

Comparative Study on Beta-Glucan Content and Proximate Composition of Spring Barley Seeds Genotypes Obtained in Different Crop Systems

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RESEARCH ARTICLE

Abstract

This paper explores the proximate composition of spring barley seeds and the β -glucan's content in various two-rowed spring barley genotypes cultivated using different agricultural systems. The genotypes originated from both autochthonous and foreign sources and were grown under conventional, ecological, and no-treatment conditions. The proximate analysis of spring barley seeds was performed using near-infrared spectrometry, while the β -glucan content was determined enzymatically. The data analysis included principal component analysis and cluster analysis to identify ideal candidates for specific applications. The results indicated that the conventional cultivation system yielded higher levels of starch, sugar, protein and ash content; conversely, the ecological and no-treatment systems showed variations in nutritional parameters, with the no-treatment approach resulting in significantly higher β -glucan and fat content. In line with previous research, this study highlights the influence of genotype and agricultural practices on the barley seeds' composition. Overall, this research contributes to a better understanding of the nutritional composition of barley seeds and offers insights into selecting specific barley genotypes for various applications in the food, feed, and brewing industries; it also underscores the potential for utilizing spring barley's β -glucan to enhance the nutritional value of various products, promoting cardiovascular and digestive health.

Keywords: spring barley, beta-glucan, proximate composition, chemometry, analysis, quality

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INTRODUCTION

Barley (*Hordeum vulgare*) is an important cereal grain with a rich history and numerous applications; its economic importance remains steadfast today, serving as an important crop for food, animal feed and the brewing industry (Ahmad et al., 2021; El-Hashash and El-Absy, 2019). Barley is known for its remarkable adaptability as a cereal grain species, thriving at higher latitudes and altitudes, and exhibiting resilience in diverse climatic and environmental conditions (Badea and Wijekoon, 2021); its culinary significance lies in regions where other cereals struggle to flourish under similar conditions but can still yield satisfactory results. Despite a waning interest in barley cultivation in recent years, it currently holds the fifth position worldwide in terms of harvested area among all crops, following wheat, maize, rice and soybean (FAO). Barley is recognized for its rich nutritional profile, featuring notable levels of proteins and carbohydrates, moderate fat

content and substantial dietary fiber, primarily β -glucan; the major carbohydrate in barley is starch, making it a valuable complex carbohydrate provider (Din et al., 2018; Gani et al., 2012; Gupta et al., 2010; Loskutov and Khlestkina, 2021). On the microcomponent side, it offers essential minerals such as calcium, iron, magnesium, phosphorus, potassium, and zinc, along with trace elements like copper, manganese and molybdenum; additionally, it is a source of B-vitamins (Abeshu and Abbrha, 2017; Din et al., 2018; Shvachko et al., 2021).

Barley seeds' proximate composition was assessed over the last decades using a wide range of techniques, such as: oven drying (Soares et al., 2016; Sologubik et al., 2013), Kjeldahl (Angelino et al., 1997; Qi et al., 2006; Tokhetova et al., 2023), Soxhlet (Garg et al., 2023; Park et al., 2023) or near infrared spectrometry (NIRS) (Albanell et al., 2021; Cozzolino, 2021; Lin et al., 2014). β -glucan analysis was accomplished with enzymatic approaches (Goudar et al., 2020; Islam et al., 2021; McCleary and Codd, 1991) or more recently using NIRS (Abeshu, 2021; Albanell et al., 2022; Ghizzoni et al., 2022; Meenu et al., 2021; Tsige et al., 2020). Among these, NIRS holds numerous advantages in the proximate analysis due to its speed and efficiency, non-destructive nature preserving original samples, reduced chemical waste, simultaneous analysis of multiple components, high accuracy and precision, cost-efficiency over time, real-time monitoring capabilities and resilience to sample variability; it proved to be a valuable tool for cereal quality control and research, contributing to faster and more environmentally friendly analysis processes.

