

## VARIABILITY OF AGRONOMIC TRAITS IN VEGETABLE PEA (*PISUM SATIVUM* L.) GENOTYPES

Srdan G. Zec<sup>1\*</sup>, Janko F. Červenski<sup>1</sup>, Aleksandra D. Savić<sup>1</sup>,  
Dario Đ. Danojević<sup>1</sup>, Žarko M. Ilin<sup>2</sup> and Maja V. Ignjatov<sup>1</sup>

<sup>1</sup>Institute of Field and Vegetable Crops, Novi Sad, Serbia

<sup>2</sup>Faculty of Agriculture, University of Novi Sad, Novi Sad, Serbia

**Abstract:** In this study, a total of 12 vegetable pea genotypes of different growing seasons were subjected to phenotypic characterization. The vegetable pea genotypes are a part of the collection maintained at the Institute of Field and Vegetable Crops Novi Sad. The plant material included 10 promising lines and two released cultivars, Tamiš and Dunav. The trial was carried out in 2022. It was set up at the Rimski Šančevi site, as a randomized block design in five replications. A total of 14 agronomic traits were analyzed. The obtained research results revealed divergence in the investigated plant material. The statistical significance of all sources of variation was determined by the LSD test. The height of the first fertile node was found to be the most variable feature, with a coefficient of variation of 40.54%. The tested genotypes were clustered into two groups and two subgroups within the second group. The correlation analysis of the examined quantitative traits revealed the presence of several statistically significant positive and negative correlations. Some of the most significant positive correlations were established between the grain weight per plant and the number of grains per plant and the yield of technologically mature grain, while the pod width and the number of fertile nodes per plant had the most negative correlations with the other tested traits.

**Key words:** vegetable pea, phenotypic characterization, genotype, correlations, divergence.

### Introduction

Vegetable pea (*Pisum sativum* L.) is an annual plant from the legume family (Dozet et al., 2018). Peas used in human nutrition are mainly grown for their grain, less often for their pods. In addition to the seasonal use of fresh grains, large quantities of grain are preserved by sterilization and freezing. The importance and the quantity of the processed pea products placed peas among the major vegetable crops in the food canning industry (Đorđević et al., 2021). Peas have long been

---

\*Corresponding author: e-mail: [srdjan.zec@ifvcns.ns.ac.rs](mailto:srdjan.zec@ifvcns.ns.ac.rs)

consumed because of their nutritional value, namely their high content of protein, starch, fibre, minerals and vitamins (Castaldo et al., 2021). As a rich and affordable source of protein for human and livestock nutrition, peas are a strategically important commodity for global food security. In addition, when included in crop rotation, peas enable the fixation of atmospheric nitrogen and have a beneficial effect on soil physical properties (Pavan et al., 2022). One of the most important tasks in pea breeding is the development of high-yielding and stable pea varieties (Kumar et al., 2022). Different plant traits affect pea yield, which depends on both the specific genotype and environmental conditions (Đinović, 1986). When a new cultivar is developed, knowledge of effective yield traits saves time and labor, and improves the chances of success (Ceyhan and Avci, 2015). To this end, researchers have already studied various traits that affect the yield of a pea. Đinović (1986) lists the following as the most important traits that affect the yield of pea grains: number of pods per plant, number of grains per plant, number of grains per pod, absolute weight and grain yield. Timmerman-Vaughan et al. (2005) describe pea grain yield as the result of four components: number of plants per unit area, number of pods per plant, number of grains per pod and grain weight. Greveniotis et al. (2021) measure the following traits in their studies: grain yield (kg/ha), 1000-grain weight (g), number of pods per plant, number of grains per pod, pod length (cm), pod width (mm), number of branches per plant, and plant height (cm). These traits vary depending on the genotype and the agroecological conditions.

During the breeding process, breeders use diverse material (wild relatives, populations, lines and cultivars) that are expected to contain variability in different traits. However, for some of these genotypes to be used, they should be well described to give the researcher an insight into their breeding value. The description and knowledge of the genotypes is a prerequisite for their use (Kumar et al., 2018). According to Ton et al. (2022), the description of some traits of local genotypes is very important for pea breeding. The first step in the description and classification of the germplasm is morphological characterization (Smith and Smith, 1989). The aim of the research was to determine the correlation between the tested traits, to assess the relative contribution of the variability of the tested traits to the total variability of the studied pea genotypes, and ultimately to group the divergent genotypes and thereby facilitate breeding work.

## Material and Methods

### Field trial and plant material

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

19°50'14.9" E and 86 m above sea level). The experiment was set up as a randomized block design with five replications. The main plot consisted of two rows of plants with a distance of 20 cm between the rows, 5 cm in a row and a length of 3 m. The distance between the two plots was 80 cm for easier manipulation and tillage between the rows during the growing season.

The sample for the analysis consisted of 10 plants per replication, i.e., a total of 50 plants per one genotype. The examined material is part of the collection of the species *Pisum sativum* L. of the Institute of Field and Vegetable Crops Novi Sad. The research included 12 genotypes consisting of 10 prospective lines and 2 domestic varieties (Tamiš and Dunav) of vegetable peas. The lines were named S-1 to S-10, and the Tamiš and Dunav lines were designated S-T and S-D. Spring vegetable pea lines, which differ significantly in terms of several morphological and quantitative characteristics, were selected based on earlier observation and the determination of certain parameters important in pea breeding.

