Food Chemistry 491 (2025) 144713

Contents lists available at ScienceDirect

Food Chemistry

journal homepage: www.elsevier.com/locate/foodchem

Identifying semi-polar co-passengers in commercial plant protein ingredients

Pauline F.R. Damhof, Jean-Paul Vincken, Wouter J.C. de Bruijn *

[a] *Wageningen University & Research, Laboratory of Food Chemistry, Bornse Weilanden 9, 6708, WG, Wageningen, the Netherlands*

ARTICLE INFO

Keywords:
Phytochemical analysis
Lipid oxidation intermediates
Plant protein ingredients
RP-UHPLC-PDA-MS/MS
Co-extraction
Anti-nutritional factors

ABSTRACT

One of the main challenges in the transition from animal to plant proteins is the presence of undesired non-volatile co-passengers in plant protein ingredients, including off-tastants. Despite this, data on the non-volatile composition of commercial plant protein concentrates and isolates is lacking. Therefore, our main aim was to systematically identify and quantify the semi-polar co-passengers present in commercial soy, pea, oat, potato, and almond protein isolates or concentrates. Our RP-UHPLC-MS analysis of the semi-polar co-passengers in the plant protein ingredients indicated that saponin content varied: 0.105 g/kg, 0.270–0.595 g/kg, and 0.891–1.096 g/kg, for oat, pea, and soy, respectively. Additionally, potato protein isolates contained trace amounts of glycoalkaloids. Other semi-polar co-passengers in the investigated plant protein ingredients were mainly polar lipids, comprising oxylipins, lysophosphatidylethanolamines, and lysophosphatidylcholines. We conclude that saponins, lysophospholipids, and oxylipins are the main undesired semi-polar non-volatile co-passengers in commercial plant protein ingredients.

1. Introduction

In the past few years, alternative protein sources to supplement or replace the traditional meat and dairy protein sources have gained popularity. They are becoming more relevant as the projected population growth of the world, as well as the loss in farmland due to climate change, will lead to an additional protein deficiency in 150 million people in the near future (Medek et al., 2017; Shukla et al., 2019). To limit the rising protein deficiency, consumers and industry have turned to plant material with high protein content as a potential protein source. Traditionally, protein is extracted using pH-assisted precipitation, ultrafiltration, extraction with salt solutions, dry fractionation, or a combination thereof (Hewage et al., 2022). Depending on the efficiency of the process, this will yield a protein concentrate or protein isolate, with a protein content of 60–80 % and > 80 %, respectively. However, in both final products, non-protein compounds are co-extracted. These co-extracted compounds include undesired non-volatiles, often referred to as co-passengers. Some of these co-passengers are semi-polar compounds that exhibit a strong off-taste and can contribute to an overall undesired flavour for consumers (Cosson et al., 2022; Trindler et al., 2021). These semi-polar off-tastants limit consumer acceptance of food products that are produced from these plant-based protein sources.

Previous studies have focused on characterization of undesired semi-polar off-tastants present in the plant raw material. It is currently assumed that the semi-polar off-tastants that are present in the plant raw material are also the main undesired semi-polar co-passengers in the final plant protein ingredient, i.e. the isolate or concentrate, after protein extraction and purification. Off-tastes in plant raw materials are generally described as bitter, astringent, and metallic (Gunther-Jordanland et al., 2020; Price et al., 1985). The main culprits of these off-tastes in plant raw materials are reported to be isoflavones, saponins, phenolic acids, tannins, and oxylipins (i.e. oxidized fatty acids) (Roland et al., 2017; Soares et al., 2018; Soares et al., 2020). Some of these off-tastants—specifically glycoalkaloids, saponins, and tannins—are coincidentally also anti-nutritional factors, meaning that they can negatively affect nutrient uptake (Friedman, 2006; Jenkins & Atwal, 1994; Samtiya et al., 2020; Yoshiki et al., 1998). Amongst others, anti-nutritional factors are suggested to inhibit digestive enzymes (Ercan & El, 2016; Lee et al., 2015; Mehansho et al., 1992), thereby potentially limiting the appeal of plant protein ingredients. While polar co-passengers, like phytic acid, and apolar co-passengers, like triacylglycerides and phospholipids, can also be present in plant protein ingredients (Keuleyan et al., 2023; Samtiya et al., 2020), they are not typically reported to be off-tastants and thus were not the focus of the present study.

* Corresponding author.
E-mail address: wouter.debruijn@wur.nl (W.J.C. de Bruijn).

https://doi.org/10.1016/j.foodchem.2025.144713
Received 31 January 2025; Received in revised form 28 April 2025; Accepted 9 May 2025
Available online 15 May 2025

Only limited research exists in which plant protein ingredients have been analysed for the presence of these undesired semi-polar co-passengers. It is therefore unclear which and how much of these undesired off-tastants from the plant protein raw material are present in the final commercial plant protein ingredient. Some undesired off-tastants from the raw material may be partially removed during protein extraction and purification, whereas others may be concentrated. Additionally, similar off-taste may exist across plant families. To date, no comparison of the types and quantities of semi-polar non-volatile co-passengers in commercial plant protein ingredients from different plant sources exists.

Identifying the undesired semi-polar non-volatile co-passengers in commercial plant protein ingredients will provide leads for their removal, which can ultimately contribute to improving the properties of these ingredients. For this project soy, pea, oat, potato, and almond were selected, since they are all already commonly used as, or promising sources for, plant protein ingredients (Aiking, 2011; Day, 2013; Dijkstra et al., 2003; Shan et al., 2019). Moreover, they represent four different plant families, namely legumes (Fabaceae), cereals (Poaceae), nightshades (Solanaceae), and the rose family (Rosaceae). Therefore, our main objectives were (i) to systematically identify semi-polar non-volatile co-passengers that potentially contribute to off-tastes in commercial plant protein ingredients from soy, pea, oat, potato, and almond; and (ii) to quantify these co-passengers in the selected commercial plant protein ingredients. These semi-polar non-volatiles will be extracted with aqueous methanol, followed by extensive analysis with reversed-phase ultra-high performance liquid chromatography coupled mass spectrometry (RP-UHPLC-MS). It was hypothesized that the main off-tastants present in the plant raw materials are also the main undesired co-passengers in commercial plant protein ingredients. Additionally, we expected that the main culprits associated with off-taste in commercial plant protein ingredients from different plant families would be members of the same common compound classes.

2. Materials and methods

2.1. Commercial plant protein ingredients and chemicals

2.1.1. Commercial plant protein ingredients

Soya Protein Isolate (SoyPI1), Organic Soy Protein (SoyPI2), in-house soy protein (SoyPI3) were obtained from Bulk™ (Colchester, United Kingdom), Body & Fit Sportsnutrition B.V. (Heerenveen, The Netherlands), and through in-house purification (Wageningen University, The Netherlands). PISANE™ C9 (PeaPI1), NUTRALYS (PeaPI2), and Pisane HD (PeaPI3) were obtained from Cosucra (Warcoing, Belgium), Roquette (Breda, The Netherlands), and Quest International (Maarssen, The Netherlands), respectively. Solanic® 100 (PotPI1), Solanic® 200 (PotPI2), PrOatein (OatPC), and Almond Protein Powder (AlmPC) were purchased from Royal Avebe U.A. (Veendam, The Netherlands), Lantmännen Functional Foods (Stockholm, Zweden), and Blue Diamond Almonds (Sacramento, USA), respectively. Given that all the samples, except SoyPI3, are commercial plant protein ingredients, processing conditions are not readily available. SoyPI3 was produced through in-house purification using pH assisted precipitation/wet-extraction. For the protein concentrates, OatPC and AlmPC, a brief description of the processing is available from the suppliers' websites. OatPC was obtained by wet milling of the oat bran, whereas AlmPC was obtained by mechanical processing. Royal Avebe U.A. relies on adsorption chromatography to purify their potato protein ingredients, as described in patent WO 2008/069650 (Giuseppin et al., 2008). Protein content of all commercial plant protein ingredients was determined using the Dumas method. The methods and results of this determination can be found in the supplementary data (section S1, Fig. S1).

2.1.2. Chemicals

ULC-MS grade methanol, acetonitrile (ACN), formic acid 99 % (*v*/v), ACN with 0.1 % (v/v) formic acid, and water with 0.1 % (v/v) formic acid were obtained from Biosolve (Valkenswaard, The Netherlands). Water for all purposes other than UHPLC was prepared using a Milli-Q water purification system (Millipore, Billerica, MA). Soyasaponin Bb, 13-oxo-9*Z*,11*E*-octadecadienoic acid (13-Oxo-ODE), and epicatechin were purchased from Cayman Chemical (Ann Arbor, MI, USA). Avenacoside A, α-solanine, α-chaconine, daidzein, and genistein were purchased from Sigma-Aldrich (St. Louis, MO, USA). 18:1a/lysoPC, 18:1a/lysoPE, and 18:0a/lysoPE were purchased from Avanti Polar Lipids, Inc. (Alabaster, AL, USA). Soyasapogenol A and soyasapogenol B were purchased from Phyproof® (Vestenbergsgreuth, Germany). Additionally, avenanthramide 2c, avenanthramide 2p, and avenanthramide 2f, were previously synthesized in our laboratory (van Zadelhoff et al., 2022).

2.2. Sample preparation

Extraction was conducted in triplicate. The commercial plant protein ingredients were extracted with 80 % (*v*/*v*) methanol (1:20 [*w*:*w*]) during five sequential cycles. To ensure a homogeneous particle size, lysing matrix C (MP Biomedicals, Irvine, CA, USA) was added and, after solvent addition, all samples were mixed for 30 s at 30 Hz with a Cryomill MM 400 (Retsch, Haan, Germany). Hereafter, extraction was assisted by treatment in an ultrasonic bath at room temperature for 10 min per cycle. After each cycle, samples were centrifuged at 15,000 ×*g* for 10 min at 4 °C. The supernatants were dried overnight using N_2-flow and weighed to determine the dry extract yield per cycle. The extracts from the separate cycles were resolubilized with 1 mL 80 % (*v*/*v*) methanol and combined to obtain a representative pool for further analysis. The pooled samples were dried overnight using N_2-flow, followed by re-solubilization in 80 % (*v*/*v*) methanol to a concentration of 2–5 mg/mL for reversed-phase ultra-high performance liquid chromatography coupled to mass spectrometry (RP-UHPLC-MS). Samples for Orbitrap MS were additionally diluted thirty times (final concentrations 67–167 μg/mL). Prior to injection into the RP-UHPLC-MS, all extracts and standards were centrifuged at 15,000 ×*g* for 5 min at 4 °C.

