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Breeding for protein content and quality in rapeseed: a mini review☆

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Abstract – The global challenge of meeting future protein and oil demand requires innovative solutions, and rapeseed emerges as a key player. Its potential as a dual-purpose crop, providing both high-quality oil and protein, positions it as an essential component of strategies to address the protein gap, reduce reliance on imported soybeans, and meet sustainability objectives. Leveraging advancements in breeding, processing, and utilization can unlock rapeseed's full potential, ensuring its role in a resilient and sustainable global food system. This mini review provides a summary of the efforts to enhance protein content and quality in rapeseed through breeding, integrating traditional and modern genomic approaches.

Keywords: Rapeseed protein / protein content / molecular breeding / processing

Résumé – **La Sélection du colza selon la teneur et la qualité de ses protéines : une mini-revue.** Le défi mondial que représente la réponse à la demande future en protéines et en huile nécessite des solutions innovantes, et le colza se présente comme un acteur essentiel. Sa capacité à fournir à la fois de l'huile et des protéines de haute qualité en fait une culture à double usage essentielle pour répondre au déficit en protéines, réduire la dépendance au soja importé et atteindre les objectifs de durabilité. Les avancées dans les domaines de la sélection, de la transformation et de l'utilisation peuvent permettre de libérer tout le potentiel de cette culture et de garantir son rôle dans un système alimentaire européen et mondial résilient et durable. Ce mini-bilan résume les efforts déployés pour améliorer la teneur en protéines et la qualité du colza par sélection, en intégrant des approches génomiques traditionnelles et modernes.

Mots clés : Protéines de colza / teneur en protéines / sélection moléculaire / transformation industrielle

Highlights

Rapeseed is crucial for global protein/oil demand. Advancing rapeseed breeding for protein, yield, and quality by integrating genetics, molecular tools, and processing innovations is key to sustainable protein production and will unlocks its potential in food, feed, and industrial uses, supporting global protein demand.

Le colza est essentiel pour répondre à la demande mondiale en protéines et en huile. Pour une production durable de protéines, il est essentiel de faire progresser la sélection du colza en matière de protéines, de rendement et de qualité, en intégrant la génétique, les outils moléculaires et les innovations en matière de transformation. Cela permettra de libérer son potentiel dans les domaines de l'alimentation humaine et animale, ainsi que dans les utilisations industrielles, afin de répondre à la demande mondiale de protéines.

☆ Contribution to the Topical Issue: "Diversity of Plant Proteins extracted from Oil & Protein Crop / Diversité des protéines végétales issues des oléoprotéagineux".

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1 Future protein and oil demand: the role of rapeseed in addressing global challenges

The growing global population, projected to exceed 8.5 billion by 2030 (United Nations, 2024), alongside rising living standards, will intensify the demand for dietary diversification. This shift is expected to drive significant increases in both protein and oil consumption. In 2030, plant-based protein demand is forecasted to rise by 43%, with South Asia and Sub-Saharan Africa contributing the largest shares to this growth. Developed regions such as Europe, North America, and Oceania will also experience moderate increases, reflecting secondary nutritional transitions toward balanced diets. Simultaneously, the demand for animal-based proteins is projected to grow by over 30% in developing regions, particularly in East Asia. This trend will substantially elevate the need for oilseed meals used in animal feed, predicted to rise by 53%, as well as vegetable oil and protein for food, which is expected to grow by nearly 40%. However, a supply shortfall of 58 million tonnes in oilseed meals by 2030 highlights a critical challenge for global meat production and consumption systems.