Barley seeds find diverse applications, such as in human food production, livestock feed and health support due to their nutritional value, while they also play a role in biomass and ethanol production. Barley is commonly used in human diets: it can be processed into various food products, such as barley flour for baking bread, barley flakes for cereals and barley pearls for soups and stews. Meanwhile, it is a crucial ingredient in the beer and whiskey production processes (Lukinac and Jukić, 2022; Shvachko et al., 2021). Barley is a valuable source of nutrition for livestock, including cattle, poultry and pigs; it provides significant energy and protein, making it a staple in animal feed formulations (Badea and Wijekoon, 2021; Babatunde et al., 2021). Barley also offers a wide range of health benefits: it is a good source of dietary fiber, B vitamins, minerals and antioxidants, being often included in diets to support overall health and digestive function (Geng et al., 2022; Gangopadhyay et al., 2015; Sharma et al., 2022); it reduces cholesterol (β -glucan has been linked to lowering LDL cholesterol levels, which can reduce the risk of heart disease), enhances gut health and facilitates digestion (Ho et al., 2016; Hughes and Grafenauer, 2021; Ryan et al., 2007). Moreover, some varieties of barley are bred to have lower gluten content and are used in the production of gluten-free products, making them suitable for individuals with gluten sensitivity (Tanner et al., 2016). Last but not least, barley straw and residues can be used for biomass energy production and as a feedstock for bioethanol production (Raud et al., 2021). Overall, barley seeds offer a wide range of valuable compounds that contribute significantly to human nutrition and health status, standing out particularly as an excellent source of β -glucan. Leveraging the potency of barley's β -glucan, the food industry has the opportunity to enhance the nutritional profile of cereals, bread, pasta, snacks and other fiber-enriched products, thereby supporting cardiovascular wellness and digestive health.

The research objectives of this study align with the broader goal of enhancing the nutritional quality of food products: 1) to assess the proximate composition and the β -glucan content of eight two-rowed spring barley genotypes obtained in different crop systems; 2) to identify ideal candidates among these genotypes for the production of functional foods.

MATERIALS AND METHODS

Plant material

Spring barley seeds (*Hordeum vulgare* ssp. *distichum*) were harvested in 2022 from eight two-rowed spring barley cultivars - 4 genotypes of autochthonous origin creation of ARDS Turda (Turdeana, Aura, Daciana and Romanita) and 4 genotypes of foreign origin (Su Lilly, Tatum, Sunshine and Armada), originating from field trials performed at Agricultural Research and Development Station Turda (a research unit located in the western part of the Transylvanian Plateau of Romania). Three crop system approaches were employed: conventional (utilizing 150 kg/ha Nitrocalcar), ecological (using 1000 kg/ha Fertildung) and a no-treatment control group; the experiment was organized in a randomized block design with three replicates.

Proximate analysis

Representative barley grains were screened for impurities, being then subjected to near infra-red spectrometric measurements using a Tango spectrometer with rotating sample cup (Bruker Optics GmbH, Ettlingen, Germany), calibrated to provide data for moisture, protein, sugar, starch, fat and ash.

β -glucan determination

Barley grains were ground in a centrifugal mill, then passed through a 0.5 mm sieve to obtain a consistent powder; samples of ~100 mg were weighed and subjected to enzymatic analysis using the Megazyme mixed linkage

kit (Megazyme International Ireland Ltd., Bray, Ireland), compliant with AOAC 995.16 and AACC 32-21.01 methods; the spectrophotometric measurements were performed at 510 nm on a T80+ UV/VIS spectrophotometer (PG Instruments, Ltd., Lutterworth, UK).

Data analysis

The NIR's instrument control, data acquisition and data analysis were accomplished using the Opus software (Bruker Optics GmbH, Ettlingen, Germany). Microsoft Excel (Microsoft, USA) was used for processing data matrices and for descriptive statistics. Principal component analysis (PCA) and cluster analysis were performed after mean center preprocessing of the experimental data using MatLab (The Mathworks Inc., USA). Each sample was analyzed in triplicate and mean values were reported.

RESULTS AND DISCUSSIONS

Spring barley seeds originating from the conventional culture system (Table 1) are relatively similar in terms of moisture (ranging from 11.08% to 11.39%) and ash (1.50% to 1.90%). They are low in fat (1.56% to 2.47%), rich in protein (9.33% to 10.93%) and primarily composed of starch (ranging from 49.63% to 60.54%) with varying sugar levels (3.10% to 5.06%) and β -glucan's content (from 3.87 to 4.73 %).