2.3. Reversed-phase ultra-high performance liquid chromatography with photodiode array detection (RP-UHPLC-PDA)

The analytes were separated on a Thermo Vanquish UHPLC system (Thermo Scientific, San Jose, CA) equipped with a pump, degasser, autosampler, and photodiode array (PDA) detector. Separation was conducted using water (A) and ACN (B), both acidified with 0.1 % formic acid, as eluents. The flow rate was set at 400 μL/min at a column temperature of 35 °C. All samples (1 μL) were injected on a Waters Acquity BEH C18 column (150 mm × 2.1 mm i.d., 1.7 μm particle size) with a VanGuard guard column of the same material (5 mm × 2.1 mm i.d., 1.7 μm particle size) (Waters, Milford, MA, USA). The elution program was as follows: 0–1.09 min isocratic at 5 % B, 1.09–26.98 min linear gradient from 5 to 100 % B, 26.98–32.43 min isocratic at 100 % B, 32.43–33.52 min linear gradient to starting conditions, and 33.52–38.97 min isocratic at 5 % B. Detection wavelengths for the PDA detector were set to monitor the range between 190 and 680 nm.

2.4. Electrospray ionisation ion trap mass spectrometry (ESI-IT-MS/MS)

Low resolution mass spectrometric data were acquired using an LTQ Velos Pro linear ion trap mass spectrometer (Thermo Scientific) equipped with a heated ESI probe coupled in-line to the Vanquish UHPLC system. Data was collected in the negative ionisation (NI) and positive ionisation (PI) mode in the *m*/*z* range of 150–1500. Data-dependent MS/MS analyses by collision-induced dissociation (CID) were performed with a normalized collision energy (NCE) of 35 %. MS/MS fragmentation was performed on the most intense product ion in the MS/MS^{-1} spectrum. Dynamic exclusion with a repeat count of 3, repeat duration of 10 s, and an exclusion duration of 15 s was used to obtain MS/MS spectra of multiple different ions present in full MS at the same time.

Most settings were optimized by automatic tuning using LTQ Tune Plus 4.2 (Thermo Scientific). The ion-transfer tube temperature was 350 °C, the source heater temperature was 425 °C, and the source voltage was 3.5 kV.

2.5. Electrospray ionisation hybrid quadrupole orbitrap mass spectrometry (ESI-FT-MS/MS)

Accurate mass data were acquired using a Thermo Q Exactive Focus hybrid quadrupole-Orbitrap Fourier transform mass spectrometer (FT-MS) (Thermo Scientific) equipped with a heated ESI probe. For quantification, data was collected in full MS for NI and PI mode, both in the *m/z* range of 120–1500, with resolution set to 70,000. The source conditions used were: capillary temperature of 254 °C, probe heater temperature 408 °C, source voltage of 2.5 kV, and S-Lens RF level of 50. For identification, pools of each sample were also analysed by full MS and MS^2 with higher-energy collisional dissociation (HCD) fragmentation, recorded at 70,000 and 35,000 resolution, respectively. NCE was 35 %. Data-dependent MS^2 fragmentation was performed on the most intense product ion in the full MS spectrum.

2.6. Data processing: Identification and quantification

All data was processed using Xcalibur 4.1 (Thermo Scientific, USA). Tentative identifications of several compounds were confirmed by comparison with authentic standards. Other compounds' tentative identifications were corroborated by comparison of their MS^1 and MS^2 data from RP-UHPLC-PDA-ESI-IT-MS/MS and RP-UHPLC-PDA-ESI-FT-MS/MS analysis with literature. Additionally, Compound Discoverer 3.3 (Thermo Scientific) was used to search for spectral matches in several databases, including mzCloud (HighChem LLC, Slovakia), LipidMaps Structure database (Sud et al., 2007), and the integrated Endogenous Metabolites database (Shimadzu, Japan). Quantification of the tentatively identified compounds was conducted using TraceFinder (Thermo Scientific).

Solanidine was quantified based on α-solanine equivalents (quantification range: 0.001–0.956 μg/mL). The avenacosides where quantified based on avenacoside A equivalents (quantification range: 0.004–4.901 μg/mL). Soyasaponins were quantified based on soyasaponin Bb equivalents (quantification range: 0.005–4.683 μg/mL). Lysophospholipids and oxylipins were quantified based on 18:1a/lysoPC equivalents, 18:0a/lysoPE equivalents, and 13-oxo-ODE equivalents for lysophosphatidylcholines (quantification range: 0.001–1.040 μg/mL), lysophosphatidylethanolamines (quantification range: 0.002–1.011 μg/mL), and oxylipins (quantification range: 0.002–1.008 μg/mL), respectively.

3. Results and discussion

3.1. Characterization of non-volatiles in commercial plant protein ingredients

In the present study, the semi-polar non-volatile profiles of soy protein isolates (SoyPIs), pea protein isolates (PeaPIs), oat protein concentrate (OatPC), almond protein concentrate (AlmPC), and potato protein isolates (PotPIs) were characterized. The base peak chromatograms of one representative sample from each protein source can be seen below (Fig. 1). The full *m/z* range base peak chromatograms of all samples can be found in supplementary data (section S2, Fig. S2).

The combined results of analysis using RP-UHPLC-PDA-ESI-IT-MS/MS with CID fragmentation and RP-UHPLC-PDA-ESI-FT-MS/MS with HCD fragmentation resulted in the (tentative) identification of 71 compounds. The spectral data and (tentative) identifications are presented in Table 1. Comparison of retention times, MS^1 data, and MS^2 CID and HCD spectra with those of standards led to the unambiguous identification of 12 compounds. Additionally, the percentage of the total peak area for each protein source that was covered by the tentatively identified compounds can be found in supplementary data (section S2, Fig. S3).

The initial identification of lysophospholipids was based on previously published research (Fang et al., 2003) and supported by database searches. Lysophosphatidylcholines (LPCs) were tentatively identified based on their accurate masses in MS^1 based upon FT-MS analysis, in combination with relative abundance of $[M + H - H_2O]^+$ and [polar headgroup]$^+$ in MS^2 upon CID fragmentation (for CID-MS/MS spectral data, see supplementary data section S4, Table S1). Our HCD fragmentation data showed the presence of *m/z* 184.073 as the most abundant fragment for all LPCs, followed by *m/z* 104.107 for *sn*-1 or *m/z* 86.097 for *sn*-2 LPC isomers. Additionally, apart from the five 18:2-LPC isomers found by Fang et al. (2003), we detected six possible isomers of 18:2-OH LPC. The identification of lysophosphatidylethanolamines (LPEs) followed the same principle as for LPCs and relied on the relative abundance of $[M + H - H_2O]^+$ and $[M + H - 141]^+$ upon CID fragmentation. HCD fragmentation showed the presence of $[M + H - 141]^+$ as the most abundant fragment for all LPEs. LPE identification was based on the relative abundance of $[M\text{-}H - 180]^-$ upon CID fragmentation. In the commercial plant protein ingredients investigated in the present study, 27 lysophospholipids were tentatively identified. The majority (67 %) of the lysophospholipids were LPCs, the others were LPEs.

For the SoyPIs and PeaPIs, soyasaponins were identified similarly to the lysophospholipids, using previous research (Baiseitova et al., 2022; Krishnamurthy et al., 2014; Tsuno et al., 2018), and by corroborating tentative identifications based on trends in fragmentation of the soyasaponin Bb standard (supplementary data section S3, Fig. S4). DDMP group soyasaponins commonly present in legume species (Heng, Vincken, van Koningsveld, et al., 2006) could not be found in PeaPIs, and only trace amounts were identified in SoyPIs. The absence of DDMP group soyasaponins can be explained by their inherent instability (Heng, Vincken, Hoppe, et al., 2006), resulting in decomposition of DDMP soyasaponins to group B soyasaponin during the processing of raw material to protein isolates. For the oat protein concentrate, the unambiguous identification of avenacoside A was based on its authentic standard. Presence of other avenacosides, their aglycons, and their derivatives described in literature (Gunther-Jordanland et al., 2016) was screened for, but these compounds were not detected. Flavonoids and related compounds previously found in plant protein isolates (Cosson et al., 2022; Fahim et al., 2019) were identified in AlmPC and all three SoyPIs, but could not be found in either of the PeaPIs. Avenanthramides 2p, 2c, and 2f could be identified in OatPC, but their quantities were below the limit of quantification.

For PotPIs, trace amounts of α-solanine and α-chaconine were confirmed based on alignment of their accurate mass and retention time with those of the authentic standards. Additionally, oxylipins, such as 13-Oxo-ODE and its isomers, were mainly present in the PotPIs.

For the almond protein concentrate, trace amounts of epicatechin were confirmed based on alignment of its accurate mass and retention time with that of the authentic standard. Interestingly, no proanthocyanins, other flavonoids, or phenolic acids were found. These phenolic compounds are frequently reported to be present in almond and almond-derived ingredients (Bolling, 2017; Milbury et al., 2006; Xie et al., 2012), but were not present in the concentrate. MALDI-TOF-MS analysis was used to investigate whether any larger molecular mass tannins were present that could not be detected by LC-MS. The outcomes of the MALDI-TOF-MS analysis supported those of LC-MS and showed no compounds at higher *m/z* ranges (supplementary data S4, Table S2 and Fig. S5). The absence of tannins can be explained by the fact that they are mainly present in the skin of the almond (Bolling, 2017), which is most likely physically removed before extraction of the almond protein.

