Journal of Agricultural Sciences (Belgrade)
Vol. 69, No. 3, 2024
Pages 271-286

https://doi.org/10.2298/JAS2403271C
UDC: 635.656:575.22(497.11)"2022"
Original scientific paper

CHEMICAL AND TECHNOLOGICAL COMPOSITION OF SPRING GREEN PEA (*PISUM SATIVUM* VAR. *HORTENSE* L.) GENOTYPES

Janko F. Červenski[*], **Srđan D. Zec, Biljana M. Kiprovski, Dario Đ Danojević, Gordana M. Tamindžić, Maja V. Ignjatov and Dragana Đ. Miljaković**

Institute of Field and Vegetable Crops, National Institute of the Republic of Serbia,
Maksima Gorkog 30, 21000 Novi Sad, Serbia

Abstract: Through the chemical-technological analysis of (technologically) mature spring pea genotypes, we examined the following traits: moisture content, ash, oil, total nitrogen, protein, total sugars, starch, cellulose, and content of total soluble solids (Brix) (eight lines and two varieties). This research aimed to determine the chemical and technological characteristics of the selected spring pea genotypes, assess the variability structure of pea genotype characteristics, and therefore assess the contribution of the individual characteristics to the overall variability. The field trial was set up in 2022 at the Rimski Šančevi site on a chernozem-type soil in an irrigation system in the Department of Vegetable and Alternative Crops, Institute of Field and Vegetable Crops, Novi Sad. The lines with a higher protein content SK-1, SK-5, and SK-10 as well as the lines with a higher sugar content SK-4, SK-5, and SK-8, which are included in the development of pea varieties, have a special value in the selection of vegetable peas with a high protein and sugar content. Pea genotypes SK-6, SK-7, and SK-8 with a higher Brix value can be used for the earlier selection of sweeter peas suitable for fresh or early spring consumption. Based on the cluster analysis, the pea genotypes were classified into individual groups to assess the impact on the variability of each trait. Principal component analysis revealed that the four separate components cumulatively explained 91.91% of the total variability.

Key words: garden pea, seeds, PCA, cluster.

Introduction

Spring green pea (*Pisum sativum* var. *hortense* L.) is an annual cool-season herbaceous legume that belongs to the *Fabaceae* family. It is one of the nutritionally most important vegetable crops, as it contains a high percentage of proteins, essential amino acids, and a significant content of vitamins, minerals, and

---

[*] Corresponding author: e-mail: janko.cervenski@ifvcns.ns.ac.rs

carbohydrates. The rapid growth of the world's population today also requires an increase in food supply (Červenski et al., 2021; Tamindžić et al., 2023). In this regard, peas are rich in proteins (20–35%), sugars (8–12%), low amounts of fat (0.5–4.0%), and high amounts of starch (about 30–48%), vitamins A and C, calcium and phosphorus and a small amount of iron (García Arteaga et al., 2021; Kumar et al., 2021).

Peas are one of the most widely produced legumes, accounting for 26% of the total global production of legumes. As a leguminous crop, peas fix nitrogen in the soil and are thus also beneficial in agriculture **(**Červenski et al., 2017). It is also one of the most commonly consumed and cultivated legumes (Shen et al., 2022). With the change in people's dietary habits, the availability of garden peas in the market is demanded by customers throughout the year. In addition to the seasonal use of fresh grain, it is also consumed as a processed product, whether canned, dehydrated or frozen for off-season consumption (Nasir et al., 2023). Regarding the importance and quantity of processed products, peas occupy one of the first places in the vegetable canning industry (Đorđević et al., 2021). Pea production has a long tradition as an industrial crop in Serbia. Short growing seasons, relatively simple production, pleasant taste, and high nutritional value of the grain stimulate the production and consumption of peas. It has a nutritionally favorable composition concerning macronutrients: low fat, high fiber and protein content, and starch with a low glycemic index (Jovićević et al., 2008). The fact that the energy value of peas is 339 kJ shows the importance of this crop for human nutrition (Vlahović, 2015).

This research aimed to determine the chemical and technological properties of the selected spring green pea genotypes, look into the structure of the variability of the characteristics of the pea genotypes, and assess the contribution of the individual characteristics to the total variability.

Material and Methods

Study area

The field trial was set up in 2022 at the Rimski Šančevi site on a chernozem-type soil in an irrigation system in the Department of Vegetable and Alternative Crops, Institute of Field and Vegetable Crops, Novi Sad (45°19'55.7"N, 19°50'14.9"E, and 86 masl).

The experiment was conducted using a randomized block design with five replications. The basic plot comprised two rows of pea genotypes spaced 20 cm apart between the rows and 5 cm apart within the rows, with a row length of 3 meters. The distance between the two plots was 80 cm to facilitate manipulation and tillage between the rows during the growing season. Harvesting was done manually at the time of technological maturity of all examined pea genotypes.

Sampling procedure

Under favorable conditions, the phase of optimal technological maturity usually lasts from 2 to 5 days, depending on the variety. Harvesting is carried out when 75% to 80% of the peas are technologically ripe, which is characterized by a sweet taste, uniform color, uniform consistency and characteristic smell. These organoleptic quality parameters correspond to the optimal content of dry matter, a certain ratio of sugar and starch, the amount of alcohol-insoluble substances (ANS) and grain hardness. Compliance with these quality parameters is achieved with a sugar content of 5.5 to 6.5, a starch content of 6% to 7%, and a content of nitrogenous substances of around 5%. This ratio of the main ingredients is achieved when the dry matter amounts to 16 to 22%, depending on the pea variety (Vračar, 2001; Ilić et al., 2007; Jovićević et al., 2008; Červenski et al., 2021).

