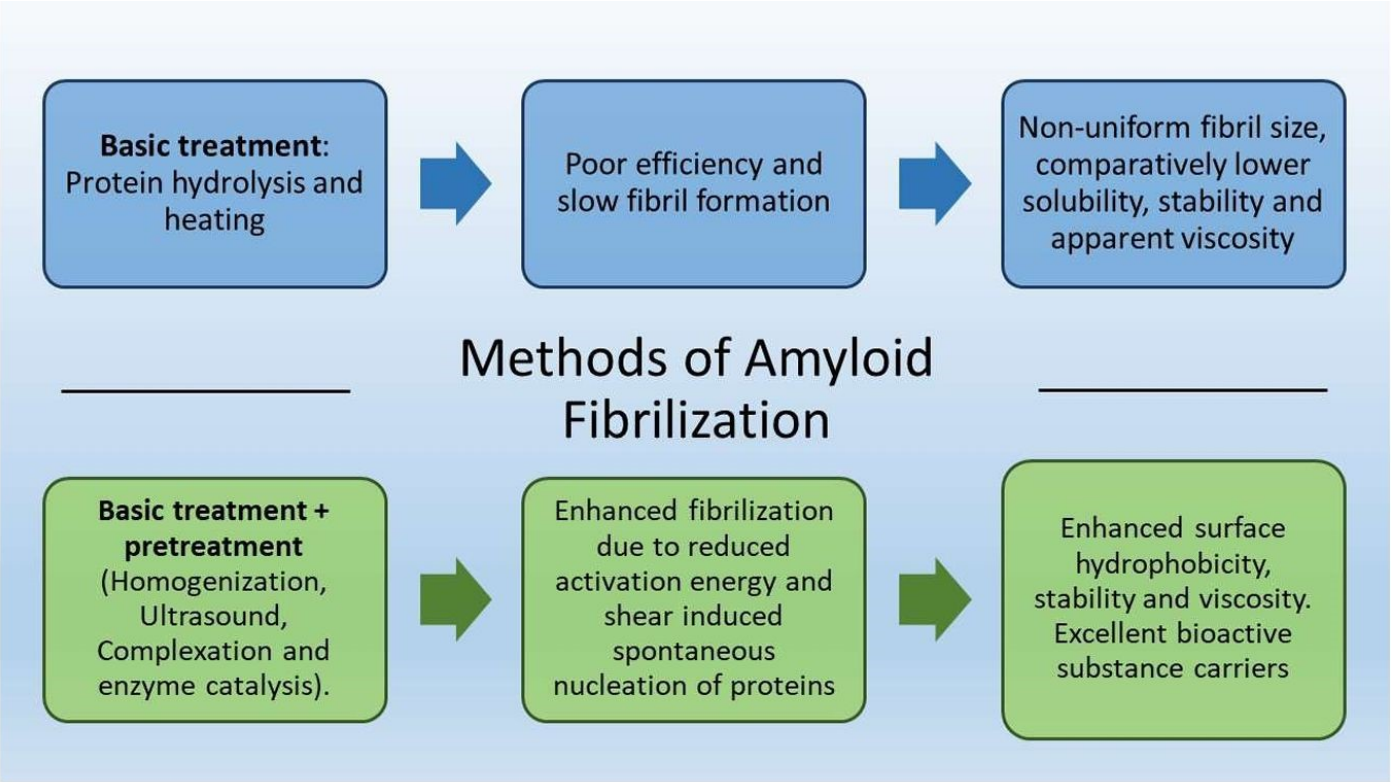

Figure 3. Role of pretreatment on amyloid fibrilization (*Adapted from Chen et al. [195]*).

The formation of amyloid fibrils from different globular proteins, such as ovalbumin [196], lysozyme [197], and β-lactoglobulin [198] has been developed under specified conditions for their utilization in food and biotechnology sector. Other protein sources, such as soybean, potato, wheat gluten, pea, hemp, zein, maize, etc., can also form fibrils. Despite its enormous potential and easy availability of plant proteins, research on amyloid fibrils is still lacking.

3.2. Mechanism of Formation of Amyloid Fibrils

The formation of amyloid fibrils can be performed using three mechanisms: (i) nucleated polymerization, (ii) nucleated conformational conversion, and (iii) downhill polymerization (Figure 4) [199].