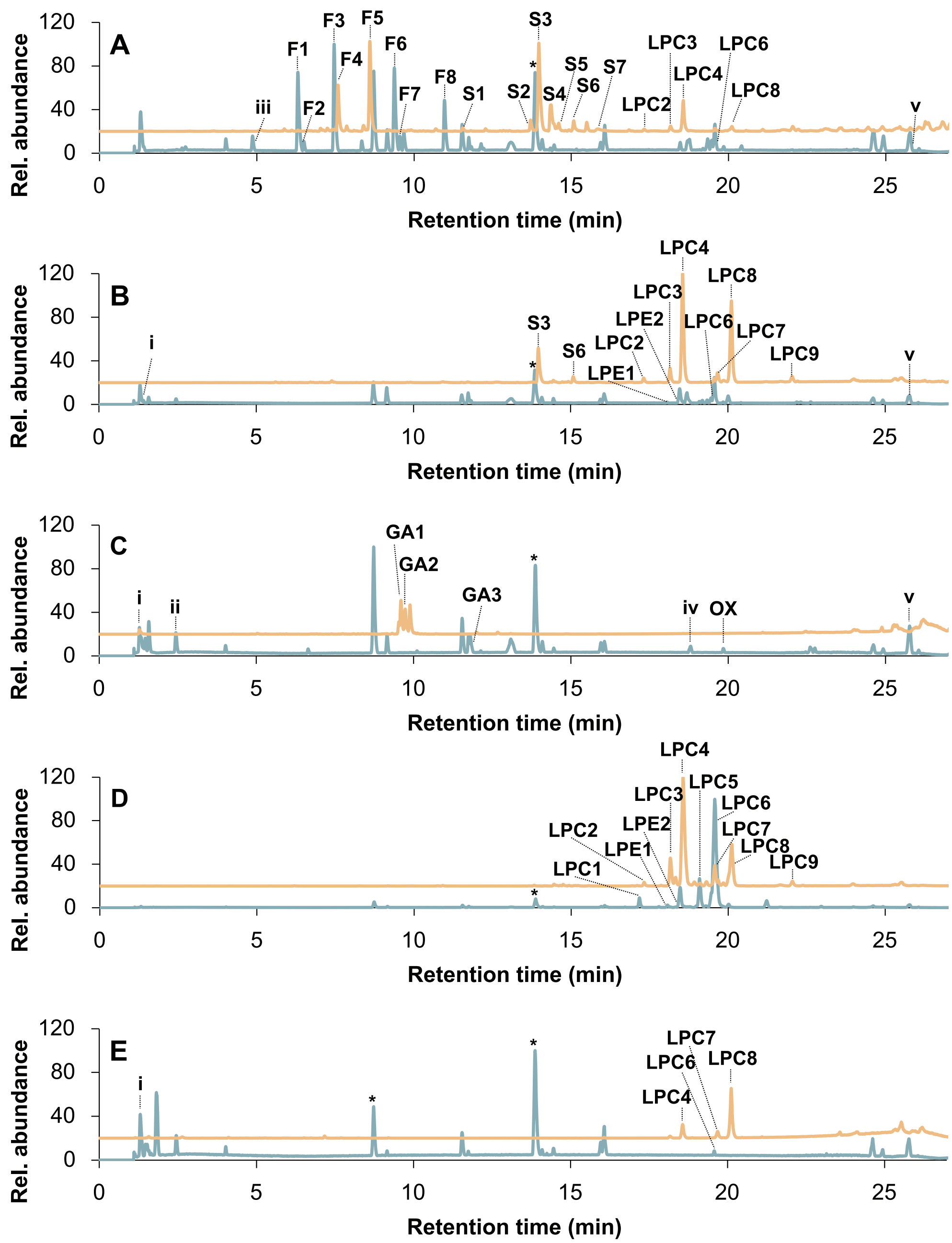

Fig. 1. RP-UHPLC-PDA-ESI-FT-MS/MS (positive ionisation mode) base peak chromatograms of 80 % methanol extracts of one representative sample for each protein source. SoyPI1 (A), PeaPI1 (B), PotPI2 (C), OatPC (D), and AlmPC (E). Blue line: m/z 120–500, orange line: m/z 500–1000. Peak labels mean the following: F, flavonoid; S, saponin; LPC, lysophosphatidylcholines; LPE, lysophosphatidylethanolamines; GA, glycoalkaloid; OX, oxylipin; i-v, other; *, system peak. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 1

Tentative identifications of flavonoids, avenanthramides, steroidal (glyco)alkoloids, saponins, lysophosphatidylcholines, lysophosphatidylethanolamines, and other co-passengers with their corresponding chromatographic and mass spectrometric data obtained using RP-UHPLC-PDA-ESI-FT-MS/MS (positive ionisation mode) with HCD fragmentation. Labels correspond to labels used in Fig. 1. CID-MS/MS spectral data is available in supplementary data (section S4, Table S1). ✓ indicates qualitative presence in corresponding sample, × indicates not detected in corresponding sample.

Label [a]	RT (min)	MS^1 [M+H]$^+$	HCD-MS/MS (rel. abundance) [b]	(Tentative) ID	ID level [c]	Theoretical formula	Theoretical [M+H]$^+$	Mass error (ppm)	SoyPI			PeaPI			PotPI		OatPC	AlmPC	Refs. [d]
									1	2	3	1	2	3	1	2			
(iso) Flavonoids																			
	4.23	291.0864	below threshold	catechin	2	$C_{15}H_{14}O_6$	291.08631	-0.41	×	×	×	×	×	×	×	×	×	✓	
	4.85	291.0864	below threshold	epicatechin	1	$C_{15}H_{14}O_6$	291.08631	-0.17	×	×	×	×	×	×	×	×	×	✓	
F1	6.31	417.1183	**255.0650** (100), 256.0684 (18), 199.0753 (13), 137.0233 (8), 227.0702 (6)	daidzin	2	$C_{21}H_{20}O_9$	417.11801	-0.79	✓	✓	✓	×	×	×	×	×	×	×	1
F2	6.50	447.1283	285.0754 (100), 270.0519 (20), 286.0787 (19), 229.0857 (5), 225.0544 (4)	glycitin	2	$C_{22}H_{22}O_{10}$	447.12857	0.56	✓	✓	✓	×	×	×	×	×	×	×	1
F3	7.46	433.1135	**271.0599** (100), 272.0632 (17), 89.0602 (9), 215.0702 (9), 197.0597 (5)	genistin	2	$C_{21}H_{20}O_{10}$	433.11292	-1.32	✓	✓	✓	×	×	×	×	×	×	×	1
F4	7.58	503.1188	**255.0651** (100), 199.0755 (3)	malonyl-daidzin	3	$C_{24}H_{22}O_{12}$	503.11840	-0.80	✓	✓	✓	×	×	×	×	×	×	×	2, 4
F5	8.59	519.1143	**271.0597** (100), 153.0181 (2)	malonyl-genistin	3	$C_{24}H_{22}O_{13}$	519.11332	-1.91	✓	✓	✓	×	×	×	×	×	×	×	2, 4
F6	9.37	255.0656	91.0547 (100), 137.0233 (53), 152.0620 (45), 181.0647 (41), 153.0701 (33)	daidzein	1	$C_{15}H_{10}O_4$	255.06519	-1.53	✓	✓	✓	×	×	×	×	×	×	×	
F7	9.55	475.1237	**271.0600** (100), 272.0633 (18), 215.0703 (3), 153.0182 (3), 243.0652 (2)	acetyl-genistin	3	$C_{23}H_{22}O_{11}$	475.12349	-0.46	✓	✓	✓	×	×	×	×	×	×	×	
F8	10.97	271.0603	91.0547 (100), 153.0182 (54), 68.9979 (25), 141.0699 (23), 65.0394 (19)	genistein	1	$C_{15}H_{10}O_5$	271.06010	-0.63	✓	✓	✓	×	×	×	×	×	×	×	
Avenanthramides																			
A1	8.30	316.0819	below threshold	avenanthramide 2c	1	$C_{16}H_{13}NO_6$	316.08156	-1.20	×	×	×	×	×	×	×	×	✓	×	
A2	9.23	300.0867	119.0493 (100), 91.0548 (92), 147.0441 (39), 120.0527 (10), 55.9353 (9)	avenanthramide 2p	1	$C_{16}H_{13}NO_5$	300.08665	-0.17	×	×	×	×	×	×	×	×	✓	×	
A3	9.60	330.0972	117.0336 (100), 145.0283 (75), 89.0391 (45), 149.0597 (27), 134.0362 (10)	avenanthramide 2f	1	$C_{17}H_{15}NO_6$	330.09721	0.15	×	×	×	×	×	×	×	×	✓	×	
									1	2	3	1	2	3	1	2			
Steroidal (glyco)alkoloids																			
GA1	9.59	868.5049	868.5049 (100), 869.5085 (47), 870.5237 (1), 727.4632 (1), 636.5011 (1)	α-solanine	1	$C_{45}H_{73}NO_{15}$	868.50530	0.48	×	×	×	×	×	×	✓	✓	×	×	
GA2	9.66	852.5107	852.5095 (100), 853.5126 (51), 86.0969 (1), 213.2501 (1), 184.0734 (1)	α-chaconine	1	$C_{45}H_{73}NO_{14}$	852.51038	-0.42	×	×	×	×	×	×	✓	✓	×	×	
GA3	11.80	398.3421	398.3420 (100), 98.0970 (42), 399.3453 (35), 126.1280 (2), 99.1003 (2)	solanidine	2	$C_{27}H_{43}NO$	398.34174	-0.98	×	×	×	×	×	×	✓	✓	×	×	1
Saponins																			
	10.75	1225.5853	below threshold	avenacoside B	3	$C_{57}H_{92}O_{28}$	1225.58479	-0.43	×	×	×	×	×	×	×	×	✓	×	3
	10.91	1063.53311	431.3155 (100), 413.3050 (58), 271.2055 (35), 129.0548 (21), 85.0290 (18)	avenacoside A	1	$C_{51}H_{82}O_{23}$	1063.53197	-1.04	×	×	×	×	×	×	×	×	✓	×	
	8.17	1269.6118	**439.3566** (100), 457.3671 (60), 421.3461 (56), 615.3885 (28), 440.3600 (25)	non-acetylated soyasaponin Ab	2	$C_{59}H_{96}O_{29}$	1269.61100	-0.64	✓	✓	✓	×	×	×	×	×	×	×	2
	10.69	959.5211	**439.3571** (100: 421.3461 (76), 457.3676 (62), 85.0290 (42), 141.0183 (35)	soyasaponin A derivative	3				✓	✓	✓	×	×	×	×	×	×	×	
S1	11.55	957.5050	437.3409 (100), 455.3514 (93), 438.3443 (29), 419.3305 (27), 456.3547 (27)	soyasaponin Bd	3	$C_{48}H_{76}O_{19}$	957.50536	0.37	✓	✓	✓	✓	✓	✓	×	×	×	×	2
	13.29	1029.5265	423.3616 (100), 424.3651 (29), 405.3512 (23), 85.0289 (14), 581.3829 (12)	malonyl-soyasaponin Bb	3	$C_{51}H_{80}O_{21}$	1029.52649	-0.01	✓	✓	✓	✓	✓	✓	×	×	×	×	4
S2	13.70	959.5208	423.3618 (100), **441.3724** (77), 163.0600 (54), 141.0182 (33), 145.0495 (29)	soyasaponin Ba	2	$C_{48}H_{78}O_{19}$	959.52101	0.22	✓	✓	✓	×	×	×	×	×	×	×	5

