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The potential and limitations for applications of oat proteins in the food industry

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Abstract. Oat proteins have gained high attractive popularity in the market as future protein alternatives in various food products. The extracted oat protein fractions are characterised by a relatively high protein content and a unique amino acid profile compared to other cereal grains. From another aspect, the oat protein is separated unintentionally during the production of oat flours, oat drinks, and oat flakes which encourages the incorporation of oat proteins in the food industry to valorise the food wastes. Therefore, commercial oat proteins possess poor techno-functionality and water solubility in the usual environmental conditions for most food products; therefore, modification of oat proteins functionalities is highly recommended. Several modification methods, including chemical, physical and enzymatic, have been proposed to improve the techno-functionality of native oat proteins and their biological activities. This review highlights the nutritional value of the oat protein fractions, their techno-functional properties and their food industrial challenging limitations. Additionally, it summarises several prospective methods effective for boosting the functionality of oat protein fractions and broadening their application in a range of food industries (bakery, dairy, meat, and their alternative products) with an overview of their impact on humans, animals, and environmental health.

Key words: oat proteins, nutritional benefits, biological activity, techno-functionality, modification methods, food industrial application.

INTRODUCTION

In the last decade, consumer awareness regarding a healthy lifestyle and dietary protein sources has increased (Boukid, 2021a). As a result, the market demand for innovative healthy food products rich in alternative non-animal proteins has increased remarkably (Sterna et al., 2020; Boukid, 2021a). Meanwhile, the proteins derived from plant sources are attracting enormous food industrial interest owing to health, religious, ethical, cost, and dietary habits for some consumers (vegetarian, vegan, flexitarian), in

addition to sustainable and environmental concerns (Nieto-Nieto et al., 2014; Boukid, 2021b).

The comparison of Boukid (2021a) between the nutritional composition of grains and seeds (cereals, legumes, oil seeds) highlighted the particularly high protein content in oat grains among the whole major cereal categories. The protein content of oat groats ranges from 15 to 20% by weight, depending on genotype and growing environment (David, 2011; Kruma et al., 2018), in contrast to the protein contents of wheat (10.69–13.68%), brown rice (7.50%), barley (9.91%), sorghum (10.62%), millet (11.02%) and rye (10.34%) (Kumar et al., 2021). The main storage protein of most cereals (wheat, barley, and rye) is prolamin except for oat grains, where the predominant storage protein is globulin (which represents 70–80% of the total oat protein fraction) (Nieto-Nieto et al., 2014; Sargautis et al., 2021). Oat globulin is characterised by having a better amino acids composition, which is significantly higher in essential ones such as lysine and threonine, for human and animal nutrition than the prolamin of the other cereals (David, 2011; Nieto-Nieto et al., 2014). From the biological activity aspect, the oat globulin is characterized by particular bioactive peptides sequences such as angiotensin-converting enzyme inhibitor, antiamnestic (PEP-inhibitor), DPP-IV-inhibitor, antioxidant, and hypotensive peptides (Cavazos & Gonzalez de Mejia, 2013). Moreover, oat protein is a gluten-free source that suits the requirements of people suffering from coeliac disease (Kumar et al., 2021).

The annual marketing observations have indicated a prominent increment for oat protein acceptance by consumers compared to the other plant protein alternatives such as soy, pea, and lupine proteins since no off-flavours concerns are raised (Boukid, 2021a). Therefore, the research and markets (2019) predict growth in the global oat protein market at a CAGR of 1.22% during the forecast period (2019–2024). Furthermore, from the sustainability and the environmental perspectives, Mogensen et al. (2020) confirmed the potential reduction in greenhouse gas emissions by 8% and the land use by 14% if 24% of animal-based food is replaced by oat protein concentrate-based food. In this regard, the oat grains became valuable and attractive for research and commercial interests as a superior cereal source of low-cost dietary proteins with a prominent demand for its oat protein fractions in all the food industries (Boukid, 2021a).