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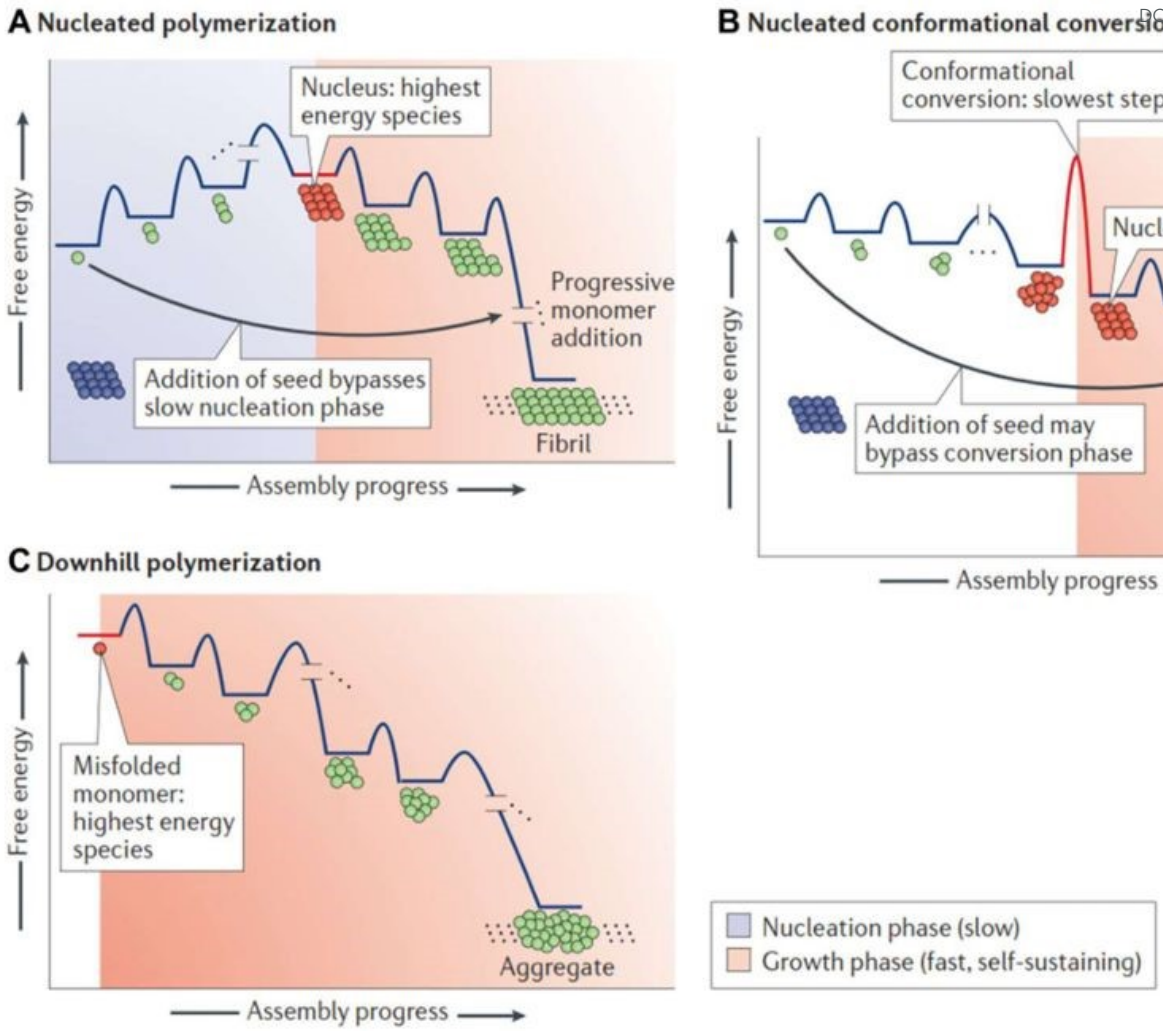

Figure 4. Mechanisms of protein aggregation and formation of thermodynamically stable amyloid fibrils (*adapted with permission from Eisele et al. [199]*).

Nucleation-dependent polymerization or nucleated polymerization is a technique where protein aggregation takes place through the formation of a nucleus, which is a high-energy species. The nucleus is rich in oligomeric species; however, monomeric species are also found and consist of a β-sheet structure. After the formation of the nucleus, monomeric species (seeds) are added, and aggregation proceeds progressively to form fibrils, as no nucleation is needed at that stage. The formation of amyloid fibrils under very low pH or acidic conditions can be explained by this process.

