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Title	Novel food ingredients from Cyperus rotundus L.: an ancient famine food and the world's pernicious weed coming back on the table
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Publication date	2026-10-01
Original Citation	Giorgi, G, Sahin, A W, Patriarca, A, Sciubba, F, Massimi, L, Zannini, E, Miccheli, A, Tomassini, A & Brasili, E 2026, 'Novel food ingredients from Cyperus rotundus L.: an ancient famine food and the world's pernicious weed coming back on the table', Food Research International, vol. 241, 119741, pp. 1-11. https://doi.org/10.1016/j.foodres.2026.119741
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://www.scopus.com/pages/publications/105041851191 - 10.1016/j.foodres.2026.119741
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Download date	2026-11-06 20:01:36
Item downloaded from	https://hdl.handle.net/10468/19555

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Food Research International 241 (2026) 119741

Contents lists available at ScienceDirect

Food Research International

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

Novel food ingredients from *Cyperus rotundus* L.: an ancient famine food and the world's pernicious weed coming back on the table

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ARTICLE INFO

Keywords:
Cyperus rotundus
Edible weeds
Novel food
Techno-functional properties
^{1}H-NMR based metabolic profile

ABSTRACT

The increasing vulnerability of global food systems has led to an interest in the rediscovery of underutilised plant species as alternative and resilient food resources. Among these species, edible weeds such as *Cyperus rotundus* L., may represent a promising resource. Even though *C. rotundus* has been considered as one of the most invasive weed species, it produces energy-rich tubers that have been traditionally consumed but remain poorly characterised from a nutritional and technological perspective. This study provides a comprehensive evaluation of the chemical and metabolomic profile, techno-functional properties, digestive behaviour, and phenolic content. Proximate analysis revealed high total dietary fibre content (39.05 ± 1.23 g/100 g FW), dominated by insoluble fibre, followed by starch (15.00 ± 0.53 g/100 g FW), alongside moderate protein levels (8.44 ± 0.14 g/100 g FW). Elemental analysis performed by ICP-MS revealed a mineral profile dominated by nutritionally relevant macronutrients, particularly Ca, K, P, and Mg, and allowed the determination of microelements and trace potentially toxic elements (PTEs), including As, Cd, Pb, and Ni, which were detected only at low concentrations.

The untargeted ^{1}H NMR metabolomic analysis identified 37 metabolites, including free sugars, organic acids, fatty acids, sterols, amino acids, and bioactive compounds such as arginine, γ-aminobutyric acid (GABA), and luteolin-7-O-glycoside. Techno-functional analysis showed favourable water- and oil-holding capacities, and stable pasting behaviour, moderate foaming capacity with high foam stability, and suitability for coarse emulsion systems. *In vitro* digestion demonstrated slow starch hydrolysis, with reducing sugar release closely matching that of the low-digestible starch fraction, suggesting a potential low-glycaemic response. Total phenolic content was 4.71 ± 0.04 mg GAE/g DW. Overall, these findings indicate *C. rotundus* tubers as a promising candidate for valorisation within modern food and feed systems, where resilient and underutilised species are increasingly essential to face future climate and security challenges.

1. Introduction

The current agricultural system heavily relies on the cultivation of a limited number of plant species, with the majority of human caloric intake derived from just three crops: wheat, rice and maize (Farooq et al., 2023). Climate change poses a significant threat to this already vulnerable system, which suffers from low agrobiodiversity and the ongoing erosion of genetic resources. Therefore, guaranteeing the production, yield and quality needed to meet the demands of a growing global population, currently exceeding 8 billion, represents one of the main challenges of modern agriculture (Laghari et al., 2025). In this context, the integration of underutilised or novel plant species into agricultural and dietary systems could play a key role in alleviating global food insecurity (Phillips et al., 2025). Among underutilised plant species, edible weeds may represent a promising resource due to their local availability and low-input ecological resources. Although they are typically considered a major threat to crops as they reduce yields by competing for light, space, nutrients, and water (Horvath et al., 2023), the use of weeds in human nutrition could enhance the resilience of food systems while helping to meet the nutritional needs of a growing global

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https://doi.org/10.1016/j.foodres.2026.119741
Received 18 February 2026; Received in revised form 27 May 2026; Accepted 12 June 2026
Available online 13 June 2026
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population (Ebel & Menalled, 2025; Prosperi, 2025). With approximately 950 species, the genus *Cyperus* (family Cyperaceae) is mainly regarded as a group of invasive weeds, despite its traditional medicinal and nutritional applications (Taheri et al., 2021). Among this group, *Cyperus rotundus* L. (family Cyperaceae) has been recognised as one of the world's most problematic weed species (Holm et al., 1977). *C. rotundus* is a highly invasive C_4 herbaceous plant with strong resistance to conventional control methods. Its invasiveness is driven by aggressive growth and reproductive strategies, including competition for essential resources, release of allelopathic compounds and extensive tuber production, along with the formation of a dense network of roots and rhizomes (Peerzada, 2017). Indeed, its aggressiveness arises from the ability to form tubers with energy-rich substances capable of giving rise to a rapid and cyclical re-colonization of the agroecosystem. These tubers, in addition to being highly vigorous, are characterised by a dense vertical arrangement (about 0–40 cm soil depth), with a strong capacity for the rapid development of a horizontal arrangement through tuber–rhizome chains (Benvenuti, 2025). Tubers represent an important food source for both humans and animals, as their high carbohydrate content allows them to generate more energy per hectare per day than many other food crops, even under adverse growing conditions (Scott et al., 2000). However, less attention has been paid to other metabolites that contribute significantly to their nutritional quality, such as amino acids, fatty acids and lipid derivatives. Therefore, considering that a healthy and conscious diet is fundamental for continuous provision of nutrients required by the human body, the compositional analysis of tubers should extend beyond their energetic profile to include a broader range of nutritionally relevant metabolites. Even though *C. rotundus* has been included in human diets ever since the late Palaeolithic Era (Hillman, 1996), its consumption is currently restricted to specific regions where it serves as a constituent in culinary preparations, including curry, pickling spices and baked goods in Asia; or as a dietary supplement during drought periods in Africa (Mugera et al., 2017; Wang et al., 2023). While its phytochemistry and its pharmacological applications have been extensively studied (Xue et al., 2023) (Bezerra & Pinheiro, 2022), its possible applications in food remain largely unexplored, with scarce information on its compositional analysis and technological performance, with only a few studies initiating preliminary research in this field (Algboory et al., 2021; Devi et al., 2020; Eltilib et al., 2016; Umerie & Ezeuzo, 2000). In addition to their energetic and phytochemical composition, the mineral profile of edible tubers represents a key aspect for evaluating their nutritional quality and safety. Essential macro- and micronutrients contribute significantly to the physiological and nutritional value of plant-derived foods, whereas the occurrence of trace potentially toxic elements (PTEs) may represent a limitation for their use in human and animal nutrition. Despite the increasing interest in *C. rotundus* as a potential underutilised food resource, information regarding its elemental composition remains scarce and fragmentary. Therefore, the characterisation of both essential mineral nutrients and trace PTEs is necessary to better assess the nutritional potential and safety of *C. rotundus* tubers within future food and feed systems. In this context, ICP-MS elemental analysis was performed to determine the concentration of macro- and micronutrients as well as the occurrence of PTEs in *C. rotundus* tubers.