Recently, oat protein preparations have been produced industrially (Fig. 1) in the following forms: oat protein isolates (OPI), oat protein concentrates (OPC), and fraction rich-in-proteins. The oat protein isolates (containing ≈ 90% protein) are extracted by wet methods (alkaline iso-electrically extraction, saline extraction, and acidic extraction) or an enzymatically isolation method (Boukid, 2021a; Immonen et al., 2021; Kumar et al., 2021). Oat protein concentrates (containing ≈ 70% protein) are produced with a production yield of up to 5% as the by-product of oat flour dry fractionation (including fine milling and air classification) into oat bran, oat starch, and β-glucan (Jiang et al., 2015; Immonen et al., 2021; Kumar et al., 2021). Additionally, the oat protein concentrates can be recovered as a by-product from the industrial production of β-glucan isolates (Brückner-Gühmann et al., 2019a).

The dry fractionation process is incorporated in the production of a fraction rich in proteins containing 42% protein (Boukid, 2021a). The study of Kumar et al. (2021) illustrated the unintentional removal of oat proteins during the physical separation step

of fibres in the production processes of oat flours, oat flakes and oat drinks that have a potential in oat protein fraction preparation. Theoretically, the oat protein possesses potential functional properties that contribute to the production of plant protein-enriched food products characterised by their improved quality (Jiang et al., 2015; Mäkinen et al., 2017; Kumar et al., 2021).