The vegetation period length of the studied vegetable pea genotypes was: S1 – 65 days, S2 – 61 days, S3 – 60 days, S4 – 66 days, S5 – 65 days, S6 and S7 – 70 days, S8 – 72 days, S9 and S10 – 76 days, ST – 63 days and SD – 64 days.

The tested genotypes were harvested manually at the time of technological maturity. The degree of maturity was determined with a tenderometer, where the degree of grain hardness is expressed in tenderometric values (TV) (Jovičević et al., 2009; Červenski et al., 2021). According to the tests, a grain hardness of 100 to 180 TV was deemed acceptable (Đinović et al., 1984). The tenderometric values at harvest in the tested genotypes ranged from 100 to 135.

The traits were examined based on morphological descriptors for peas in the protocol for distinctness, uniformity and stability tests UPOV. Quantitative traits were not assessed according to the UPOV protocol, but were measured and expressed according to the International System of Units (SI). The studied agronomic traits included: stem length (cm) and height of the first fertile node (cm) – measured using a meter; number of nodes per plant, number of fertile nodes per plant, number of pods per plant, number of pods per stem; pod length (mm) and pod width (mm) – measured with a ruler; number of grains per pod, number of grains per plant; grain weight per pod (g) and grain weight per plant (g) – measured using a precise analytical scale; yield of technologically mature grain (kg/ha) – determined based on the total grain weight obtained from each plot for each genotype; vegetation period from sprouting to technologically mature grain (expressed as number of days).

During the trial, cultivation practices were carried out to control weeds, diseases and harmful insects. Sprinkler irrigation (a system of sprinklers) was used three times during the growing season with a watering rate of 35 mm. Watering peas is necessary at localities with poor distribution of precipitation, as well as in extremely dry years. The time and rate of watering are determined as needed. At

low soil moisture, crops are irrigated at germination and during the initial stages of plant development with a smaller amount of water. The irrigation norm of 10 mm is sufficient for wetting the top soil layer, connecting with winter moisture reserves and preventing the formation of soil crust. On average, 1–2 irrigations during flowering, fertilization and pod formation, with a watering rate of 30–40 mm can significantly increase the yield (the number of pods and grains), as well as improve the quality of pea seeds (Ćervenski et al., 2021).

#### Agrometeorological conditions

The meteorological conditions at the trial locality and during the trial period were represented by the following meteorological parameters: minimum and maximum monthly air temperature (°C), average monthly air temperature (°C) and ten-year average precipitation sum (mm). The values of the analyzed parameters were compared with the corresponding values of the multi-year average for the reference period from 1964 to 2014. The number of days during the growing season with maximum temperatures over 25°C stands out as an important parameter in vegetable pea production. The meteorological parameters for the examined locality were provided by the Republic Hydrometeorological Service of Serbia.

Tables 1, 2 and 3 show the precipitation deficit compared to the multi-year average during the entire vegetation period. Average temperatures during March were lower compared to the multi-year average, but slightly higher in mid-May and June with maximum temperatures above 25°C, which can have a negative effect on plant development during and shortly after flowering.

Table 1. Mean values of maximum, minimum and average air temperatures (°C) per 10-day periods at the investigated location during the growing season.

Month	Maximum (°C)			Minimum (°C)			Mean (°C)			Multiannual average (°C)		
	Period									I	II	III
	I	II	III	I	II	III	I	II	III			
February	18.0	18.4	18.1	-3.3	-3.8	-1.7	5.8	7.7	6.2	1.3	1.6	2.6
March	9.2	16.6	23.3	-4.5	-9.4	-6.3	2.5	4.3	10.3	4.3	6.2	8.8
April	22.3	24.8	23.2	-2.5	-1.4	1.6	10.4	9.3	13.1	10.8	10.8	13.5
May	26.0	31.4	32.3	8.5	6.0	11.7	17.2	19.6	19.7	15.8	17.2	17.9
June	33.0	33.7	36.2	12.8	12.4	15.3	23.2	22.0	24.9	19.2	20.0	20.9

Table 2. Precipitation sum (mm) per 10-day period at the investigated location during the growing season.

Month	Period			Sum	Multiannual sum
	I	II	III		
February	8	5	16	29	34.2
March	1	0	0	1	38.8
April	18	2	17	37	47.5
May	0	3	17	20	64.6
June	8	23	12	43	87.7

Table 3. Number of days with maximum temperatures above 25 °C.

Month	Period		
	I	II	III
February	0	0	0
March	0	0	0
April	0	0	0
May	1	9	6
June	10	10	8

#### Statistical data analysis

In view of the main statistical indicators for the analyzed traits, the following values were calculated: minimum and maximum values, mean value, standard error of the arithmetic mean, and coefficient of variation (%).

The least significant difference test (LSD) was conducted for all traits, at the significance threshold of 0.05 and 0.01.

The Pearson's correlation coefficient was calculated to determine the mutual dependence of the examined quantitative traits. The correlations between traits based on the intensity of the Pearson's coefficient values were divided according to Evans (1996):

$r = 0.00-0.19$  (very low);

$r = 0.20-0.39$  (low);

$r = 0.40-0.59$  (medium);

$r = 0.60-0.79$  (high);

$r = 0.80-1.00$  (very high).