Therefore, this research aims to advance the understanding of the nutritional properties of *C. rotundus* tubers and to investigate their potential applications in the food sector, considering their use as an emergency food source or a sustainable alternative in the view of future climate and food crises. To this end, tubers of *C. rotundus* were analysed for their chemical composition, metabolomic profile, techno-functional properties, susceptibility to digestive enzymes, and phenolic content.

2. Materials and methods

2.1. C. rotundus harvesting and sample preparation

C. rotundus tubers were harvested from Aureli Mario S.S. Agricola company (Ortucchio, AQ, Italy) in the Fucino Plain (41°52′ N, 12°12′ E; 680 m AMSL). The tubers were carefully brushed to remove soil residuals then treated with liquid nitrogen and freeze-dried for 48 h in Lyovapor L-200 (Buchi Italia s.r.l., Cornaredo, MI, Italia). The tubers were then stored under vacuum conditions until use to avoid moisture changes. For the following experiments, the tubers were manually ground using a pestle.

All chemicals were purchased from Sigma- Aldrich (St. Louis, MO, USA) unless stated otherwise. All experiments were conducted in triplicate, results are expressed as mean ± standard deviation.

2.2. Compositional analysis

Protein content was determined using Kjeldahl method (AACC Method 46–12) with a nitrogen conversion factor of 6.25. Soluble Dietary Fibre (SDF), Insoluble Dietary Fibre (IDF) and Total Dietary Fibre (TDF) were determined using the K/RINTDF enzyme assay kit (Megazyme, Bray, Ireland), following methods AOAC method 2022.01 with minor amendments, as reported by Sahin et al. (2023). Megazyme rapid-resistant starch assay kit (K-RAPRS, Megazyme, Bray, Ireland) was used to determine the resistant starch content of the sample. Moisture and ash contents were determined following the 44–15.02 and the AOAC 923.03, respectively.

2.3. Elemental analysis

For elemental analysis, *C. rotundus* tubers were dried in a ventilated oven at 70 °C for 24 h until constant weight was achieved. The dry biomass was weighed and subsequently homogenised through thermal mineralisation in a muffle furnace at 550 °C for 5 days. After complete combustion of the organic matrix, the resulting ash was weighed. The ash fraction corresponded to 4.22% of the initial dry biomass.

The obtained ash was homogenised and subdivided into five analytical replicates. Approximately 50 mg of ash (dry mass) from each replicate were subjected to acid digestion using a mixture of HNO_3 (2 mL; 65%, analytical grade) and H_2O_2 (1 mL; Suprapur grade). Digestion was performed using a microwave-assisted system (Ethos Touch Control, Milestone, Italy) equipped with a high-pressure rotor operating at 180 °C for 30 min. After digestion, the solutions were quantitatively transferred and diluted to a final volume of 330 mL with ultrapure deionized water (18.2 MΩ cm). All samples were filtered through 0.45 μm cellulose nitrate membrane filters prior to analysis. Five method blanks were included in each digestion batch to assess potential contamination during sample preparation.

Elemental concentrations were determined by inductively coupled plasma mass spectrometry (ICP-MS; PlasmaQuant MS Q, Analytik Jena, Germany) equipped with a concentric glass nebulizer (0.4 mL min^{-1}) and a cyclonic spray chamber. Instrumental operating conditions were optimised daily to maximize sensitivity while minimizing oxide formation and doubly charged ions. A total of 37 elements (Al, As, B, Ba, Be, Bi, Ca, Cd, Ce, Co, Cr, Cs, Cu, Fe, Ga, K, La, Li, Mg, Mn, Mo, Na, Nb, Ni, P, Pb, Rb, Sb, Sn, Sr, Ti, Tl, U, V, Zn, and Zr) were quantified.

External calibration was performed using multi-element standard solutions (1000 ± 2 mg L^{-1}) prepared by serial dilution in the same acid matrix as the samples. Yttrium (Y) was used as an internal standard to correct for instrumental drift, signal instability, and matrix effects. The internal standard was continuously introduced online and monitored throughout the analytical sequence.

Limits of detection (LODs) for each element were calculated as the mean concentration of five method blank measurements plus three times the standard deviation (SD). All samples were analysed in randomised

order to minimise systematic bias. Instrumental performance was verified through repeated analysis of calibration standards and quality control solutions during each analytical run. Calibration linearity was assessed for all analytes ($R^2 > 0.999$), and recalibration was performed whenever deviations exceeded ±5%. Precision was evaluated through replicate analyses, with relative standard deviations (RSDs) generally below 15%, confirming the high analytical reproducibility of the dataset.

Elemental concentrations were first calculated on the ash dry mass basis and subsequently normalized to the original dry biomass considering the ash yield percentage (4.22%). Final concentrations are therefore expressed as μg g^{-1} dry weight (DW) of the original tuber biomass.

2.4. ^{1}H-NMR analysis

C. rotundus tubers were extracted following a modified Bligh-Dyer protocol (Giampaoli et al., 2021). In detail, a total of 0.5 g of each sample was mixed with 2 mL of cold methanol (≥ 99.8%, ACS reagent grade), 2 mL of cold chloroform ($CDCl_3$) (99.4%, GC grade) and 1.5 mL of deionized water. Samples were vortexed after each solvent addition, stored at 4 °C overnight and then centrifuged for 30 min at 4 °C, with a rotation speed of 8900 g. The upper hydrophilic and lower lipophilic phase were carefully separated and dried under nitrogen flow. The hydrophilic phase was resuspended in 0.7 mL of D_2O containing 3-(trimethylsilyl)-propionic-2,2,3,3-d_4 acid sodium salt (TSP, 2 mM) as internal and chemical shift reference standard, while the lipophilic phase was resuspended in 0.7 mL of $CDCl_3$ containing hexamethyldisiloxane (HMS, 2 mM), as an internal and chemical shift reference standard. The hydrophilic and the lipophilic phases were then analysed by ^{1}H NMR. The experiments were performed using a JNM-ECZ 600R spectrometer (JEOL Ltd., Tokyo, Japan) operating at a proton frequency of 600 MHz and equipped with a multinuclear z-gradient inverse probe, maintained at 298 K. One-dimensional ^{1}H spectra of the hydrophilic phase were acquired using a pre-saturation pulse sequence to suppress the water signal, using a time length of 2 s, a spectral width of 9.03KHz, 64 k data points and an acquisition time of 5.81 s. The 90° pulse length was set to 8.3 μs, and the recycling delay was 5.72 s. The lipophilic phase was analysed using the same protocol, except that water suppression was not applied. Two-dimensional ^{1}H—^{1}H TOCSY and ^{1}H- ^{13}C HSQC experiments were carried out for spectral assignment according to Spinelli et al. (2022). Compound quantities were expressed in mg/100 g by comparing the signal intensities with those of the standards, normalized by the number of protons contributing to each signal (9 protons for TSP, 18 protons for HMS), adjusted according to the sample's weight and then expressed in mg/100 g as a mean ± standard deviation (S.D.). Metabolite assignment was done employing the protocol reported for two-dimensional experiments by Sciubba et al. (2020). Putative assignment was carried out with databases such as the Biological Magnetic Resonance Data Bank (BMRB, https://bmrb.io) (Hoch et al., 2023) and the Natural Products Magnetic Resonance Database (NP-MRD; https://np-mrd.org) (Wishart et al., 2025).