(*continued on next page*)

Table 1 (*continued*)

Label [a]	RT (min)	MS[1] [M+H]+	HCD-MS/MS (rel. abundance) [b]	(Tentative) ID	ID level [c]	Theoretical formula	Theoretical [M+H]+	Mass error (ppm)	SoyPI 1	SoyPI 2	SoyPI 3	PeaPI 1	PeaPI 2	PeaPI 3	PotPI 1	PotPI 2	OatPC	AlmPC	Refs. [d]
S3	13.98	943.5236	423.3618 (100), **441.3724** (81), 85.0290 (34), 141.0182 (31), 424.3653 (29)	soyasaponin Bb	1	$C_{48}H_{78}O_{18}$	943.52609	2.64	✓	✓	✓	✓	✓	✓	×	×	×	×	
S4	14.33	913.5151	423.3617 (100), **441.3723** (84), 141.0181 (30), 424.3650(29), 85.0289 (25)	soyasaponin Bc	2	$C_{47}H_{76}O_{17}$	913.51553	0.47	✓	✓	✓	✓	✓	✓	×	×	×	×	2
	14.36	797.4683	141.0183 (100), 423.3622 (81), 203.1796 (54), 184.0735 (52), 163.0601 (43)	soyasaponin Bb'	2	$C_{42}H_{68}O_{14}$	797.46818	-0.15	✓	✓	✓	✓	✓	✓	×	×	×	×	2
S5	14.60	767.4560	141.0182 (100), 423.3622 (84), 203.1795 (71), 109.1015 (41), 217.1951 (39)	soyasaponin Bc'	3	$C_{41}H_{66}O_{13}$	767.45762	2.11	✓	✓	✓	✓	✓	✓	×	×	×	×	
S6	15.08	941.5085	**439.3570** (100), 421.3464 (58), 440.3604 (29), 85.0295 (26), 141.0183 (21)	soyasaponin Be	2	$C_{48}H_{76}O_{18}$	941.51044	2.06	✓	✓	✓	✓	✓	✓	×	×	×	×	2
	15.19	1069.5588	**423.3618** (100), 145.0495 (46), 424.3652 (27), 405.3513 (23), 127.0391 (12)	soyasaponin βg	2	$C_{54}H_{84}O_{21}$	1069.55779	-0.95	✓	✓	✓	×	×	×	×	×	×	×	2, 5
	15.48	795.4525	141.0181 (100), 421.3460 (75), **439.3572** (70), 245.1895 (39), 219.1742 (33)	soyasaponin Be'	2	$C_{42}H_{66}O_{14}$	795.45253	0.04	✓	✓	✓	✓	✓	✓	×	×	×	×	5
	15.49	1039.5480	**423.3617** (100), 145.0495 (41), 424.3651 (26), 405.3512 (21), 85.0289 (12)	soyasaponin βa	2	$C_{53}H_{82}O_{20}$	1039.54722	-0.75	✓	✓	✓	×	×	×	×	×	×	×	2, 5
	15.51	911.4990	**439.3569** (100), 421.3462 (58), 440.3602 (31), 184.0734 (28), 85.0290 (26)	soyasaponin Bg	2	$C_{47}H_{74}O_{17}$	911.49988	0.97	✓	✓	✓	✓	✓	✓	×	×	×	×	5
S7	15.84	923.5001	**423.3622** (100: 145.0496 (69), 127.0392 (28), 424.3656 (28), 405.3517 (28)	soyasaponin ϒg	2	$C_{48}H_{74}O_{17}$	923.49988	-0.24	✓	✓	✓	×	×	×	×	×	×	×	2
Lysophosphatidylcholines (LPCs)																			
	13.82	536.3356	184.0733 (100), 104.1074 (83), 86.0970 (31), 125.0000 (12), 60.08160 (9)	18:2-OH LPC isomer 1	2	$C_{26}H_{50}NO_8P$	536.33468	-1.72	×	×	×	×	×	×	×	×	✓	×	6
	14.16	536.3353	184.0734 (100), 86.0970 (22), 104.1074 (17), 125.0000 (10), 185.0768 (5)	18:2-OH LPC isomer 2	2	$C_{26}H_{50}NO_8P$	536.33468	-1.16	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	14.46	536.3347	184.0733 (100), 104.10737 (80), 86.0970 (30), 125.0000 (12), 60.0816 (9)	18:2-OH LPC isomer 3	2	$C_{26}H_{50}NO_8P$	536.33468	-0.04	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	14.54	536.3348	184.0733 (100), 104.1074 (77), 86.0970 (31), 125.0000 (12), 60.0816 (8)	18:2-OH LPC isomer 4	2	$C_{26}H_{50}NO_8P$	536.33468	-0.22	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	14.75	536.3346	184.07329 (100), 104.1074 (47), 86.0970 (26), 125.0000 (10), 60.0816 (8)	18:2-OH LPC isomer 5	2	$C_{26}H_{50}NO_8P$	536.33468	0.15	×	×	×	✓	✓	✓	✓	✓	✓	✓	6
	15.10	536.3350	184.0733 (100), 104.1074 (84), 86.0970 (32), 125.0000 (12), 60.0816 (9)	18:2-OH LPC isomer 6	2	$C_{26}H_{50}NO_8P$	536.33468	-0.60	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	16.71	468.3087	184.0732 (100), 86.0970 (44), 125.0000 (24), 60.0812 (9), 185.0767 (5)	lyso/14:0a-PC	2	$C_{22}H_{46}NO_7P$	468.30847	-0.49	✓	✓	✓	✓	✓	✓	×	×	✓	✓	6
	16.94	518.3243	184.0733 (100), 86.0970 (30), 125.0000 (14), 60.0816 (7), 185.0768 (5)	lyso/18:3a-PC	2	$C_{26}H_{48}NO_7P$	518.32412	-0.35	✓	✓	✓	✓	✓	✓	✓	✓	✓	×	6
LPC1	17.17	468.3083	104.1074 (100), 184.0733 (95), 86.0970 (58), 125.0000 (29), 60.0816 (19)	14:0a/lysoPC	2	$C_{22}H_{46}NO_7P$	468.30847	0.36	✓	✓	✓	✓	✓	✓	×	×	✓	✓	6
LPC2	17.33	518.3236	184.0731 (100), 104.1073 (84), 86.0969 (40), 124.9999 (18), 60.0815 (12)	18:3a/lysoPC	2	$C_{26}H_{48}NO_7P$	518.32412	1.00	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC3	18.16	520.3408	184.0737 (100), 86.0972 (28), 125.0002 (12), 60.0817 (6), 185.0771 (5)	lyso/18:2a-PC	2	$C_{26}H_{50}NO_7P$	520.33977	-1.98	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC4	18.57	520.3395	184.0733 (100), 104.1073 (94), 86.0970 (40), 125.0000 (17), 60.0816 (13)	18:2a/lysoPC	2	$C_{26}H_{50}NO_7P$	520.33977	0.52	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC5	19.09	496.3395	184.0732 (100), 86.0970 (34), 125.0000 (17), 60.0816 (7), 185.0767 (5)	lyso/16:0a-PC	2	$C_{24}H_{50}NO_7P$	496.33977	0.54	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6

(*continued on next page*)

Table 1 (*continued*)