Addressing this protein deficit presents a formidable task for the agricultural sector, particularly in Europe, which faces a notable supply gap in plant protein production for both human nutrition and animal feed. Rapeseed (*Brassica napus*), the second most significant vegetable oil crop globally, offers a promising avenue to mitigate this deficit. Traditionally valued for its oil content, rapeseed is increasingly recognized for its potential as a high-quality plant protein source. Enhancing the utilization of rapeseed meal could reduce dependency on soybean meal, improve protein security in Europe, and support the region's sustainability goals amid growing market pressures (Fig. 1). To fully exploit rapeseed's potential as a protein source, addressing its nutritional and functional challenges is essential. Rapeseed protein boasts a favorable amino acid profile, competitive with soybean protein, particularly due to its high levels of essential sulfur-containing amino acids, such as methionine and cysteine (Sosulski, 1979; Wittkop *et al.*, 2009; Aider and Barbana, 2011). These amino acids contribute 3–4% of the total protein content, aligning rapeseed protein closely with FAO recommendations for human nutrition (Ohlson and Anjou, 1979). Additionally, rapeseed protein's two primary storage proteins, cruciferin and napin, contribute to its superior nutritional value. Cruciferin, constituting 60% of total seed protein, is rich in glutamine and asparagine, while napin, comprising 20%, is distinguished by its elevated cysteine, methionine, and lysine content. These attributes make rapeseed a viable candidate for targeted breeding programs aimed at improving its amino acid composition and digestibility (Crouch and Sussex, 1981; Höglund *et al.*, 1992). Despite these advantages, rapeseed protein's relatively low concentration in seeds and the presence of anti-nutritional factors, such as fiber and phenolic compounds, remain significant barriers to broader applications. Overcoming these challenges requires advancements in breeding techniques and processing technologies to enhance seed protein content and reduce anti-nutritional components. Innovations in rapeseed meal processing could unlock its full potential for both human and animal diets, providing a sustainable alternative to soybean meal and addressing the looming global protein deficit.

2 Breeding for protein content in seed and meal

The major constituents of Brassicaceae seeds are water, oil, proteins and residues (RES), which mainly comprise carbohydrates, fibre, minerals and ash (for review see Nesi *et al.*, 2008). The meal that results from oil extraction contains over 35% protein and shows a relatively balanced amino acid profile (Krzymanski, 1998; Dimov *et al.*, 2012). A high oil content in the seed and a high protein content in the meal are therefore major targets for Brassica breeding. To date, research has focused mainly on the metabolism of reserve lipids (Ruuska *et al.*, 2002; Beisson *et al.*, 2003). In addition, genetic control of seed oil content has been widely described in oilseed rape (for review see Delourme *et al.*, 2018) and Arabidopsis (O'Neill *et al.*, 2003, 2012; Hobbs *et al.*, 2004; Jasinski *et al.*, 2018). The high number of loci identified reflects the complexity of the trait, with each locus explaining on average less than 10% of the total variability of the trait.

Conversely, protein content in the seed or in the meal (Meal Proteins, MP) has been the subject of less research and breeding effort, as the meal was until recently often considered to be a by-product of oil extraction. However, with the recent revival of interest in plant proteins, and in particular those derived from rapeseed, it is necessary to consider the protein content and yield as targets for rapeseed breeding programmes. The strong negative correlation classically observed between oil and protein content in the seed in Brassicaceae (Grami and Stefansson, 1977); Zhao *et al.*, 2006; Jolivet *et al.*, 2013; Bouchet *et al.*, 2014), suggests that seed filling in these species is highly constrained and that increasing one of the two fractions inexorably leads to a decrease in the other. However, new observations show that there is considerable scope for improving seed quality in Brassicaceae. On the one hand, certain Arabidopsis mutants affected in the accumulation of oil or protein do not show compensation for the other reserve compounds (Lécureuil *et al.*, 2024), which suggests that the biosynthesis and accumulation pathways for oil and protein are independent. On the other hand, although many loci involved in seed quality affect both oil and protein with opposite allelic effects, some QTL nevertheless show independent segregations for these two traits (Mahmood *et al.*, 2006; Bouchet *et al.*, 2014; Jasinski *et al.*, 2018). Finally, there are genotypes for which a deviation in the oil/protein ratio is observed in favour of the accumulation of either lipids or proteins, or both fractions.

