



# Sensory screening of pea (*Pisum sativum* L.) seeds and correlations to seed quality

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## ARTICLE INFO

### Keywords:

*Pisum sativum*

Taste

Sensorics

Pea flour

Diversity panel

Nutrients

Antinutritional factors

## ABSTRACT

Growing demand for environmentally sustainable protein sources is shifting dietary preferences toward plant-derived alternatives such as legumes. Pea (*Pisum sativum* L.) seeds offer great potential for expanded human consumption, but sensory quality is key for consumer acceptance and cultivar development. In this study, a diversity panel of 15 pea accessions was evaluated for nutrients and phytochemicals (protein, resistant and non-resistant starch, fatty acids, choline, phytate, saponins, and sucrose) and their sensory attributes (taste, aroma, mouthfeel, and aftertaste). Among the sensory attributes, mouthfeel and aroma contributed most to the variation. Principal component analysis revealed two large, distinct clusters, primarily separated by seed coat (testa) colour. Accessions with a dark-coloured testa were generally perceived more odour intense and with more texture, while accessions with light-coloured testa were sweeter and juicier. Accessions with wrinkled seeds stood out in their content of non-resistant starch, sucrose, total choline, and phytate, when compared to smooth and dimpled seeds. Shorter cooking times were positively correlated to the perception of higher bitterness. This study highlights the potential in combining seed compositional analysis and sensory evaluations for screening pea accessions suitable for the development of future food products.

## Introduction

A cultural shift toward more plant-dominated diets is ongoing in Western societies, largely driven by health benefits, concerns for animal welfare, and the detrimental impacts of meat production on climate and the environment (Aschemann-Witzel et al., 2021). Legumes, a rich source of 'green protein', have the potential to replace a substantial part of animal-derived protein in the human diet. Pea is a vital legume crop in this regard, with a global annual production of approximately 15 million tonnes dry (mature) peas and 20 million tonnes green (immature) peas (FAOSTAT 2022; [www.fao.org/faostat](http://www.fao.org/faostat)). Peas, like other legumes, are environmentally beneficial crops within cultivation systems due to their ability to fix atmospheric nitrogen, reducing the need for synthetic fertilisers compared to other crops. Furthermore, pea offers several health benefits including improved gastrointestinal function and reduced glycaemic index (Dahl et al., 2012). Dry peas can be consumed in their whole form after sufficient soaking and cooking, in the form of starch or protein isolates, for instance, in products like cheese (Masiá et al., 2022),

or ground into flour as a gluten-free alternative for making bread and cakes (Noguera et al., 2022; Wu et al., 2023).

Sensory evaluation of pulses (mature legume seeds) in different forms is crucial for driving consumer acceptance of new food products, a key aspect of the dietary shift toward a higher share of plant-based proteins. Improving seed quality to enhance sensory perception should be an important target for plant breeding of pulses. Shifting to more plant-based diets poses challenges when consumers face unfamiliar tastes, aromas, flavours, and trigeminal sensations, which may affect their acceptance of pulses and pulse-derived ingredients (Chigwedere et al., 2022; Wang et al., 2022). Nutrients and phytochemicals can influence sensory perception. Evaluating the sensory attributes of mature pea seeds in relation to their seed quality, which includes nutrients and phytochemicals, can therefore guide the selection of varieties that are perceived more favourably (Subasi et al., 2024). For example, off-taste has been associated with lipoxygenase (LOX)-catalysed degradation of unsaturated fatty acids (Roland et al., 2017; Zhang et al., 2020), while bitterness in pea has been associated with saponins, especially DDMP

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<https://doi.org/10.1016/j.fufo.2025.100691>

Received 28 January 2025; Received in revised form 18 June 2025; Accepted 20 June 2025

Available online 21 June 2025

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saponin (Cosson et al., 2022; Heng et al., 2006b).

Starch is the main component in pea and is important for textural properties, including functional properties when used in food applications (Guindon et al., 2021; Liu et al., 2015). While high protein content is a key factor for replacing animal-derived protein and is often sought after, it is important to recognise that some undesirable taste and flavour components may bind to the protein and become concentrated during protein fractionation (Gläser et al., 2020, 2021; Subasi et al., 2024). It also is important to identify varieties that have desirable levels of health-related compounds. Resistant starch, which resists hydrolysis and enzymatic degradation in the stomach, offers health benefits by acting as dietary fibres (Ratnayake et al., 2002). Choline is important as a methyl donor and is required through the diet (Obeid and Karlsson, 2023). Conversely, phytate is widespread in pulses, including peas, and can inhibit the absorption of divalent minerals due to its strong chelating abilities; it is therefore considered an antinutritional factor (Bangar et al., 2017). Based on a diversity panel of 15 pea accessions, the primary objectives of this study were (1) to quantify the levels of various seed storage compounds of the accessions in the panel, (2) to evaluate the sensory attributes of cooked peas, and (3) to identify potential correlations between these factors to be used as a tool for the development of pea cultivars for human consumption.

Materials and methods

Plant material

A diversity panel of 15 pea (*Pisum sativum* L.) accessions (Table 1) was selected to capture the large variation within a germplasm collection of 300 accessions, which is part of a large pre-breeding initiative. Except for three accessions (BR\_SweGBA1, BR\_SweGBA2, and LR\_SweGRP2), all seeds were multiplied in field 2022 in Lönnstorp (Sweden; 55.6669°N, 13.1085°E) with plots measuring 1 × 1 m as described in Dueholm et al. (2024). These three accessions were derived from a mixture of batches from seeds multiplied at both Lönnstorp and

Table 1

Seed characteristics and cooking properties of 15 pea accessions. The accession IDs are defined according to plant material type: CV – cultivar, BR – breeding material, LR – landrace; geographical origin: Fin – Finland, Ukr – Ukraine, Swe – Sweden, Gre – Greece, Fra – France, Ind – India, Arg – Argentina; and pea type: GBA – Genebank accession (unknown type), DYP – dry yellow pea, SNP – snow pea, GRP – grey pea, FOP – fodder pea, SSP – sugar snap pea, and MFP – marrowfat pea. The table includes data on thousand-seed weight (TSW), seed profile area, seed morphology, testa colour, and cooking time. Wrinkled seeds have deep curvatures in their seed coat and very low levels of amylopectin, while dimpled seeds have small depressions in their seed coat and smooth seeds have no seed-coat depressions. Testa colours are defined according to Pavelková et al. (1986) with light brown, brown, and black testa defined as dark, and other colours defined as light. Seed IDs and cooking times are based on Dueholm et al. (2024).