Label [a]	RT (min)	MS^1 $[M+H]^+$	HCD-MS/MS (rel. abundance) [b]	(Tentative) ID	ID level [c]	Theoretical formula	Theoretical $[M+H]^+$	Mass error (ppm)	SoyPI			PeaPI			PotPI		OatPC	AlmPC	Refs. [d]
									1	2	3	1	2	3	1	2			
LPC6	19.57	496.3407	184.0736 (100), 104.1076 (90), 86.0972 (46), 125.0001 (20), 60.0817 (13)	16:0a/lysoPC	2	$C_{24}H_{50}NO_7P$	496.33977	-1.87	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC7	19.69	522.3565	184.0737 (100), 86.0972 (27), 125.0002 (13), 60.0817 (6), 185.0771 (5)	lyso/18:1a-PC	2	$C_{26}H_{52}NO_7P$	522.35542	-2.07	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC8	20.12	522.3550	184.0731 (100), 104.1073 (89), 86.0969 (38), 124.9998 (17), 60.0816 (12)	18:1a/lysoPC	1	$C_{26}H_{52}NO_7P$	522.35542	0.80	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
	21.56	524.3716	184.0729 (100), 86.0968 (25), 124.9997 (11), 185.0763 (6), 60.0815 (5)	lyso/18:0a-PC	2	$C_{26}H_{54}NO_7P$	524.37107	-1.01	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
LPC9	22.04	524.3707	184.0730 (100), 104.1072 (82), 86.0968 (36), 124.9997 (15), 60.0815 (11)	18:0a/lysoPC	2	$C_{26}H_{54}NO_7P$	524.37107	0.71	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
Lysophosphatidyl ethanolamines (LPEs)																			
	16.61	426.2611	57.0707 (100), 71.0862 (64), 95.0859 (40), 85.1017 (33), 57.0343 (31)	lyso/14:0a-PE	2	$C_{19}H_{40}NO_7P$	426.26152	1.10	✓	✓	✓	✓	✓	✓	✓	×	✓	✓	6
	17.07	426.2614	57.0707 (100), 71.0863 (77), 95.0860 (46), 85.1018 (41), 62.0609 (39)	14:0a/lysoPE	2	$C_{19}H_{40}NO_7P$	426.26152	0.19	✓	✓	✓	✓	✓	✓	✓	×	✓	✓	6
LPE1	18.07	478.2939	81.0705 (100), 67.0550 (87), 95.0860 (83), 69.0706 (64), 55.0551 (42)	lyso/18:2a-PE	2	$C_{23}H_{44}NO_7P$	478.29282	-2.15	✓	✓	✓	✓	✓	✓	×	✓	✓	✓	6
LPE2	18.47	478.2928	67.050 (100), 81.0705 (99), 95.0860 (82), 62.0609 (60), 69.0706 (47)	18:2a/lysoPE	2	$C_{23}H_{44}NO_7P$	478.29282	0.13	✓	✓	✓	✓	✓	✓	×	✓	✓	✓	6
	18.99	454.2930	57.0708 (100), 71.0863 (68), 85.1018 (41), 95.0861 (41), 57.0344 (31)	lyso/16:0a-PE	2	$C_{21}H_{44}NO_7P$	454.29282	-0.46	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	19.47	454.2935	57.0709 (100), 71.0864 (65), 85.1020 (52), 62.061 (35), 95.0863 (34)	16:0a/lysoPE	2	$C_{21}H_{44}NO_7P$	454.29282	-1.39	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	19.59	480.30945	below threshold	lyso/18:1a-PE	3	$C_{23}H_{46}NO_7P$	480.30847	-2.04	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	6
	20.01	480.3081	69.0706 (100), 83.0861 (71), 95.0859 (65), 62.0608 (64), 81.0705 (61)	18:1a/lysoPE	1	$C_{23}H_{46}NO_7P$	480.30847	0.83	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
	21.45	482.3244	below threshold	lyso/18:0a-PE	3	$C_{23}H_{48}NO_7P$	482.32412	-0.58	✓	✓	✓	✓	✓	✓	×	×	✓	✓	6
	21.94	482.3247	309.2978 (100), 308.2944 (25), 310.3001 (16), 57.0707 (11), 71.0862 (10)	18:0a/lysoPE	1	$C_{23}H_{48}NO_7P$	482.32412	-1.16	✓	✓	✓	✓	✓	✓	×	×	✓	✓	
Oxylipins																			
	19.19	295.2268	67.0550 (100), 79.0548 (82), 91.0547 (66), 93.0703 (64), 81.0704 (61)	13-oxo-ODE	1	$C_{18}H_{30}O_3$	295.22677	-0.03	✓	✓	✓	✓	✓	✓	✓	×	✓	×	
	19.34	295.2263	67.0550 (100), 79.0549 (89), 55.0501 (69), 91.0548 (69), 93.0704 (65)	oxo-ODE isomer	2	$C_{18}H_{30}O_3$	295.22677	1.52	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
	19.54	295.2267	81.0341 (100), 67.0550 (90), 53.0395 (64), 79.0549 (60), 55.0551 (58)	oxo-ODE isomer	2	$C_{18}H_{30}O_3$	295.22677	0.17	✓	✓	✓	✓	✓	✓	✓	×	✓	✓	
OX	19.85	295.2268	81.0341 (100), 67.0549 (58), 53.0394 (57), 79.0548 (50), 81.0704 (49)	oxo-ODE isomer	2	$C_{18}H_{30}O_3$	295.22677	-0.03	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
Others																			
i	1.30	268.1042	136.0616 (100), 137.0458 (14), 119.0354 (10), 137.0649 (6), 94.0404 (5)	adenosine	2	$C_{10}H_{13}N_5O_4$	268.10403	-0.67	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	1
iii	4.86	295.1289	67.0550 (100), 120.0809 (97), 55.0551 (78), 79.0549 (74), 81.0705 (64)	aspartame	2	$C_{14}H_{18}N_2O_5$	295.12885	-0.10	✓	✓	✓	×	✓	✓	×	✓	✓	×	1
ii	2.44	166.0864	56.9656 (100), 103.0546 (40), 95.0496 (37), 84.9602 (24), 91.0547 (16)	L-phenylalanine	2	$C_9H_{11}NO_2$	166.08626	-0.54	✓	✓	✓	✓	✓	✓	✓	✓	✓	×	1
iv	18.80	279.2320	67.0550 (100), 81.0705 (61), 95.0860 (31), 79.0549 (23), 55.0551 (14)	(alpha/beta) eleostearic acid	2	$C_{18}H_{30}O_2$	279.23186	-0.61	×	×	×	×	×	✓	✓	✓	✓	×	1
v	25.77	310.3104	55.0051 (100), 69.0707 (83), 57.0708 (55), 83.0862 (34), 67.0551 (28)	stearoyl ethanolamide -H2O	2	$C_{20}H_{39}NO$	310.31044	0.16	✓	✓	✓	✓	✓	✓	✓	✓	✓	×	1
	26.20	786.5998	184.0732 (100), 185.0767 (5), 86.0969 (3), 124.9999 (1), 60.0816 (1)	PC (18:1/18:1)	2	$C_{44}H_{84}NO_8P$	786.60073	1.20	✓	✓	✓	✓	✓	✓	✓	×	×	✓	7

[a] Labels are related to peaks visible in Fig. 1. If no peak label is present, the compound is only visible in an extracted ion chromatogram. [b] Key diagnostic fragments for different compound classes are highlighted by bolding or underlining them: for flavonoids one diagnostic fragment, **[aglycone + H]$^+$**; for saponins two diagnostic fragments, **[aglycone – H_2O + H]$^+$** and [aglycone – 2 H_2O ± H]$^+$. [c] Level of identification, based on Schymanski et al. (Schymanski et al., 2014). [d] Used references: 1 = mzCloud (HighChem LLC, Slovakia), 2 = (Baiseitova et al., 2022), 3 = (Gunther-Jordanland et al., 2016), 4 = (Krishnamurthy et al., 2014), 5 = (Tsuno et al., 2018), 6 = (Fang et al., 2003), and 7 = LipidMaps Structure database (Sud et al., 2007).

3.2. Saponin and glycoalkaloid quantification and implications for off-taste

Saponins and glycoalkaloids were identified and quantified in our extracts (Fig. 2). As shown in Fig. 2, soy protein isolates had a considerably higher saponin content compared to pea protein isolates. Taste recognition thresholds vary in literature, though 0.4 g/kg is generally accepted (Aldin et al., 2006; Heng, Vincken, van Koningsveld, et al., 2006). Assuming the mentioned threshold, the overall soyasaponin content of the SoyPIs and PeaPIs, except for PeaPI2 and PeaPI3, were above the threshold. However, even lower taste recognition thresholds were reported by Okubo and co-workers, who also made the following ranking: soyasaponins group A < soyasaponins group B < soyasaponins group E (Okubo et al., 1992). This would imply that the taste of all soy protein isolates and pea protein isolates analysed in the current study is affected by soyasaponin, resulting in an undesired off-taste for consumers. Additionally, saponins may limit nutrient absorption and reduce digestibility and are therefore also considered to be anti-nutritional factors (Samtiya et al., 2020; Yoshiki et al., 1998).

Fig. 2 shows that the total glycoalkaloid content of PotPI2 was considerably lower than that of PotPI1, 0.014 g/kg and 0.056 g/kg, respectively. Both were below the taste perception threshold reported at 0.1 g/kg (Taylor et al., 2007), which is likely due to specific breeding and processing practices targeted at limiting their content in final products to meet regulatory guidelines regarding glycoalkaloid toxicity in potato products. Glycoalkaloids, apart from being bitter, are also considered toxic, with the lowest observed adverse effect level of 1 mg per kilogram of body weight per day (Schrenk et al., 2020). Depending on the country, the maximum acceptable content of glycoalkaloids in potato products varies between 0.10 and 0.25 g/kg. Both potato protein isolates had glycoalkaloid levels below this range. Based on the content of total glycoalkaloids, it is not expected that they will significantly contribute to off-taste.

The total avenacoside (i.e. oat saponin) content (0.105 g/kg) of the oat protein concentrate was approximately a factor 20 above the bitterness (0.007 g/kg) and astringency (0.003–0.005 g/kg) thresholds that were previously reported (Gunther-Jordanland et al., 2016) for these compounds. Therefore, these saponins potentially contribute to the bitter off-taste in oat protein concentrate, as well as being an anti-nutritional factor.

3.3. Lysophospholipids and oxylipins quantification, and implications for off-flavour

Previously identified lysophospholipids and oxylipins were quantified based on 18:1a/lysoPC equivalents, 18:0a/lysoPE equivalents, and 13-Oxo-ODE equivalents for lysophosphatidylcholines, lysophosphatidylethanolamines, and oxylipins, respectively. Fig. 3 shows the overall quantification of lysophospholipids and oxylipins in commercial plant protein ingredients.

The major types of polar lipids in all plant protein ingredients were lysophosphatidylcholines followed by lysophosphatidylethanolamines, with the exception of the potato protein isolates, which solely contained oxylipins. It has to be noted that lysophospholipids and oxylipins are generally not the overall major lipid constituents of plant protein ingredients (Boatright & Hettiarachchy, 1995; Keuleyan et al., 2023; Sargautis et al., 2023), and that the overall lipid content was not established in the present study. As shown in Fig. 3, AlmPC, SoyPIs, and PotPIs have an overall low lysophospholipids and oxylipins content. This can be attributed to lipid extraction (i.e. defatting) prior to the extraction of commercial plant protein ingredients from soy and almond. Potato fruit juice, which was used for the protein extraction of PotPI1 and PotPI2, already has a relatively low polar lipid content (van Koningsveld, 2001). To the best of the authors' knowledge, to date, oxylipins and lysophospholipids are not considered to be anti-nutritional factors. Oxylipins may contribute to off-taste, as some are described as bitter (Lainer et al., 2019). It is unknown whether lysophospholipids contribute to off-taste but this seems unlikely, as evidence for a possible taste of these compounds is lacking in the literature. However, based on findings for oxidation of phospholipids, literature suggests that

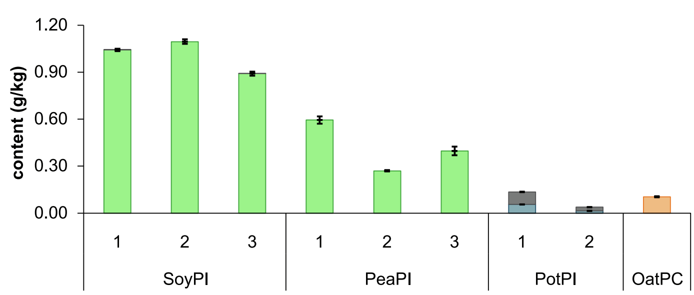

Fig. 2. Quantification of glycoalkaloids, avenacosides, soyasaponins and their respective aglycons in commercial soy, pea, oat, almond, and potato protein ingredients. Colours correspond to: total soyasaponins (green), total glycoalkaloids (blue), and total avenacosides (orange). If the corresponding aglycon was detected, it is depicted in grey. Error bars display the standard deviation based on triplicates. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