Cluster analysis was conducted to group the genotypes based on similarities and differences in the tested traits. Cluster analysis is a multivariate method that allows the determination of clustering in a data set.

The obtained research results were statistically processed using the Statistica program version 14.0.1.25.

## Results and Discussion

The basic statistical indicators and mean values of the examined traits are shown in Tables 4 and 5. The statistical significance of all sources of variation at both levels of significance (0.05 and 0.01) was determined by the LSD test for the examined agronomic traits of the studied genotypes.

Table 4. Main statistical indicators of the examined agronomic traits of the studied vegetable pea genotypes.

Trait	Minimum	Maximum	Mean $\pm$ Se	CV (%)
SL	51.42	84.42	60.4 $\pm$ 2.92	16.76
HFFN	19.24	65.24	33.38 $\pm$ 3.91	40.54
NNPP	9.66	17.1	13.09 $\pm$ 0.67	17.79
NFNPP	4.94	6.7	5.81 $\pm$ 0.17	10.4
NPPP	5.94	10.66	8.84 $\pm$ 0.4	15.65
NPPS	1.19	1.89	1.54 $\pm$ 0.07	14.89
PL	58.23	82.46	67.48 $\pm$ 2.13	10.95
PW	11.7	14.13	12.7 $\pm$ 0.18	4.87
NGPPo	5.82	8.3	7.05 $\pm$ 0.19	9.34
GWPPo	1.6	3.34	2.55 $\pm$ 0.15	20.62
NGPP	36.04	63.22	51.75 $\pm$ 2.51	16.79
GWPP	9.3	21.8	17.63 $\pm$ 1.28	25.09
YTM	3627.78	8502.78	6848.4 $\pm$ 501.8	25.38
LVP	60	76	67.33 $\pm$ 1.56	8.04

SL – stem length (cm); HFFN – height of the first fertile node (cm); NNPP – number of nodes per plant; NFNPP – number of fertile nodes per plant; NPPP – number of pods per plant; NPPS – number of pods per stem; PL – pod length (mm); PW – pod width (mm); NGPPo – number of grains per pod; GWPPo – grain weight per pod (g); NGPP – number of grains per plant; GWPP – grain weight per plant (g); YTM – yield of technologically mature grain (kg/ha); LVP – vegetation period from sprouting to technologically mature grain.

The height of the first fertile node (HFFN) was found to be the most variable trait with a coefficient of variation of 40.54%, ranging from 19.24 cm in genotype S-T to 65.24 cm in genotype S-7. According to the LSD test, no mutually significant difference was found between genotype S-T and genotypes S-1 and S-2, while being significantly different compared to the other examined genotypes. Significant variability for this trait was also noted by Ton et al. (2022). Literature sources state that the average values in vegetable peas for the HFFN range from 9.22 to 74.5 cm (Singh and Dhall, 2018; Kalapchieva and Yankova, 2019; Ton et al., 2022). The yield of technologically mature grain (YTM) varied significantly, with a coefficient of variation of 25.38% and an interval of variation from 3627.78 kg/ha (S-T) to 8502.78 kg/ha (S-9). Compared to the other tested genotypes, a significantly higher YTM was found in genotypes S-1, S-5, S-6, S-7, S-8, S-9 and S-10, while a significantly lower yield was achieved by genotypes S-3 and S-T. On

average, the YTM was 6848.4 kg/ha. In the studies of other authors, the reported average values of technologically mature vegetable pea grain yield ranged from 1100 to 17900 kg/ha (Đorđević et al., 2001; Uher et al., 2009; Stanimirović et al., 2011; Červenski et al., 2016; Kanižai Šarić et al., 2016; Kumar et al., 2017; Dozet et al., 2018; Arunadevi et al., 2022). Plant productivity is determined by multiple factors that directly affect each other, so yield variability can be high and difficult to predict (Woźniak, 2013). A high coefficient of variation (25.09%) was determined for grain weight per plant (GWPP), with a variation interval of 9.3 g (S-T) to 21.8 g (S-9).

Table 5. Mean and LSD values of the examined agronomic traits of the studied pea genotypes.