The reserve proteins in rapeseed are cruciferins (12S globulins) and napins (2S albumins), which account for more than 70% of total protein (Crouch and Sussex, 1981), with the remainder mainly comprising oleosins (Purkrtova *et al.*, 2008; Jolivet *et al.*, 2009) and lipid transfer proteins. The amino acid composition of rapeseed proteins is excellent, although there is a slight deficit in essential amino acids (Wanasundara, 2011). With 3–4% more sulphur residues, the quality of rapeseed proteins would be close to the FAO recommendations for human consumption. As 2S proteins are richer in sulphur and aromatic residues than 12S proteins (8.1% cysteine + methionine

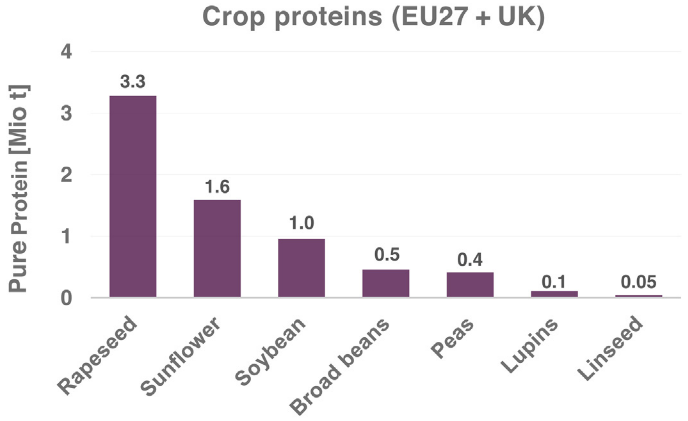

Fig. 1. Potential availability of protein from domestic sources in the EU27 and the UK. The numbers are the product of the production volume (2021) and protein content of the plants. However, the EU currently imports a lot of soy, mainly from Brazil and the USA, rather than using domestic proteins. (Source: FAO; adapted by J. Lübeck).

vs. 2.7%), they are of greater interest for food applications. They also have functional properties that make them attractive to the food industry. The 2Ss are therefore the preferred targets for improving the composition of rapeseed reserve proteins.

3 Use of rapeseed protein: Impact of other seed constituents

A major problem for the use of rapeseed meal in animal feed also lies in the low digestibility of the proteins compared with those of soya meal. (Patridge *et al.*, 1987) The composition of the seed, and in particular the presence of fibre and so-called anti-nutritional factors, has a significant impact on the availability and digestibility of proteins *in vivo* (Toutirais *et al.*, 2024). On the one hand, fibres or parietal polysaccharides are the third molecular family of the seed, representing 20-28% of the dry mass of rapeseed seeds. They are present mainly in the seed coat and to a lesser extent in the albumen and embryo. Their composition and structure vary according to tissue, stage of development and genotype. These variations can have a direct impact on the physicochemical properties of these polymers and therefore on their technological and/or nutritional qualities. Fibres in the teguments can hinder digestibility but can also potentially improve pressability, while fibres in the albumen and embryo are more fermentable and therefore have a potential biological role (prebiotic). Condensed tannins (CTs), sinapins and phytates are anti-nutritional factors, and reducing their content in seeds leads to better-quality oilcake. Numerous teams have worked on CTs and yellow-seeded rapeseed varieties (without CTs) have reduced fibre content and better quality (increased oil, seed and meal protein) (Simbaya *et al.*, 1995). Such varieties are grown in Canada but have certain agronomic shortcomings (susceptibility to disease, yield, seed conservation, etc.). A major challenge is therefore to obtain a detailed characterisation of the fibre and anti-nutritional factor composition of rapeseed and meal, and to describe the variability that exists within the genetic diversity of rapeseed.