In nucleated conformational conversion, an equilibrium was maintained between monomeric and heterogeneously structured oligomeric species, which are more stable. The oligomers are converted into nuclei and then into fibrils, which then convert neighboring monomers into fibrils by conformation.

The above two processes both require the formation of a nucleus, which, when aggregated, forms fibrils, whereas in downhill polymerization, the step-by-step addition of unfolded/partially unfolded/misfolded monomer is the focus. This subsequent monomeric addition leads to the formation of amorphous aggregation, which further develops fibrils. The cross β-sheet structured amyloid fibrils are developed in a downhill polymerization process, which may or may not be available in nucleated polymerization or nucleated conformational polymerization.

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3.3. Structure

These amyloid fibrils have a cross β-sheet structure formed from strands of β-sheet with fibrils attached by hydrogen bonds perpendicular to them [108,200]. Morphologically, they consist of protofilaments (2–6), with a diameter of 2–5 nm, associated laterally or twisted together to form unbranched, long fibrils [185]. Amyloid fibrils can vary in size and shape and can range from a few nanometers to several micrometers in length. They typically have a highly ordered and regular structure, with a uniform diameter and a straight, linear shape. The fibrils are usually highly soluble in water and tend to aggregate in a parallel arrangement, leading to the formation of fibril bundles.

The persistence length of amyloid fibrils is a measure of the stiffness or rigidity of the fibril and is typically in the range of tens to hundreds of nanometers. The persistence length is defined as the length over which the orientation of the fibril is correlated. The shape of amyloid fibrils can be a long narrow type or short curly type depending upon the source of plant protein [108,201]. In a study by Li et al. [108], a worm or curly-like structure was found in cowpea, kidney beans, mung bean, and black bean, whereas a straight narrow structure was found in pumpkin seeds, lentils, and chickpeas (Figure 5). The persistence length for curly fibrils is in the range of 50–150 nm, and straight long fibrils in the range of 500–3000 nm or more. Overall, it can be seen that beans mostly carry worm-like curly structures due to their specific protein composition. The proteins dominant in the 7S or 8S fraction have lower denaturation temperatures (69–73 °C) were hydrolyzed to form small peptides and require small energy gain, thus forming small curly worm-like fibrils [108,202]. On the other hand, the proteins dominant in 11S fractions have a higher denaturation temperature (76–77 °C), require more energy for fibrillization, and form longer straight fibrils [108,203].

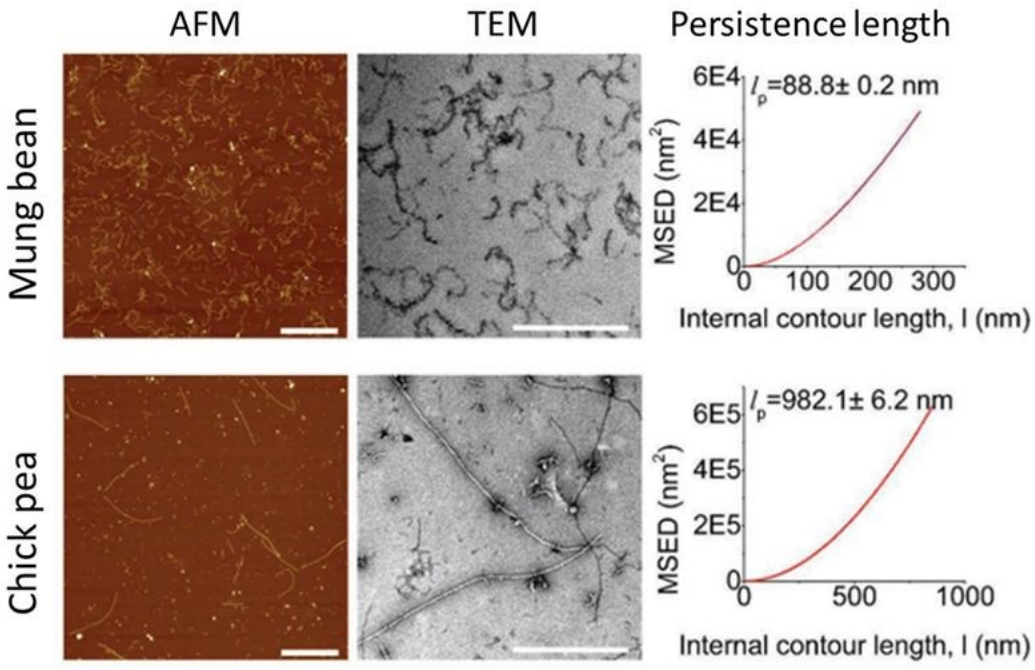

Figure 5. AFM, TEM, and persistence length of mung bean and chickpea (*adapted with permission from Li et al. [108].*