Genotype	SL	HFFN	NNPP	NFNPP	NPPP	NPPS	PL	PW	NGPPo	GWPPo	NGPP	GWPP	YTM
S-1	54.12	21.26	10.6	5.94	7.9	1.31	71.56	13.32	6.88	3.34	43.6	20.50	7850.7
S-2	51.42	20.26	11.72	6.7	8.06	1.20	58.23	11.70	5.82	1.60	46.24	12.53	4814.94
S-3	54.98	26.98	9.66	5.02	5.94	1.19	64.03	14.13	6.07	1.79	36.04	10.40	3978.78
S-4	63.98	31.08	13.6	6.2	10.66	1.75	59.4	12.26	6.74	2.46	59.04	18.18	7024.68
S-5	61.16	26.02	11.94	5.78	9.74	1.7	67.94	13.14	7.04	2.72	54.42	19.59	7582.38
S-6	73.34	51	14.66	5.4	9.08	1.79	66.48	12.42	7.4	2.88	55.42	20.07	7947.42
S-7	84.42	65.24	17.1	4.94	9.2	1.89	62.88	12.6	7.2	2.83	54.64	21.23	8257.86
S-8	56.82	33.3	15.26	6.46	10.58	1.65	63.1	12.68	7.26	2.56	63.22	21.55	8402.94
S-9	66.06	40.24	16.06	6.7	10.16	1.53	79.8	12.94	7.58	2.86	60.58	21.80	8502.78
S-10	55.02	36.26	13.7	5.4	9.02	1.66	82.46	12.36	8.3	2.87	59.86	19.41	7568.34
S-T	51.44	19.24	11.42	5.7	7.54	1.33	65.72	12.46	7.42	1.89	41.9	9.30	3627.78
S-D	52.22	29.64	11.36	5.48	8.24	1.51	68.18	12.42	6.94	2.82	46.08	16.98	6622.2
Mean	60.42	33.38	13.09	5.81	8.84	1.54	67.48	12.70	7.05	2.55	51.75	17.63	6848.4
LSD <sub>0.01</sub>	3.295	3.175	0.782	0.754	1.301	0.130	3.177	0.520	0.551	0.375	8.248	2.720	1061.06
LSD <sub>0.05</sub>	2.504	2.413	0.594	0.573	0.989	0.099	2.415	0.395	0.419	0.285	6.268	2.067	806.40

SL – stem length (cm); HFFN – height of the first fertile node (cm); NNPP – number of nodes per plant; NFNPP – number of fertile nodes per plant; NPPP – number of pods per plant; NPPS – number of pods per stem; PL – pod length (mm); PW – pod width (mm); NGPPo – number of grains per pod; GWPPo – grain weight per pod (g); NGPP – number of grains per plant; GWPP – grain weight per plant (g); YTM – yield of technologically mature grain (kg/ha).

On the other hand, S-1, S-6, S-7, S-8 and S-9 had significantly higher GWPP compared to the other genotypes, but not compared to each other, while S-T and S-3 had significantly lower GWPP. The average GWPP was 17.63 g. According to the sources, the average grain weight per plant ranges from 1.52 to 118.4 grams (Ghafoor et al., 2005; Ceyhan et al., 2008; Siddika et al., 2013; Kumari et al., 2015; Barcchiya et al., 2018; Singh and Dhall, 2018; Kalapchieva and Yankova, 2019; Kumar et al., 2022; Singh and Prakash, 2022; Ton et al., 2022). The lowest grain weight per pod (GWPPo) of 1.6 g was measured in genotype S-2, while the highest

GWPPo of 3.34 g was found in genotype S-1. According to the LSD test, S-2, S-3 and S-T had significantly lower GWPPo compared to the other genotypes, while the S-1 genotype showed significantly higher GWPPo compared to the other genotypes. The mean value for this trait was 2.55 g, with a coefficient of variation of 20.62%. According to the literature, the average value of GWPPo ranged from 1.52 to 48.22 grams (Ghafoor et al., 2005; Ceyhan et al., 2008; Siddika et al., 2013; Kumari et al., 2015; Kalapchieva and Yankova, 2019; Kumar et al., 2022; Ton et al., 2022; Singh and Prakash, 2022).

The trait with the lowest value of the coefficient of variation (4.87%) was the pod width (PW), considering the narrow range from 11.7 mm in genotype S-2 to 14.13 mm in genotype S-3. A similar coefficient of variation for PW was also obtained by Singh and Dhall (2018). The PW in different studies ranged from 9.3 to 23.7 mm (El-Hak et al., 2012; Siddika et al., 2013; Afreen et al., 2017; Singh et al., 2017; Kumar et al., 2017; Singh and Dhall, 2018; Bardisi and Zyada, 2021).

The variability of different agronomic traits in plant material is an important source and factor in breeding work.

From the aspect of the indirect selection of traits correlated with the main breeding objectives and for a simultaneous selection of multiple traits, the assessment of correlation coefficients is important for plant breeders (Radinović et al., 2022). Correlation coefficients shown in Table 6 make it possible to identify direct connections between the examined agronomic traits of vegetable pea genotypes.

Table 6. The Pearson's correlation coefficients of the examined agronomic traits of the studied vegetable pea genotypes.

	NFFN	NNPP	NFNPP	NPPP	NPPS	PL	PW	NGPP	GWPP	NGPP	GWPP	YTM
SL	0.79**	0.68**	0.07	0.35**	0.46**	0.02	0.03	0.15**	0.21**	0.37**	0.47**	0.47**
HFFN		0.66**	-0.26**	0.07**	0.46**	0.07	-0.08	0.20**	0.24**	0.15**	0.30**	0.30**
NNPP			0.27**	0.46**	0.40**	0.10*	-0.13**	0.28**	0.16**	0.50**	0.50**	0.50**
NFNPP				0.73**	-0.12**	-0.01	-0.04	-0.01	-0.06	0.63**	0.46**	0.46**
NPPP					0.56**	0.02	-0.08*	0.12**	0.07	0.85**	0.71**	0.71**
NPPS						0.02	-0.11**	0.20**	0.17**	0.48**	0.49**	0.49**
PL							0.30**	0.52**	0.41**	0.15**	0.26**	0.26**
PW								0.03	0.09*	-0.05	0.03	0.03
NGPP									0.41**	0.32**	0.32**	0.32**
GWPP										0.16**	0.44**	0.44**
NGPP											0.83**	0.83**
GWPP												1.00**

SL – stem length (cm); HFFN – height of the first fertile node (cm); NNPP – number of nodes per plant; NFNPP – number of fertile nodes per plant; NPPP – number of pods per plant; NPPS – number of pods per stem; PL – pod length (mm); PW – pod width (mm); NGPPo – number of grains per pod; GWPPo – grain weight per pod (g); NGPP – number of grains per plant; GWPP – grain weight per plant (g); YTM – yield of technologically mature grain (kg/ha).