ID	TSW (g)	Profile area (mm <sup>2</sup> )	Seed morphology	Testa colour	Cooking time
CV_FinGBA	267.34	56.9	Smooth	Light	12
CV_UkrGBA	204.77	42.8	Smooth	Light	25
BR_SweGBA1	200.19	43.4	Dimpled	Dark	25
CV_SweDYP3	111.91	29.3	Smooth	Light	30
CV_GreGBA	193.82	37.1	Smooth	Dark	30
CV_SweDYP2	202.42	45.3	Smooth	Light	30
CV_FraSNP	262.24	46.0	Dimpled	Dark	30
LR_SweGRP2	204.81	37.1	Smooth	Dark	30
CV_SweDYP1	167.87	31.6	Smooth	Light	40
CV_SweFOP	207.82	38.6	Smooth	Dark	40
CV_IndSSP	212.26	38.5	Dimpled	Dark	45
CV_ArgGRP	224.19	39.5	Smooth	Dark	45
LR_SweMFP	265.08	50.7	Wrinkled	Light	50
LR_SweGRP1	183.67	35.2	Dimpled	Dark	50
BR_SweGBA2	176.77	41.4	Wrinkled	Light	70

Lanna (Sweden; 58.3467°N, 13.1255°E) during 2022. The field trials in Lanna followed the same protocol as those in Lönnstorp, except that the plots in Lanna measured 0.5 × 2 m.

The mean profile seed area of each accession was determined by loading approximately 200 seeds per accession using a Marvin ProLine I seed analyser (MARViTECH, Wittenburg, Germany). Thousand-seed weight (TSW), a common agronomic measurement for comparing seed batches, was determined using seeds from the same sample. Seeds within each accession were ground into a fine, homogeneous flour using a centrifugal ZM 200 mill (Retsch GmbH, Haan, Germany) at 10,000 rpm and passed through a 0.5 mm sieve. The moisture content of the flour was then determined. Prior to the analysis of storage compounds, the flour was lyophilised and kept at −18 °C, while whole seeds for sensory evaluation were stored at 15 °C at approximately 35 % humidity.

Nutrient analysis

Resistant and non-resistant starch content

Starch (resistant and non-resistant) was determined as described in Hefni et al. (2021b). In brief, duplicate flour samples (100 mg) were incubated overnight in 4 mL sodium malate buffer (100 mmol L<sup>−1</sup>, pH 6.0) containing pancreatic α-amylase and amyloglucosidase, and then analysed according to the official method AACC 32-40.01/AOAC 2002.02 using the K-RSTAR kit (Megazyme, Bray, Ireland).

Simple-sugar content

Sucrose, D-glucose, and D-fructose were extracted from duplicate samples of 5 mg flour in 100 µL 96 % EtOH. The mixtures were heated at 80 °C for 10 min. Following heating, 100 µL Milli-Q water was added to each sample. The mixtures were then sonicated for 10 min and centrifuged at 4500 g for 10 min. Supernatants (50 µL) were analysed using the K-SUFRG kit (Megazyme, Bray, Ireland) in cuvettes with a Multiskan GO spectrophotometer (Thermo Scientific, Waltham, USA) at a wavelength of 340 nm.

Protein content

Protein was determined by the Dumas method via total nitrogen (N) analysis. Duplicate samples of 5 mg lyophilised flour were weighed into tin capsules using a XP6 microbalance (Mettler Toledo, Columbus, USA). The samples were analysed using a Flash 2000 Elemental Analyzer combustion system (Thermo Scientific, Waltham, USA). The protein content was calculated using the average nitrogen-to-protein conversion factor of N × 6.25.

Fatty acid content

Total fatty acid content was determined in duplicate lyophilised flour samples using acidic methylation followed by gas chromatography (GC) of fatty acid methyl esters (FAMES). For this analysis, 100 mg flour was scaled up into each glass tube, 2 mL of 2 % (v/v) H<sub>2</sub>SO<sub>4</sub> in dry MeOH was added, and the tubes were sealed with screw caps. The glass tubes were then incubated at 90 °C for 60 min on a heating block. After cooling, 300 nmol of internal standard heptadecanoic acid methyl ester (Larodan, Solna, Sweden) was added to each tube. FAMES were extracted by adding 1.5 mL heptane and 2 mL Milli-Q water, followed by vortexing thoroughly and centrifuging for 2 min at 1400 g. Aliquots (300 µL) of the heptane phase were transferred to GC vials, which were stored at −20 °C until further analysis. FAMES were finally separated on a CP-wax 58 column (FFAP-CB, 50 m, 0.32 mm inner diameter, 0.20 µm film) (Varian, Palo Alto, USA) using an 8860 gas chromatograph (Agilent Technologies, Santa Clara, USA) with hydrogen (>99.999 % purity) as the mobile phase and with the following temperatures: Injector at 250 °C,

oven from 150 °C to 210 °C (at a rate of 4 °C/min) then increasing up to 250 °C (at a rate of 10 °C/min), and flame ionization detector at 260 °C. The quantification of FAMES (in nmol) was performed relative to the internal standard, and the fatty acid content was calculated as the percentage of the dry weight (DW) based on the molecular weight of each fatty acid.

#### Choline content

Choline, including both free and total, was quantified from duplicate flour samples (250 mg, homogenized in 10 mL of 1 mol L<sup>-1</sup> HCl) using a HILIC column on a 1200 HPLC system (Agilent Technologies, Santa Clara, USA) coupled with a single quadrupole mass spectrometer (Agilent 6130) equipped with an APCI-ES source, as described in [Hefni et al. \(2021a\)](#).