4 Molecular breeding approaches

The advent of crop genome sequencing has revolutionized molecular breeding. Over a decade ago, the first genome sequence of a crop plant was published (Bolger *et al.*, 2014), and in 2014, the rapeseed (*Brassica napus* L.) genome was sequenced (Chalhoub *et al.*, 2014). Despite some gaps in completeness, this resource has become invaluable for advancing basic and applied research, including marker-assisted selection (MAS), genome-wide association studies (GWAS) and genomic selection. Continued resequencing efforts of diverse genotypes are enhancing marker utility, enabling SNP-based annotations, and improving breeding strategies through functional allele mining. For over 25 years, molecular markers have been employed to link genetic loci to phenotypic traits. Bulked segregant analysis (BSA) has been a cornerstone in this effort, leveraging DNA polymorphisms in segregating populations to identify loci of interest (Cantu *et al.*, 2011). While precise, BSA has historically been limited by marker density. However, next-generation sequencing (NGS) has addressed these limitations by providing massive DNA sequence datasets. Approaches like “mapping by sequencing” (MBS) combine BSA with high-throughput sequencing, rapidly identifying causal mutations in pooled populations (Schneeberger *et al.*, 2009; Schneeberger and Weigel, 2011). These methods, now refined for crops like barley (Mascher *et al.*, 2014) and sugar beet (Ries *et al.*, 2016), are being successfully applied to rapeseed breeding.

A major challenge is to understand the genetic and molecular determinism of the strong negative correlation between oil and seed, in order to break or reduce this link so that oil and protein can be manipulated independently. Characterising the genetic factors that regulate the oil/protein ratio provide some answers. Innovations such as GWAS, coupled with haplotype diversity analyses, now allow a deeper understanding of complex traits. Haplotype-based GWAS provides higher resolution than single-SNP analyses, as demonstrated in recent studies (Qian *et al.*, 2016). Similarly, the integration of mutagen-induced polymorphisms has proven useful in identifying functional genes within uniform genetic backgrounds (Abe *et al.*, 2012; Hartwig *et al.*, 2012). Recent work has advanced understanding of metabolic and regulatory networks in rapeseed. For example, studies in *Arabidopsis thaliana* have identified key genes in the phenylpropanoid biosynthesis pathway, such as flavonol synthase (FLS), flavanone 3-hydroxylase (F3H), and anthocyanin synthase (ANS). Mutations in these genes re-channel metabolic flux, producing novel compounds with potential applications, such as bitter-masking metabolites (Schilbert *et al.*, 2024). Transferring these insights to rapeseed could open avenues for optimizing flavor and reducing off-tastes in protein products. Moreover, transcription factors like R2R3-MYBs (*e.g.*, BnaMYB12 and BnaMYB111) have been implicated in flavonol biosynthesis regulation in rapeseed (Schilbert and Glover, 2022). Concurrently, glycosyltransferases are being investigated for their roles in modifying off-taste compounds, offering additional targets for breeding.

Phenomic Selection (PS) has emerged as a cost-effective alternative to Genomic Selection (GS) for complex traits (Rincent *et al.*, 2018; Zhu *et al.*, 2021). Unlike GS, which relies on genotypic data, PS uses non-destructive, high-throughput phenotyping methods, such as near-infrared spectroscopy (NIRS), to derive trait predictors. Preliminary studies in rapeseed suggest that PS can predict seed yield with comparable accuracy to GS (Roscher-Ehrig *et al.*, 2024). However, optimizing prediction accuracy for traits like protein content and integrating PS across diverse breeding populations remains an area for further research.