Based on the intensity of the obtained Pearson's coefficient values, at both levels of significance (0.05 and 0.01), a very strong positive correlation was established between the following traits: GWPP and YTM (1.00), number of pods per plant (NPPP) and the number of grains per plant (NGPP) (0.85), the NGPP and the GWPP (0.83), the NGPP and the YTM (0.83). Khan et al. (2017) also noted a high positive correlation between the NGPP and the GWPP. Contrary to our results, Khan et al. (2017) found that the stem length (SL) had a highly significant negative correlation with pod length (PL) and a negative correlation with the NGPPo. This research suggests that grain yield could be improved through the selection of genotypes with high GWPP and high NGPP.

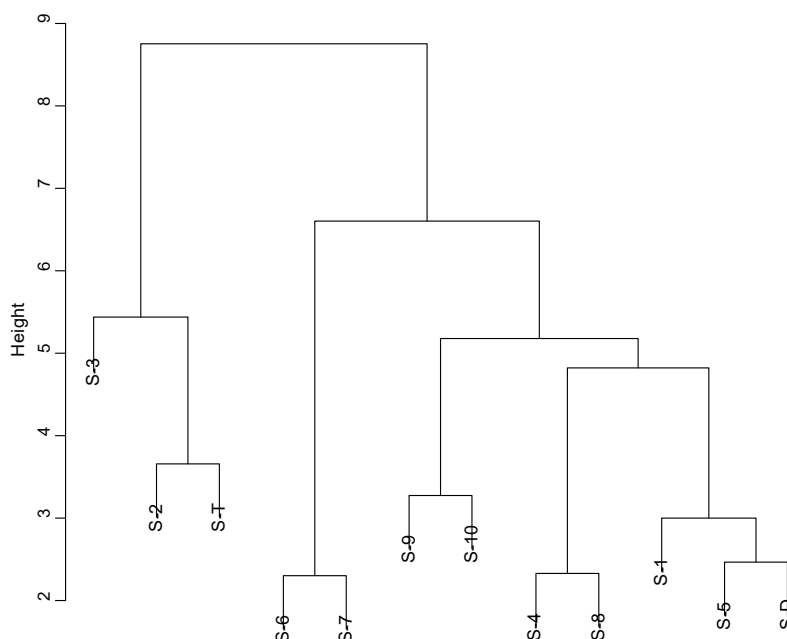
A strong positive correlation was established between: SL and the HFFN (0.79), the number of fertile nodes per plant (NFNPP) and the NPPP (0.73), the NPPP and the GWPP (0.71), the NPPP and the YTM (0.71), the SL and the number of nodes per plant (NNPP) (0.68), the HFFN and the NNPP (0.66), the NFNPP and the NGPP (0.63). Similar to the results of our research, Dozet et al. (2011) found that the SL had a highly significant positive correlation with the HFFN. In the research conducted by Arunadevi et al. (2022), the NPPP showed a highly significant positive correlation with the YTM, which is in agreement with the results of this research. However, Arunadevi et al. (2022) also reported a highly significant positive correlation between the NPPP and the number of grains per pod (NGPPo), and a significant positive correlation between the NPPP and the PL, which is not in accordance with our results.

Panwar et al. (2018) stated that the NPPP had a negative correlation with the NGPPo. The most significant negative correlations in our research (with the height of the reciprocal ratio  $>-0.3$ ) at both levels of significance (0.05 and 0.01) were found between the following traits: the HFFN and the NFNPP (-0.26), the NNPP and the PW (-0.13), the NFNPP and the number of pods per stem (NPPS) (-0.12), the NPPS and the PW (-0.11). The negative correlation between the NPPP and the PW (-0.08) was only significant at the 0.05% significance level. Both PW and the NFNPP exhibited the most negative correlations with the tested vegetable pea traits.

The distribution of genotypes by clusters and the mean values of the investigated agronomic traits for each cluster are presented in Graph 1. Using the complete linkage method, the vegetable pea genotypes were clustered into two groups and two subgroups, while the similarity between genotypes was determined based on Euclidean distances.

The first group (I), which consisted of genotypes S-2, S-3 and S-T, was characterized by the smallest NGPPo with 6.44 grains, the smallest GWPPo with 1.76 g, the smallest NGPP which was 41.39 on average, the smallest GWPP with 10.74 g, and the lowest YTM, which was 4140.5 kg/ha in group I. This group was also characterized by the lowest average SL of 52.61 cm, HFFN of 22.16 cm,

NNPP of 10.93 nodes, NPPS of 1.24 pods, and PL of 62.66 mm. All three genotypes in group I were characterized by the shortest vegetation period (LVP) compared to the other examined genotypes, with an average vegetation period of 63.33 days.