#### Antinutrient analysis

##### Saponin content

For determining the saponin content, soyasaponin Bb (SSB, also referred to as saponin B or soyasaponin I; Merck, Darmstadt, Germany) was used as a reference compound while ginsenoside Rb1 (AdooQ Bioscience, Los Angeles, USA) served as an internal standard (IS). Stock solutions were prepared to 220 mg L<sup>-1</sup> MeOH for both these compounds. Saponins were extracted from 20 mg of triplicate lyophilised flour samples using 400 µL aqueous MeOH (80 %) containing 2.2 mg L<sup>-1</sup> IS, first by vortexing for 15 s and then by constant shaking at 1500 rpm on a VXR shaker (IKA-Werke, Staufen, Germany) fitted with a VX 2E.n rack for 3 h at room temperature. The samples were centrifuged at 20,000 g for 5 min and supernatants (200 µL) were carefully aliquoted into vials. Samples (5 µL) were injected into a 1260 Infinity HPLC system (Agilent Technologies, Santa Clara, USA) fitted with a reverse-phase Triart C18 ExRS column (3 µm, 150 × 3.0 mm, 8 nm) (YMC, Kyoto, Japan). The column temperature was 35 °C, which is below the temperature at which elevated degradation of DDMP saponin to SSB has been observed ([Heng et al., 2006a](#)). A gradient method was used with acidified water (0.1 % formic acid) as solution A and acetonitrile:MeOH (3:1) as solution B. With a flow rate of 0.600 mL min<sup>-1</sup>, the method was as follows: a linear increase at 20–80 % B (v/v) at 0–10 min, 80–90 % B at 10–13 min, 90–20 % B at 13–14 min and constant at 20 % B from 14–15 min. The IS eluted at 6.57 min, SSB at 8.73 min, and DDMP saponin at 9.67 min. The HPLC was coupled to a 6120 quadrupole mass spectrometer (Agilent Technologies, Santa Clara, USA) in SIM mode targeting only IS, SSB, and DDMP saponin. Negative ion mode (API-ES) was used for ionisation, the mass range was set at 900–1200 m/z, the capillary voltage set to 4000 V, dry gas (nitrogen) flow set to 12 L min<sup>-1</sup>, dry temperature set to 300 °C, and nebulizing gas set to 50 p.s.i. The ion counts of SSB in all samples were normalised to the mean IS ion count in blank samples ( $n = 3$ ) as well as the weight of added DW flour. A standard curve of ten concentrations was run for SSB (2.2–44.0 ng µL<sup>-1</sup>). Since DDMP saponin (soyasaponin βg,  $m/z$  1067.5432 [ $M - H$ ]) is commercially unavailable, SSB ( $m/z$  941.5115 [ $M - H$ ]) was used for quantifying the content of both saponin types.

##### Phytate content

Phytate content was determined on duplicate flour samples (250 mg, hydrolysed in 5 mL of 0.66 mol L<sup>-1</sup> hydrochloric acid) using the K-PHYT kit (Megazyme, Bray, Ireland).

#### Sensory screening

Mature seeds of all the accessions were soaked for 20 h in water (1:2 w:v) and then cooked in 1.5 L of unsalted water. Cooking times reflected those of [Dueholm et al. \(2024\)](#), ranging from 12 min for the

fastest-cooked accession (CV\_FinGBA) to 70 min for the slowest-cooked accession (BR\_SweGBA2) ([Table 1](#)). All seeds had a spherical shape after soaking and cooking. Fifteen assessors, part of a professional sensory panel (Ipsos Sensory and Product Testing, Stockholm, Sweden), screened the 15 pea accessions on 18 attributes ([Table A1](#)) on taste (sweet, bitter, starchy, intensity, off), mouthfeel (floury, dry, juicy, chewy, rubbery, thick-shelled), aroma (earthy, grassy, yeasty, sweet, intensity), and aftertaste (off, bitter) using a RATA (rate-all-that-apply) scale (0–10, [Table A2](#)) based on the study of [Nleya et al. \(2014\)](#) originally developed for assessing the sensory quality of green peas. Assessors in the panel were selected according to the selection process of the ISO standard for sensory analysis (ISO 5492 and ISO 11132:2021) and were trained in assessing foods. The panel had expertise in assessing plant-based products but had not been trained specifically for this study. The screening was conducted within a single 2-h session. Each assessor was served approximately 30 g of cooked pea with the accessions presented using randomised three-digit codes ([Figure A1](#)). The assessors were instructed to neutralise their palates with water and neutral biscuits between samples.

#### Statistical analysis

A previous study by [Dueholm et al. \(2024\)](#), which included the 15 accessions analysed in the present study, found that wrinkled seeds were highly different on multiple parameters, including starch content and quality, water absorption capacity, cooking quality, and seed-coat hardness, when compared to non-wrinkled seeds. To assess significant differences between wrinkled and non-wrinkled seeds in the present study, two-sample *t*-tests ( $\alpha \leq 0.05$ ) were used.

To visualise patterns (e.g. clusters) and variation in the sensory data, a principal component analysis (PCA) was performed on the 18 sensory scores across all 15 pea accessions. A biplot was used to visualise the relationship between sensory attributes and accessions. For correlating the chemical properties and sensory scores, canonical correlation analysis (CCA) was employed, which is a multivariate approach to explore correlations between two datasets acquired on the same experimental units ([González et al., 2008](#)). Canonical correlation is achieved by maximising the correlation between linear combinations of the variables (chemical components) in the first dataset and the variables (sensory scores) in the second dataset, giving rise to canonical variates that represent a new space of shared correlation ([González et al., 2009](#)). The canonical variate pair with the greatest correlation is the first component, while next canonical variate (uncorrelated to the first variate pair) is the second component. As the number of variables in the two datasets exceeded the number of accessions ([Table A1](#)), there was a risk of generating singular covariance matrices in the inversion procedure. Therefore, a regularised version of CCA (rCCA) was used to mitigate this issue, and for the regularisation, leave-one-out cross-validation (CV) was performed to make the two datasets invertible ([Lê Cao et al., 2009](#)). The tuning parameters used, after multiple refinements, were  $\lambda_1 = 0.00201$  and  $\lambda_2 = 0.03862$ , which gave a CV-score of 0.98 ([Figure A2](#)). A variable plot was used to visualise the first two canonical variate pairs (components 1 and 2). Statistical analyses were carried out using the factoextra package ([Kassambara and Mundt, 2020](#)) and the mixOmics package ([Rohart et al., 2017](#)) in R v4.3.0 ([R Core Team, 2023](#)). The data for the PCA and rCCA were centred and scaled prior to analysis.