2.5. Viscosity changes

For the determination of viscosity changes during heating and cooling a ViscoQuick Analyzer (Brabender, Version 2.1.8 CV 6) was used. Ten grams of the sample were mixed with 40 mL of deionized water and heated at a rate of 20 °C/min from 30 °C to 93 °C, maintained at 93 °C for 5 min, cooled at a rate of −15.09 °C/min, and held for 1 min at 50 °C, cooled at a rate of −5 °C/min from 50 °C to 30 °C, and then held at 30 °C for 1 min before the test ended. Peak viscosity, breakdown viscosity, and final viscosity were evaluated.

2.6. Water and oil holding capacity

The water and oil holding capacities (WHC and OHC, respectively), defined as the amount of water or oil retained per unit mass of sample, were determined using a modified method based on Boye et al. (2010). Briefly, 0.5 g of sample was weighed into 15 mL centrifuge tubes. Subsequently, 3 mL of distilled water or oil was added to each tube. The mixtures were vortexed for 5 min to ensure thorough dispersion. Samples were then allowed to stand at room temperature (RT) for 1 h, followed by centrifugation at 4000 rpm for 45 min at 20 °C. After centrifugation, the supernatant (water or oil) was carefully decanted, and the tubes were inverted onto absorbent paper for 30 min to allow excess liquid to drain. The tubes were then weighed, and the holding capacity was expressed using the following calculation:

$$WHC\ or\ OHC(\%) = \frac{Weight\ of\ tube\ and\ pellet - Weight\ of\ tube - Weight\ of\ the\ ingredient}{Weight\ of\ the\ ingredient}\ x\ 100$$

2.7. Foaming capacity and foam stability

Foaming capacity and foam stability were determined based on Alonso-Miravalles et al. (2019) method, with slight modifications. The sample was dispersed in distilled water at 2% *w*/w and left to hydrate at 4 °C overnight. The initial sample height was then measured. The sample was frothed using the Ultraturrax T10 with S10N-10G dispersing element for 30 s at maximum speed. The height of the foam was then measured at 0 min and after 60 min. Foaming capacity and foam stability were calculated according to the following equations:

$$Foaming\ capacity\ (\%) = \frac{Foam\ height\ at\ 0\ min}{Initial\ sample\ height}\ x\ 100$$

$$Foam\ stability\ (\%) = \frac{Foam\ height\ at\ 60\ min}{Foam\ height\ at\ 0\ min}\ x\ 100$$

2.8. Emulsion stability

Emulsion stability was determined using the method described by Jaeger et al. (2023) with some adaptations. Aqueous sample dispersions of 1% w DM/w concentration were prepared and hydrated by shaking at 250 rpm at 4 °C overnight. Emulsions were prepared by adding sunflower oil with a ratio of 1:10. Samples were sheared using an Ultra-Turrax equipped with a S10N-10G dispersing element (IKA Labortechnik, Janke and Kunkel GmbH, Staufen, Germany) at maximum speed for 2 min. Stability was measured using an analytical centrifuge (LUMiSizer, LUM GmbH, Berlin, Germany) with parameters of 100 rcf for 15 min at 15 °C. The results are reported as separation rate (%/min) and transmission profiles over the entire measurement range.

2.9. pH & TTA

The pH and TTA were determined based on the method reported by Jaeger et al. (2023) with slight modifications. In detail, 1 g of the sample was weighed into a beaker, followed by the addition of 9.5 mL of

distilled water and 0.5 mL of acetone. The mixture was stirred until fully dispersed. The pH was measured using a pH meter (Mettler Toledo, Columbus, OH, USA) and TTA was determined by titration with 0.1 M NaOH until a pH of 8.5 was reached. The TTA is expressed as mL 0.1 M NaOH.

2.10. Susceptibility towards digestive enzymes

An *in vitro* digestion assay was conducted following the method described by Sempio et al. (2024). Briefly, 4 g of sample was subjected to proteolytic digestion using a pepsin solution for 30 min. Subsequently, a pancreatic α-amylase solution was added, and the samples were transferred into dialysis tubing, suspended in a sodium-potassium phosphate buffer (pH 6.9), and incubated for 5 h. Aliquots were collected from the phosphate buffer every 30 min, while the dialysis tubes were manually inverted four times every 15 min. For reducing sugar quantification, 100 μL of each aliquot was mixed with 100 μL of 40 mM 3,5-dinitrosalicylic acid (DNS) solution, heated at 100 °C for 15 min, and then diluted with 1 mL of deionized water. Absorbance was measured at 546 nm. Reducing sugar release (RSR%) was calculated using the following formula:

$$RSR\ (\%) = \frac{(A_{sample} \times 500 \times 0.95)}{(A_{malt_ose} \times available\ carbohydrate)} \times 100$$

where A_{sample} is the sample absorbance, 500 is the total volume of the solution, 0.95 is the conversion factor from maltose to starch, $A_{maltose}$ is the absorbance of the 1 mg/mL maltose standard, while available carbohydrate refers to the digestible starch present in 4 g of the sample.

2.11. Total phenolic content

Total phenolic content was quantified following the method reported by Pasquet et al. (2024) with some adaptations. Briefly, 1 g of the sample was suspended in 20 mL of MeOH/Milli-Q H_2O (80/20 *v/v*), vortexed and incubated at 40 °C for 40 min. After that, samples were centrifugated for 10 min at 4000 x g and supernatants collected and diluted 1:5 with MeOH/Milli-Q H_2O (80/20 *v/v*). 100 μL of the diluted sample was then added to 50 μL of Folin-Ciocalteu reagent and 700 μL of Milli-Q H_2O. After 5 min of incubation, 150 μL of $NaCO_3$ (7.5%) was added. The mixtures were incubated for 30 min in the dark, and absorbance was measured at 760 nm. Quantification was based on a calibration curve prepared with gallic acid standard at concentrations of 0, 25, 50, 75, 100, and 130 μg/mL. Results were expressed as mg gallic acid equivalents (GAE)/g of sample.

3. Results and discussion

3.1. Compositional analysis

C. rotundus tubers contained 8.44 ± 0.14% protein and 39.05 ± 1.23% total dietary fibre. Of the total fibre, 35.98 ± 1.3% was insoluble dietary fibre (IDF), 2.61 ± 0.31% was represented by high molecular weight soluble dietary fibre (SDFP), while 0.47 ± 0.01% was low molecular weight soluble dietary fibre (SDFS). The starch content was 15.00 ± 0.53%, comprising 12.73 ± 0.49% digestible starch (DS) and 2.27 ± 0.11% resistant starch (RS). Moisture and ash contents were 6.58 ± 0.02% and 4.22 ± 0.06%, respectively. All values are reported as is.

The starch content of *C. rotundus* tubers was within the average range reported for *S. tuberosum* (9.1–22.6 g/100 g FW) by Burlingame et al. (2009), but lower than other literature data (24.1 g/100 g DW) and that of *C. esculentus* (29.93 ± 2.24 g/100 g FW) (Sabah et al., 2019; Umerie & Ezeuzo, 2000). These discrepancies may be attributed to differences in analytical methodologies, as Umerie and Ezeuzo (2000) quantified starch following isolation and purification of the starch fraction, while Sabah et al. (2019) determined starch content using a polarimetric method. In addition, sources of variability may be also represented by differences in climatic conditions and plant developmental stage at harvest.