Plant material

The examined material is part of the genetic collection of *Pisum sativum* L., which belongs to the Institute of Field and Vegetable Crops, Novi Sad. Eight pea lines and two commercial spring green pea cultivars, Tamiš (ST) and Danube (SD) were included in this research. The tested spring green pea genotypes were selected based on previous studies/observations and the determination of specific parameters important for pea breeding.

Measurements

The working sample for the chemical and statistical analyses consisted of 10 plants per replication, i.e., a total of 50 plants per genotype. Fresh pea seeds were homogenized (using IKA T 10 basic ULTRA-TURRAX®) and further used for the analyses of the contents of ash, proteins, oil, cellulose, starch, total sugars, Brix (Bx). Moisture and ash contents were determined gravimetrically (dried for 3 h at 105°C and ignited for 2 h at 600°C) according to Ph. Eur. (2013). Total nitrogen was determined using the Kjeldahl method (manufacturer's specification Gerhardt, 2003), while total protein content was calculated using the conversion value of 6.25. The oil content was determined by the Soxhlet extraction (8 h, 70°C) (Ph. Eur., 2013). The cellulose content was determined by the modified Scharrer method (SRPS ISO 6541:1996) (identical to ISO 6541:1981). The starch content was determined by the polarimetric method (ISO 10520:1997). Total sugar was determined according to the Luff-Schoorl method (Official Gazette, 41/87). All seed traits were expressed as g per 100 g of the dry weight (g 100 g^{-1} d.w.) and moisture content (%). The Balling Relative Intensity Index (Brix, °Bx), the sugar content of an aqueous solution (g sucrose/100 g of the sample), was determined directly using a digital refractometer (ATR ST Plus, Schmidt + Haensch, Germany) and expressed as % of the fresh pea seeds.

Statistical analysis

The basic statistical indicators for quantitative traits were calculated using the InfoStat ver. 2011 program. The following values were determined: minimum, maximum, mean values, and coefficient of variation. The Jamovi 2.3.24 software was used for cluster analysis (CA) and principal component analysis (PCA) to group the genotypes based on similarities and differences in quantitative traits. For CA, the Euclidean distance measure and the complete clustering method were used as options in the snow cluster module. For the component loadings, no rotation method was selected in the factor module, and the snow cluster module was used for the PCA biplot.

Results and Discussion

Botanically mature grain has a low water content and a higher energy value and is a significant source of protein in the diet (Červenski et al., 2021). Peas are essential for human nutrition due to their high protein, sugar and starch content and high energy value. As the grain ripens, the content of sugar and peptides decreases, the content of protein and starch increases, and the grain becomes firmer, with higher tenderometric values and therefore becomes unfavorable for all forms of processing. As the degree of maturity increases, the sugar is transformed into starch and the grain acquires a harder consistency and a floury taste and is less acceptable. Considering that the pea grain is of better quality when the sugar content is higher, great attention is paid to the degree of maturity (Jovićević et al., 2008).

Seeds play a crucial role in creating optimal yield through pathogen-free crop production. Healthy seeds, free from seed-transmitted pathogens, are a prerequisite for successful production and an optimal plant population (Milosević et al., 2023).

The values of the analyzed traits of the tested spring green pea genotypes are listed in Table 1.

Moisture content in spring green pea seeds

The moisture content of the green pea genotypes in this research ranged from a minimum of 61.31% (SK-6) to a maximum of 72.22% (SK-5) (Table 1). These values are slightly higher compared to the results of Borah et al. (2021), who stated that the moisture content ranged between 58.51% and 62.31%. Research by Ganjloo et al. (2018) has found that the initial moisture content of green peas is up to 75.15%. They also state that all physical properties of green pea seeds depend on moisture content. Hatamipour and Mowla (2003) note that green peas have a natural moisture content of about 75%. The variation of moisture content of green peas in the range from 71.25% to 79.2% was obtained in the study of Senapati et al. (2019).

Table 1. Values of chemically and technologically analyzed contents of ash, proteins, oil, cellulose, starch, total sugars, Brix expressed as g per 100 g of the dry weight (g 100 g^{-1} d.w.) and moisture content (%) of fresh (a) and dry (b) seeds.

Pea genotype	Moisture content[a]	Ash[b]	Oil[b]	Total nitrogen[b]	Proteins[b]	Total sugars[b]	Starch[b]	Cellulose[b]	Brix[ad]
ST	64.98	3.67	7.58	5.03	31.43	8.32	48.87	15.21	17.6
SD	64.55	3.38	6.99	3.99	24.96	8.58	53.20	10.17	16.5
SK-1	70.80	3.75	10.11	4.57	28.55	6.51	53.69	9.94	11.9
SK-4	69.11	3.93	8.99	3.68	22.97	13.15	41.89	6.79	14.5
SK-5	72.22	3.84	7.23	4.78	29.89	12.80	48.63	8.82	12.6
SK-6	61.31	3.43	3.91	3.43	21.44	5.28	56.80	9.54	16.0
SK-7	62.28	3.44	6.67	4.06	25.36	5.02	63.38	8.12	16.7
SK-8	66.38	3.59	7.39	4.11	25.70	11.38	38.63	9.28	17.6
SK-9	67.64	3.67	14.60	3.59	22.43	6.10	47.17	18.31	15.4
SK-10	63.43	3.62	8.62	4.29	26.80	5.68	35.98	10.20	15.8
Mean	66.27	3.63	8.21	4.15	25.95	8.28	48.82	10.64	15.4
Minimum	61.31	3.38	3.91	3.43	21.44	5.02	35.98	6.79	11.9
Maximum	72.22	3.93	14.60	5.03	31.43	13.15	63.38	18.31	17.6
CV[c]	5.48	4.94	33.88	12.58	12.58	37.78	17.24	32.56	12.4

Coefficient of variation (%),[d] (°Bx).