Recent studies have identified significant genetic variability in the cruciferin-to-napin ratio in doubled haploid populations (Schatzki *et al.*, 2014). Mapping of quantitative trait loci (QTL) linked to this trait provides a promising avenue for optimizing the protein quality of rapeseed by modifying storage protein composition. Given the distinct structural, thermal, and functional properties of cruciferin and napin, targeted breeding can enhance the balance of these proteins to improve rapeseed protein applicability in diverse nutritional contexts. Despite its high-quality amino acid profile, the utilization of rapeseed protein is further limited by the presence of secondary metabolites, including phenolics, which can impart off-tastes and reduce palatability. Overcoming these barriers requires advancements in breeding strategies and processing technologies to reduce anti-nutritional factors while preserving protein quality. In this minireview we highlight the latest advancement in breeding for rapeseed protein for human nutrition.

Studies aimed at increasing 2S content in oilseed rape by introducing genes coding for exogenous 2S (Guerche *et al.*, 1990, Altenbach *et al.*, 1992) or by inactivating endogenous 12S genes (Kohno-Murase *et al.*, 1995) show that transgenic plants accumulate more cysteine, methionine and lysine. Furthermore, the increase in 2S in these plants was offset by a decrease in 12S content, suggesting the existence of a fine control of the 12S/2S balance in rapeseed. Conversely, little work has been done to date on the natural variability of reserve protein composition in oilseed rape. In the 2000s, however, J. Guéguen's team at INRA Nantes showed that the 12S/2S ratio varies between 0.7 and 2 (Malabat *et al.*, 2001; Malabat *et al.*, 2003) and that it is significantly higher in modern 00-varieties. These results were confirmed by French researchers on a collection of 103 winter oilseed rape accessions registered between 1958 and 2005 (Nesi, per. Commun.). A strong negative correlation between glucosinolates (GSL) and the 12S/2S ratio is also described in a population of doubled haploids of oilseed rape (Schatzki *et al.*, 2014). These same authors describe the co-localisation of a GSL content QTL with a QTL controlling 12S, 2S content and the 12S/2S ratio. Finally, the identification of 2S QTL showed that for 3 regions out of 7, the majority allele in the population tested is the unfavourable allele, mainly present in recent 00-varieties.

These results show that there is room for improvement in the 2S content of rapeseed. However, at present, the methods for extracting and measuring reserve proteins are still cumbersome and limit selection for these traits. A major challenge is therefore to develop medium-high throughput methods for quantifying reserve proteins (2S and 12S) in rapeseed. Finally, progress in understanding the genetic, molecular and/or metabolic basis of the relationship between GSL content and the 12S/2S ratio in the seed is also a research issue.

5 Identification, quantitation, and sensory analysis of off-taste components

The incorporation of plant protein isolates or concentrates in food products often faces low consumer acceptance due to their lingering bitter and astringent off-taste (Ismail *et al.*, 1981; Naczk *et al.*, 1998). This off-taste is typically attributed to non-covalently bound phytochemicals, including: Glucosinolates and their breakdown products (GBP) (Ismail *et al.*, 1981; Pallida *et al.*, 2007), quaternary ammonium compounds (Ismail *et al.*, 1981), Tannins and phenolic acids (Kozlowska *et al.*, 1990; Naczk *et al.*, 1998). Despite these findings, existing data on the sensory attributes of individual purified phytochemicals and their specific contribution to the off taste of protein isolates are inconsistent or incomplete. Furthermore, no comprehensive studies have investigated the intrinsic taste properties of rapeseed storage proteins, napin and cruciferin, leaving the primary contributors to the off-taste unknown. To fill these knowledge gaps, the SENSOMICS approach has been successfully applied to identify key molecules responsible for specific off tastes. This method integrates activity-guided identification of compounds with dose-activity relationships and taste re-engineering to confirm the impact of identified molecules. Researchers at the Technical University of Munich have employed this approach addressing diverse taste challenges in food products such as carrots, coffee, and apples. This research has resulted in over 40 patents. In rapeseed protein isolates the SENSOMICS approach identified kaempferol glycosides—notably kaempferol-3-O-(2”’-O-sinapoyl-sophoroside) (K3OSS)—as the main contributors to the bitter taste in rapeseed protein isolates (Hald *et al.*, 2018; Walser *et al.*, 2024). These findings marked a breakthrough in understanding the molecular basis of rapeseed protein's off-flavor, providing insights for improving consumer acceptance (Fig. 2A, B). By identifying and quantifying the key off-taste components, the SENSOMICS approach offers valuable tools for refining extraction processes and formulating plant-based protein products with improved sensory profiles. This methodology could guide the reduction or elimination of bitter compounds, making rapeseed protein isolates more palatable and suitable for wider food applications.