## Results and discussion

The goal of the present study was to explore the nutritional quality and sensory diversity present in pea by screening a diversity panel including wrinkled, dimpled, and smooth accessions ([Table 1](#)). In addition, the panel included different types of peas: grey peas (GRP), snow (SNP) and sugar snap peas (SSP), dry yellow peas (DYP), marrowfat peas (MFP), and fodder peas (FOP). Accessions without known type were labelled as GBA (genebank accession). The accessions

were previously shown to be genetically diverse, based on a neighbour-joining (NJ) tree constructed using genome-wide SNP markers (Brhane and Hammenhag, 2024) and are distributed across several genetic clusters. In Sweden, approximately 95 % of the produced peas are used for fodder (Statistics Sweden, 2022; Subasi et al., 2024). As consumer interest in plant-based foods grows and the demand for sustainable protein sources increases, peas are well-positioned to become a key ingredient in diverse food products. Their versatility, combined with potential advances in breeding for improved taste and quality, offers opportunities to elevate peas from primarily fodder use to a staple in plant-based nutrition. Expanding their use in food production could also contribute to more sustainable agriculture and a greater diversity of protein sources in diets worldwide.

### Seed storage compounds

The first objective of this study was to determine the levels of seed storage compounds in the diversity panel. Seed storage compounds were quantified using untreated wholegrain flour with levels comparable to those reported in previous studies (Table 2, Fig. 1A). Protein content ranged from 20.37 to 25.98 g 100 g<sup>-1</sup> DW while total starch (resistant and non-resistant combined) ranged from 32.06 to 53.30 g 100 g<sup>-1</sup> DW (Table A1). Starch and protein levels were negatively correlated ( $r = -0.55$ ;  $P = 0.035$ ), supporting earlier studies (Dueholm et al., 2024; Tao et al., 2017). Protein has been reported higher in wrinkled peas than in smooth peas (Coyne et al., 2005). Although protein was high in the two wrinkled accessions (LR\_SweMFP and BR\_SweGBA2), it was rivalled by several of the non-wrinkled accessions and not significantly higher ( $P = 0.086$ ; two-sample  $t$ -test). The wrinkled phenotype is caused by a mutation in starch-branching enzyme I (SBEI; located at the *r* (*rugosus*) locus in the pea genome). This mutation leads to a stark reduction in amylopectin biosynthesis which lowers total starch content and alters starch granule morphology (Yu et al. 2022). The two accessions identified as wrinkled (LR\_SweMFP and BR\_SweGBA2) also displayed the expected biochemical characteristics associated with the *r* locus mutation, namely lower total starch content and a higher amylose:amylopectin ratio (Dueholm et al., 2024), further supporting the likelihood that they carry the SBEI mutation. Consequently, these two accessions with wrinkled seeds therefore had a lower level of non-resistant starch ( $P = 0.0004$ ; two-sample  $t$ -test). Resistant starch content ranged from 1.91 to 8.56 g 100 g<sup>-1</sup> DW, close to what has been reported in other studies (Wu et al. 2022) with no difference observed between wrinkled and non-wrinkled seeds ( $P = 0.58$ ; two-sample  $t$ -test). The levels of D-glucose and D-fructose were below the sensitivity level of the kit with the majority of the measured simple sugars in the form of sucrose. Sucrose content ranged from 1.44 to 4.85 g 100 g<sup>-1</sup> DW with the highest content

in the two accessions with wrinkled seeds ( $P < 0.0001$ ; two-sample  $t$ -test).

Total choline ranged from 0.12 to 0.18 g 100 g<sup>-1</sup> DW. Total choline levels were higher in the wrinkled accessions ( $P = 0.0002$ ; two-sample  $t$ -test), while free choline content aligned more with accessions featuring dark-coloured testa. Choline is a desirable component in pulses, as it serves as a methyl donor in many enzymatic reactions of functioning cells and is primarily acquired through dietary intake (Obeid and Karlsson, 2023).

The average content of total saponin (SSB and DDMP saponin combined) across all 15 pea accessions was 2.86 ( $\pm 0.41$ ) mg g<sup>-1</sup> DW, of which 0.80 ( $\pm 0.22$ ) mg g<sup>-1</sup> DW was SSB and 2.06 ( $\pm 0.27$ ) mg g<sup>-1</sup> DW was DDMP saponin. Total saponin content varied from 2.23 to 3.57 mg g<sup>-1</sup> DW. These levels were similar to those reported in previous studies, for instance, 1.9 mg g<sup>-1</sup> DW (Heng et al., 2006b), 2.32 mg g<sup>-1</sup> DW (Sagrati et al., 2013), and 2.99 mg g<sup>-1</sup> DW (Hodgins et al., 2024). Daveby et al. (1997) reported up to 2.5 mg g<sup>-1</sup> DW in mature seeds, but a concentration of SSB around 4 mg g<sup>-1</sup> DW in immature peas.

The phytate level was also determined, ranging from 0.78 to 1.24 g 100 g<sup>-1</sup> DW. Phytate, being relatively heat-stable can inhibit mineral uptake in the gastrointestinal tract (Shi et al., 2018); hence, having varieties naturally lower in phytate could increase the bioavailability of essential minerals. Dry yellow pea (DYP) accessions showed levels of phytate around 1 g 100 g<sup>-1</sup> DW, whereas many of the accessions with dark-coloured testa showed slightly lower phytate levels, around 0.8–0.9 g 100 g<sup>-1</sup> DW. Phytate in wrinkled seeds was slightly higher ( $P = 0.024$ ; two-sample  $t$ -test) than in non-wrinkled seeds.

As for sucrose, total choline, and phytate, levels of fatty acids were also higher in wrinkled seeds ( $P < 0.0001$ ; two-sample  $t$ -test) compared to non-wrinkled seeds. Total fatty acid content across the accessions ranged from 1.35 to 2.57 g 100 g<sup>-1</sup> DW. Levels of all of the main types of fatty acids, palmitic acid (16:0), oleic acid (18:1(9)), linoleic acid (18:2), and linolenic acid (18:3), were higher in the wrinkled seeds ( $P = 0.0001$ ,  $P < 0.0001$ ,  $P < 0.0001$ , and  $P = 0.02$ , respectively; two-sample  $t$ -test) compared to the smooth and dimpled seeds (Fig. 1B). However, the relative proportions of these fatty acids remained consistent across accessions (Figure A3). It can be noted that the fatty acid content measured in this study was determined through methylation of whole flour. Consequently, the specific contributions of storage lipids (triacylglycerols) or membrane lipids to the total fatty acid content remain unknown. To elucidate potential cultivar differences in triacylglycerol content further detailed lipid analyses of the flour is needed.