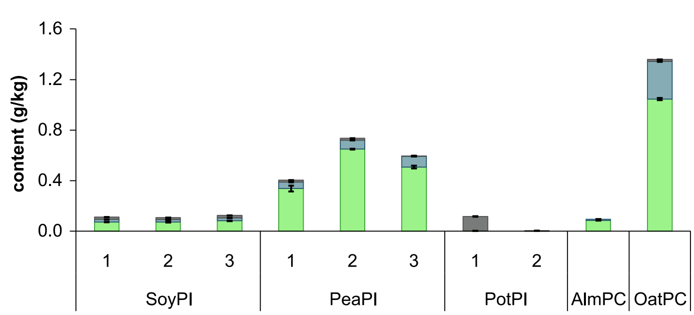

Fig. 3. Quantification of total lysophosphatidylcholines (green), lysophosphatidylethanolamines (blue) and oxylipin (grey) content in commercial soy, pea, oat, almond, and potato protein ingredients. Error bars display the standard deviation based on triplicates. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

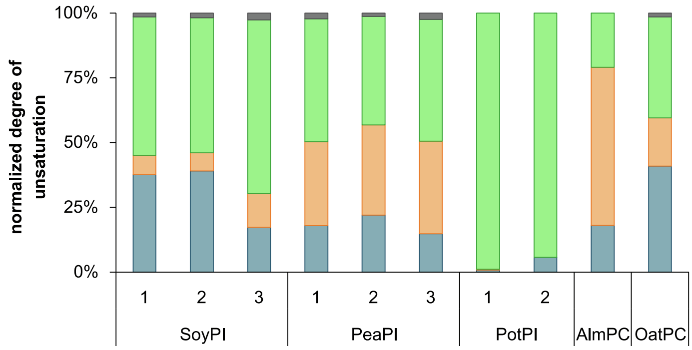

Fig. 4. Quantification of lysophospholipids in commercial soy, oat, pea, potato and almond protein ingredients based on their degree of unsaturation. Colours correspond to degree of unsaturation of 0 (blue), 1 (orange), 2 (green) and 3 (grey), respectively. Degree of unsaturation was normalized and expressed as the average of triplicates. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

lysophospholipids can contribute to off-odour formation through lipid oxidation, which is also undesired (Damodaran & Arora, 2013; Jacobsen, 1999; Zhou et al., 2025).

Lipids containing polyunsaturated fatty acids (PUFAs) in particular are susceptible to lipid oxidation. Depending on the degree of unsaturation, the detected lysophospholipids can partake in lipid oxidation, leading to off-odours resulting in beany and rancid notes. Therefore, for the quantification of lysophospholipids, a distinction was made in the degree of unsaturation (Fig. 4).

Fig. 4 shows that lysophospholipids in all commercial plant protein ingredients had relatively high amounts of PUFA-containing lysophospholipids. Interestingly, compared to the other commercial plant protein ingredients, the almond protein concentrate was the only sample that had a low content of PUFA-containing lysophospholipids and oxylipins, which might indicate that it is less prone to lipid oxidation, potentially resulting in less off-odour in applications.

3.4. Future of plant protein ingredients in food production: Strategies for off-flavour removal

In this work, we showed that the main semi-polar non-volatile co-passengers that may contribute to off-flavour of common commercial plant protein ingredients derived from soy, pea, oat, almond, and potato were saponins and polar lipids, comprising lysophospholipids and oxylipins (Fig. 5). Since these co-passengers may affect both off-taste and off-odour, we intentionally use the term off-flavour, which encompasses both taste and odour. Our findings contradict previous research on plant raw materials, which assumed that phenolic compounds, such as tannins and flavonoids, were the main culprits regarding off-tastes in commercial plant protein ingredients (Roland et al., 2017; Soares et al., 2018;

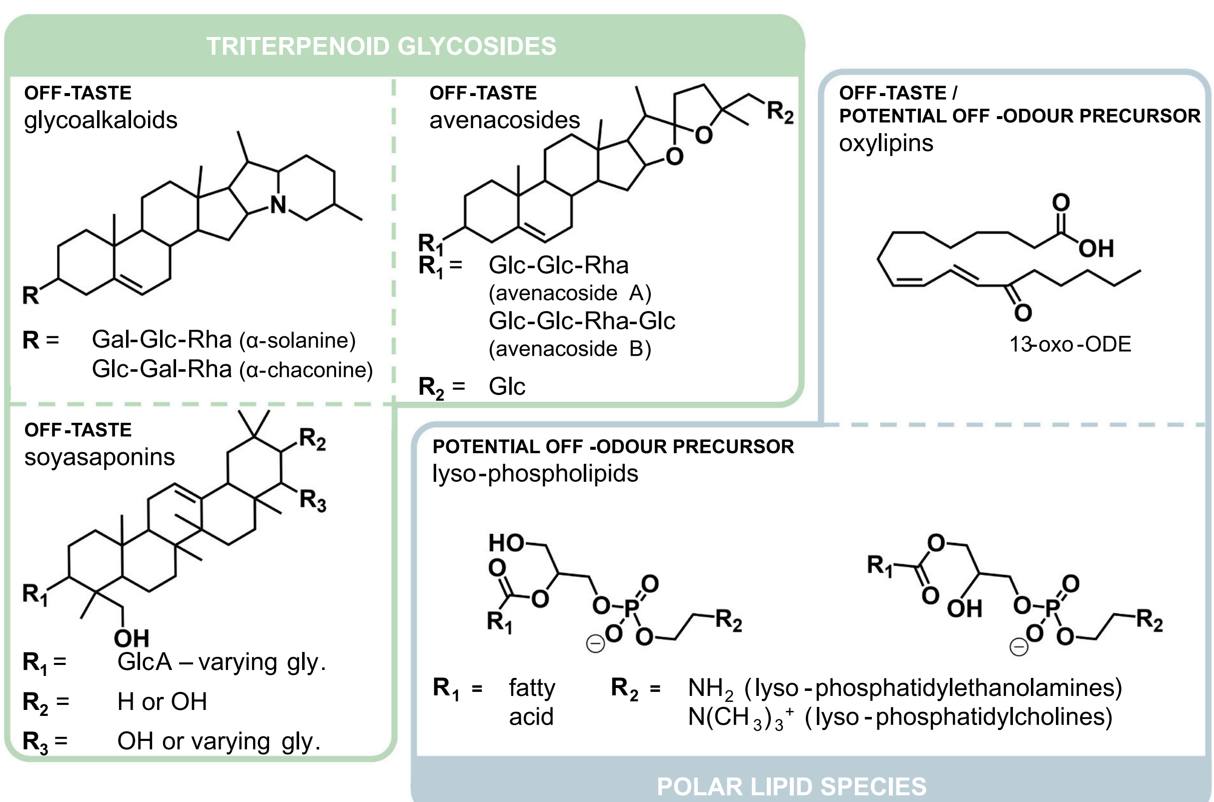

Fig. 5. The main semi-polar non-volatile co-passengers that may contribute to off-flavour of commercial plant protein ingredients derived from soy, pea, oat, almond, and potato. Abbreviation used: Gly, glycosylation.

Soares et al., 2020). Follow-up studies that include sensory evaluation are necessary to verify the impact of the semi-polar non-volatiles identified in our work. Nonetheless, our findings offer insights into potential off-flavours, which may guide targeted sensory evaluation in subsequent research.

The protein extraction process itself is designed to maximize protein yield and overall purity, without specifically focussing on the removal of undesired co-passengers. Current strategies for removal of undesired co-passengers from commercial plant protein ingredients are typically divided into three categories: pre-treatment (e.g. germination, soaking), mechanical (e.g. dehulling), and post-processing treatments (e.g. thermal treatment) (Manzanilla-Valdez et al., 2024; Samtiya et al., 2020). The dehulling step, which is commonly performed prior to plant protein extraction, may explain both the lack of oligo- and polymeric phenolics (such as tannins in almonds), as well as the absence of smaller phenolics in commercial soy, pea, and almond protein ingredients. These compounds are mainly reported to be present in the skin, hulls, and shells of the raw material, which are usually removed by dehulling (Bolling, 2017; Tsuno et al., 2018) Additionally, the smaller phenolics can only form relatively weak non-covalent interactions with the protein and may be removed relatively easily during steps like soaking or ultra-filtration. Therefore, these phenolics might be less of an issue as off-tastants in commercial plant protein ingredients than previously thought. Saponins, however, are not affected by dehulling, as they are mainly present in the hypocotyl and cotyledon of soybeans (Tsuno et al., 2018) and oat grains (Pecio et al., 2013). Moreover, saponins are suggested to form relatively strong non-covalent interactions with proteins, limiting their removal during subsequent extraction steps (Zhao et al., 2022; Zhu et al., 2020). No specific information is currently available about strategies for the removal of lysophospholipids and oxylipins. Yet, our results show that these polar lipids are not (completely) removed by the processes (e.g. defatting) that are currently used to obtain commercial plant protein ingredients. Based on our results, we can conclude that lysophospholipids, oxylipins, and saponins are co-passengers of commercial plant protein extraction. There are currently no established strategies for the effective removal of these specific semi-polar co-passengers from commercial plant protein ingredients. Thus, development of new strategies for their removal will be key in obtaining commercial plant protein ingredients with desirable flavour and limited anti-nutritional properties. To this end, we may find inspiration in processes used to remove undesired co-passengers in other agriculture and food applications.

Literature shows that the aglycons of soyasaponins (i.e. soyasapogenols) are perceived as less bitter than their respective soyasaponins (Okubo et al., 1992). Analogous to the debittering of citrus products by deglycosylation of bitter flavonoids via naringinase treatment (Muñoz et al., 2022; Puri et al., 1996), a potential strategy in the reduction of bitterness from saponins in commercial soy, pea, and oat protein ingredients could therefore be the hydrolysis of these saponins to their aglycons. A similar strategy has already been established in industry for glycoalkaloid reduction, by hydrolysing potato glycoalkaloids to their less toxic and less bitter aglycons (Edens et al., 1997). Alternatively, the potential use of bio-purification using micro-organisms in the removal or degradation of undesired co-passengers may be explored. This practice is already widely applied in industry, for example for the removal of undesired contaminants, such as mycotoxins, from agricultural raw materials (Ji et al., 2016). Nonetheless, applying the same concept to plant proteins in the food industry requires the use of food-grade micro-organisms devoid of protease activity. It has been shown that lactic acid bacteria and yeasts are suitable as candidates for bio-purification agents in food (Ahlberg et al., 2015; Król et al., 2018; Shetty & Jespersen, 2006). The use of bio-purification for the removal of undesired volatiles, such as aldehydes and ketones, from commercial plant protein ingredients resulted in improved sensory properties, with limited effects on protein functionality (Nugroho et al., 2024). However, it remains unknown whether bio-purification can also be used for the removal of semi-polar non-volatile co-passengers in commercial plant protein ingredients.