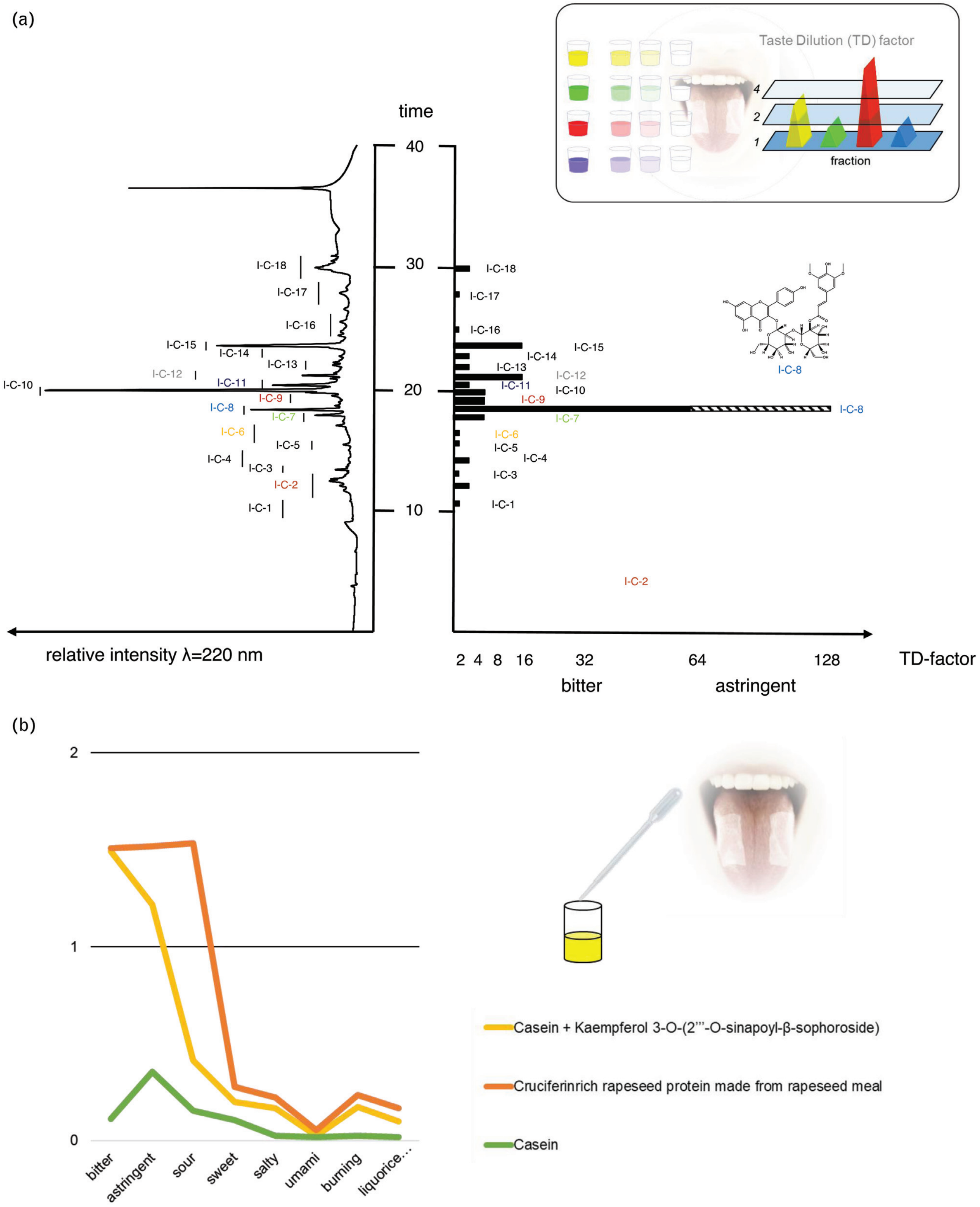

Fig. 2. A: Identification of kaempferol glycosides—notably kaempferol-3-O-(2‴-O-sinapoyl-sophoroside I-C-8) (K3OSS)—as the main contributors to the bitter taste in rapeseed protein isolates (Courtesy from Hald *et al.*, 2018 and Walser *et al.*, 2024). B: Flavour characteristics of casein and cruciferin rich fraction made from rapeseed meal and recombination experiment of K3OSS with casein fraction demonstrating the bitterness of K30SS (Courtesy from Hald *et al.*, 2018 and Walser *et al.*, 2024).

6 Technical processing and valorisation of rapeseed proteins

The successful valorisation of rapeseed proteins requires careful optimization of extraction parameters and a comprehensive understanding of how processing influences both quantitative yields and qualitative properties (Hewage *et al.*, 2022). Conventional alkali extraction, typically using alkali solutions at various pH values is commonly used, due to its ability to disrupt hydrogen bonds and enhance protein solubility (Cui *et al.*, 2017; Zhang *et al.*2020). Additionally, parameters like solid-to-liquid ratio are critical, as they influence mass transfer and overall extraction efficiency (Fetzer *et al.*, 2018). Studies have demonstrated that optimized conditions can yield high protein recoveries at demonstration scale, although scaling up these processes often leads to reduced yields due to altered mass transfer dynamics (Wongsirichot *et al.*, 2024). Therefore, alternative solvents and methodologies including aqueous extraction, enzyme-assisted extraction, and high-pressure or pulse electric field-assisted extraction have been investigated to improve yield and efficiency and to preserve protein techno-functionality during extraction (Hewage *et al.