The Kjeldahl method used for the estimation of protein content is widely regarded as the reference procedure; however, it quantifies total organic nitrogen, rather than true protein and therefore it requires a conversion factor which depends on the amino acid composition (Hayes, 2020). In the present study, protein content was calculated using the standard conversion factor of 6.25. This factor has been previously applied to other tubers, such as potatoes, for which Burlingame et al. (2009) reported protein content ranging from 0.85 to 4.2 g/100 g FW. Lower protein content for *C. rotundus* have been reported by Emelugo et al. (2011) (1.75 ± 0.55 DW) using the Folin-Lowry method and the same conversion factor. While comparable protein contents have also been reported for *C. rotundus* (7.8 g/100 g FW Ibrahim & Abdullahi, 2013) and *C. esculentus* (8.51 g/100 g FW Suleiman et al., 2018) using the Kjeldahl method. However, the conversion factor was not explicitly reported in those studies, limiting the accuracy of direct comparisons.

Fibre content exceeded the values reported for *C. esculentus* (14.8 ± 0.113 g/100 g FW Sabah et al., 2019), *S. tuberosum* (2.2 g/100 g FW Furrer et al., 2018) and those found in the literature (17.48 g/100 g DW Emelugo et al., 2011). These profound differences between literature and experimental data may be again related to variations in analytical methodologies or to differences in the matrix. In this study, dietary fibre was quantified using AOAC Method 2022.01, the most recent standardised procedure, which enables the analysis of insoluble and soluble dietary fibre across a wide range of matrices. This method is considered more robust and reproducible than earlier approaches thus improving analytical reliability (McCleary & McLoughlin, 2023). Ash content was lower than the literature reference value (7.87 ± 0.92 g/100 g DW Emelugo et al., 2011), but higher than those reported for *C. esculentus* (2.23 ± 0.052 g/100 g FW Sabah et al., 2019) (1.18 g/100 g FW Suleiman et al., 2018) and *S. tuberosum* (1.53 ± 0.04 g/100 g DW Arshad et al., 2021). Overall, the observed differences in the proximate composition of the tubers could be related to the intrinsic diversity of the species, as in the case of *C. esculentus* and *S. tuberosum*. However, they may also result from the use of different analytical methodologies or from variations in the physical conditions under which the samples were collected. As previously reported by Xue et al. (2023) *C. rotundus* tubers exhibit regional variability with chemical composition influenced by both harvesting period and geographical origin. In this study, tubers were harvested at the flowering stage in October 2024 in the Fucino Plain (Italy), a ~200 km^2 endorheic intermontane basin composed mainly of clay–silt alluvial and lacustrine sediments, locally interbedded with sand (Cavinato et al., 2002). The year was marked by record-high temperatures (+1.9 °C above the 1991–2020 average) and three severe heatwaves (36–41 °C), along with precipitation 25% below average, leading to prolonged summer–autumn drought (Autorità di bacino distrettuale dell'Appennino Centrale (AUBAC), 2025). Overall, these factors may have influenced the composition and properties of *C. rotundus* tubers. However, the extent of these influences remains unclear due to the lack of comparative data for this species across different years, seasons and soil conditions. Moreover, the lack of literature data and the use of different methodologies for the proximate composition analysis represent an additional source of uncertainty and prevent reliable comparison among studies. Furthermore, our study represents the characterisation of a single experimental condition without comparative group analysis, and therefore comparisons with the available literature should be considered descriptive rather than confirmatory or validation-based.

3.2. Elemental analysis

The elemental composition of *C. rotundus* tubers is reported in Table 1. No concentrations below the LODs were observed for the quantified elements. The mineral profile of the analysed tubers was

Table 1
Elemental composition of *C. rotundus* tubers. Values are expressed as μg g^{-1} dry weight (DW) of the original biomass.

Element	LOD (μg g^{-1})	Mean ± SD (μg g^{-1} DW)	RSD (%)
Al	0.15	680 ± 87	13
As	0.042	0.16 ± 0.01	7
B	0.57	2.0 ± 0.25	12
Ba	0.0040	3.1 ± 0.38	12
Be	0.0012	0.031 ± 0.0043	14
Bi	0.0058	0.0093 ± 0.0010	11
Ca	2.8	6760 ± 660	10
Cd	0.00060	0.13 ± 0.018	13
Ce	0.00037	0.68 ± 0.085	13
Co	0.0023	0.20 ± 0.033	12
Cr	0.22	1.0 ± 0.14	13
Cs	0.00036	0.077 ± 0.010	13
Cu	0.026	6.7 ± 0.82	12
Fe	3.0	290 ± 38	13
Ga	0.00060	0.14 ± 0.018	13
K	12	4510 ± 560	12
La	0.00023	0.35 ± 0.044	13
Li	0.0032	1.1 ± 0.16	13
Mg	0.64	1310 ± 160	12
Mn	0.00099	9.2 ± 1.1	12
Mo	0.21	0.51 ± 0.066	13
Na	19	120 ± 14	12
Nb	0.0097	0.021 ± 0.0011	5
Ni	0.0036	1.7 ± 0.21	12
P	2.0	2200 ± 270	12
Pb	0.0015	0.33 ± 0.037	11
Rb	0.0018	1.6 ± 0.22	13
Sb	0.00020	0.012 ± 0.0015	13
Se	0.14	0.067 ± 0.0031	0
Sn	0.0043	0.022 ± 0.0018	8
Sr	0.0022	5.6 ± 0.69	12
Ti	0.016	12 ± 1.3	11
Tl	0.00027	0.0047 ± 0.00064	14
U	0.0029	0.075 ± 0.0081	11
V	0.070	4.1 ± 0.48	12
Zn	0.017	20 ± 2.6	13
Zr	0.086	0.44 ± 0.043	10

dominated by nutritionally relevant macronutrients, particularly Ca, K, P, and Mg.

Calcium was the most abundant element detected (6760 ± 660 μg g^{-1} DW), followed by K (4510 ± 560 μg g^{-1} DW), P (2200 ± 270 μg g^{-1} DW), and Mg (1310 ± 160 μg g^{-1} DW). These concentrations are consistent with the physiological role of underground storage organs, which function as reservoirs for mineral nutrients involved in osmotic regulation, energy transfer, carbohydrate metabolism, and structural stabilisation. The relatively elevated concentrations of Ca and K suggest an efficient mineral accumulation capacity of *C. rotundus* tubers and are in line with values commonly reported for mineral-rich tuberous and rhizomatous plant species including *C. rotundus* as reported by Rao et al. (2019) that estimated a range of 4.467–14.728 mg/g and 8.038–18.794 mg/g for Ca and K respectively. Similarly, P and Mg concentrations were within the expected ranges for underground storage tissues and indicate a nutritionally relevant mineral composition. In *C. esculentus*, P concentrations in tubers have been reported within ranges of 1.56–3.57 mg/g) (Kouamé et al., 2024) and Mg levels within ranges 0.1907–1.2295 mg/g (Voica et al., 2025).

Among micronutrients, Fe represented the most abundant (290 ± 38 μg g^{-1} DW), followed by Zn (20 ± 2.6 μg g^{-1} DW), Mn (9.2 ± 1.1 μg g^{-1} DW), and Cu (6.7 ± 0.82 μg g^{-1} DW). Iron concentrations were comparable with values previously reported for *Cyperus* species and wild geophyte plants. Zinc, manganese, and copper concentrations were within typical physiological ranges reported for non-contaminated edible plant matrices, indicating balanced micronutrient accumulation without evidence of anomalous enrichment (Rao et al., 2019).