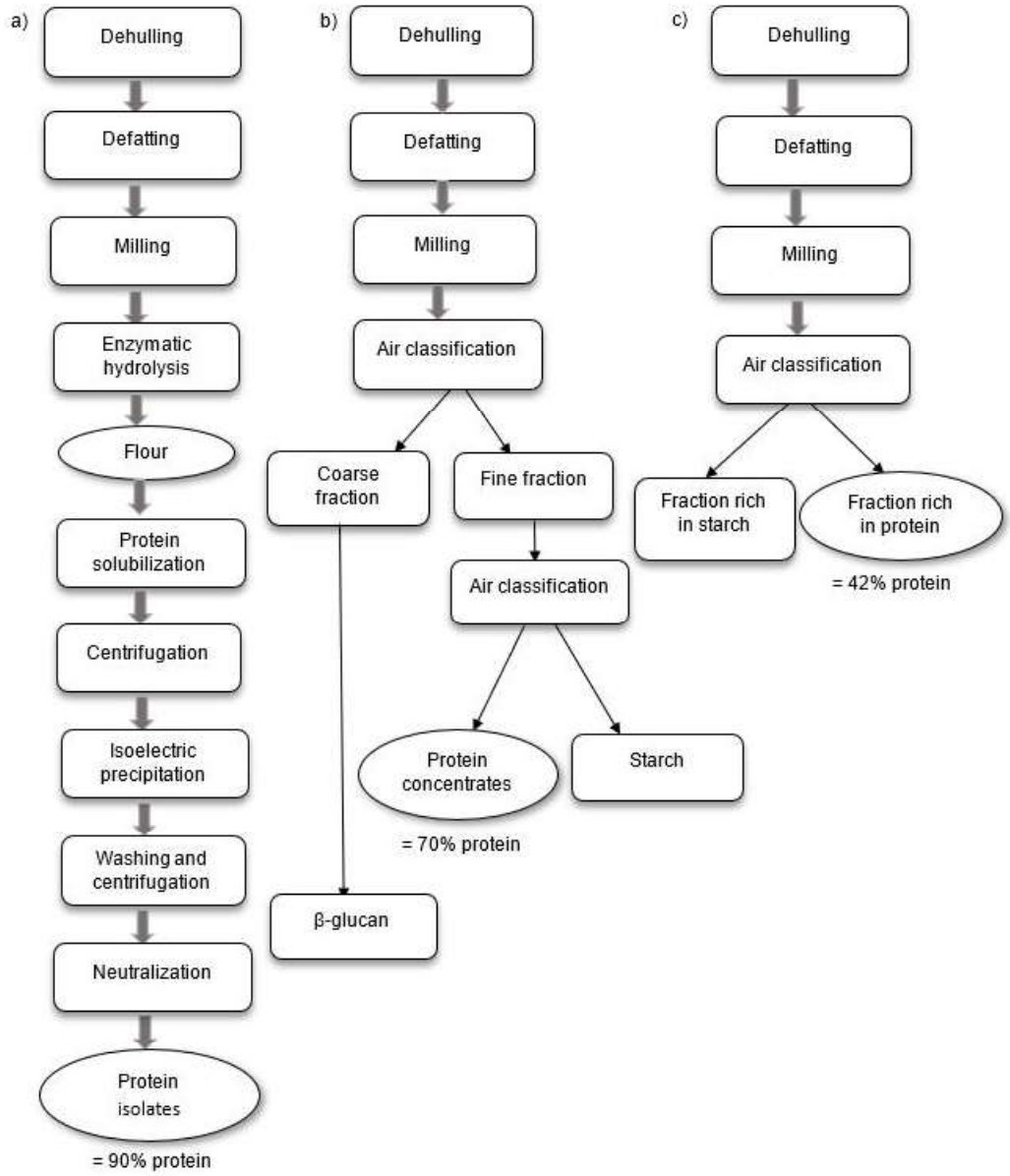

Figure 1. Schematic demonstration of the three potential industrial processing methods for producing oat protein preparations: a) alkaline extraction method, b) eecovery of oat concentrate from *β*-glucan production chain, and c) dry fractionation (Boukid, 2021a).

Although the market availability for the oat protein preparations and its unique proteinaceous profile and good amino acid compositions, the oat protein utilisation in the food industry remains limited and challenging due to the limited techno-functionality of the native oat protein under the typical aqueous food conditions (Mäkinen et al., 2017; Li & Xiong, 2020; Kumar et al., 2021). Thus, the demand has increased for the development of new modification strategies to enhance the techno-functionality of oat proteins and boost their application in various food industries (Brückner-Gühmann et al., 2018; Boukid, 2021a). Therefore, the purpose of this review is to demonstrate the nutritional value of the oat protein fractions, their biological activities, their techno-functional properties, and their food industrial challenging limitations. Additionally, this study summarises several prospective methods effective for boosting the functionality of oat proteins and broadening their application in various food industries with an overview of their impact on humans, animals, and environmental health.

The unique nutritional value of oat proteins and their biological activities

Typically, oat proteins have the following distribution in the layers of oat groats: 12% protein in the starchy endosperm, 18–30% in the bran, and 29–38% in the germ (Immonen et al., 2021). Four different varieties of proteins have been discovered in the oat grains based on the Osborne classification: globulins (70–80%), prolamins (4–14%); in oats called avenins, albumins (1–12%) and glutelins (< 10%), each as a percentage of the total oat proteins (Immonen et al., 2021; Spaen & Silva, 2021). Moreover, the essential amino acid composition in oat proteins is basically the same as the standard required for the daily intake of the human body, which can effectively promote the growth and development of the human body, in parallel to its regular consumption helps in treating the lysine deficiency (Tang et al., 2022).

The globulins represent the major fraction in oat proteins. Their amino acid profile is typically more valuable when compared to glutelin rich crops such as wheat or maize (Kruma et al., 2016). The amino acid composition for oat globulin is similar to soya glycinin, with the exception of tyrosine and phenylalanine, which were higher in oat globulin, and aspartic acid, proline, and lysine which were lower (Sargautis et al., 2021).

The distribution of oat amino acids varies between the structural parts of the grain (the germ, the endosperm, and the husk). The lysine content was found higher in oat germs than in either endosperm or the husk (Kumar et al., 2021). Mäkinen et al. (2017) identified higher glutamic acid and proline content in oat endosperm, particularly in comparison with the husk. In contrast, the same research found that the phenylalanine husk content is higher than in both the embryo and endosperm. Sterna et al. (2016) reported that the dehulled oat grains (45.60 g kg^{-1}) usually have a more significant amount of essential amino acids than the hulled grains (38.65 g kg^{-1}).