Ash content in spring green pea seeds

Ash content is a raw parameter, which is considered an indicator of the mineral content in the edible part of the grain, which includes essential elements for human life (Mohammed et al., 2018). As for this parameter, the values varied between genotypes. The lowest value of ash content was recorded in the Dunav variety (SD) at 3.38 g (100 g)$^{-1}$, in the pea line SK – 4 g (100 g)$^{-1}$, and the ash content was 3.93 g (100 g)$^{-1}$ (Table 1). According to previous literature reports, the ash content in peas varied and ranged from 2.3 to 5.2 g (100 g)$^{-1}$ (Wang and Daun, 2004; Boye et al., 2010; Nikolopoulou et al., 2007; Wendy et al., 2012; Piecyk et al., 2012; Wani and Kumar, 2014; Jadwisieńczak et al., 2014; Červenski et al., 2017).

Oil content in spring green pea seeds

There were significant differences between green pea genotypes in terms of fatty oil content. The value of fatty oil content ranged from 3.91 (SK-6) to 14.60 g (100 g)$^{-1}$ (SK-9) (Table 1). The tested genotypes had a significantly higher fatty oil content compared to literature data, indicating that the fatty oil content in peas ranges from 0.6 to 3.95 g (100 g)$^{-1}$ (Wang and Daun, 2004; Nikolopoulou et al., 2007; Boye et al., 2010; Wendy et al., 2012; Pratap and Kumar, 2011; Piecyk et al., 2012; Wani and Kumar, 2014; Jadwisieńczak et al., 2014; Červenski et al., 2017). When analyzing 96 different pea samples, Hacisalihoglu et al. (2020) obtained a variation in the oil content in the grain of 5.7–21.4 g (100 g)$^{-1}$, which indicates peas with an extremely high oil content. They stated that several studies had discussed the value of developing peas as a low-cost oilseed for cultivation in colder climates, such as Canada and Northern Europe. Peas have a lower oil content (<40 g (100 g)$^{-1}$) compared to other legumes such as soybean, which has an average oil content of 200 g (100 g)$^{-1}$. Screening of potentially high-value lines such as the SK-9 line based on oil content can be used in selection to produce pea varieties with a high oil content.

Total nitrogen and protein contents in spring green pea seeds

The total nitrogen content in our research ranged between 3.43 g (100 g)$^{-1}$ (SK-6) and 5.03 g (100 g)$^{-1}$ (SD) (Table 1). These results are in agreement with Urbano et al. (2005), Gvozdenović et al. (2011), Červenski et al. (2017) and Borah et al. (2021), who have stated that the total nitrogen content ranges up to 4.49 g (100 g)$^{-1}$. The increase in the total nitrogen content can be due to temperature and water conditions as well as morphological and useful characteristics that are subject to change by breeding (Gautam et al., 2017).

Proteins are essential macronutrients and an important part of a healthy diet. High-quality pea proteins are a significant source of essential amino acids such as histidine, lysine, phenylalanine, and threonine (Gomes et al., 2021). Peas are increasingly used as a protein source in plant-based products (García Arteaga et al., 2021). Increasing attention is being paid to plant proteins due to the growth of the world’s population, the growing protein deficiency, and their diverse ecological, functional, nutritional, and health benefits (Shen et al., 2022).

The values of protein content in our research ranged from 21.44 g (100 g)$^{-1}$ (SK-6) to 31.43 g (100 g)$^{-1}$ (SD) (Table 1). A review of the previous literature revealed that the protein content in pea seeds ranged between 15.8 g (100 g)$^{-1}$ and 34.7 g (100 g)$^{-1}$ (Wang and Daun, 2004; Stanek et al., 2004; Nikolopoulou et al., 2007; Boye et al., 2010; Pratap and Kumar, 2011; Wendy et al., 2012; Piecyk et al., 2012; Wani and Kumar, 2014; Jadwisieńczak et al., 2014; Sepehya et al., 2015; Khichi et al., 2017; Barcchiya et al., 2018; Singh and Dhall, 2018; Červenski et al., 2017; Borah et al., 2021), which is in agreement with our results. The overall phenotypic expression of protein content depends on environmental and genotypic components, and cultivars originating from different geographical areas manifest a range of protein content levels (Dhaliwal et al., 2021).

Total sugar content in spring green pea seeds

When harvested as a young grain, while the endosperm is still soft, peas are rich in vitamins and sugars. This phase of development is relatively short, and the higher production of young grains is achieved by successive sowing of the same pea cultivar or simultaneous sowing of pea cultivars with different vegetation periods (Ambrose, 2008).

In this research, a significant variation in the content of total sugar was observed between the tested pea genotypes (Table 1). The values of the total sugar content ranged between 5.02 g (100 g)$^{-1}$ for SK-7 and 13.15 g (100 g)$^{-1}$ for SK-4. The range of total sugar content from 0.7 g (100 g)$^{-1}$ to 28.59 g (100 g)$^{-1}$ has been established in the literature (Wang and Daun, 2004; Urbano et al., 2005; Nikolopoulou et al., 2007; Pratap and Kumar, 2011; Wendy et al., 2012; Jadwisieńczak et al., 2014; Sepehya et al., 2015; Červenski et al., 2017; Singh and Dhall, 2018; Borah et al., 2021).

Starch content in spring green pea seeds

Starch makes up about 45–50 g (100 g)$^{-1}$ of the dry weight of pea seeds and consists of several fractions, which are usually classified according to their structure and digestibility (Robinson and Domoney, 2021). The pea genotypes used in this research included lines that produce seeds with different starch content. According to the obtained results, the starch content in this research ranged from a minimum of 35.98 (SK-10) to a maximum of 63.38 g (100 g)$^{-1}$ (SK-7) (Table 1), which is similar to previous findings (Wang and Daun, 2004; Urbano et al., 2005; Nikolopoulou et al., 2007; Pratap and Kumar, 2011; Wendy et al., 2012; Piecyk et al., 2012; Sepehya et al., 2015; Červenski et al., 2017; Borah et al., 2021). Pea starch is commonly used in the diet due to its relatively low degree of digestibility and high content of resistant starch, and thus these results are of great importance.