Potentially toxic elements (PTEs), including As, Cd, Pb, and Ni, were detected only at trace concentrations. Arsenic showed the lowest concentrations among t he investigated PTEs (0.16 ± 0.01 μg g^{-1} DW), while Cd and Pb concentrations were 0.13 ± 0.02 and 0.33 ± 0.04 μg g^{-1} DW, respectively. Nickel concentrations were also relatively low (1.7 ± 0.2 μg g^{-1} DW) and within the range commonly reported for edible and wild plant species growing under non-contaminated environmental conditions (Al-Huqail et al., 2023) .

The overall elemental profile indicates that *C. rotundus* tubers may represent a potentially valuable source of essential mineral nutrients while maintaining limited accumulation of PTEs. Variability in elemental concentrations is likely influenced by environmental and agronomic factors including soil geochemistry, mineral availability, irrigation regime, climatic conditions, and organic matter content, all of which are known to affect elemental uptake and storage in underground plant organs.

3.3. ^{1}H-NMR-based metabolic profile

Representative ^{1}H NMR spectra from aqueous and organic extracts of *C. rotundus* tubers with resonance assignment are shown in Supporting

Table 2
C. rotundus tubers ^{1}H-NMR metabolomic profile. Mean and standard deviation (SD) of metabolites identified and quantified in tubers and expressed as mg/100 g.

Compound	mg/100 g
Amino acids	
Leucine	0.21 ± 0.09
Isoleucine	0.34 ± 0.16
Valine	1.1 ± 0.49
Alanine	6.56 ± 3.07
Arginine	319.08 ± 140.87
Glutamic acid	66.46 ± 29.57
Glutamine	5.88 ± 2.76
Aspartic acid	28.86 ± 13.26
Asparagine	118.62 ± 55.98
Tyrosine	2.03 ± 0.96
GABA	15.56 ± 6.74
Organic acids and derivatives	
Malic acid	24.52 ± 7.45
Fumaric acid	1 ± 0.48
4-Hydroxyphenylacetic acid	0.8 ± 0.34
Formic acid	0.42 ± 0.18
Lactic Acid	3.99 ± 1.82
Succinic acid	7.38 ± 3.16
Citric acid	41.22 ± 18.03
Sugars	
Glucose	619.68 ± 272.23
Sucrose	7146.55 ± 3115.41
Fatty acids and lipid derivatives	
b-Sitosterol	2.84 ± 1.1
Campesterol	0.42 ± 0.14
Omega 9	205.26 ± 81.31
Omega 6	47.67 ± 19.24
Omega 3	1.44 ± 0.58
Monoacylglycerids	1.27 ± 0.55
Diacylglycerids	1.09 ± 0.4
Triacylglycerids	27.34 ± 10.21
Total Saturated Fatty Acids	103.09 ± 37.3
Others	
Trigonelline	2.75 ± 1.19
Uracil	0.26 ± 0.26
Uridine	0.58 ± 0.55
Inosine	1.57 ± 0.62
Luteolin-7-O-Glycoside	15.49 ± 4.97
Choline	3.03 ± 1.27
Dihydroxyacetone	1.09 ± 0.5
NAD	1.09 ± 0.57

figs. S1-S6. Bidimensional $^{1}H—^{1}H$ TOCSY and $^{1}H—^{13}C$ HSQC used for assignment are reported in Supporting figs. S7-S10. The untargeted ^{1}H NMR analysis enabled the identification and quantification of 37 metabolites, including both primary and secondary compounds (Table 2). The list of the identified metabolites and relative chemical shifts of the resonances are reported in Supplementary Table S1.

The most intense spectral signals were attributed to carbohydrates including glucose and sucrose. Minority signals were associated with other metabolites such as amino acids (leucine, isoleucine, valine, alanine, arginine, glutamic acid, glutamine, aspartic acid, asparagine, tyrosine and γ-aminobutyrate (GABA)), ionized organic acids and derivatives such as malic acid, fumaric acid, 4-hydroxyphenylacetic acid, formic acid, trigonelline lactic acid, succinic acid and citrate, as well as fatty acids and lipid derivatives such as b-sitosterol, campesterol, Omega-3, Omega-6, Omega-3, mono-, di-, and triacylglycerols, and total saturated fatty acids and other compounds (uracil, uridine, inosine, luteolin-7-O-glycoside, choline, dihydroxyacetone and NAD).

The ground tubers contained three essential amino acids (isoleucine, valine, and leucine), as well as alanine, glutamic acid, glutamine, aspartic acid, tyrosine, and γ-aminobutyric acid (GABA). Arginine (319.08 ± 140.87 mg/100 g) and asparagine (118.62 ± 55.98 mg/100 g) were the most abundant amino acids, exhibiting a pattern similar to that reported for specific *Solanum tuberosum* cultivars, where these two amino acids also predominated (*e.g.* asparagine 286 ± 3 mg/100 g and arginine 112 ± 7 mg/100 g) (Orsák et al., 2021). Although arginine is not classified as an essential amino acid since it can be synthesized from glutamine/glutamate and proline, its endogenous production may not always meet physiological demands, making dietary intake necessary. Arginine benefits, including vascular and metabolic improvements, occur at supplemental doses of 3–30 g/day (Wu et al., 2021), beyond typical dietary intake (2.5–5 g/day). At 319.08 ± 140.87 mg/100 g FW in *C. rotundus* tubers (Table 2), realistic portions (*e.g.*, 100–200 g) contribute modestly (~0.3–0.6 g), supporting overall nutrition but insufficient for therapeutic effects; synergies with other amino acids like GABA enhance potential in blended foods (Viribay et al., 2020). However, high levels of arginine in tubers must be carefully monitored during food processing, as this amino acid serves as a primary nitrogen reserve and correlates with elevated asparagine levels, as observed in this study, significantly increasing the risk of acrylamide formation through the Maillard reaction. Indeed, during high-temperature cooking (above 120 °C), asparagine reacts with reducing sugars (glucose and fructose) to form acrylamide (Muttucumaru et al., 2017). Although arginine does not directly convert into acrylamide, its massive presence competes with or accompanies critical precursors, influencing the kinetics of the Maillard reaction and the final browning of the product.

Unlike *S. tuberosum*, *C. rotundus* tubers did not contain all nine essential amino acids (Pandey et al., 2023). Nonetheless, previous studies (Kadum, 2019) and unpublished data (not shown) have reported the presence of lysine, which was not detected in the present analysis. These discrepancies may be related to differences in the harvest time of the tubers, as previously reported.

Similarly, the organic acids profile of *C. rotundus* was similar to that reported for *S. tuberosum* (Ingallina et al., 2020) with citric acid (41.22 ± 18.03 mg/100 g) as the predominant component, followed by malic acid (24.52 ± 7.45 mg/100 g) and, in lower amount, succinic acid, lactic acid, trigonelline, fumaric acid, 4-hydroxyphenylacetic acid, and formic acid. Organic acids constitute an important class of bioactive compounds that contribute to the sensory characteristics and the nutritional value of foods. They are widely used in the food industry as additives due to their preservative, acidity-regulating and antioxidants properties. Moreover, organic acids have demonstrated significant inhibitory effects against foodborne pathogens (Karpiński & Ożarowski, 2024), exhibiting a broad spectrum of action against gram-positive bacteria, Gram-negative bacteria, fungi and yeasts (Ben Braïek & Smaoui, 2021). In addition to their antimicrobial properties, numerous studies have demonstrated significant health-promoting effects, including anti-inflammatory activity, prevention of osteoporosis, modulation of immune responses, stimulation of intestinal hormone secretion, anti-obesity effects, regulation of inflammatory processes, enhancement of calcium absorption, and inhibition of platelet aggregation (Shi et al., 2022).