Both albumin and globulin in the oat grains play essential roles as contributors of lysine, and these have been found to have greater lysine contents, about 8.18 and 5.53 g amino acid 16 g^{-1} of N, respectively (Kumar et al., 2021). Furthermore, Spaen & Silva (2021) determined that the prolamins of oats are rich in sulphur and contain high amounts of glutamic acid.

Apart from the nutritional value of oat proteins, the isolated oat protein fractions characterized by high digestibility (90.3–94.2%), biological value (74.5–79.6%) as well as net protein utilisation rate (69.1–72.4) (Kumar et al., 2021). The high utilisation rate

of the oat protein in the human body was reported by Tang et al. (2022), in addition to the superior oat protein efficiency ratio (PEP) that exceeds 2.0, compared to wheat and maize's PEP (< 1.5). Recent studies showed the presence of a bioactive peptides sequence in oat globulins that have the following biological activities: ACE-inhibitor, antiamnestic (PEP-inhibitor), DPP-IV-inhibitor, antioxidant, hypotensive peptides, antidiabetic peptides and antithrombotic peptides (Cavazos & Gonzalez de Mejia, 2013; Ramírez-Fuentes et al., 2021). An *in-vivo* study by Zhang et al. (2015a) showed that oat peptides, at a high dosage, had a hypoglycaemic effect on STZ-induced diabetic mice stimulating insulin secretion, increasing insulin sensitivity and elevating glycogenesis. Sánchez-Velázquez et al. (2021) explained the dependence of the biological activity and the functionality of oat protein on its solubility and digestibility, which can be enhanced by the digestive enzymes in the GIT (gastrointestinal tract). Consequently, oat protein modifications, especially limited proteolytic hydrolysis, are highly recommended for unfolding the complex structure of native oat protein and promoting its solubility and bioactivity (Sánchez-Velázquez et al., 2021). The previous nutritional profile and bioactivity of oat proteins justify its potential future application in the food industry and its particular techno-functional properties.

The techno-functional properties of oat proteins and their challenging limitations in the food industries

The functionality of the various oat protein fractions has a promising value in the novel healthy food industry. Kumar et al. (2021) and Spaen & Silva (2021) reported the oat proteins' functional properties, including gelling ability, emulsification properties, water-holding capacity (WHC), fat-binding capacity (FBC) and foaming properties, which enable the oat proteins to function as thickeners, emulsifiers, texture modifiers, and stabilisers in food products. Furthermore, the similar structure between the oat 12S globulin and the soya glycinin 11S globulin, which is known for its good gelling and emulsifying properties, suggesting the potential of oat protein to act as a gelling agent (Nieto-Nieto et al., 2015; Li & Xiong, 2020).

However, the functionality of native proteins is poor and limited in neutral and slightly acidic pH conditions (4−7), which is the typical pH range for food products, and consequently restricts its utilisation in many food industries (Mäkinen et al., 2017; Kumar et al., 2021). The reason for functionality limitation is that the oat globulins are insoluble under slightly acidic and neutral conditions due to their unfolding structure, resulting in transition from β-sheet to a random coil conformation and the formation of insoluble aggregates (Brückner-Gühmann et al., 2019a; Ma et al., 2000). Further explanation was illustrated by Mäkinen et al. (2017), who attributes the solubility difference between the oat globulins and the soya glycinins to some changes in the oat globulin surface properties. These changes arise from the existing glutamine-rich repeats of eight amino acids near the C-terminus of the acidic polypeptide exposed to solvents. Thus, these surface changes render the oat globulins less hydrophilic compared to other globulins, and explain the higher salt concentrations needed for solubilizing the oat globulin.