Graph 1. Dendrogram of the tested vegetable pea genotypes for the tested agronomic traits.

In the second group (II), two genotypes were distinguished (S-6 and S-7), which separately formed subgroup IIa. What distinguishes these two genotypes from the others at first glance is precisely their “main” characteristic of the SL, which averaged 78.88 cm in this subgroup. The genotypes of this subgroup were characterized by the highest values for the HFFN, which was 58.12 cm, the NNPP with 15.88 nodes, the NPPS of 1.8 pods, the NGPPo with 7.3 grains, the GWPPo of 2.86 g, and the GWPP which was 20.65 g.

Subgroup IIb was characterized by the highest NFNPP with 5.99 fertile nodes, the highest NPPP with 9.47 pods, the greatest PL of 70.35 mm, and the highest NGPP with 55.26 grains. Although the average YTM in subgroup IIb was lower compared to subgroup IIa, genotypes S-8 and S-9 from subgroup IIb achieved the highest average YTM in the trial with 8402.94 kg/ha and 8502.78 kg/ha, respectively.

Grouping peas using multivariate techniques can provide breeders with considerable advantages, as many researchers have applied these techniques to group vegetable pea genotypes based on different traits (Singh et al., 2017; Hanci, 2019; Mohamed et al., 2019). Clustering genotypes into the groups based on similarities and differences between the examined traits will help breeders to select parental pairs for future crosses to breed for different traits.

### Conclusion

The obtained research results indicate the presence of divergence with a medium level of phenotypic variability in the investigated plant material. The statistical significance of all sources of variation was determined by the LSD test for the examined agronomic traits. The Pearson's correlation matrix indicates that traits such as the grain weight per plant and the number of grains per plant can be used as selection criteria for the development of new high-yielding pea varieties. On the other hand, pod width and the sum of fertile nodes per plant had the most negative correlations with the tested pea traits, which directly indicates of the possibility to obtain weaker or lower values in the selection based on these traits. The examined genotypes were clustered into two groups based on similarities and differences between the examined traits, with the second group divided into two subgroups. The formation of homogeneous groups based on a combination of the examined agronomic traits will help breeders to select parental pairs for future crosses to breed for different traits.

### Acknowledgements

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

- Afreen, S., Singh, A.K., Moharana, D.P., Singh, V., Singh, P., & Singh, B. (2017). Genetic evaluation for yield and yield attributes in garden pea (*Pisum sativum* var. *hortense* L.) under North Indian gangetic plain conditions. *International Journal of Current Microbiology and Applied Sciences*, 6 (2), 1399-1404. <http://dx.doi.org/10.20546/ijcmas.2017.602.158>.
- Arunadevi, K., Singh, M., Franco, D., Prajapati, V. K., Ramachandran J., & Maruthi S.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://dx.doi.org/10.22271/chemi>.