Table 1. Comparative proximate composition and β -glucan content of barley genotypes (%) originating from the conventional culture system

ID	β -glucan	Moisture	Ash	Fat	Protein	Starch	Sugar
Turdeana	4.73	11.12	1.69	1.56	10.93	54.19	5.06
Aura	4.58	11.10	1.69	1.68	10.91	54.95	4.50
Daciana	4.28	11.39	1.77	2.41	10.44	56.33	3.38
Romanita	4.03	11.14	1.59	2.26	10.38	59.28	3.40
Su Lilly	3.98	11.08	1.72	2.47	10.90	58.70	4.36
Tatum	4.61	11.22	1.50	2.05	9.33	60.54	3.43
Sunshine	3.87	11.18	1.61	2.11	9.43	56.39	3.30
Armada	4.72	11.22	1.90	2.51	9.59	49.63	3.10
average	4.35	11.18	1.69	2.13	10.24	56.25	3.82
min	3.87	11.08	1.50	1.56	9.33	49.63	3.10
max	4.73	11.39	1.90	2.51	10.93	60.54	5.06

Spring barley seeds originating from the ecological culture system (Table 2) are characterized by lower ranges of protein (8.62% to 9.59%), moisture (10.96% to 11.22%) and ash (1.40% to 1.68%) and lower average β -glucan (4.30%), starch (55.54%) and sugar (2.63%) contents in comparison with those from the conventional system, but they are slightly higher in fat range (1.81% to 2.60%). The smaller content in β -glucan in a similar context was reported in research targeting conventional and organic systems (Menkovska et al., 2017).

Table 2. Comparative proximate composition and β -glucan content of spring barley genotypes (%) originating from the ecological culture system

ID	β -glucan	Moisture	Ash	Fat	Protein	Starch	Sugar
Turdeana	4.54	10.96	1.68	2.16	9.45	54.43	2.32
Aura	4.66	11.21	1.64	2.35	9.12	53.95	2.76
Daciana	4.45	11.22	1.40	2.30	9.07	58.33	2.80
Romanita	4.09	10.97	1.59	2.60	9.59	56.55	3.41
Su Lilly	4.18	10.96	1.45	2.09	8.62	56.16	3.90
Tatum	4.22	11.05	1.55	2.29	8.74	54.01	2.50
Sunshine	3.97	11.02	1.54	2.37	9.36	55.76	3.46
Armada	4.25	11.13	1.52	1.81	9.20	55.15	1.83
average	4.30	11.07	1.55	2.24	9.14	55.54	2.87
min	3.97	10.96	1.40	1.81	8.62	53.95	1.83
max	4.66	11.22	1.68	2.60	9.59	58.33	3.90

The no-treatment approach yielded notably higher average levels of β -glucan (4.48%) and fat (2.34%) in the examined spring barley genotypes. Conversely, the remaining parameters demonstrated reduced values, underscoring that refraining from chemical fertilizer interventions can foster the development of a nutritionally enriched spring barley crop (Table 3).

Table 3. Comparative proximate composition and β -glucan content of spring barley genotypes (%) originating from the no treatment culture system

ID	β -glucan	Moisture	Ash	Fat	Protein	Starch	Sugar
Turdeana	5,01	11,04	1,61	2,30	9,44	56,76	2,21
Aura	4,74	11,02	1,51	2,50	9,52	56,23	2,57
Daciana	4,81	11,41	1,41	2,28	8,85	58,14	2,08
Romanita	4,25	11,10	1,58	2,24	8,73	53,13	2,64
Su Lilly	4,06	11,02	1,42	2,42	8,91	57,35	3,82
Tatum	4,61	11,14	1,53	2,21	8,41	55,13	2,17
Sunshine	4,06	11,16	1,47	2,49	8,68	56,08	3,23
Armada	4,32	11,24	1,60	2,27	9,33	54,12	2,28
average	4.48	11.14	1.52	2.34	8.99	55.87	2.63
min	4.06	11.02	1.41	2.21	8.41	53.13	2.08
max	5.01	11.41	1.61	2.50	9.52	58.14	3.82

This study revealed that the conventional treatment approach yielded the highest average values for starch, sugar, protein, and ash content, suggesting that conventional cultivation methods may have varying effects on specific nutritional parameters, making them more suitable for particular applications. Although the eight genotypes have the same nutrients, some stands out for particular characteristics. The Tatum and Daciana genotypes had a higher content of carbohydrates, considering it important for nutrition and the malting industry. The Turdeana, Romanita and Daciana genotypes showed high protein content; this parameter is significant for the feed industry and human nutrition. Su Lily, Romanita and Aura are the genotypes with the highest fat content, while Turdeana and Aura are the ones with the highest β -glucan content.