The oat protein preparations (OPC and OPI) could be used as an additional source of proteins to enrich dairy alternative products (Spaen & Silva, 2021) and producing meat analogue products (Mäkinen et al., 2017; Boukid, 2021a), or as a replacement for

skimmed milk powder in hybrid (dairy/plant based) yoghurt production (Brückner-Gühmann et al., 2019b). However, the main commercially available oat protein preparations (OPC and OPI) have poor techno-functionality and solubility in most relevant liquid and semi-solid food products (Spaen & Silva, 2021). Brückner-Gühmann et al. (2019b) investigated the potential of substituting skimmed milk powder with an oat protein preparation OPC (containing 43% protein and 33% starch) or OPI (containing 90% protein and less than 1% starch) in a cow's milk-based yoghurt. The results showed a decrease in syneresis with an increment in the viscosity and the sensorial characteristics of yoghurt containing OPC (43% proteins and 33% starch). Brückner-Gühmann and co-workers attributed this observation to the high amount of starch in the OPC rather than to the aggregated gelatinous oat protein particles due to their poor functionality and solubility (Brückner-Gühmann et al., 2019b; Spaen & Silva, 2021). Mäkinen et al. (2017) reported results of producing wheat bread containing OPC (3% and 6%) or OPI (5%) based on total flour weight. The trial outcomes showed increments in the loaf volume containing OPC, in contrast to a significant reduction in the loaf volume containing OPI which also had an increment in bread hardness and chewiness. Thus, modifying the oat protein preparations, especially the OPI, functionality, is critical for broadening their food application.

The good solubility of oat protein is a critical precondition property to achieve good emulsifying, foaming, and gelling properties (Jiang et al., 2015; Zhang et al., 2021). The US patent, US2016/0309762A1 (Chen, 2016) described the very weak gel formation and the poor water-holding capacity for oat proteins in acidic and neutral pH conditions. However, the oat proteins' gelling properties improve from a pH value of 8, and strong gels can be formed at pH 9–10 (Nieto-Nieto et al., 2015; Chen, 2016). The oat proteins' compact structure and heat stability explain the high-temperature (90–100 °C) needed to initiate a limited oat globulin dissociation into subunits to ameliorate its solubility and gelation properties (David, 2011). Nevertheless, this heating temperature doesn't suit a wide range of food systems, except those requiring high thermal stability, and consequently limits the utilisation of oat proteins in food products (David, 2011; Nieto-Nieto et al., 2015). Furthermore, the solubility and functionality of protein fractions vary by the extraction method used, where the alkaline method is the most efficient compared to both the saline and acidic methods (Kumar et al., 2021). In short, the alteration in the functionality of oat protein depends on its molecular size, structure, and charge distribution, as well as the presence of other components (lipids, starch, *β*-glucans) in association (Mäkinen et al., 2017). Therefore, various investigations have evaluated several modification procedures of the native oat protein to enhance its physicochemical and functional properties in typical food industrial conditions (Nieto-Nieto et al., 2014; Kumar et al., 2021).

The industrial modification procedures of oat protein to broaden its food application

Several chemical, physical and enzymatic modification methods (Table 1) have been studied to change the net charge and the hydrophilicity of proteins, leading to improvements in the solubility, surface properties and overall techno-functionality of oat protein fractions (Mäkinen et al., 2017; Brückner-Gühmann et al., 2018).

Table 1. Highest potential modification methods to enhance oat protein techno-functionality

Modification categories	Modification methods	Impact on oat protein structure	References
Chemical modifications	Acetylation	Formation of acyl linkage	Kumar et al., 2021
	Succinylation	Transfer the succinyl group and add negative charge	Mäkinen et al., 2017
	Acidity regulator or Ionic salts	Altering the surface distribution of protein charges	Li & Xiong, 2020
	Acidic deamidation	Degradation of protein and change its charge	Jiang et al., 2015
Physical modifications	Glycation by controlled Maillard reaction	Enable the conjugation of protein with polysaccharides (dextrin, β-glucan, inulin)	Zhang et al., 2015b; Nieto-Nieto et al., 2015
	Cold-set gelation	Proteins' denaturation followed by adding Ca^{2+} or glucono-δ-lactone	Chen, 2016; Boukid, 2021a
Enzymatic modifications	Partial protein hydrolysis with trypsin or alcalase	Changing the molecular size and the conformation of tertiary protein structure	Spaen & Silva, 2021; Nieto-Nieto et al., 2014
	Protein-glutaminase	Catalyse the deamidation of the side chain amino group of protein-bound glutaminyl residues	Jiang et al., 2015
	Transglutaminase	Catalyse the formation of an isopeptide linkage between a glutamine and the amino group of protein-bound lysine	Mohamed et al., 2009