Cellulose content of spring green pea seeds

As for the cellulose content, the values in this research ranged from a minimum of 6.79 (SK-4) to a maximum of 18.31 g (100 g)$^{-1}$ (SK-9) (Table 1). According to the literature sources, the cellulose content varied among the pea cultivars and ranged between 2.0 and 15.0 g (100 g)$^{-1}$ (Wang and Daun, 2004; Stanek et al., 2004; Boye et al., 2010; Pratap and Kumar, 2011; Wendy et al., 2012; Wani and Kumar, 2014; Jadwisieńczak et al., 2014; Shen et al., 2022). The SK-9 line had the highest cellulose content, which ranks it among the peas with increased fiber content compared to the literature data. According to the recommendation of Dodevska et al. (2013), green peas have great potential for medical nutrition therapy that requires a higher fiber intake as they are an excellent source of total dietary fiber.

Brix

The sugar content, of course, influences sweetness, an important component of product quality. However, sugar is the most abundant soluble solid in many vegetable juices. Therefore, Brix values primarily represent estimates of the sugar content in vegetables. Nevertheless, it is important to note that sweetness can be overwhelmed by other aspects of flavor. Therefore, a high Brix value does not guarantee a sweet flavor (Ahmed et al., 2022). The content g (100 g)$^{-1}$ of total soluble solids (or Bx) in spring green peas indicates the possibility of selecting the appropriate source material for crop improvement. The tested genotypes showed a significant variation in total soluble solids in spring green peas. The pea line SK-1 had a minimum of 11.9 g (100 g)$^{-1}$, while the maximum values of total soluble solids were recorded in SK-8 and ST – 17.6 g (100 g)$^{-1}$ (Table 1). Previous studies have also found a significant difference in total soluble solids between different cultivars, with Brix values ranging from 6.81 to 25.33 g (100 g)$^{-1}$ (Sepehya et al., 2015; Khichi et al., 2017; Barcchiya et al., 2018; Borah et al., 2021; Gautam et al., 2017; Sharma et al., 2020; Yathish et al., 2021; Arunadevi et al., 2022).

Statistical analysis of the tested quality parameters of spring green pea seeds

Ash and moisture contents were the traits with the lowest coefficient of variation (4.94% and 5.48%, respectively), which could indicate a low selection gain for ash content in future generations, while the low moisture content showed that the genotypes were similar in terms of maturity date and the samples were taken at the same time for analysis (Table 1). The high coefficient of variation was noted for total sugar (37.78%), oil (33.88%), and cellulose content (32.56%), indicating high variability among genotypes for these traits.

Table 2. Principal component analysis of the studied traits.

Trait	PC 1	PC 2	PC 3	PC 4
Moisture	0.933			
Ash	0.905			
Oil	0.402	-0.805	0.340	
Total nitrogen	0.560	0.603	0.561	
Proteins	0.560	0.603	0.561	
Total sugars	0.668		-0.476	0.385
Starch	-0.444			-0.748
Cellulose		-0.544	0.771	
Brix	-0.660			0.665

*Values below 0.3 are not shown.

The principal components analysis reduced the original eight variables to four artificial, uncorrelated variables, i.e., the principal components. The principal component method concentrated the variability on the first principal component. The first principal component explained most of the variability of all the investigated properties. The first component was mainly defined by the following properties: moisture, ash, and total sugars. The second component had the highest correlation with fatty oil, total nitrogen, and protein content. The cellulose content was defined as the third component. The fourth component consisted of starch and Brix (Table 2).

The four extracted components cumulatively explained 91.9% of the total variability. The individual contribution of each of the mentioned components to the total variability was 39.54 %, 20.42%, 18.38% and 13.56 %, respectively (Table 3).

Table 3. Eigenvalue and percentage of variance using four principal components (PCs).

PC	Eigenvalue	Total variance, %	Cumulative, %
1	3.5589	39.54	39.54
2	1.8376	20.42	59.96
3	1.6545	18.38	78.34
4	1.2210	13.56	91.90

In this regard, by analyzing the chemical composition of winter pea grains, the authors (Shen et al., 2022) obtained three separate components, which collectively explained 81.59% of the total variability. Moreover, the results of Espósito et al. (2007) obtained for pea genotypes for the first two components explained 67.7% of the variability in the first trial season and 69.8% of the variability in the second trial season.

The factor loading > 0.70 was used as a criterion for extracting the variables that defined most of the extracted components. The factor loadings are correlations between the individual variables and factors that indicate the degree of correspondence between the variables and the factors.

Based on the cluster analysis, the genotypes were divided into four individual groups. The first observed group of spring pea genotypes (SK-10, SK-8, ST) had four maximum values among the observed properties, namely: total nitrogen content (ST), protein (ST) and Brix (ST and SK -8). In this group, one of the lowest values of the observed properties was recorded for the starch content (SK-10 and SK-8). The contents of moisture, ash, oil, and total sugars were mainly around the average value determined for the observed properties (Figure 1).

The second group of spring pea genotypes (SK-9) was obtained by separating the mentioned genotypes from the others based on the highest content of oil and cellulose. The values of the other properties were around the observed average values, although they were mostly slightly less than the arithmetic mean of the observed properties (Figure 1).

In the third group of spring green pea genotypes (SK-7, SD, SK-6), the highest value among the observed genotypes was obtained only for starch content (SK-7). The minimum values of the examined traits of the pea genotypes defined this group, such as moisture (SK-6, SK-7), ash (SD, SK-6, SK-7), oil (SK-6, SK-7, SD), total nitrogen (SK-6), protein (SK-6), and total sugar contents (SK-7, SK-6). The cellulose content was slightly lower than the arithmetic mean value, while the Brix values were a bit higher than the arithmetic mean of the observed pea genotypes.