Free sugars were dominated by sucrose (7146.55 ± 3115.41 mg/100 g), while glucose (619.68 ± 272.23 mg/100 g) was the second most abundant, in agreement with values reported for *S. tuberosum* (Ingallina et al., 2020). This high concentration of available sugars may serve as a suitable substrate for microbial fermentation (Madsen et al., 2021), suggesting a possible food application through fermentation process. The lipid profile was dominated by omega-9 fatty acids (205.26 ± 81.31 mg/100 g), which have recently received wide attention due to emerging studies and discoveries regarding their biological benefits in attenuating inflammatory, lipid, cardiovascular and cancer disorders (Farag & Gad, 2022). Other major lipid components included omega-6 fatty acids (47.67 ± 19.24 mg/100 g) and triacylglycerols (27.34 ± 10.21 mg/100 g). Minor constituents comprised β-sitosterol, omega-3 fatty acids, monoacylglycerols, diacylglycerols, and campesterol. In comparison with *S. tuberosum*, the total lipid content of *C. rotundus* tubers appears elevated relative to the typical low lipid content (~0.15–0.5% fresh weight) reported for potato tubers (Lal et al., 2020). Additionally, the sterol profile in *C. rotundus*, which includes β-sitosterol and campesterol, is qualitatively consistent with that of potatoes, with β-sitosterol as one of the main constitutes of the sterol fraction (Lee et al., 2017). Finally, it is interesting to note the presence of the luteolin-7-O-glycoside, a flavone known for its anti-inflammatory (Park & Song, 2018), anti-diabetic (Zang et al., 2016) and antioxidant activities (Episkopou et al., 2025).

3.4. Techno-functional properties

The ground *C. rotundus* tubers had a pH of 6.62 ± 0.01, and a TTA value of 1.13 ± 0.06 mL 0.1 M NaOH. The changes of viscosity profile of the ground tubers during heating and cooling is presented in Fig. 1. Gelatinisation began at 54.33 ± 12.2 °C. The peak viscosity, defined as the maximum viscosity observed during the heating phase leading to paste formation, was reached at 77.7 ± 2.3 °C with a value of 614.33 ± 67.9 BE. The breakdown viscosity, calculated as the difference between the peak viscosity and the minimum viscosity during the holding phase, was 158.00 ± 46.5 BE. This value indicates the stability of the sample under prolonged heating and mechanical shear. The final stage of the pasting profile consisted of a holding period at constant temperature, during which the viscosity increased until reaching a steady state. This value, referred to as the final viscosity or end-point viscosity, was 870.33 ± 92.1 BE. Although starch primarily drives pasting behaviour, proteins, dietary fibres, and lipids can modulate viscosity and stability by limiting swelling, binding water, or forming amylose-lipid complexes, highlighting the combined influence of starch properties and the non-starch matrix on paste behaviour, texture, and potential digestibility (Li et al., 2024; Náthia-Neves et al., 2024; Zhang et al., 2025). Specifically, insoluble fibre (35.98 g/100 g FW) competes for water, delaying swelling and reducing peak viscosity (614 BE), similar to fibre blends lowering pasting in wheat (Santiago-Ramos et al., 2018). Proteins (8.4%) aggregate post-denaturation, accelerating breakdown/setback and restricting starch gelatinisation (Teobaldi et al., 2025); lipids (*e.g.*, omega-9 at 205 mg/100 g) form complexes stabilising hot paste (final viscosity 870 BE) per Li et al. (2024). Resistant starch (2.27%) further limits digestibility, modulating texture in high-fibre applications (Reddy et al., 2013).

The WHC of the ground tubers is defined as the ability of the sample to retain water against gravity (Mariod, 2018), similarly, OHC reflects the sample's capacity to retain oil. They represent important functional properties in food processing, as they contribute to texture enhancement/stability and influence the sensory characteristics of the final product (Du et al., 2014; Ijarotimi et al., 2018). In this study, WHC was

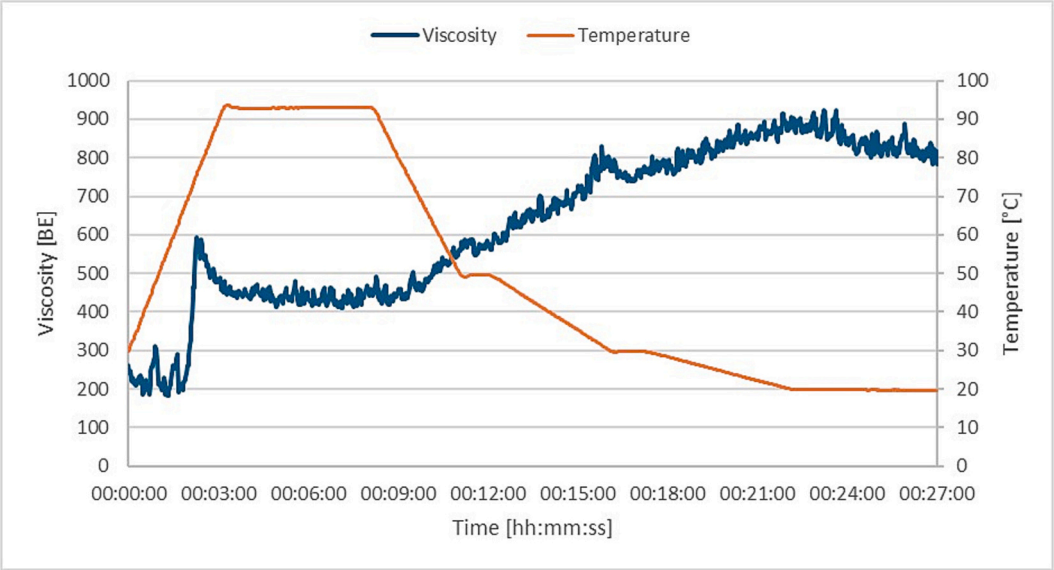


Fig. 1. Viscosity profile of the ground tubers during heating and cooling.

219.06 ± 5.26%, while OHC was 106.80 ± 5.6%. These results are in line with reports for *C. esculentus*, such as those by Ijarotimi et al. (2018) (*e.g.* 295 ± 5% WHC; 162 ± 4% OHC), but higher than those reported by Oladunjoye and Olaoluwa (2024) (*e.g.* 110 ± 3% WHC; 93 ± 3% OHC). The superior WHC (219.06 ± 5.26%) stems predominantly from IDF (35.98 ± 1.3 g/100 g FW), which absorbs water *via* hydroxyl groups and insoluble matrix entrapment, reducing free water availability during centrifugation (McCleary & McLoughlin, 2023). Proteins (8.44 ± 0.14 g/100 g FW) further enhance retention through surface hydrophilicity and denaturation-induced gelation (Bellissent-Funel et al., 2016), yielding values exceeding *C. esculentus* reports (Oladunjoye & Olaoluwa, 2024).