The chemical modifications by acetylation and succinylation were reported by Jiang et al. (2015) and Immonen et al. (2021) as efficient methods of altering the isoelectric point and the functionality profiles of oat protein. Protein acetylation includes adding an acetyl group to a specific amino acid of a protein in an esterification reaction with acetic acid or acetic anhydride to change the basic groups into neutral groups (Kumar et al., 2021). The succinylation process comprises attaching a succinyl group to proteins in a reaction with succinic anhydride to change the positive groups into negative groups (Mirmoghtadaie et al., 2009). Both modifications render the net charge towards the negative, leading to an increment in the negative charge repulsion and subunits dissociation (Mäkinen et al., 2017; Kumar et al., 2021). Of both treatments, succinylation was more effective in improving the techno-functionalities of modified oat protein, including its solubility, emulsification, gelation hardness, fat-binding capacity, and foaming properties (Mirmoghtadaie et al., 2009; Mohamed et al., 2009). The acetylation treatment showed improvement in the emulsification activity index of the native protein isolate (NPI) from 60.8 $m^2\ g^{-1}$ protein to 76.2 $m^2\ g^{-1}$ protein; however, it decreased the emulsion stability index of NPI from 29.0 min to 12.1 min (Mohamed et al., 2009; Spaen & Silva, 2021). Otherwise, these modifications still have legal issues related to the utilisation of succinic anhydride and acetic anhydride in food protein processing and other food safety concerns (Jiang et al., 2015; Zhang et al., 2015b). David (2011) mentioned the linoleate/potassium linoleate treatment's ability to modify the oat protein solubility at pH 4–7, in addition to its emulsifying capacity and stability. The potential factors of the aqueous environment affecting the oat protein functionality are the pH and

the ionic strength. In industrial operations, the addition of ionic salts (sodium chloride (NaCl) or sodium phosphate (Na_2HPO_4 / NaH_2PO_4)) or acidity regulators (dipotassium phosphate or trisodium citrate) in food formulations promote the protein solubility and the formation of firm gel with a smooth texture and good water-holding capacity (Li & Xiong, 2020; Vikenborg & Stensson, 2020). Chemical deamidation can be done by mild acid or alkaline treatment to increase the negative charge of the protein and lead to changes in its functionality (Mäkinen et al., 2017). The acidic deamidation is recognised to perform severe degradation to the protein which negatively affects some protein functionality and results in a bitter taste (Jiang et al., 2015).

Some physical modification methods were noticed to be effective in strengthening and altering oat protein techno-functionality. Glycation is a promising way for oat protein modification which is achieved by the Maillard reaction under controlled dry-heating conditions to enable the oat protein conjugation with several polysaccharides such as *Pleurotus ostreatus* β-glucan, inulin, and dextran (Zhang et al., 2015b; Boukid, 2021a). The conjugated form of isolated oat protein-β-glucan exhibits improved solubility, emulsifying capacity and thermo-stability compared to unconjugated oat protein (Boukid, 2021a). A promising industrial future for the conjugated protein-β-glucan form is in the β-carotene encapsulation process to increase its stability, bioavailability, and antioxidant activity (Zhong et al., 2019). The dextran-linked oat protein isolate had more effective emulsification properties than its native protein (Zhang et al., 2015b). The inulin associated oat protein-containing low concentration inulin (0.1–0.5%) resulted in strong oat protein gels formation at neutral pH (Nieto-Nieto et al., 2015). A novel physical method was described by Chen (2016) as an alternative gelling method for oat protein named cold-set gelation. This method consists of two steps; initially a heating step to enable proteins denaturation and then polymerization followed by a cooling and the addition of Ca^{2+} or glucono- ε -lactone (GDL), resulting in the formation of three-dimensional soluble protein aggregates (a gel network) at ambient temperature (Chen, 2016; Boukid, 2021a). The oat protein cold-set gel is characterised by its resistance to acidic juice and pepsin digestion, thereby protecting against both α-amylase enzyme activity and the viability of probiotics in harsh gastric conditions, that is why it has the potential to be used as a delivery vehicle for sensitive compounds in food production (Boukid, 2021a). A stronge effect of the homogenisation process on oat protein functionality was observed by Vikenborg & Stensson (2020) and indicated improvement in the protein solubility from approximately 4% for the non-homogenised proteins to approximately 6% for the homogenised proteins. The investigation of the same study explained the solubility changes resulting from the effect of homogenization on decreasing the protein particle size to < 10 µm and disrupting the aggregates with their enabling to refold (Vikenborg & Stensson, 2020). Effect of homogenisation promoted the stability and solubility of oat protein concentrate, in parallel with the addition of the β-glucan extract, in the smoothie and the pudding products rich in protein and fibres (Vikenborg & Stensson, 2020). The physical deamidation of oat protein carried out by dry heating at 70 °C, for 2 h in an aqueous phase boosted some functional properties such as solubility, foaming capacity, and emulsifying activity and decreased the foaming stability and the emulsion stability (Mirmoghtadaie et al., 2009).