4. Conclusion

In the present work, we identified the undesired semi-polar co-passengers in commercial soy, pea, potato, oat, and almond protein ingredients. It was hypothesized that the main off-tastants in plant raw materials are also the main undesired co-passengers in commercial plant protein ingredients. However, based on our research, this is not fully the case. Our RP-UHPLC-MS analysis of the commercial plant protein ingredients indicated that saponins, glycoalkaloids, lysophospholipids, and oxylipins were the main semi-polar co-passengers present in commercial plant protein ingredients. Avenacosides and soyasaponins likely contribute to the bitter off-taste in oat and pea or soy, respectively, as their content in the samples exceeded the taste recognition thresholds. These saponins are also considered to be anti-nutritional factors, making their presence in commercial plant protein ingredients even less desirable. Additionally, the presence of oxylipins may potentially contribute to this bitter off-taste as well. The presence of phenolic compounds in commercial pea, oat, almond, and potato protein ingredients was very limited, contradicting our expectation, which was based on previous publications, that phenolics would be major off-tastants and potential anti-nutritional factors in plant protein ingredients. Therefore, it is highly unlikely that, for these commercial plant protein ingredients, the off-taste originates from phenolic compounds. Furthermore, oxylipins and lysophospholipids may partake in lipid oxidation, which potentially leads to off-odour formation. Future research should explore potential strategies to remove saponins, lysophospholipids, and oxylipins, which will be key in obtaining desirable flavour and limited anti-nutritional properties of commercial plant protein ingredients.

CRediT authorship contribution statement

Pauline F.R. Damhof: Writing – original draft, Visualization, Methodology, Investigation, Conceptualization. **Jean-Paul Vincken:** Writing – review & editing, Supervision. **Wouter J.C. de Bruijn:** Writing – review & editing, Supervision, Methodology, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Pauline F.R. Damhof reports financial support was provided by Top Consortia for Knowledge and Innovation. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This work was supported by Topconsortium voor Kennis en Innovatie (TKI, grant number LWV19212), as part of the “Bio-purification of plant proteins”-project. This project receives financial support from the Top Sector Agri & Food. Research partners at NIZO food research B.V., HAS Hogeschool, and VU University Amsterdam. Business partners include Groupe Bel, DMK Group, Glanbia, IFF, General Mills, and Ruitenberg Ingredients. None of the business partners participated in the analysis and interpretation of results, and all of them agreed to submit the article for publication. Part of the presented results were obtained using a Vanquish UHPLC coupled to a Q Exactive Focus hybrid quadrupole-Orbitrap Fourier transform mass spectrometer and an autoflex maX MALDI-TOF mass spectrometer, which are owned by WUR-Shared Research Facilities. Investment by WUR-Shared Research Facility was made possible by the ‘Regio Deal Foodvalley’.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.foodchem.2025.144713.

Data availability

Data will be made available on request.

References

Ahlberg, S. H., Joutsjoki, V., & Korhonen, H. J. (2015). Potential of lactic acid bacteria in aflatoxin risk mitigation. *International Journal of Food Microbiology, 207*, 87–102. https://doi.org/10.1016/j.ijfoodmicro.2015.04.042

Aiking, H. (2011). Future protein supply. *Trends in Food Science & Technology, 22*(2–3), 112–120. https://doi.org/10.1016/j.tifs.2010.04.005

Aldin, E., Reitmeier, H. A., & Murphy, P. (2006). Bitterness of soy extracts containing isoflavones and saponins. *Journal of Food Science, 71*(3), S211–S215. https://doi.org/10.1111/j.1365-2621.2006.tb15643.x

Baiseitova, A., Ban, Y. J., Kim, J. Y., Lee, G., Shah, A. B., Kim, J. H., … Park, K. H. (2022). Soybean phytochemicals responsible for bacterial neuraminidase inhibition and their characterization by UPLC-ESI-TOF/MS. *Food & Function, 13*(13), 6923–6933. https://doi.org/10.1039/D2FO00537A

Boatright, W., & Hettiarachchy, N. (1995). Effect of lipids on soy protein isolate solubility. *Journal of the American Oil Chemists' Society, 72*, 1439–1444. https://doi.org/10.1007/BF02577835

Bolling, B. W. (2017). Almond polyphenols: Methods of analysis, contribution to food quality, and health promotion. *Comprehensive Reviews in Food Science and Food Safety, 16*(3), 346–368. https://doi.org/10.1111/1541-4337.12260

Cosson, A., Meudec, E., Ginies, C., Danel, A., Lieben, P., Descamps, N., Cheynier, V., Saint-Eve, A., & Souchon, I. (2022). Identification and quantification of key phytochemicals in peas–linking compounds with sensory attributes. *Food Chemistry, 385*, Article 132615. https://doi.org/10.1016/j.foodchem.2022.132615

Damodaran, S., & Arora, A. (2013). Off-flavor precursors in soy protein isolate and novel strategies for their removal. *Annual Review of Food Science and Technology, 4*, 327–346. https://doi.org/10.1146/annurev-food-030212-182650

Day, L. (2013). Proteins from land plants–potential resources for human nutrition and food security. *Trends in Food Science & Technology, 32*(1), 25–42. https://doi.org/10.1016/j.tifs.2013.05.005

Dijkstra, D. S., Linnemann, A. R., & van Boekel, T. A. (2003). Towards sustainable production of protein-rich foods: Appraisal of eight crops for Western Europe. PART II: Analysis of the technological aspects of the production chain. *Critical Reviews in Food Science and Nutrition, 43*(5), 481–506. https://doi.org/10.1080/10408690390246332

Edens, L., Souppe, J., Schipper, D., & Helena, M. (1997). *Process for the modification of toxic and/or off-flavour compounds G.-B. B.V*.

Ercan, P., & El, S. N. (2016). Inhibitory effects of chickpea and Tribulus terrestris on lipase, α-amylase and α-glucosidase. *Food Chemistry, 205*, 163–169. https://doi.org/10.1016/j.foodchem.2016.03.012

Fahim, J. R., Attia, E. Z., & Kamel, M. S. (2019). The phenolic profile of pea (*Pisum sativum*): A phytochemical and pharmacological overview. *Phytochemistry Reviews, 18*(1), 173–198. https://doi.org/10.1007/s11101-018-9586-9

Fang, N., Yu, S., & Badger, T. M. (2003). LC-MS/MS analysis of lysophospholipids associated with soy protein isolate. *Journal of Agricultural and Food Chemistry, 51*(23), 6676–6682. https://doi.org/10.1021/jf034793v

Friedman, M. (2006). Potato glycoalkaloids and metabolites: Roles in the plant and in the diet. *Journal of Agricultural and Food Chemistry, 54*(23), 8655–8681. https://doi.org/10.1021/jf061471t

Giuseppin, M. L. F., van der Sluis, C., & Laus, M. C. (2008). *Native potato protein isolates*. U.A: C. A.

Gunther-Jordanland, K., Dawid, C., Dietz, M., & Hofmann, T. (2016). Key phytochemicals contributing to the bitter off-taste of oat (*Avena sativa* L.). *Journal of Agricultural and Food Chemistry, 64*(51), 9639–9652. https://doi.org/10.1021/acs.jafc.6b04995

Gunther-Jordanland, K., Dawid, C., & Hofmann, T. (2020). Quantitation and taste contribution of sensory active molecules in oat (*Avena sativa* L.). *Journal of Agricultural and Food Chemistry, 68*(37), 10097–10108. https://doi.org/10.1021/acs.jafc.0c04022

Heng, L., Vincken, J.-P., Hoppe, K., Van Koningsveld, G., Decroos, K., Gruppen, H., Van Boekel, M., & Voragen, A. (2006). Stability of pea DDMP saponin and the mechanism of its decomposition. *Food Chemistry, 99*(2), 326–334. https://doi.org/10.1016/j.foodchem.2005.07.045

Heng, L., Vincken, J.-P., van Koningsveld, G., Legger, A., Gruppen, H., van Boekel, T., Roozen, J., & Voragen, F. (2006). Bitterness of saponins and their content in dry peas. *Journal of the Science of Food and Agriculture, 86*(8), 1225–1231. https://doi.org/10.1002/jsfa.2473

Hewage, A., Olatunde, O. O., Nimalaratne, C., Malalgoda, M., Aluko, R. E., & Bandara, N. (2022). Novel extraction technologies for developing plant protein ingredients with improved functionality. *Trends in Food Science & Technology, 129*, 492–511. https://doi.org/10.1016/j.tifs.2022.10.016

Jacobsen, C. (1999). Sensory impact of lipid oxidation in complex food systems. *Lipid/Fett, 101*(12), 484–492. https://doi.org/10.1002/(SICI)1521-4133(199912)101:12<484::AID-LIPI484>3.0.CO;2-H

Jenkins, K. J., & Atwal, A. (1994). Effects of dietary saponins on fecal bile acids and neutral sterols, and availability of vitamins a and E in the chick. *The Journal of Nutritional Biochemistry, 5*(3), 134–137. https://doi.org/10.1016/0955-2863(94)90084-1

Ji, C., Fan, Y., & Zhao, L. (2016). Review on biological degradation of mycotoxins. *Animal Nutrition, 2*(3), 127–133. https://doi.org/10.1016/j.aninu.2016.07.003

Keuleyan, E., Gélébart, P., Beaumal, V., Kermarrec, A., Ribourg-Birault, L., Le Gall, S., Meynier, A., Riaublanc, A., & Berton-Carabin, C. (2023). Pea and lupin protein ingredients: New insights into endogenous lipids and the key effect of high-pressure homogenization on their aqueous suspensions. *Food Hydrocolloids, 141*. https://doi.org/10.1016/j.foodhyd.2023.108671

van Koningsveld, G. A. (2001). *Physico-chemical and functional properties of potato proteins*. Wageningen University and Research.