In the fourth group of spring green pea genotypes (SK-5, SK-1, SK-4), maximum values were obtained for the contents of moisture, ash, and total sugars (SK-4 and SK-5). SK-4 achieved the minimum value for the cellulose content, while all three genotypes had the minimum values for the Brix property. Other trait values for this group were around the arithmetic mean of the individual properties (Figure 1).

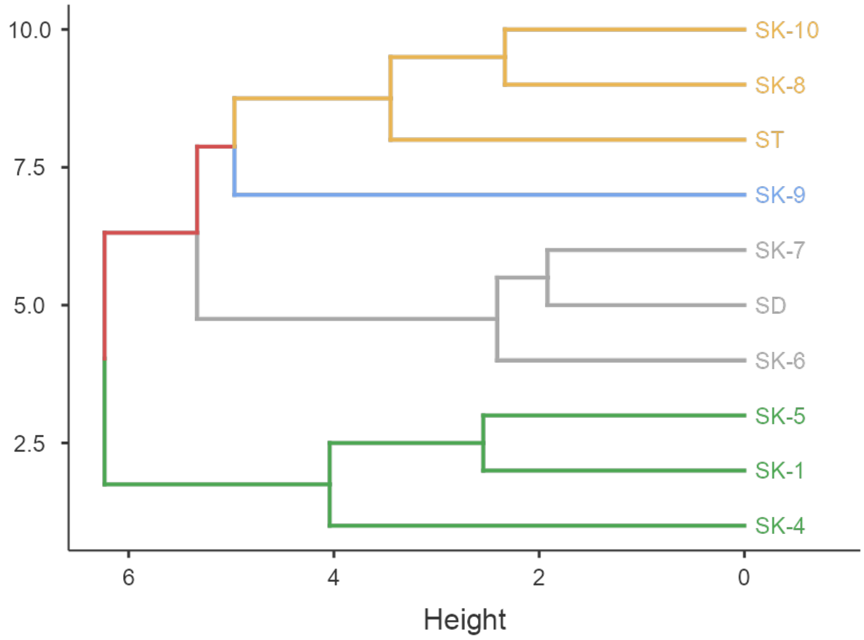

Figure 1. The cluster dendrogram of the studied spring green pea genotypes.

The PCA-biplot summarized the arrangement of the properties and the tested pea genotypes based on the PC analysis.Thus the connection between the observed properties and the pea genotypes can be seen based on the highest % of the explained variance of the first two main components (Figure 2).

The lower left quadrant of the PCA-biplot graph is defined by the highest cellulose content of the pea genotype SK-9, and therefore this genotype is separated into a separate group on the dendrogram (Figure 2).

The upper left quadrant of the PCA-biplot graph is defined by the pea genotypes SK-6, SK-7, and SD. SK-7 had the highest starch content value. The contents of ash, oil, and moisture are the furthest away from the mentioned genotype group because they achieved the minimum values of these properties (Figure 2).

The group of genotypes SK-1, SK-4, and SK-5 achieved maximum values for moisture content, ash, and total sugars, which is why they are located at a corresponding distance on the graph (Figure 2).

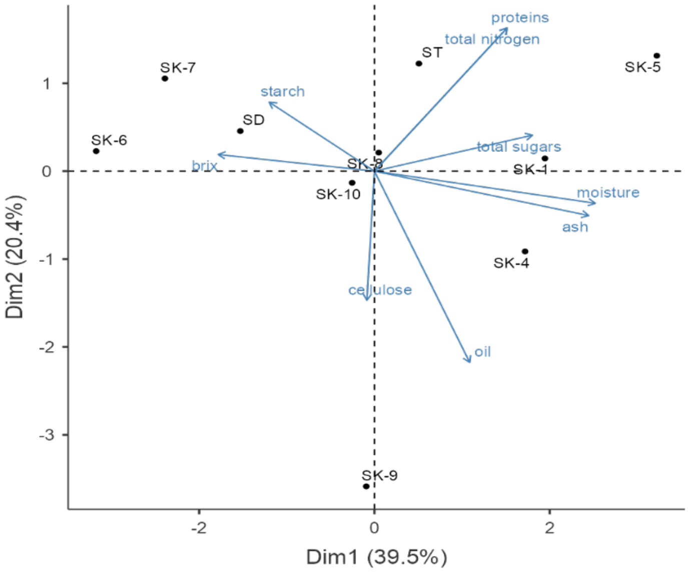

Figure 2. The PCA-biplot graph of the studied spring green pea genotypes.

Conclusion

This research aimed to determine the chemical and technological characteristics of the selected spring green pea genotypes. Through the chemical-technological analysis of the (technologically) mature spring pea genotypes, we examined the following traits: moisture content, ash, oil, total nitrogen, protein, total sugars, starch, cellulose and Brix. The tested pea genotypes were better studied and grouped according to the aforementioned analysis.

The lines with a higher protein content SK-1, SK-5 and SK-10, as well as the lines with a higher sugar content SK-4, SK-5 and SK-8, which are included in the development of pea varieties, will have a special value in the selection of vegetable peas with a high protein and sugar content.

The pea genotypes SK-6, SK-7 and SK-8 with a higher Brix can be used for an earlier selection of high sugar peas suitable for fresh, i.e., early spring consumption.

The research results have confirmed that the use of Brix in the selection of vegetable peas is mainly an indicative value for the assessment of the sweetness of the fresh grain of the lines. Using principal component analysis, four separated components explained a total of 91.912% of the total variability. The first component was defined to the greatest extent: the content of moisture, ash and total sugars. The second component was highly correlated with the content of fatty oil, total nitrogen, and protein. The third component was defined by the content of cellulose, while the fourth component was the content of starch and Brix.

The PCA-biplot graph shows the association of traits and pea genotypes based on the largest percentage of the explained variance of the first two principal components.