Currently, the modification category which is under investigation for oat protein modification includes enzymatic treatments. Studies have pointed out that enzymatic hydrolysis is a powerful tool to improve the techno-functionalities of oat protein fractions (Nieto-Nieto et al., 2014; Mäkinen et al., 2017). Studies were performed to evaluate the solubility and the gelling properties of oat protein treated with trypsin (Guan et al., 2007; Sargautis et al., 2021). The evaluations' results showed the formation of a weak gel structure and no change in functionality after the trypsin treatment due to the development of protein molecules with a small size that can no longer associate to form a strong gel matrix (Nieto-Nieto et al., 2014). Guan et al. (2007) mentioned that the harsh excessive enzymatic hydrolysis modification could impair the oat protein functionality. Nevertheless, limited enzymatic proteolysis can improve the functional properties of proteins by changing the molecular size, conformation, and strength of the inter-and intramolecular bonds of the protein molecules (Nieto-Nieto et al., 2014). Therefore, the proteolysis reaction must be carefully monitored and controlled in order to manufacture oat protein isolated products with desired functionality (Guan et al., 2007). For example, the effect of limited trypsin hydrolysis was cited by Spaen & Silva (2021), where the oat protein solubility at pH 5 increased from 7.3% in its native form into 68.2% in its trypsin-treated form with a degree of hydrolysis (DH) of 8.3%. In addition, the improved solubility of limited trypsin modified oat protein promoted improvement of the emulsifying activity index and the foaming ability (Guan et al., 2007). The same solubility observation at pH 4 was reported by Brückner-Gühmann et al. (2018). However, that the solubility of trypsin-treated oat protein was not improved at pH 7 was explained by the exposure of hydrophobic patches and subsequent protein-protein interactions and aggregation. Further inspection for the partial hydrolysis of oat protein isolate was carried out by alcalase which changed the native protein solubility at pH 4 from 17.6% without treatment to 50.3% with trypsin treatment (DH = 3%) (Spaen & Silva, 2021). Nieto-Nieto et al. (2014) reported that the partial enzymatic hydrolysis by trypsin or alcalase could improve the gelling properties of oat protein fractions by encouraging the gel formation from plant origin with similar properties to those from animal proteins such as egg white. Therefore, oat protein value increases in the industry as new plant gelling ingredients in food formulations such as meat binding and fat replacer or in meat analogues (Nieto-Nieto et al., 2014; Kumar et al., 2021). In the baking industry, partially hydrolysed OPI resulted in similar mechanical properties and water-holding capacity in wheat bread to that of egg white (Mäkinen et al., 2017). This could enable the use of OPI as a texturizing and structure-forming ingredient to replace animal protein in bakery products (Mäkinen et al., 2017).