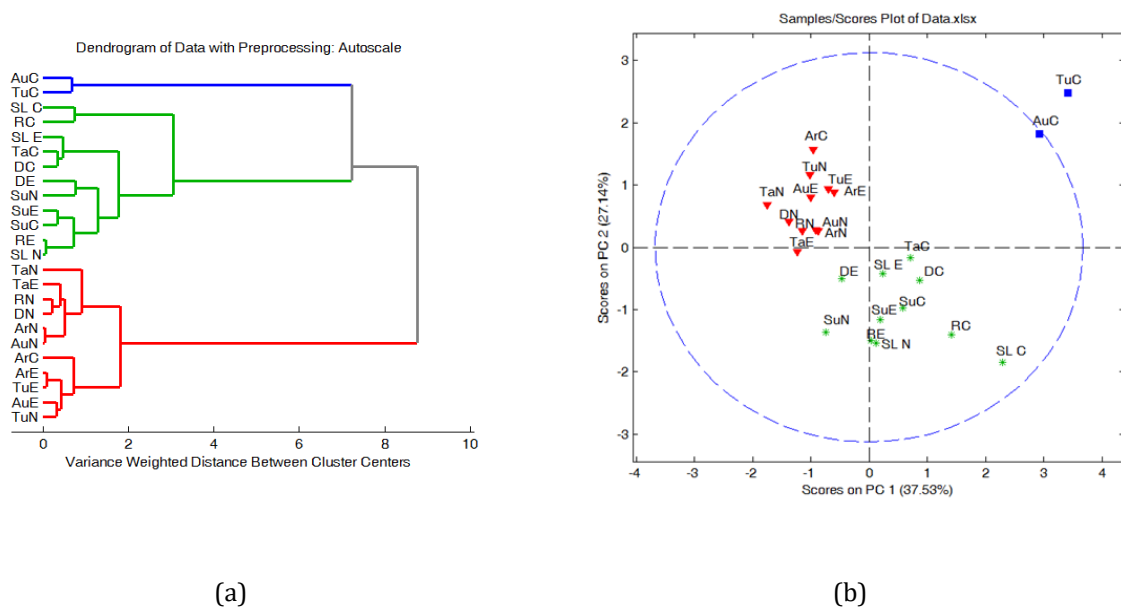
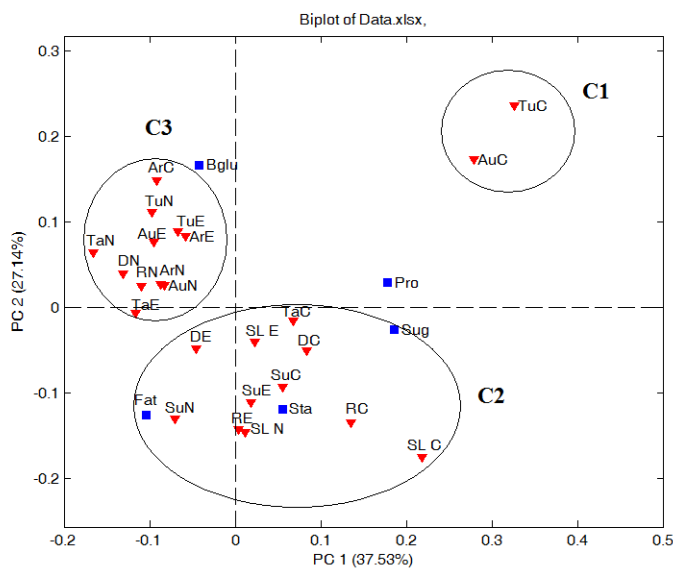


Figure 1. Dendrogram resulted from cluster analysis (a) and score's plot (b) for spring barley seeds data

PCA of the experimental data was conducted using five key variables (the content of β -glucan, protein, starch, fat, and sugar); the resulted model comprised three principal components, with first two accounting for 64.67% of the data's variability; PCA coupled with cluster analysis unveiled a data structure characterized by three clusters, as depicted in Figure 1. The biplot illustrated in Figure 2 serves as a useful tool for the fast selection of spring barley genotypes for specific applications: cultivars from cluster C2, characterized by lower β -glucan content and moderate protein levels are suitable for brewing applications, where an excessive β -glucan content can lead to complications such as increased viscosity and negative effect on the beer clarity and stability. In contrast, genotypes from clusters C1 and C3 are deemed most suitable for the production of functional foods.



Clusters:
 C1 – genotypes with the highest content of protein & sugars;
 C2 – genotypes with the lowest β -glucan's content;
 C3 – genotypes with the highest β -glucan's content.