Foaming properties play a critical role in food formulation by influencing texture, volume, and overall sensory quality in aerated products (Amagliani et al., 2021). Foaming capacity and foam stability largely depend on the protein-generated interfacial film that keeps air bubbles dispersed and limits coalescence (Du et al., 2014). The foaming capacity of the sample was 13.29 ± 1.4%, slightly lower than the 18.83 ± 0.29% reported for *C. esculentus*. In contrast, its foam stability was 64.4 ± 3.8, which was higher than the 43.96 ± 0.83% reported for *C. esculentus* (Oladunjoye & Olaoluwa, 2024).

The modest foaming capacity (13.29 ± 1.4%) reflects limited protein solubility (8.44 g/100 g FW) for interfacial film formation, compounded by high IDF (35.98 g/100 g FW) that elevates suspension viscosity and physically interferes with air incorporation during high shear mixing (Amagliani et al., 2021). Insoluble fibre particles disrupt continuous protein adsorption at the air-water interface, increasing surface tension and limiting foam expansion, unlike more soluble *C. esculentus* matrices (18.83 ± 0.29%) (Oladunjoye & Olaoluwa, 2024). Conversely, superior foam stability (64.4 ± 3.8% *vs.* 43.96 ± 0.83%) arises from IDF network consolidation during drainage, where partially hydrated fibre aggregates bridge and stabilise lamellae through capillary entrapment, while denatured proteins form cohesive, viscoelastic films that resist coalescence (Du et al., 2014). This stability-fibre interference trade-off positions *C. rotundus* for dense foam applications (*e.g.*, batters, meringues) rather than high-volume foams.

The Lumisizer transmission profile for *C. rotundus* ground tubers is displayed in Fig. 2. Analytical centrifugation offers a fast and reliable

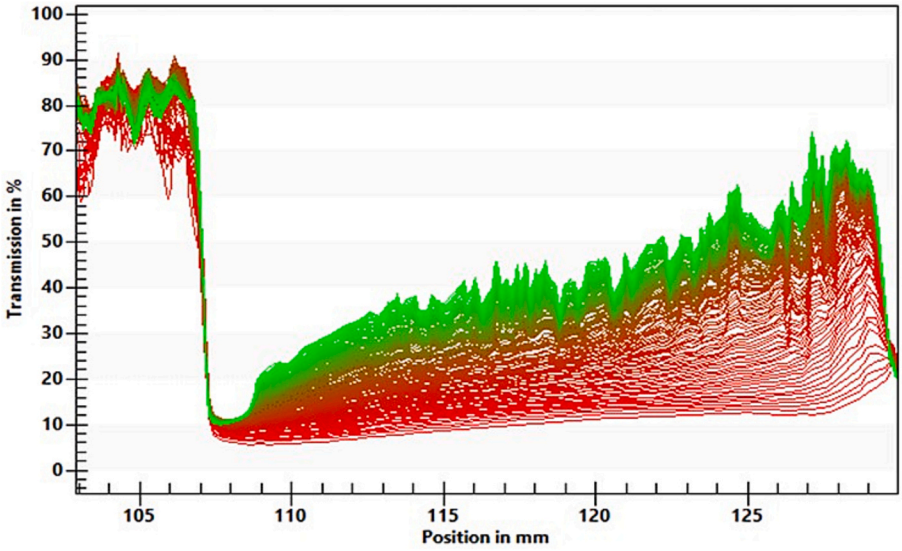


Fig. 2. Lumisizer transmission profile of *C. rotundus* tubers.

approach for evaluating the stability of dispersions, as it can simulate gravitational separation processes. The applied centrifugal force corresponds to roughly two months of sedimentation under normal gravity conditions (Vogelsang-O'Dwyer et al., 2022). The sample showed a separation rate of 2.47 ± 0.15 (%/min). A decrease in light transmission in the upper region of the cell and a corresponding increase in the lower region over time were observed. This behaviour suggests upward migration of the dispersed phase, leading to the formation of a thin cream layer. In addition, a minor presence of sediment particles was observed. Food emulsions function either as stable end-products or as structural components in complex foods, where droplet stability or controlled destabilisation defines product texture. Accordingly, emulsification represents a fundamental process in food formulation and processing (Xiao et al., 2025). The separation rate of 2.47 ± 0.15 min^{-1} and transmission profile indicating creaming with minor sedimentation result from partial interfacial coverage by proteins (8.44 g/100 g FW) and polar lipids (monoacylglycerols 1.27 mg/100 g, diacylglycerols 1.09 mg/100 g), which adsorb rapidly during Ultra-Turrax shearing (2 min, max speed) but form incomplete viscoelastic films due to low solubility in 1% DM dispersions (Du et al., 2014). High IDF content (35.98 g/100 g FW) causes depletion flocculation as non-adsorbing colloids generate attractive osmotic gradients between droplets (Vogelsang-O'Dwyer et al., 2022), while abundant ω-9 fatty acids (205.26 mg/100 g FW) partially saturate the oil-water interface, moderating coalescence rates compared to protein-only systems (Xiao et al., 2025). The thin cream layer formation aligns with low emulsifier loading (1% DM, 1:10 oil: aqueous) where droplet stabilisation relies primarily on Pickering-type stabilisation from partially wetted IDF particles rather than molecular surfactants, positioning *C. rotundus* for coarse emulsion applications (dressings, sauces) rather than fine mayonnaises.

3.5. Susceptibility towards digestive enzymes

The release of reducing sugars during the simulated *in vitro* digestion is presented in Fig. 3. The curve exhibits a nonlinear upward trend over the five-hour digestion period, with a faster rate of release after approximately 2 h. By the end of the incubation, the cumulative release of reducing sugars reached 15.11 ± 0.7%. This value is in close agreement with the starch fractionation analysis, which showed 12.73% digestible starch and 2.27% of resistant starch. The non-linear release profile, with a slow initial phase and a faster hydrolysis after ~2 h, indicates that enzymatic accessibility might be initially limited by structural constraints such as intact granule crystallinity, fibre entrapment, and cell wall remnants (Magallanes-Cruz et al., 2017). Cooking and processing (*e.g.* fine milling, fermentation) could modify starch availability and change the profile of reducing sugar release (Zhang & Hamaker, 2009). The relatively slow release of reducing sugars observed during *in vitro* digestion, together with the presence of resistant starch fractions, may suggest reduced starch susceptibility to enzymatic hydrolysis and a potential low-glycaemic response. However, these findings should be interpreted cautiously, as the present assay was designed as an exploratory assessment of starch digestibility behaviour rather than a full physiological simulation of gastrointestinal digestion. Future studies should implement harmonised INFOGEST-based digestion protocols combined with starch digestibility kinetic modelling to better predict glycaemic response and further validate the nutritional functionality of *C. rotundus* tubers.