A second enzymatic category to improve the oat protein functionality without causing severe hydrolysis is the oat protein deamidation with a food-grade commercial enzyme ‘protein-glutaminase’ (PG) that specifically catalyses the deamidation of the side chain amino group of protein-bound glutaminyl residues (Jiang et al., 2015; Immonen et al., 2021). The PG deamidation was able to double the protein water solubility compared to its native form (Jiang et al., 2015; Sargautis et al., 2021). Moreover, PG deamidated oat protein (59% deamidation degree) assisted the stability of the emulsion for longer than 30 days (Jiang et al., 2015). The transglutaminase, a protein cross-linking enzyme, can also induce deamidation with high enzyme to substrate ratios (Mohamed et al., 2009). The Transglutaminase mechanism catalyses the formation of an isopeptide

linkage between a glutamine and the amino group of protein-bound lysine (Mäkinen et al., 2017). The transglutaminase effectively increased protein solubility, foaming properties and emulsification (Boukid, 2021a). All the previous modifications aimed to change the oat protein fraction's surface properties to boost their techno-functionality and broaden their food industrial applications (dairy, meat, bakery, and their alternative products).

Impact of oat protein modification methods on humans, animals and the environment

The effect of oat protein modification methods may have important effects on human and animal health, in parallel to those on the environment. Due to the modification methods of oat proteins being understudied recently, their impact on humans, animals and the environment is only partially understood. It has been established that the chemical deamidation, acetylation and succinylation methods have drawbacks for human and animal health and may pollute the environment (Kutzli et al., 2021). The drawbacks of these modification methods are concerning problems with food-safety regulations arising from the requirement for various chemicals, which in some cases are toxic (Jiang et al., 2015; Kutzli et al., 2021). Mohamed et al. (2009) cited non-alteration in the nutritional value of the acylated oat proteins while its digestibility was significantly increased.

Oat and pea protein glycation significantly affect protein digestibility, which can be increased or reduced depending on the carbohydrate types and the conditions of protein glycation (Kutzli et al., 2021). The causative agents of coeliac disease(prolamins and glutelins) are very low in oat compared to other cereals (Rasane et al., 2015). However, enzymatic deamidation was reported to decrease the allergenicity of plant-based proteins, including the prolamins and glutelins (Nikbakht Nasrabadi et al., 2021). The most popular method for the oat protein modification is enzymatic treatment, particularly for incorporating the modified proteins in food production, since this process is environmentally friendly and less energy-consuming without the production of toxic by-products (Nikbakht Nasrabadi et al., 2021). In addition to the modulation of oat protein functionality, enzymatic treatment has the ability to improve the protein's nutritional quality including digestibility, bioavailability, and its biological activity such as antioxidant and antimicrobial properties (Nikbakht Nasrabadi et al., 2021; Sargautis et al., 2021). Tang et al. (2022) identified the formation of a new type of angiotensin-converting enzyme (ACE), an inhibitory peptide with strong antioxidant activity when the oat protein is hydrolysed by trypsin. The influence of the oat protein modification methods on different aspects are still not well known, which is why further detailed research needs to be carried out in the near future.

CONCLUSIONS

In the framework of mapping new sources of alternative proteins of plant origin, the oat protein concentrates, and isolates have been shown to have a potential future in various food industries. Oat protein could be considered a good plant-derived protein source from its relatively superior amino acid and nutritional profiles compared with other cereal grains (wheat, barley, and rye). Moreover, the oat protein preparations possess good functional properties such as solubility, emulsification, foaming and

gelling properties, additionally to valued bioactivities. Noteworthily, native oat proteins present poor techno-functionality in most food products' typical production conditions, which restricts in its use in industrial food production. Therefore, several research studies have investigated the potential of diverse modification methods to improve the oat protein functionality and expand its industrial food incorporation. The common proposed modification categories include chemical, physical, and enzymatic treatments, where the enzymatic methods have been shown to be a powerful safe and environmentally friendly strategy to change the functionality and promote the oat protein as a novel nutritious plant protein source without the production of toxic by-products. More investigations are required to optimise the extraction methods of oat protein fractions from food by-products for their valorisation and promote their modification methods for boosting their quality to meet the food industry requirements.

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