Acknowledgments

This research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, grant number: 451-03-47/2023-01/200032.

References

Ahmed, M.E, Ahmed Taha, G.E, Ibrahim, K.A, Mohamed, M.T, & Zeen Elabedeen, H.E. (2022). Evaluation of Digital Brixmeter Performance for Brix Measurement In Raw Sugar Solution. *Journal of Engineering Sciences, 50* (3), 1-10. https://doi.org/10.21608/JESAUN.2022.115375.1108

Ambrose, M. (2008). Garden pea. In: Prohens, J., Nuez, F. (eds) Vegetables II: Handbook of Plant Breeding, vol 2. (pp. 3-26). New York, NY: Springer New York. https://doi.org/10.1007/978-0-387-74110-9_1

Arunadevi, K., Singh M., Franco, D., Prajapati V. K., Ramachandran J., & Maruthi Sankar G. R. (2022). Real Time Soil Moisture (RTSM) Based Irrigation Scheduling to Improve Yield and Water-Use Efficiency of Green Pea (Pisum sativum L.) Grown in North India. *Agronomy 12*, (2), 278. https://doi.org/10.3390/agronomy12020278

Barcchiya, J., Naidu, A.K., Mehta, A.K., & Upadhyay, A. (2018). Genetic variability, heritability and genetic advance for yield and yield components in pea (*Pisum sativum* L.). *International Journal of Chemical Studies*, 6 (2), 3324-3327. https://www.chemijournal.com/archives/?year=2018&vol=6&issue=2&ArticleId=2360&si

Borah, L., Saikia, J., & Abstractary, A.B. (2021). Consequences of foliar zinc application on soil properties and quality of garden pea (*Pisum sativum* l.) İn assam condition. *The Pharma Innovation Journal, 10* (7), 1219-1223. https://www.thepharmajournal.com/archives/?year=2021&vol=10&issue=7&ArticleId=7038

Boye, J., Zare, F., & Pletch, A. (2010). Pulse proteins: Processing, characterization, functional properties and applications in food and feed. *Food research international, 43* (2), 414-431. https://doi.org/10.1016/j.foodres.2009.09.003

Červenski, J., Danojević, D., & Savić, A. (2017). Chemical composition of selected winter green pea (*Pisum sativum* L.) genotypes. *Journal of the Serbian Chemical Society*, *82* (11), 1237-1246. https://doi.org/10.2298/JSC170323094

Červenski, J., Medić-Pap, S., & Ignjatov, M. (2021). Proizvodnja konzumnog graška. *Zbornik referata*, 55. Savetovanje agronoma i poljoprivrednika Srbije (SAPS), (pp. 23-32). Zlatibor, https://fiver.ifvcns.rs/handle/123456789/2637

Dhaliwal, S.K., Salaria, P., & Kaushik, P. (2021). Pea seed proteins: A Nutritional and Nutraceutical Update. In Jimenez-Lopez, J.C. (Ed.). *Grain and Seed Proteins Functionality,* Chapter 7. (pp. 105-114). London: BoD–Books on Demand.

Dodevska, M.S., Djordjevic, B.I., Sobajic, S.S., Miletic, I.D., & Djordjevic, P.B. (2013). Dimitrijevic-Sreckovic VS. Characterisation of dietary fibre components in cereals and legumes used in Serbian diet. *Food Chemistry, 141* (3), 1624-1629. https://doi.org/10.1016/j.foodchem.2013.05.078

Đorđević, R., Cvikić, D., Đurić, N., Gavrilović, B., Đorđević-Melnik, O., Živanović, T., & Prodanović, S. (2021). Selekcija industrijskih sorti graška u Institutu za povrtarstvo Smederevska Palanka. *Biotehnologija i savremeni pristup u gajenju i oplemenjivanju bilja, Zbornik radova*. (pp. 123-128). Smederevska Palanka.

Espósito. M.A., Milanesi, L.A., Martin, E.A., Cravero, V.P., Lopez, A.F., & Cointry, E.L. (2007). Principal component analysis based on morphological characters in pea (Pisum sativum L.). *International Journal of Plant Breeding, 1* (2), 135-137.

Ganjloo, A., Bimakr, M., Zarringhalami, S., Safaryan, M.J., & Ghorbani, M. (2018). Moisture-dependent physical properties of green peas (*Pisum sativum* L.). *International Food Research Journal, 1*, 25 (3), 1246-1252.

García, Arteaga, V., Kraus, S., Schott, M., Muranyi, I., Schweiggert-Weisz, U., & Eisner, P. (2021). Screening of twelve pea (*Pisum sativum* L.) cultivars and their isolates focusing on the protein characterization, functionality, and sensory profiles. *Foods*, *2*, 10 (4), 758. https://doi.org/10.3390/foods10040758

Gautam, K.K., Syamal, M.M., Singh, A.K., & Gupta, N. (2017). Variability, character association and path coefficient analysis of green pod yield and its related traits in pea (*Pisum sativum* L.). *Legume Research - An International Journal, 40* (5), 818-823. https://doi.org/10.18805/lr.v0iOF.9104

Gomes, D.D., Rosa, L.S., Cordoba, L.D., Fiorda-Mello, F., Spier, M.R., & Waszczynskyj, N. (2021). Development of muffins with green pea flour and their physical and sensory evaluation and essential amino acid content. *Ciência Rural, 17*, 52:e20200693. http://doi.org/10.1590/0103-8478cr20200693

Gvozdenović, Đ., Červenski, J. Gvozdanovic-Varga, J., Vasić, M., Jovićević, D., Bugarski, D., & Takač, A. (2011). *Semenarstvo III.* Institut za ratarstvo i povrtarstvo Novi Sad, SP Print, Novi Sad.