- Bardisi, S., & Zyada, H. (2021). Combining ability and heterosis for yield and quality traits in pea (*Pisum sativum* L.). *Scientific Journal of Agricultural Sciences*, 3 (2), 78-86. <https://doi.org/10.21608/sjas.2021.106304.1167>.
- Castaldo, L., Izzo, L., Gaspari, A., Lombardi, S., Rodríguez-Carrasco, Y., Narváez, A., Grosso, M., & Ritieni, A. (2021). Chemical Composition of green pea (*Pisum sativum* L.) pods extracts and their potential exploitation as ingredients in nutraceutical formulations. *Antioxidants*, 11 (1), 105. <https://doi.org/10.3390/antiox11010105>.
- Ceyhan, E., Avci, M.A., & Karadas, S. (2008). Line x tester analysis in pea (*Pisum sativum* L.): Identification of superior parents for seed yield and its components. *African Journal of Biotechnology*, 7 (16), 2810-2817.
- Ceyhan, E., & Avci, M.A. (2015). Determination of some agricultural characters of developed pea (*Pisum sativum* L.) lines. *International Journal of Agricultural and Biosystems Engineering*, 9 (12), 1235-1238. [doi.org/10.5281/zenodo.1110331](https://doi.org/10.5281/zenodo.1110331).
- Červenski, J., Gvozdanović-Varga, J., Vasić, M., Stojanović, A., Medić-Pap, S., Danojević, D., & Savić, A. (2016). Home gardens and backyards – suitable area for vegetable production. *Acta Horticulturae*, 1142, 179-186. <https://doi.org/10.17660/ActaHortic.2016.1142.28>.
- Červenski, J., Medić-Pap, S., & Ignjatov, M. (2021). Proizvodnja konzumnog graška. In A.M. Jeromela (Ed.), *Zbornik referata, 55. Savetovanje agronoma i poljoprivrednika Srbije (SAPS)* (pp. 23-32). Zlatibor, Serbia.
- Dozet, G., Bošković, J., Galonja-Coghill, T., Zečević, V., Cvijanović, G., Jovičević, D., & Đukić, V. (2011). Effect of genotype and pre-sowing fertilization on yield of garden pea. *Genetika*, 43 (2), 229-238. <https://doi.org/10.2298/GENSR1101041P>.
- Dozet, G., Stanojević, S., Cvijanović, G., Ugrenović, V., Ugrinović, M., Jakšić, S., & Abuatwarat, S. (2018). Uticaj sorte i mikrobioloških đubriva na prinos baštenskog graška u organskom povrtarenju. In G. Cvijanović & S. Savić (Ed.), *Radovi sa XXXII savetovanja agronoma, veterinarara, tehnologa i agroekonomista* (pp. 153-160). Bačka Topola, Srbija.
- Dinović, I., Lešić, R., Krsmanović, Ž., Perić, B., Ipša, F., Gligorijević, B., Kojić, Z., & Čermak, N. (1984). *Grašak*. Beograd: Novinsko-izdavačka radna organizacija Zadruga.
- Dinović, I. (1986). *Nasleđivanje komponenti prinosa zrna graška, proteina i vitamina u recipročnim ukrstanjima Pisum sativum var. Medullare x Pisum sativum ssp. Saccharatum*. Univerzitet u Novom Sadu, Poljoprivredni fakultet, Novi Sad, Srbija.
- 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. *Zbornik radova, Biotehnologija i savremeni pristup u gajenju i oplemenjivanju bilja, Nacionalni naučno-stručni skup sa međunarodnim učešćem*, (pp. 123-129). Smederevska Palanka, Srbija.
- Đorđević, R., Damjanović, M., & Milošević, S. (2001). Golijat-srednje kasna afila sorta graška. *Savremena poljoprivreda*, 50 (1-2), 221-224.
- El-Hak, S.G., Ahmed, A.M., & Moustafa, Y.M.M. (2012). Effect of foliar application with two antioxidants and humic acid on growth, yield and yield components of peas (*Pisum sativum* L.). *Journal of horticultural science & ornamental plants*, 4 (3), 318-328. <https://doi.org/10.5829/idosi.jhsop.2012.4.3.262>.
- Evans, J.D. (1996). *Straightforward statistics for the behavioral sciences*. Monterey, CA, USA: Thomson Brooks/Cole Publishing Co.
- Ghafoor, A., Ahmad, Z., & Anwar, R. (2005). Genetic diversity in *Pisum sativum* and a strategy for indigenous biodiversity conservation. *Pakistan Journal of Botany*, 37 (1), 71-77.
- Greveniotis, V., Bouloumpasi, E., Zotis, S., Korkovelos, A., & Ipsilandis, C.G. (2021). Yield components stability assessment of peas in conventional and low-input cultivation systems. *Agriculture*, 11 (9), 805. <https://doi.org/10.3390/agriculture11090805>.

- Guidelines for the conduct of tests for distinctness, uniformity and stability. International Union for the Protection of New Varieties of Plants (UPOV). Geneva, (Pea, UPOV Code: PISUM\_SAT (*Pisum sativum* L.) TG/7/10, 2009-04-01, www.upov.int).
- Hanci, F. (2019). Genetic variability in peas (*Pisum sativum* L.) from Turkey assessed with molecular and morphological markers. *Folia Horticulturae*, 31 (1), 101-116. <https://doi.org/10.2478/fhort-2019-0007>.
- Jovičević, D., Jokanović, R.M., Gvozdanović-Varga, J., & Tepić, A., (2009). Characteristics and suitability of some pea (*Pisum sativum* L.) varieties for processing. *Acta Horticulturae*, 830 (1), 83-90. <https://doi.org/10.17660/ActaHortic.2009.830.9>.
- Kalapchieva, S., & Yankova, V. (2019). Opportunities for growing of garden pea in organic production systems. *Zemdirbyste-Agriculture*, 106 (3), 227-232. <https://doi.org/10.13080/z-a.2019.106.029>
- Kanižai, Šarić, G., Milaković, Z., Rapčan, I., Majić, I., Šeput, J., & Kojić, D. (2016). Rast i prinos graška (*Pisum sativum* L.) pod utjecajem bakterizacije i gnojidbe dušikom. *Agronomski glasnik: Glasilo Hrvatskog agronomskog društva*, 78 (5-6), 205-214.
- Khan, M.R.A., Mahmud, F., Reza, M.A., Mahbub, M.M., Shirazy, B.J., & Rahman, M.M. (2017). Genetic diversity, correlation and path analysis for yield and yield components of pea (*Pisum sativum* L.). *World Journal of Agricultural Sciences*, 13 (1), 11-16. <https://doi.org/10.5829/idosi.wjas.2017.11.16>.
- Kumar, M., Jeberson, M., Singh, N., Sharma, R., & Patel, R.S. (2018). Analysis of trait association and principal component of variability in field pea (*Pisum sativum* L.) genotypes. *The Pharma Innovation Journal*, 7 (8), 437-441.
- Kumar, S., Ali, B., Ahmed, W., Islam, R., Rahman, M.M., Chakma, M., & Miah, M.S. (2022). Assessment of the Genetic Variability for various Agronomic Traits of Pea (*Pisum sativum* L.) Genotypes. *Plant Archives*, 22 (1), 87-94. <https://doi.org/10.51470/PLANTARCHIVES.2022.v22.no1.013>.
- Kumar, V., Kumar, A., Singh, M.K., Kumar, M., & Kumar, U. (2017). Growth and Yield of Pea (*Pisum sativum* L.) cv. Azad P-1 as Influenced by NADEP Composts Prepared by Using Different Raw Materials. *International Journal of Current Microbiology and Applied Sciences*, 6 (11), 2260-2267. <https://doi.org/10.20546/ijcmas.2017.611.268>.
- Kumari, J., Dikshit, H.K., Singh, B., & Singh, D. (2015). Combining ability and character association of agronomic and biochemical traits in pea (*Pisum sativum* L.). *Scientia Horticulturae*, 181, 26-33. <https://doi.org/10.1016/j.scienta.2014.10.051>
- Mohamed, A., García-Martínez, S., Loumerem, M., Carbonell, P., Ruiz, J.J., & Boubaker, M. (2019). Assessment of genetic diversity among local pea (*Pisum sativum* L.) accessions cultivated in the arid regions of Southern Tunisia using agro-morphological and SSR molecular markers. *Genetic Resources and Crop Evolution*, 66 (6), 1189-1203. <https://doi.org/10.1007/s10722-019-00784-8>.
- Panwar, A., Mishra, A.C., & Negi, S. (2018). Correlation studies on seed quality, pod and seed yield in germplasm of pea (*Pisum sativum* L.). *International Journal of Bio-resource and Stress Management*, 9 (1), 098-102. <https://doi.org/10.23910/IJBMS/2018.9.1.3C0753>.
- Pavan, S., Delvento, C., Nazzicari, N., Ferrari, B., D'Agostino, N., Taranto, F., Lotti, C., Ricciardi, L., & Annicchiarico, P. (2022). Merging genotyping-by-sequencing data from two ex situ collections provides insights on the pea evolutionary history. *Horticulture research*, 9. <https://doi.org/10.1093/hr/uhab062>.
- Radinović, I., Vasiljević, S., & Branković, G. (2022). Correlations of morpho-agronomic traits and forage quality properties in diverse red clover (*Trifolium pratense* L.) collections. *Journal of Agricultural Sciences (Belgrade)*, 67 (2), 139-151. <https://doi.org/10.2298/JAS2202139R>.
- Siddika, A., Islam, A.K.M.A., Rasul, M.G., Mian, M.A.K., & Ahmed, J.U. (2013). Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). *International Journal of Plant Breeding*, 7 (2), 124-128.