Several methods to identify amyloid fibrils have been developed, such as X-ray diffraction, transmission electron microscopy, nuclear magnetic resonance, and circular dichroism spectroscopy. The change in secondary structure was observed during the fibrillization process with a slight increase in unordered random coils due to the unfolding of secondary structure and hydrolysis of peptides [183]. In addition, fluorescent-based methods were also developed to identify and quantify them; for

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example, such when these fibrils are bonded with Congo red, they develop yellow-green birefringence and intense fluorescence with thioflavin T [185].

Currently, atomic force microscopy has been widely, allowing researchers to study the fibrils in detail, including their shape, size, and length and the interactions between them.

3.4. Effect on Functional Properties with Fibrillization and Applications

The formation of fibrils is a generic property of all proteins whether they are of animal origin or plant origin. The unintentional formation of amyloid fibrils in food leads to changes in physical and functional properties that can result in spoilage or quality deterioration in food. With the increase in knowledge about fibrils, researchers tried to utilize them as a tool for texturing and stabilizing food products and improving food quality and safety. It is also used as a functional ingredient for gelation, viscosity, and emulsification. The fibrillization of proteins in food can alter the texture, flavor, and appearance of food products and may also have toxic effects on human health [204].

The unfolded protein is soluble in nature when aggregates form insoluble fibers. Viscosity and gelation are two of the most important properties due to their fiber strands, which can increase viscosity and form a stronger and more stable gel. During gelling, the fibrils–polysaccharide complex has been formed under crosslinking in a water environment to form a hydrogel. The developed hydrogel contained greater elasticity and had a greater water-holding capacity [205]. (Figure 6a). Another important characteristic of amyloid fibril is that it acts as a foaming, as well as an emulsifying, agent by reducing the surface tension and forming an elastic network around the air bubble (Figure 6b,c). Fibrils help in stabilizing emulsions, thereby enhancing the biological activity of bioactives [209]. The amyloid fibril can also be used as a wall material to encapsulate bioactive compounds in drug delivery or micro/nanoencapsulation due to its larger aspect ratio and stability against environmental factors [206] (Figure 6d). The delivery system with amyloid fibrils can be made through different mechanisms, viz. protein–fibril complex, emulsion, gels, capsules, etc. Hu et al. [206] made a whey protein fibril–chitosan complex to encapsulate curcumin. Numerous studies have shown the benefits provided by fibrils in encapsulation and target delivery of bioactive compounds via various mechanisms. The presence of fibril in starch can lead to a reduction in glycemic index (GI) and can help develop low GI products that are beneficial for diabetic patients. In plant-based food such as meat or dairy alternatives, protein fibrils showed enormous potential in texturizing food products. Other applications of protein aggregation in food-processing industries are thickeners or gelling agents [207-209], ultralight aerogels [208], foaming and emulsifying agents [79,209], degradable films [210], carrier for encapsulation [206], and antimicrobials [206].