*, 2022). Indeed, protein techno-functionality is critically dependent on controlling structural properties under varying conditions. In the case of rapeseed cruciferin denatures at lower pH irrespective of temperature, whereas napin is more robust denaturing only at higher temperature and lower pH (Perera *et al.*, 2016). Thus, ensuring non-acidic and low-temperature conditions during aqueous extraction is essential to maximize protein recovery while minimizing degradation, amino acid profile alterations, and the formation of toxic by-products that can occur under high-pH conditions (Fetzer *et al.*, 2018). On the other hand, enzyme-assisted methods can significantly boost extraction yields, although the use of proteases may result in unwanted protein degradation, which is counterproductive when intact proteins are required (Hewage *et al.*, 2022).

A further key technology for the valorisation of high-quality rapeseed proteins is the hulling process (Rass and Schein, 2010, (Carré *et al.*, 2014). The rapeseed hulling process is thought to improve the oil quality by removing antinutritive ingredients with the hulls (Matthäus, 1998) and, on the other hand, to improve the press cake quality and protein quality (Eapen *et al.*, 1969; Carré *et al.*, 2016; Carré, 2021). Before hulling, the mechanical behaviour of the seed coat is transformed from a rather elastic to a brittle state through resource-intensive drying after breaking the shell, it is fractionated into shells and kernels. Before pressing, the original elastic state of the kernel fraction must be restored by remoistening. However, this moistening process is suspected of promoting the formation of antinutritive substances (Ikebudu *et al.*, 2000; Walser *et al.*, 2024). For this reason, more and more gentle processes are being investigated for the hulling of rapeseed in order to maintain the quality of the end-product.