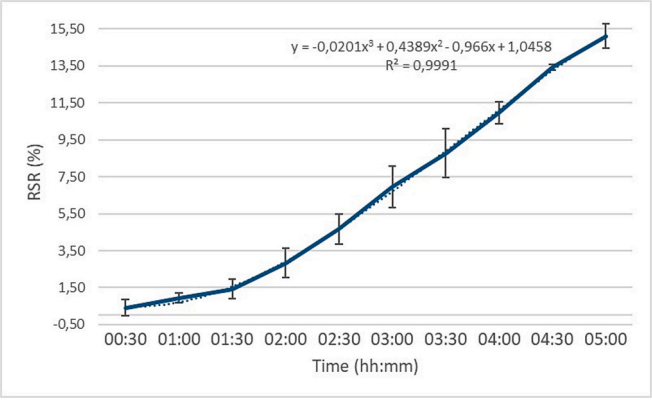


Fig. 3. Polynomial regression model of reducing sugars released during the simulated *in vitro* digestion.

3.6. Total phenolic content

Total phenolic content in *C. rotundus* tubers was 4.714 ± 0.04 (mg/g DW GAE). This value resulted lower with respect to literature data 12.33 ± 0.08 (mg/g DW GAE) for *C. rotundus*

(Hussein et al., 2021), but higher than the values reported for two different varieties of *C. esculentus* 0.223 ± 0.003 (mg/g DW GAE) and 0.3815 ± 0.017 (mg/g DW GAE) (Ahmed et al., 2025). Phenolic compounds are secondary metabolites which play an essential role in various physiological and mechanical activities of plants, contributing to their growth, development and protection mechanisms (Pratyusha, 2022). Several factors influence the abundance of these compounds, such as climatic conditions, soil composition, genotype, harvest and post-harvest processing, as well as storage (Akyol et al., 2016). Therefore, the observed differences between literature data and results obtained in this study may be related to those factors. *C. rotundus* has been extensively studied for its pharmacological applications, some of which may be correlated to the presence of phenolic compounds (Xue et al., 2023). The presence of these compounds may suggest a possible application of these tubers in the formulation of functional food.

4. Conclusion

Cyperus rotundus compositional analysis revealed that its tubers are exceptionally rich in dietary fibre, reaching nearly 40% of their dry weight, with insoluble fibre representing the majority of this fraction. This unusually high fibre content, exceeding that of several conventional tubers and even *C. esculentus*, positions *C. rotundus* as a promising candidate for products aimed at improving intestinal health, enhancing satiety, and reducing postprandial glycaemic response. Complementing this fibre-rich profile, the tubers also contain a measurable proportion of resistant starch and exhibit slow enzymatic digestibility during *in vitro* assays. After five hours of simulated digestion, only a limited fraction of starch had been hydrolysed, closely matching the low digestible starch content measured analytically. This slow release of reducing sugars may indicate potential applicability as a functional ingredient in low-glycaemic formulations, where modulating carbohydrate availability is essential for managing blood glucose levels. Such characteristics would be of interest particularly relevant in foods designed for individuals with metabolic disorders or for populations requiring sustained energy release.

The comprehensive elemental analysis of *C. rotundus* tubers provided valuable first-time baseline data characterizing the mineral profile of this yet understudied species. The measured concentrations of some minerals, particularly the elevated K, Ca, P, and Mg, demonstrate that *C. rotundus* tubers function as significant mineral reservoirs. However, the substantial deviation from previously published data for this species underscores the importance of considering local environmental factors, soil properties, and agricultural practices when interpreting mineral composition data. The presence of trace elements and potentially concerning heavy metals reinforces the need for careful site selection when cultivating *C. rotundus* for food or medicinal purposes. Future research should investigate the bioavailability of these minerals, the effects of processing methods on mineral retention, and the influences of environmental stress on mineral accumulation patterns. Additionally, the

relationship between phytic acid and essential mineral bioavailability warrants detailed investigation to fully assess the nutritional potential of *C. rotundus* tubers for human consumption and to develop strategies for enhancing nutrient bioavailability through agronomic or processing interventions. The metabolomic profile further supports the potential relevance of this species by revealing significant concentrations of arginine and GABA, alongside a spectrum of essential and non-essential amino acids. Arginine, present at notably high levels, is associated with vascular, immune, and metabolic benefits, while GABA supports stress modulation and neurological function. Although the tubers do not offer a complete essential amino acid profile, these specific components may contribute to the nutritional functionality of blended formulations or fortified foods. Despite their high fibre content, the tubers retain considerable techno-functional versatility. Their strong water- and oil-holding capacities, moderate foaming performance, and stable pasting behaviour during heating suggest possible applicability in bakery products, extruded snacks, fibre-enriched beverages, or even plant-based meat analogues without compromising texture or processing stability. In addition, the high sucrose content identified through ^{1}H NMR analysis may provide a suitable fermentable substrate for the development of fermented foods or beverages in which probiotic or postbiotic activity could further amplify the nutritional value. Nevertheless, the present study should be considered a preliminary investigation into the potential exploitation of *C. rotundus* tubers as a food ingredient. To the best of the authors' knowledge, only limited data are currently available regarding the nutrient composition of *C. rotundus* tubers, and no previous studies have specifically addressed their techno-functional properties. Consequently, further research is necessary to improve understanding of the chemical, nutritional and functional characteristics of this species and to clarify the biochemical mechanisms underlying tuber development, providing new perspectives for its management. Importantly, the present study did not include the quantitative determination of antinutritional compounds or potentially harmful constituents, such as phytates, oxalates, tannins or protease inhibitors. This represents an important methodological limitation, particularly considering the potential future use of *C. rotundus* as a food ingredient. Therefore, dedicated investigations addressing antinutritional factors, toxicological aspects and nutrient bioavailability will be necessary to fully assess the safety and nutritional suitability of the tubers for human consumption. Furthermore, all analyses performed in this study were conducted using freeze-dried and ground tubers. Different preservation methods, the use of fresh tubers, or processing techniques such as cooking, roasting, or fermentation could potentially influence and modify both the nutritional composition and the techno-functional properties of the tubers. In addition, future work including parallel analyses of reference materials under standardised conditions would improve the robustness of inter-study comparisons and support methodological validation across laboratories.

Ethical statement - studies in humans and animals

I declare that no animal or human studies have been conducted for the execution of the research work conducted by Giulia Giorgi, Aylin W. Sahin, Adriano Patriarca, Fabio Sciubba, Emanuele Zannini, Alfredo Miccheli, Alberta Tomassini and Elisa Brasili and included in the manuscript titled "Novel food ingredients from *Cyperus rotundus* L.: an ancient famine food and the world's pernicious weed coming back on the table.

CRediT authorship contribution statement

Giulia Giorgi: Writing – original draft, Investigation, Formal analysis, Data curation. **Aylin W. Sahin:** Writing – review & editing, Validation. **Adriano Patriarca:** Methodology, Investigation, Formal analysis. **Fabio Sciubba:** Writing – review & editing. **Lorenzo Massimi:** Formal analysis, Methodology. **Emanuele Zannini:** Writing – review & editing, Supervision, Project administration, Funding acquisition, Conceptualization. **Alfredo Miccheli:** Supervision, Conceptualization. **Alberta Tomassini:** Supervision, Conceptualization. **Elisa Brasili:** Writing – review & editing, Supervision, Project administration, Funding acquisition, Conceptualization.

Funding sources

We acknowledge the financial support from the Agritech National Research Center and the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR)– MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4– D.D. 1032 17/06/ 2022, CN00000022), and from Sapienza University of Rome, Grant number RG1241910EA209D0.

Declaration of competing interest

The authors 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

The authors wish to express their gratitude to Celia Segura Godoy and to Arianna Ressa for their technical assistance.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.foodres.2026.119741.

Data availability

Data will be made available on request.

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