### Sensory screening

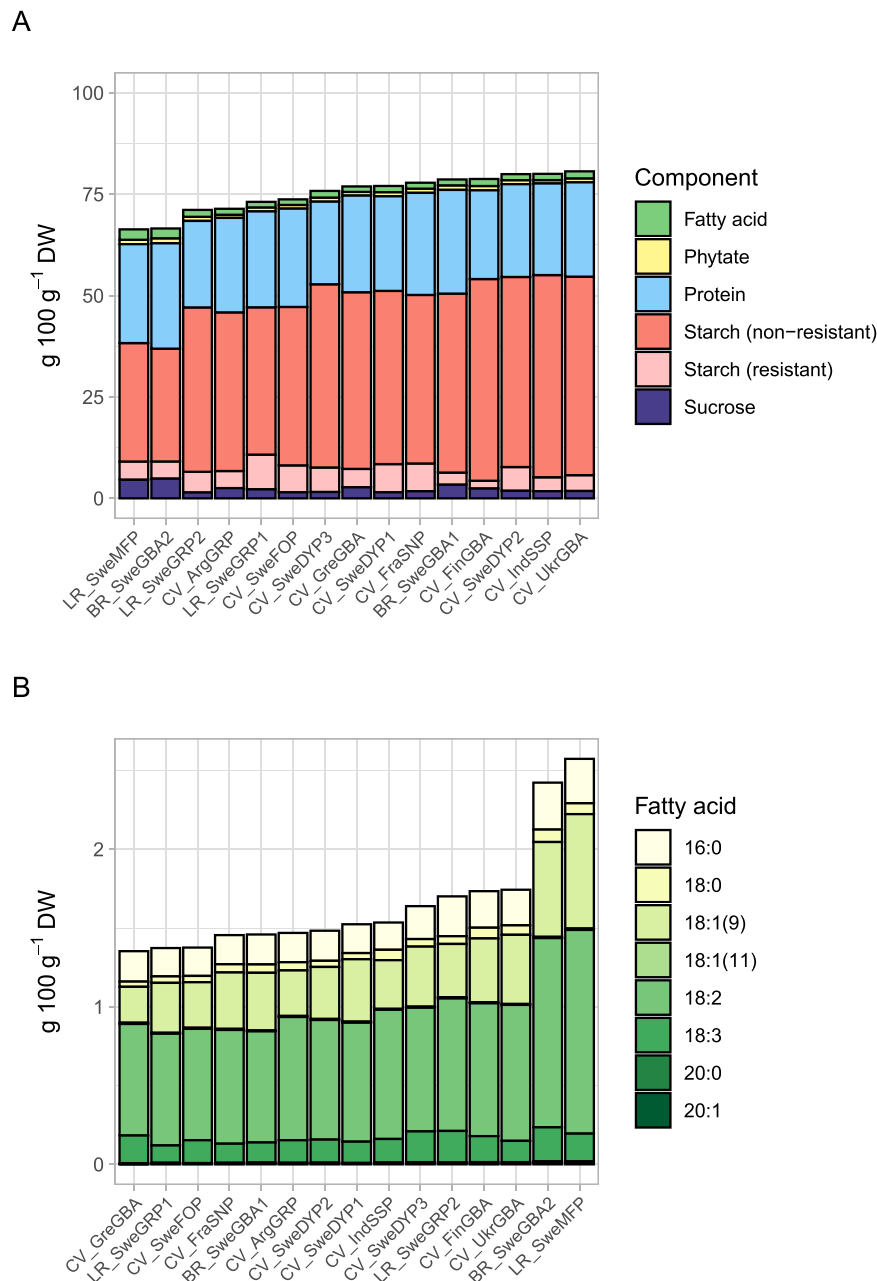
The last two objectives of this study were to evaluate the sensory attributes of cooked peas and to identify potential correlations between seed storage compounds and sensory perception. A principal component analysis (PCA) was conducted to explore the variation in the sensory evaluation of the 15 pea accessions. The variables that contributed most to the first principal component (PC1) were related to mouthfeel and aroma, while the variables that contributed most to PC2 had to do with taste and aftertaste. Overall, PC1 and PC2 accounted for 57.2 % of the variation in the data. Two larger clusters appeared within the PCA biplot from the sensory evaluation, positioned on either side of the y-axis, with accessions having light-coloured testa on the right side being perceived as juicier and sweeter, and accessions having dark-coloured testa on the left side being perceived as more odour intense and chewy (Fig. 2). In general, accessions with dark-coloured testa—light brown, brown, or black—were associated with yeasty and earthy odours, chewiness, rubbery, shell thickness, and dry mouthfeel (Fig. 2) and also had a higher percentage of DDMP saponin (DDMP\_percentage) relative to total saponin content (Fig. 3). Proanthocyanidins and the oxidation of these compounds are associated with brownish testa colouration, while anthocyanins are associated with dark-brown and black colouration (Hradilová et al., 2017). Proanthocyanidins are the chemical basis for

**Table 2**  
Mean values and ranges for seed storage compounds in 15 pea accessions.

	Mean (g 100 g <sup>-1</sup> DW)	Range (g 100 g <sup>-1</sup> DW)	Lowest level	Highest level
Protein	23.45	20.37 - 25.98	CV_SweDYP3	BR_SweGBA2
Starch (total)	46.70	32.06 - 53.30	BR_SweGBA2	CV_IndSSP
Non-resistant	41.65	27.82 - 49.86	BR_SweGBA2	CV_IndSSP
Resistant	5.05	1.91 - 8.56	CV_FinGBA	LR_SweGRP1
Sucrose	2.39	1.44 - 4.85	LR_SweGRP2	BR_SweGBA2
Saponin (total)	0.29	0.22 - 0.36	LR_SweGRP2	CV_SweDYP3
SSB <sup>†</sup>	0.08	0.05 - 0.12	LR_SweMFP	LR_SweGRP2
DDMP saponin	0.21	0.16 - 0.25	CV_FinGBA	CV_SweFOP
Choline (total)	0.15	0.12 - 0.18	CV_SweDYP1	BR_SweGBA2
Phytate	1.00	0.78 - 1.24	CV_ArgGRP	BR_SweGBA2
Fatty acids	1.66	1.35 - 2.57	CV_GreGBA	LR_SweMFP

<sup>†</sup> (soya)saponin B.