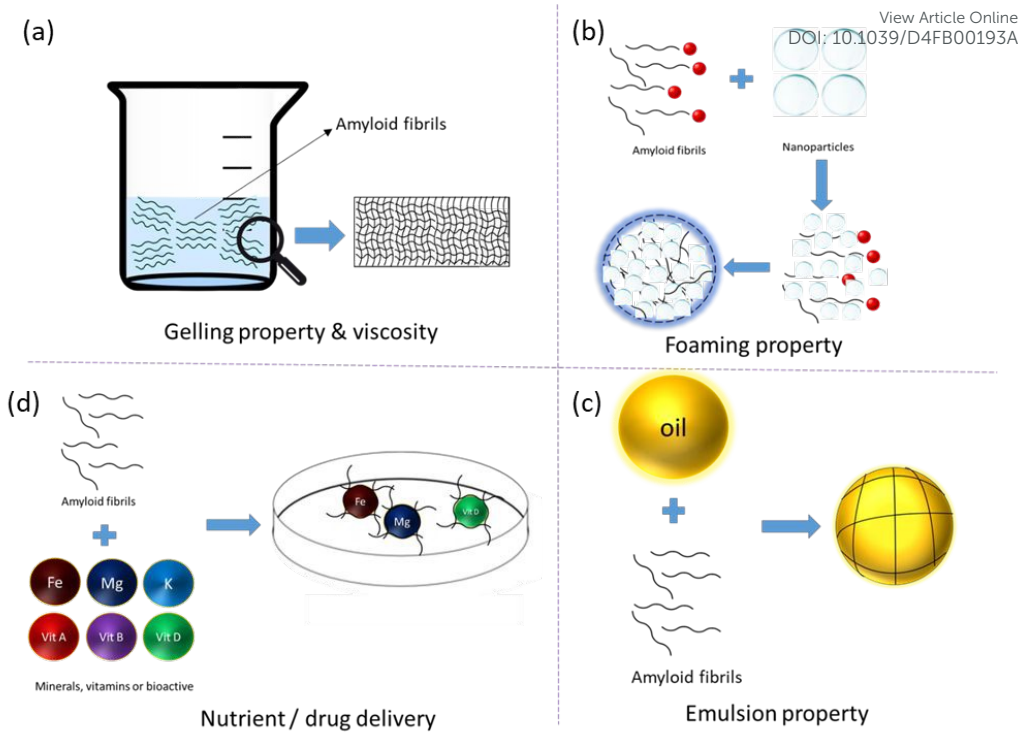

Figure 6. Functions of amyloid fibrils as (**a**) hydrogel (**b**,**c**) foaming and emulsion stabilizer and (**d**) micro/nanoencapsulating agents

3.5. Future Applications

The amyloid fibrils can also be used in biosensors to detect metal ions, microorganisms, and glucose [107]. However, a more thorough study on the application of protein fibril in a biosensor is required for its industrial application. In a study by Xiang et al. [211], fibrils were found as reducing agents. They can bind the Fe^{++}, and thus can be effective against protein malnutrition and anemia. The protein fibrils are commonly used in texturizing food products; however, their structure can help in holding and delivering flavor compounds and can even mask off-flavor in the food product which needs to be further explored. Protein fibrils have shown enormous potential in the delivery of functional ingredients. Nowadays with increasing awareness and lack of everything in a single ingredient, the use of several functional ingredients and their synergetic effect through protein fibrils need to be checked and is the future scope for nutrient delivery.

4. Conclusions and Future Scope

Proteins are widely used in many food products due to their techno-functional, as well as nutritional, properties. This review focuses on the changes in the techno-functional properties of plant-based proteins due to complexations and amyloid fibrilization. Animal-based proteins are generally preferred due to their excellent properties. However, the demand for plant proteins is increasing day by day due to environmental and nutritional concerns of the consumers in regard to animal-based products. However, when compared with the animal proteins, most of the plant-based proteins have weak techno-functional properties. For this aim, plant proteins are modified to improve their techno-functional and nutritional properties. A novel way to achieve this is to fabricate complexations of proteins with carbohydrates, polyphenols, and carbohydrate/polyphenol mixtures. Binary or ternary conjugates of proteins with effective bioactive (antioxidant, antidiabetic, antimicrobial, antifungal, etc.) and techno-functional properties are naturally present in plants and microalgae and inspired food scientists to extract such conjugates or to form conjugates artificially. Studies about the binary and ternary conjugates indicate that they have more effective

techno-functional and nutritional properties. Such conjugates can be used especially in regard to encapsulation, as they can serve as wall materials. Conjugation improves the release characteristics of the bioactive compound and helps protect against environmental factors such as heat, acidity, etc. These emerging modification techniques can prove to be an effective tool for developing engineered protein bioparticles with unique functional attributes and health aspects that can be easily incorporated into food and drug delivery systems, biosensors, and cosmetics. However, a significant knowledge gap exists regarding the impact of complexation and fibrilization conditions on plant proteins from different sources. Furthermore, there is a need to extensively study the detailed impact of these modified proteins on human health before the implementation and utilization of these technologies at a commercial level. It is necessary to have more specific details regarding the molecular, structural, and physicochemical characteristics of modified plant-protein substances. Analytical techniques like chromatography, spectroscopy, mass spectrometry, electrophoresis, microscopy, and rheology can be used to learn more about the conformational changes, bond types, and reaction mechanisms involved in the production of complexes and fibrils. It will be crucial in the future to manufacture protein-based complexes and fibrils on a large scale by utilizing materials and procedures that are economically sound. As a result, more research is needed to develop these processing activities.

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Data Availability Statement:

The original contributions presented in the study are included in the article, further inquiries can be directed to the corresponding authors.

On Behalf of all the authors,

Sincerely,

Zakir Showkat Khan*

**corresponding author*