Hacisalihoglu, G., Freeman, J., Armstrong, P.R., Seabourn, B.W., Porter, L.D., Settles, A.M., & Gustin, J.L. (2020). Protein, weight, and oil prediction by single-seed near-infrared spectroscopy for selection of seed quality and yield traits in pea (*Pisum sativum*). *Journal of the Science of Food and Agriculture, 100* (8), 3488-3497. https://doi.org/10.1002/jsfa.10389

Hatamipour, M.S., & Mowla, D. (2003). Correlations for shrinkage, density and diffusivity for drying of maize and green peas in a fluidized bed with energy carrier. *Journal of Food Engineering, 59* (2-3), 221-227. https://doi.org/10.1016/S0260-8774(02)00461-2

International organization for standardization, ISO – methods: SRPS ISO 6541:1996 Agricultural food products -Determination of crude fibre content - Modified Scharrer method.

International organization for standardization, ISO – methods: ISO 10520:1997 Native starch - *Determination of starch content - Ewers polarimetric method.*

Ilić, Z., Fallik, E., Đurovka, M., Martinovski, G., & Trajković, R. (2007). *Fiziologija i tehnologija čuvanja povrća i voća.* Kosovska Mitrovica: Z. Ilić [etc.], Novi Sad: Tampograf.

Jadwisieńczak, K.K., Choszcz, D.J., Konopka, S., Majkowska-Gadomska, J., & Głowacka, K. (2014). The content of organic compounds in pea (*Pisum sativum* L.) seeds. *Zeszyty Problemowe Postępów Nauk Rolniczych, 577*, 63-71. https://wz.izoo.krakow.pl/files/WZ_2019_2_art10.pdf

Jovićević, D., Gvozdanović-Varga, J., Vasić, M., Jokanović, M.R., & Tepić, A.N. (2008). Characteristics and Suitability of Some Pea (*Pisum sativum* L.) Varieties for Processing. *Acta Horticulturae 830,* 83-90. https://doi.org/10.17660/ActaHortic.2009.830.9

Khichi, P., Pant, R., & Upadhayay, S. (2017). Performance of garden pea varieties for their growth and yield characteristics in Vidharbha region of Maharashtra, India. *Journal of Applied and Natural Science, 1*, 9 (4), 2300-2304. http://dx.doi.org/10.31018/jans.v9i4.1527

Kumar, R., Gupta, A., Verma, K., & Singh, A. (2023). Effect of seed treatments and storage period on seed health parameters of pea (*Pisum sativum* L.) under ambient storage conditions. *Legume Research, 46*, (9), 1233-1239. https://doi.org/10.18805/LR-4634

Manufacturer specification Gerhardt (2003). Guidelines for nitrogen determination. Kjeldahl analysis.

Milosevic, D., Ignjatov, M., Nikolic, Z., Tamindzic, G., Miljakovic, D., Marinkovic, J., & Cervenski, J. (2023). Molecular Characterization of Fusarium proliferatum and F. equiseti of Pisum sativum Seed. *Legume Research, 46* (2), 233-237. https://doi.org/10.18805/LRF-695

Mohammed, Y.A., Chen, C., Walia, M.K., Torrion, J.A., McVay, K., Lamb, P., Miller, P., Eckhoff, J., Miller, J., & Khan, Q. (2018). Dry pea (*Pisum sativum* L.) protein, starch, and ash concentrations as affected by cultivar and environment. *Canadian Journal of Plant Science, 18*, 98 (5), 1188-1198. https://doi.org/10.1139/cjps-2017-0338

Nasir, G., Zaidi, S., Siddiqui, A., & Sirohi, R. (2023). Characterization of pea processing by-product for possible food industry applications. *Journal of Food Science and Technology, 60* (6), 1782-1792. https://doi.org/10.1007/s13197-023-05718-y

Nikolopoulou, D., Grigorakis, K., Stasini, M., Alexis, M.N., & Iliadis, K. (2007). Differences in chemical composition of field pea (*Pisum sativum*) cultivars: Effects of cultivation area and year. *Food chemistry*, *1*, 103 (3), 847-852. https://doi.org/10.1016/j.foodchem.2006.09.035

Official Gazette of SFRY, 41/87 (1987). *Regulation on sampling methods and methods for performing the chemical and physical analysis of cocoa beans, cocoa products, chocolate products, confectionery, cream, biscuits and biscuit related products. Method 12.*

Ph. Eur. (2013). *European Pharmacopoeia – 8th Edition* (Ph. Eur. VIII) Vol. 1. European Pharmacopoeia Commission, and the European Directorate for the Quality of Medicines & HealthCare. (EDQM), Strasbourg, France. (Methods 2.2.32. and 2.4.16.)

Piecyk, M., Wołosiak, R., Drużynska, B., & Worobiej, E. (2012). Chemical composition and starch digestibility in flours from Polish processed legume seeds. *Food Chemistry, 1*, 135 (3), 1057-1064. https://doi.org/10.1016/j.foodchem.2012.05.051

Pratap, A., & Kumar, J. (editors) (2011). *Biology and breeding of food legumes*. CABI. https://www.cabidigitallibrary.org/doi/book/10.1079/9781845937669.0000

Robinson, GH., & Domoney, C. (2021). Perspectives on the genetic improvement of health-and nutrition-related traits in pea. *Plant Physiology and Biochemistry*, *158,* 353-362. https://doi.org/10.1016/j.plaphy.2020.11.020

Senapati, A.K., Varshney, A.K., & Sharma, K.V. (2019). Dehydration of green peas: A review. *International Journal of Chemical Studies, 7* (2), 1088-1091.