Central to both traditional animal feed applications and the development of high-value protein isolates for human and technical uses is the post-extraction processing. This usually involves isoelectric precipitation to recover protein isolates. However, the diversity of protein isoelectric points in rapeseed proteins necessitates multistage precipitation for improved recovery (Dong *et al.*, 2011). Other techniques, including ultrafiltration (Fetzer *et al.*, 2020), nanofiltration, and chromatographic methods are employed for further purification (Bérot *et al.*, 2005), followed by drying methods such as freeze-drying (Dong *et al.*, 2011). The final protein isolates must exhibit favourable techno-functional properties—such as solubility, emulsification, foaming, gelation, and film-forming capabilities to meet the demands of their intended applications (Fetzer et al., 2020).

In nutritional applications, rapeseed proteins are valued (Fleddermann *et al.*, 2013), in particular for their high net postprandial protein utilization and biological value despite their relatively low ileal digestibility, which has driven much of the research into protein valorisation (Chmielewska *et al.*, 2021). However, challenges such as poor palatability and the co-extraction of antinutritional components (including glucosinolates, phenolics, phytates, and fiber) and in particular K3OSS (Hald *et al.*, 2018) must be addressed to make these proteins suitable as nutritional supplements (Wanasundara *et al.*, 2017; Fetzer *et al.*, 2020).

On the other hand, rapeseed proteins are also finding applications in various technical fields. They are being explored for use as *e.g.* adhesives, foaming agents, cosmetics additives, and emulsion stabilizers, showcasing the versatility of rapeseed proteins in industrial formulations (Popović *et al.*, 2020; Zhao *et al.*, 2023). In some cases, additional, chemical (acylation, glycation, phosphorylation, cross-linking), or biological (enzymatic hydrolysis) modifications are applied to enhance these functional characteristics (Li *et al.*, 2023).

7 Conclusion

In conclusion, breeding for protein content, yield, and quality in rapeseed is a complex but promising endeavour that holds significant potential for addressing the growing global demand for sustainable, plant-based proteins. The challenges are multifaceted, involving the harnessing of genetic variability, the utilization of advanced molecular tools, and the implementation of state-of-the-art phenotyping methods. These innovative approaches are crucial to developing new rapeseed varieties that not only deliver high yields but also provide superior protein quality, thereby enhancing both the nutritional profile and economic value of this important crop.

Furthermore, focused research into modifying seed storage protein profiles is essential for advancing (protein production and utilization?) and encouraging the wider adoption of rapeseed protein as a viable food ingredient. With rapeseed ranking as the third-most abundant oil crop worldwide, a vast, untapped value chain exists within its residual proteins. Although continuous improvements have reduced antinutritive components, the full potential of rapeseed protein for feed and food applications remains underutilized. Moreover, the promising alternative of isolating rapeseed proteins from residual press cake and meal for use in the chemical sector is attracting increasing attention in research and application. Bridging the gap between laboratory-scale success and industrial-scale production is a key challenge that necessitates further research into scalable techniques and integrated processing schemes. These schemes must facilitate oil extraction while simultaneously valorising protein products and co-extracted fractions.

Ultimately, such an integrated approach will not only improve the economic viability of rapeseed protein production but also contribute significantly to sustainable utilization in various high-value applications. Collaborative innovation across disciplines is therefore imperative to fully realize rapeseed's promise as a versatile, nutritious, and economically sustainable crop. Future breakthroughs in this field will undoubtedly transform global protein production with excellence.

Conflicts of interest

FPW, JL and AA are employees of the NPZ Innovation GmbH. FPW and AA have a patent pending for reduction of kaempferol in rapeseed seeds. All authors have no conflict of interest to declare.

Author contribution statement

AA wrote the original draft, FPW and JL reviewed and edited the paper, FPW acquire financial support from the Federal Ministry of Research, Technology and Space (BMFTR) for the RaPEQ project (Fkz-031B1305A-D).

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