Krishnamurthy, P., Lee, J. M., Tsukamoto, C., Takahashi, Y., Singh, R. J., Lee, J. D., & Chung, G. (2014). Evaluation of genetic structure of Korean wild soybean (*Glycine soja*) based on saponin allele polymorphism. *Genetic Resources and Crop Evolution, 61*, 1121–1130. https://doi.org/10.1007/s10722-014-0095-4

Król, A., Pomastowski, P., Rafińska, K., Railean-Plugaru, V., Walczak, J., & Buszewski, B. (2018). Microbiology neutralization of zearalenone using *Lactococcus lactis* and *Bifidobacterium* sp. *Analytical and Bioanalytical Chemistry, 410*(3), 943–952. https://doi.org/10.1007/s00216-017-0555-8

Lainer, J., Dawid, C., Dunkel, A., Gläser, P., Wittl, S., & Hofmann, T. (2019). Characterization of bitter-tasting oxylipins in poppy seeds (*Papaver somniferum* L.). *Journal of Agricultural and Food Chemistry, 68*(38), 10361–10373. https://doi.org/10.1021/acs.jafc.9b06655

Lee, S. S., Mohd Esa, N., & Loh, S. P. (2015). In vitro inhibitory activity of selected legumes against pancreatic lipase. *Journal of Food Biochemistry, 39*(4), 485–490. https://doi.org/10.1111/jfbc.12150

Manzanilla-Valdez, M. L., Ma, Z., Mondor, M., & Hernández-Álvarez, A. J. (2024). Decoding the duality of antinutrients: Assessing the impact of protein extraction methods on plant-based protein sources. *Journal of Agricultural and Food Chemistry, 72*(22), 12319–12339. https://doi.org/10.1021/acs.jafc.4c00380

Medek, D. E., Schwartz, J., & Myers, S. S. (2017). Estimated effects of future atmospheric CO_2 concentrations on protein intake and the risk of protein deficiency by country and region. *Environmental Health Perspectives, 125*(8), Article 087002. https://doi.org/10.1289/EHP41

Mehansho, H., Asquith, T. N., Butler, L. G., Rogler, J. C., & Carlson, D. M. (1992). Tannin-mediated induction of proline-rich protein synthesis. *Journal of Agricultural and Food Chemistry, 40*(1), 93–97.

Milbury, P. E., Chen, C.-Y., Dolnikowski, G. G., & Blumberg, J. B. (2006). Determination of flavonoids and phenolics and their distribution in almonds. *Journal of Agricultural and Food Chemistry, 54*(14), 5027–5033. https://doi.org/10.1021/jf0603937

Muñoz, M., Holtheuer, J., Wilson, L., & Urrutia, P. (2022). Grapefruit debittering by simultaneous naringin hydrolysis and limonin adsorption using naringinase immobilized in agarose supports. *Molecules, 27*(9), 2867. https://doi.org/10.3390/molecules27092867

Nugroho, A. D. W., van Schalkwijk, S., Cebeci, S., Jacobs, S., Wesselink, W., Staring, G., … Teuling, E. (2024). Biopurification using non-growing microorganisms to improve plant protein ingredients. *npj Science of Food, 8*(1), 48. https://doi.org/10.1038/s41538-024-00290-x

Okubo, K., Iijima, M., Kobayashi, Y., Yoshikoshi, M., Uchida, T., & Kudou, S. (1992). Components responsible for the undesirable taste of soybean seeds. *Bioscience, Biotechnology, and Biochemistry, 56*(1), 99–103. https://doi.org/10.1271/bbb.56.99

Pecio, Ł., Wawrzyniak-Szołkowska, A., Oleszek, W., & Stochmal, A. (2013). Rapid analysis of avenacosides in grain and husks of oats by UPLC–TQ–MS. *Food Chemistry, 141*(3), 2300–2304. https://doi.org/10.1016/j.foodchem.2013.04.094

Price, K., Griffiths, N., Curl, C., & Fenwick, G. (1985). Undesirable sensory properties of the dried pea (*Pisum sativum*). The role of saponins. *Food Chemistry, 17*(2), 105–115. https://doi.org/10.1016/0308-8146(85)90079-2

Puri, M., Marwaha, S., Kothari, R., & Kennedy, J. (1996). Biochemical basis of bitterness in citrus fruit juices and biotech approaches for debittering. *Critical Reviews in Biotechnology, 16*(2), 145–155. https://doi.org/10.3109/07388559609147419

Roland, W. S. U., Pouvreau, L., Curran, J., van de Velde, F., & de Kok, P. M. T. (2017). Flavor aspects of pulse ingredients. *Cereal Chemistry, 94*(1), 58–65. https://doi.org/10.1094/cchem-06-16-0161-fi

Samtiya, M., Aluko, R. E., & Dhewa, T. (2020). Plant food anti-nutritional factors and their reduction strategies: An overview. *Food Production, Processing and Nutrition, 2*, 1–14. https://doi.org/10.1186/s43014-020-0020-5

Sargautis, D., Kince, T., & Gramatina, I. (2023). Characterisation of the enzymatically extracted oat protein concentrate after defatting and its applicability for wet extrusion. *Foods, 12*(12), 2333. https://doi.org/10.3390/foods12122333

Schrenk, D., Bignami, M., Bodin, L., Chipman, J. K., del Mazo, J., Hogstrand, C., … Nebbia, C. S. (2020). Risk assessment of glycoalkaloids in feed and food, in particular in potatoes and potato-derived products. *EFSA Journal, 18*(8), Article e06222. https://doi.org/10.2903/j.efsa.2020.6222

Schymanski, E. L., Jeon, J., Gulde, R., Fenner, K., Ruff, M., Singer, H. P., & Hollender, J. (2014). Identifying small molecules via high resolution mass spectrometry: Communicating confidence. *Environmental Science & Technology, 48*(4), 2097–2098. https://doi.org/10.1021/es5002105

Shan, Z., Rehm, C. D., Rogers, G., Ruan, M., Wang, D. D., Hu, F. B., … Bhupathiraju, S. N. (2019). Trends in dietary carbohydrate, protein, and fat intake and diet quality among US adults, 1999-2016. *Jama, 322*(12), 1178–1187. https://doi.org/10.1001/jama.2019.13771

Shetty, P. H., & Jespersen, L. (2006). *Saccharomyces cerevisiae* and lactic acid bacteria as potential mycotoxin decontaminating agents. *Trends in Food Science & Technology, 17*(2), 48–55. https://doi.org/10.1016/j.tifs.2005.10.004

Shukla, P., Skea, J., Calvo Buendia, E., Masson-Delmotte, V., Pörtner, H., Roberts, D., Zhai, P., Slade, R., Connors, S., & Van Diemen, R. (2019). *IPCC, 2019: Climate change and land: An IPCC special report on climate change, desertification, land degradation, sustainable land management, food security, and greenhouse gas fluxes in terrestrial ecosystems*.

Soares, S., Brandao, E., Guerreiro, C., Soares, S., Mateus, N., & de Freitas, V. (2020). Tannins in food: Insights into the molecular perception of astringency and bitter taste. *Molecules, 25*(11). https://doi.org/10.3390/molecules25112590

Soares, S., Silva, M. S., Garcia-Estevez, I., Grobetamann, P., Bras, N., Brandao, E., … Meyerhof, W. (2018). Human bitter taste receptors are activated by different classes of polyphenols. *Journal of Agricultural and Food Chemistry, 66*(33), 8814–8823. https://doi.org/10.1021/acs.jafc.8b03569

Sud, M., Fahy, E., Cotter, D., Brown, A., Dennis, E. A., Glass, C. K., … Russell, D. W. (2007). Lmsd: Lipid maps structure database. *Nucleic Acids Research, 35*(suppl_1), D527–D532. https://doi.org/10.1093/nar/gkl838

Taylor, M. A., McDougall, G. J., & Stewart, D. (2007). Potato flavour and texture. *Potato biology and biotechnology, 525-540*. https://doi.org/10.1016/B978-044451018-1/50066-X

Trindler, C., Kopf-Bolanz, K. A., & Denkel, C. (2021). Aroma of peas, its constituents and reduction strategies–effects from breeding to processing. *Food Chemistry, 131892*. https://doi.org/10.1016/j.foodchem.2021.131892

Tsuno, Y., Fujimatsu, T., Endo, K., Sugiyama, A., & Yazaki, K. (2018). Soyasaponins: A new class of root exudates in soybean (*Glycine max*). *Plant and Cell Physiology, 59*(2), 366–375. https://doi.org/10.1093/pcp/pcx192

Xie, L., Roto, A. V., & Bolling, B. W. (2012). Characterization of ellagitannins, gallotannins, and bound proanthocyanidins from California almond (*Prunus dulcis*) varieties. *Journal of Agricultural and Food Chemistry, 60*(49), 12151–12156. https://doi.org/10.1021/jf303673r

Yoshiki, Y., Kudou, S., & Okubo, K. (1998). Relationship between chemical structures and biological activities of triterpenoid saponins from soybean. *Bioscience, Biotechnology, and Biochemistry, 62*(12), 2291–2299. https://doi.org/10.1271/bbb.62.2291

van Zadelhoff, A., Vincken, J.-P., & de Bruijn, W. J. (2022). Facile amidation of non-protected hydroxycinnamic acids for the synthesis of natural phenol amides. *Molecules, 27*(7), 2203. https://doi.org/10.3390/molecules27072203

Zhao, G., Zhu, L., Yin, P., Liu, J., Pan, Y., Wang, S., Yang, L., Ma, T., Liu, H., & Liu, X. (2022). Mechanism of interactions between soyasaponins and soybean 7S/11S proteins. *Food Chemistry, 368*, Article 130857. https://doi.org/10.1016/j.foodchem.2021.130857

Zhou, M., Liu, D., Tan, H., Wang, C., Yu, W., Xiong, G., Wang, L., Wu, W., & Qiao, Y. (2025). Flavor formation and phospholipids degradation of crayfish meat treated by boiling combined air-frying during accelerated storage. *Food Chemistry: X, 27*, Article 102406.

Zhu, L., Yin, P., Xie, T., Liu, X., Yang, L., Wang, S., Li, J., & Liu, H. (2020). Interaction between soyasaponin and soy β-conglycinin or glycinin: Air-water interfacial behavior and foaming property of their mixtures. *Colloids and Surfaces B: Biointerfaces, 186*, Article 110707. https://doi.org/10.1016/j.colsurfb.2019.110707