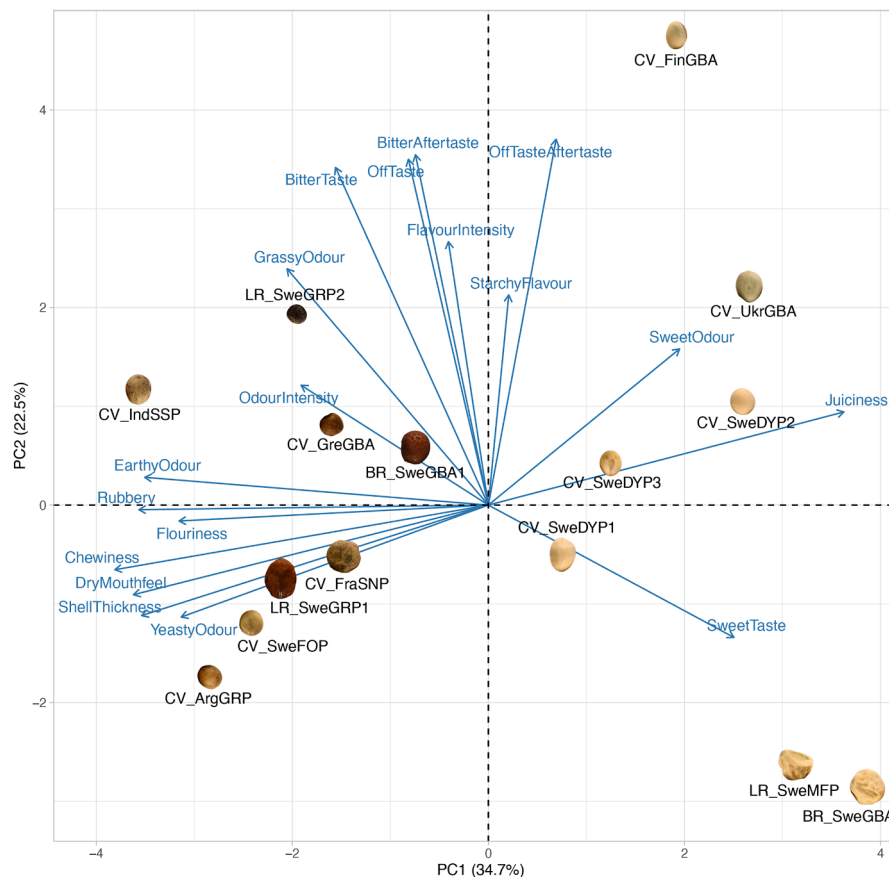


**Fig. 1.** Seed storage compounds in the 15 pea accessions with (A) contents of fatty acids, phytate, protein, starch (non-resistant and resistant), and sucrose, and (B) levels of individual fatty acids. The accession IDs are defined by plant material type: CV – cultivar, BR – breeding material, LR – landrace; geographical origin: Fin – Finland, Ukr – Ukraine, Swe – Sweden, Gre – Greece, Fra – France, Ind – India, Arg – Argentina; and pea type: GBA – genebank accession (unknown type), DYP – dry yellow pea, SNP – snow pea, GRP – grey pea, FOP – fodder pea, SSP – sugar snap pea, and MFP – marrow-fat pea.

tannins, which are linked to the perception of astringency (Troszyńska et al., 2006). Yeasty and earthy odours stem from simple, volatile compounds (Zhang et al., 2020), while many of the mouthfeel attributes are likely linked to structural seed coat traits, such as polymer composition and thickness. Dark-coloured pea seeds typically have a thicker and tougher seed coat than light-coloured ones (Dueholm et al., 2024; Smýkal et al., 2014; Zablatzká et al., 2021).

It is important to point out that while the screening was conducted by a professional sensory panel, the assessors had not been trained for this particular screening. Resistant starch showed no clear alignment with any of the sensory attributes, while the perception of starchy flavour aligned with total starch and non-resistant starch, giving merits to the sensory screening (Fig. 3). While storage compounds were determined from untreated flour, the sensory screening was conducted on cooked

whole seeds. The seeds of each accession were cooked for a duration of time that ensured they would be sufficiently soft for consumption, which meant that some seeds were cooked for approximately half an hour while others were cooked for approximately three quarters of an hour (Table 1). This variation in cooking times could have influenced the sensory evaluation as those accessions that were cooked for longer would have experienced a greater structural degradation of some or several storage compounds. For instance, DDMP saponin starts to break down at 40 °C (Heng et al., 2006a) and although DDMP saponin has been associated with the perception of bitter taste (Heng et al., 2006b; Price et al., 1985), there were no strong indications that the pre-cooking DDMP saponin levels had an impact on bitter taste; however, accessions with higher levels of DDMP saponin were also cooked for longer as seen in the close association of DDMP\_saponin and CookingTime in Fig. 3.



**Fig. 2.** PCA biplot based on the sensory evaluations. The IDs used correspond to those in Dueholm et al. (2024) with accession IDs defined according to plant material type: CV – cultivar, BR – breeding material, LR – landrace; geographical origin: Fin – Finland, Ukr – Ukraine, Swe – Sweden, Gre – Greece, Fra – France, Ind – India, Arg – Argentina; and pea type: GBA – genebank accession (unknown type), DYP – dry yellow pea, SNP – snow pea, GRP – grey pea, FOP – fodder pea, SSP – sugar snap pea, and MFP – marrow-fat pea.