Figure 2. Biplot for spring barley seeds data

The data reported in this study is consistent with findings from previous research, with inherent variations due to various factors including environmental and soil conditions, genotype and agricultural practices. Hence, the proximate composition of spring barley seeds belonging to genotypes from the Canary Islands displayed the following ranges for key parameters: moisture (11.9% - 16.2%), ash (2.43% - 2.91%), starch (52.2% - 59.2%) and protein (10.8% - 14%) following fertilization with 300 kg/ha of 15-15-15 complex NPK fertilizer (Panizo-Casado et al., 2020). In Latvia, research demonstrated protein levels ranging from 10.66% to 14.68%, fat content between 2.01% and 2.35%, starch content ranging from 62.2% to 64%, and β -glucan between 4.28% and 4.94% when applying 4470 kg/ha mineral complex fertilizer NPK 17:10 (Šterna et al., 2015). Furthermore, a study analyzing the proximate composition and energy value of five varieties of malting spring barley of Mexican origin (Castilio et al., 2019) reported high average amounts of total carbohydrates (76.84%), protein (12.47%), fiber (5.65%), fat (2.67%), ash (2.36%), and moisture (10.34%). Japanese barley genotypes exhibited varying protein content from 7.7% to 12.81%, fat content between 2.11% and 2.46%, ash ranging from 1.05% to 1.34%, starch levels between 72.86% and 77.44%, and β -glucan from 3.58% to 6.85% (Kim et al., 2016). Korean genotypes displayed protein, β -glucan and starch content within the ranges of 10.0% - 12.9%, 4.4% - 7.5%, and 49.7% - 65.3%, respectively (Lee et al., 2012); in another study, moisture, ash, protein, and starch content ranged between 7.3% - 11.1%, 1.6% - 2.2%, and 9.3% - 11.9%, and 56.1% - 67.9%, respectively (Lee et al., 2012). A study on proximate composition of barley seeds conducted in Ethiopia reported the following ranges: protein (10.07% - 14.10%), moisture (11.35% - 13.07%), ash (1.43% - 2.31%), fat (2.20% - 6.40%) and carbohydrates (45.69% - 58.45%) (Abeshu and Abhra, 2017). The reported β -glucan contents exhibited significant variability across studies, with values ranging from 2.5% to 5.4% (Papageorgiou et al., 2005), 1.37% to 6.05% (Manzali et al., 2016), 3.33% - 3.44% (Menkovska et al., 2017), 4.3% - 6.8% (Bonman et al., 2019), 4.37% - 6.5% (Lee et al., 1997), 4.6% - 6.5% (Kumar et al., 2021), 5.3% (Zielke et al., 2017), 1.86% - 5.37% (Havrlentová and Kraic, 2006) and 4.13% - 7.39% (Lee et al., 2011). These diverse findings underscore the influence of various factors on the composition of spring barley seeds in different regions and under various cultivation practices.

CONCLUSIONS

This study provides valuable insights into the nutritional composition of spring barley seeds belonging to genotypes cultivated in different agricultural systems, emphasizing the impact of cultivation methods on key nutritional parameters.

- The obtained data revealed that the choice of cultivation system significantly affects the nutritional composition of spring barley seeds. The conventional system yielded higher levels of starch, sugar, protein and ash content, making it suitable for specific applications. In contrast, the ecological and no-treatment systems exhibited variations, with the no-treatment approach leading to notably higher β -glucan and fat content, potentially contributing to the development of nutritionally enriched spring barley crops, while the conventional approach demonstrates superior outcomes for starch, sugar and ash content.

- The nutritional diversity among different spring barley genotypes opens up opportunities for genotype-specific applications: hence, genotypes with particular characteristics, such as high carbohydrate content (Tatum and Daciana), high protein content (Turdeana, Romanita, and Daciana) and high fat content (Su Lily, Romanita, and Aura), can be targeted for various applications.
- The chemometric data analysis proved to be a valuable tool for a fast selection of suitable spring barley cultivars for specific applications, supporting the development of functional foods and optimizing the brewing process.
- The resulted knowledge contributes to a deeper understanding of how to harness the potential of spring barley for enhancing human nutrition and overall well-being. The investigation underscores the impact of cultivation methods on nutritional parameters and identifies the best candidates for functional food production.

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Conflicts of Interest

The authors declare that they do not have any conflict of interest

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