Sepehya, S., Bhardwaj, S.K., & Dhiman, S. (2015). Quality attributes of garden pea (*Pisum sativum* L.) as influenced by Integrated Nutrient Management under mid hill conditions. *Journal of Krishi Vigyan, 3* (2), 78-83. https://doi.org/10.5958/2349-4433.2015.00017.3

Sharma, D., Chauhan, A., & Jarial, K. (2020). Performance of pea varieties in different altitude ranges under North-Western Himalayan Region. *International Journal of Current Microbiology and Applied Sciences, 9* (6), 3292-3302. https://doi.org/10.20546/ijcmas.2020.906.392

Shen, Y., Hong, S., & Li, Y. (2022). Pea protein composition, functionality, modification, and food applications: A review. *Advances in food and nutrition research*, *101,* 71-127. https://doi.org/10.1016/bs.afnr.2022.02.002

Singh, J., & Dhall, R.K. (2018). Genetic variability parameters of yield and quality attributes in vegetable pea (*Pisum sativum* L.). *Genetika*, *50* (1), 153-170. https://doi.org/10.2298/GENSR1801153S

Stanek, M., Zduňczyk, Z., Purwin, C., & Florek, S. (2004). Chemical composition and nutritive value of seeds of selected pea varieties. *Veterinarija ir zootechnika*, *1*, 28 (50), 71-74. https://vetzoo.lsmuni.lt/data/vols/2004/28/pdf/stanek.pdf

Tamindžić, G., Ignjatov, M., Miljaković, D., Červenski, J., Milošević, D., Nikolić, Z., & Vasiljević, S. (2023). Seed priming treatments to improve heat stress tolerance of garden pea (*Pisum sativum* L.). *Agriculture, 13*, (2), 439. https://doi.org/10.3390/agriculture13020439

Urbano, G., López-Jurado, M., Ławomir Frejnagel, S., Gómez-Villalva, E., Porres, J.M., Frías, J., Vidal-Valverde, C., & Aranda, P. (2005). Nutritional assessment of raw and germinated pea (*Pisum sativum* L.) protein and carbohydrate by in vitro and in vivo techniques. *Nutrition*, 21 (2), 230-239. https://doi.org/10.1016/j.nut.2004.04.025

Vlahović, B. (2015). *Tržište agroindustrijskih proizvoda–specijalni deo*. Poljoprivredni fakultet, Novi Sad.

Vračar, L.O. (2001). *Priručnik za kontrolu kvaliteta svježeg i preradjenog voća, povrća i pečurki i osvježavajućih pića*. Univerzitet u Novom Sadu, Tehnološki fakultet, Novi Sad.

Wang, N., & Daun, J.K. (2004). The chemical composition and nutritive value of Canadian pulses. *Canadian Grain Commission Report,* 28, 19-29.

Wani, S.A., & Kumar, P. (2014). Comparative study of chickpea and green pea flour based on chemical composition, functional and pasting properties. *Journal of Food Research and Technology, 2* (3), 124-129. http://dx.doi.org/10.13140/2.1.3470.4964

Wendy, J. D., Foster, L.M., & Tyler, R.T. (2012). Review of the health benefits of peas (Pisum sativum L.). *British Journal of Nutrition, 108*(S1), S3-S10. (https://doi.org/10.1017/S0007114512000852)

Yathish, V.C., Chowdhury, R.S., & Datta, S. (2021). Evaluation of garden pea (*Pisum sativum* var. Hortense L.) genotypes under irrigated and rainfed condition under foothills of terai agro-ecological region of West Bengal. *International Journal of Bio-resource and Stress Management, 12* (4), 332-338. https://doi.org/10.23910/1.2021.2264

Received: August 4, 2023
Accepted: August 12, 2024

HEMIJSKO-TEHNOLOŠKI SASTAV SEMENA PROLEĆNOG GRAŠKA (*PISUM SATIVUM VAR. HORTENSE* L.)

Janko F. Červenski*, Srđan D. Zec, Biljana M. Kiprovski, Dario Đ. Danojević, Gordana M. Tamindžić, Maja V. Ignjatov i Dragana Đ. Miljaković

Institut za ratarstvo i povrtarstvo, Institut od nacionalnog značaja za republiku Srbiju, Maksima Gorkog 30, 21000 Novi Sad, Srbija

Rezime

Istraživanje je imalo za cilj utvrđivanje nutritivnog kvaliteta: sadržaja vlage pepela, ulja, ukupnog azota, proteina, ukupnih šećera, skroba, celuloze i sadržaja ukupno rastvorljivih čvrstih materija (briks) semena odabranih, (tehnološki) zrelih, genotipova jarog graška (osam linija i dve sorte). Takođe, ispitana je struktura varijabilnosti analiziranih karakteristika genotipova graška i doprinos pojedinačnih karakteristika ukupnoj varijabilnosti. Poljski ogled je postavljen tokom 2022. godine na lokalitetu Rimski Šančevi na zemljištu tipa černozem, u sistemu navodnjavanja, u Odeljenju za povrtarske i alternativne biljne vrste Instituta za ratarstvo i povrtarstvo iz Novog Sada. Posebnu vrednost u selekciji povrtarskih graškova imaće linije sa većim sadržajem proteina SK-1, SK-5 i SK-10 kao i linije sa većim sadržajem šećera SK-4, SK-5 i SK-8, koje će biti uključene u stvaranje sorata graška proteinskog tipa a slađeg ukusa. Genotipovi graška SK-6, SK-7 i SK-8 sa većom vrednošću briksa možemo iskoristiti u ranijem izdvajanju graškova slađeg zrna pogodnih za svežu pijacu, tj. za rano prolećnu potrošnju. Na osnovu klaster analize, genotipovi graška su klasifikovani u četiri pojedinačne grupe na osnovu varijabilnosti ispitivanih osobina. Analizom glavne komponente, četiri odvojene komponente kumulativno su objasnile 91,91% ukupne varijabilnosti.

Ključne reči: prolećni grašak, seme, analiza glavnih komponenti, klaster.

Primljeno: 4. avgusta 2023.
Odobreno: 12. avgusta 2024.

---

[*] Autor za kontakt: e-mail: janko.cervenski@ifvcns.ns.ac.rs