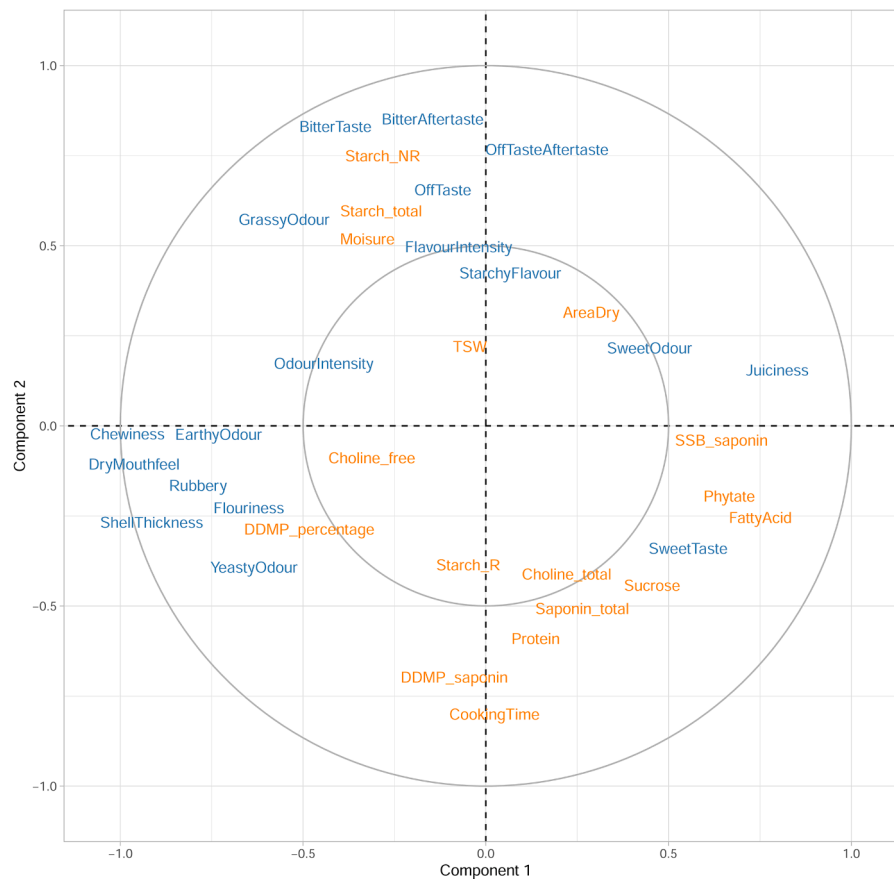
While saponins are recognised contributors to bitterness, this perception depends on their concentration relative to the bitterness recognition threshold (Dawid and Hofmann, 2012). The accession with the shortest cooking time, CV\_FinGBA (12 min) may have had a higher level of remaining DDMP saponin after its starting concentration of  $1.6 \text{ mg g}^{-1}$  DW, resulting in this accession being perceived as more bitter than other accessions (Fig. 2). Naturally, other factors not analysed in the present study (e.g. phenolic compounds) could also have contributed to the perceived bitterness. Interestingly, cut grass odorant (*cis*-3-hexen-1-ol) significantly increases the perception of bitterness in olive oil (Caporale et al., 2004). Grassy odour (GrassyOdour) also aligned closely with bitterness (BitterTaste and BitterAftertaste) in the present study. Taken together, it would have been interesting to assess how CV\_FinGBA would have been evaluated in terms of bitterness had this accession been cooked for twice as long ( $\sim 25$  min) as well as assess the level of *cis*-3-hexen-1-ol present in all 15 pea accessions and whether this variable would align with the grassy odour and bitter taste. Beyond taste, saponins may also influence texture due to their emulsifying and foaming properties (Timilsena et al., 2023) and a higher percentage of DDMP saponin (DDMP\_percentage) correlated with textural attributes such as dry mouthfeel and flouriness. However, the total level of saponin (Saponin\_total) and DDMP saponin were not correlated to textural attributes, while SSB (SSB\_saponin) was negatively correlated with textural attributes (Fig. 3).

The perception of sweet taste followed the content of sucrose (Fig. 3), in agreement with the two accessions with wrinkled seeds (LR\_SweMFP and BR\_SweGBA2) having significantly higher levels of sucrose than the accessions with non-wrinkled seeds. The long cooking times of these two accessions (50 and 70 min, respectively), likely had little impact on the

final levels of sucrose. Marrow-fat peas have been rated sweet in other studies (Malcolmson et al., 2014), but factors besides sucrose may also contribute to the perceived sweetness, such as volatile alcohols and aldehydes (Azarnia et al., 2011) or ascorbic acid (Berger et al., 2007); however, the levels of these compounds were not determined in the present study. Fatty acids also aligned with sweet taste (Fig. 3), perhaps reflecting that levels of fatty acids—like sucrose—were higher in wrinkled peas. It is possible though that the observed relationship between fatty acids and perceived sweetness is partly mediated by textural effects. During mastication, fatty acids such as palmitic, oleic, and linoleic acids can be released at concentrations sufficient to influence gustatory signalling, potentially affecting sugar perception (Kulkarni and Mattes, 2013; Martin et al., 2012). Thus, fatty acids may also contribute to the sweetness experience. On the other hand, fatty acids may also contribute to off-taste via the oxidation of unsaturated fatty acids by lipoxygenase (LOX) enzymes. The oxidative products (hydroperoxides) generated depend on the type of LOX enzymes present (Roland et al., 2017; Wang et al., 2022; Zhang et al., 2020). Oleic, linoleic, and linolenic acids have a high affiliation with lipid-oxidation-driven off-flavour formation (Subasi et al., 2024) and these fatty acids were higher in the accessions with wrinkled seeds. Although the types of LOX enzymes and their activities were not investigated in the present study, the higher levels of the aforementioned fatty acids may render these accessions more prone to developing off-taste, either due to oxidation via LOX enzymes or by alternative pathways such as auto-oxidation (Trindler et al., 2022).

### Selection of accessions for future food product development

Breeding of legumes for human consumption has created profound



**Fig. 3.** Variable plot from the rCCA analysis integrating seed-quality properties (in blue) and sensory evaluation scores (in orange). Variables farther from the origin contribute more strongly to the corresponding canonical variate, with variables close together are positively correlated, variables on opposite sides are negatively correlated, and variables at a right angle are uncorrelated. Starch\_NR, non-resistant starch; Starch\_R, resistant starch; DDMP\_percentage, percentage of DDMP saponin relative to total saponin content; AreaDry, mean profile area of dry seeds measured by the Marvin ProLine I seed analyser; TSW, thousand-seed weight.

changes in odour, taste, texture, and visual appearance, with testa pigmentation being one of the most notable changes observed across numerous parallel legume domestications (Smýkal and Parker, 2023). Fig. 2 clearly highlights this diversity in testa colouration, with clear indications that accessions with dark-coloured testa were more odour-intense and chewier while accessions with light-coloured testa were sweeter and juicier. The testa itself likely plays an important role in odour and texture attributes, as many flavour- and texture-related properties are linked to the seed coat (Klčová et al., 2024; Ku et al., 2020).

Commercial soybean is sometimes praised for its mild or neutral taste and flavour profile (Guo et al., 2022), whereas other legumes such as peas can offer a greater sensory palette, contributing to a wide range of flavour options (Westling et al., 2024). Ultimately, the goal is to identify and develop legume cultivars that can provide appealing food products that meet consumer preferences. Breeders and consumers are looking for cultivars that not only maintain sensory attributes but also align with specific culinary applications and nutritional needs. Screening a diverse selection of pea accessions can aid in the identification of useful varieties and potential breeding material that meets these criteria (Arteaga et al., 2021; Vidal-Valverde et al., 2003).

Whole pea seeds will likely constitute a considerable part of human diets (Wu et al., 2023) and fast cooking times are usually considered a positive attribute (Wood, 2017). However, despite CV\_FinGBA reaching tenderness faster than any other accession, its sensory scoring revealed less favourable results. A point of consideration in breeding for short cooking times (< 20 min) is that shorter cooking times may leave higher levels of unwarranted attributes in the cooked seeds, that could result in

perceived off-taste and bitterness. Breeding for cultivars that are low on antinutritional factors and off-flavour compounds should therefore have equal merits when breeding for short cooking times. Dry yellow pea (DYP) accessions and accessions with wrinkled seeds, although perceived as juicy and sweet, had relatively high levels of phytate. Breeding for lowering phytate in these accessions may be an advantageous avenue, as long as yield, germination rate, and other important factors are not severely compromised (Warkentin et al., 2012).

For fractionation of protein and starch isolates, accession high in protein and/or starch are particularly relevant. Based solely on protein content, the accessions with wrinkled seeds and many of the accessions with dark-coloured testa appeared promising as sources for protein isolates. However, DDMP saponin content was positively correlated with protein content (Fig. 3). Breeding for new cultivars that are high in protein but low in DDMP saponin, as well as other unwarranted off-flavour compounds, may save considerable resources in the downstream processing (Noguera et al., 2022).

The growing demand for alternative gluten-free, plant-based flour sources has driven interest in legumes, which offer a nutritious and versatile option for flour production (Schmelter et al., 2021). Legume flour based on pulses is a versatile ingredient for the production of different food and beverage items, with the global market valued at over 8,200 million USD in 2023 and projected to increase in the coming years (Verified Market Reports, 2023). From the PCA and rCCA, it was observed that some accessions scored high on odour intensity and bitterness (both in taste and aftertaste). These characteristics might negatively influence the quality of flour-based products such as bread and cookies. Consequently, accessions in the top and upper-left part of

Fig. 2 might not be ideal for flour production compared to other accessions that exhibit a more favourable sensory profile. While odour and taste components may carry over to the flour, the textural components are less likely to do so. However, this aspect requires further evaluation.

## Conclusions

Selecting varieties that are perceived more favourably is important for a greater inclusion of pulses in our daily diets. The ultimate goal is to guide future breeding efforts and product development by identifying promising pea accessions that are not only nutritionally beneficial but also have favourable sensory properties for various food applications. This study aimed to achieve this goal by determining the seed storage content of several key compounds across 15 diverse pea accessions and screening the sensory perception of their cooked seeds. Variation was found in both nutritional and sensory attributes across accessions, including links between biochemical content and perceived taste, texture, and aroma. PCA and rCCA served as effective tools in identifying both promising traits and sensory drawbacks. Accessions with wrinkled seeds had higher levels of fatty acids, sucrose, and choline but lower levels of starch than accessions with smooth and dimpled seeds. Accessions with light-coloured testa were perceived as sweeter and juicier, while accessions with dark-coloured testa were more odour-intense and chewy. However, multifaceted interactions underscore the need to consider both direct and indirect effects of chemical constituents on sensory outcomes. These results provide a foundation for selecting accessions suited for different food applications. However, the influence of cooking time and biochemical stability during preparation require further study. Future research should aim to link these phenotypes to genetic markers and assess consumer acceptance in target products. Ultimately, this study highlights the value of combining biochemical and sensory analyses to identify relevant breeding targets in legume improvement efforts.

## Ethical statement

Informed consent was obtained from the professionals participating in the sensory screening of the cooked whole peas.

The sensory screening data used in this study was provided by IPSOS, Sweden. The company conducted all sensory evaluations in compliance with relevant ethical guidelines. Ethical oversight, including obtaining informed consent from panelists, was managed entirely by the company. The data was fully anonymized prior to being shared with the authors, ensuring the privacy rights of the panelists were upheld. As the authors were not involved in the data collection process and no identifying information was accessible, no additional ethical approval was required for this study.

## Funding

The present study was made possible by a Formas grant (2022-01925) within ‘Taste and sensorics – from farm to fork’ granted to Gun Hagström, Åsa Grimberg, Cecilia Hammenhag, Mohammed Hefni, and Cornelia Witthöft.

## CRediT authorship contribution statement

**Bjørn Dueholm:** Writing – original draft, Visualization, Investigation, Formal analysis. **Åsa Grimberg:** Writing – original draft, Investigation, Funding acquisition, Formal analysis. **Mohammed Hefni:** Writing – review & editing, Investigation, Funding acquisition, Formal analysis. **Cornelia Witthöft:** Writing – review & editing, Funding acquisition, Conceptualization. **Gun Hagström:** Writing – review & editing, Funding acquisition, Conceptualization. **Cecilia Hammenhag:** Writing – original draft, Funding acquisition, Conceptualization.

## Declaration of competing interest

The authors declare that they have no competing financial or personal interests that could have influenced or biased the work presented in this manuscript.

## Acknowledgment

The authors would like to thank Karl-Erik Gustavsson (Dept. of Plant Breeding, SLU) for excellent assistance in the LC-MS method development for saponins. The authors are grateful for the competent assistance by Jenny Östberg (Dept. of Plant Breeding, SLU), Anna Nieto Esteve (Dept. of Plant Breeding, SLU), and Bindu Sunilkumar (Dept. of Biosystems and Technology, SLU) as well as Jan-Eric Englund (Dept. of Biosystems and Technology, SLU) for his valuable inputs on the statistical analysis. The authors would also like to thank Ipsos, especially Pia Holmlund, Halina Agerhem, and Mariana Ström, for setting up and conducting the sensory screening.

## Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.fufo.2025.100691](https://doi.org/10.1016/j.fufo.2025.100691).

## Data availability

Data will be made available on request.

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