- Singh, B., & Prakash, R. (2022). Genetic analysis of yield and yield attributing components in pea: Genetic analysis of yield attributes in pea. *Journal of Agri Search*, 9 (1), 6-11. <https://doi.org/10.21921/jas.v9i01.9885>.
- 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>.
- Singh, S.R., Ahmed, N., Singh, D.B., Srivastva, K.K., Singh, R.K., & Mir, A. (2017). Genetic variability determination in garden pea (*Pisum sativum* L sub sp. hortense Asch. and Graebn.) by using the multivariate analysis. *Legume Research-An International Journal*, 40 (3), 416-422. <https://doi.org/10.18805/lr.v0i0.7300>.
- Smith, J.S., & Smith, O.S. (1989). The description and assessment of distance between inbred lines of maize: The utility of morphological, biochemical and genetic descriptors and a scheme for testing of distinctiveness between inbred lines. *Maydica*, 34 (2), 151-161.
- Stanimirović, N., Koprivica, R., & Veljković, B. (2011). Visina gubitaka u žetvi zelenog graška u zavisnosti od stanja useva i režima rada kombajna. *Savremena poljoprivredna tehnika*, 37 (1), 35-44.
- Timmerman-Vaughan, G.M., Mills, A., Whitfield, C., Frew, T., Butler, R., Murray, S., Lakeman, M., McCallum, J., Russell, A., & Wilson, D. (2005). Linkage mapping of QTL for seed yield, yield components, and developmental traits in pea. *Crop Science*, 45 (4), 1336-1344.
- Ton, A., Mart, D., Karaköy, T., Türkeri, M., Torun, A., & Anlarsal, A.E. (2022). Characterization of some local pea (*Pisum sativum* L.) genotypes for agro-morphological traits and mineral concentrations. *Turkish Journal of Agriculture and Forestry*, 46 (2), 245-256. <https://doi.org/10.3906/tar-2109-89>.
- Uher, D., Štafa, Z., Blažinkov, M., Pisačić, A., & Županac, G. (2009). Prinos i kakvoća zrna novog kultivara ozimog graška cv. Maksimirski rani u smjesi s pšenicom. *Zbornik radova*, 44. hrvatski i 4. međunarodni simpozij agronoma (pp. 657-661). Opatija, Hrvatska.
- Woźniak, A., (2013). The yielding of pea (*Pisum sativum* L.) under different tillage conditions. *Acta Scientiarum Polonorum-Hortorum Cultus*, 12 (2), 133-141.

Received: April 27, 2023  
Accepted: January 29, 2024

VARIJABILNOST AGRONOMSKIH SVOJSTAVA KOD GENOTIPOVA  
POVRTARSKOG GRAŠKA (*PISUM SATIVUM* L.)

Srdan G. Zec<sup>1\*</sup>, Janko F. Červenski<sup>1</sup>, Aleksandra D. Savić<sup>1</sup>,  
Dario Đ. Danojević<sup>1</sup>, Žarko M. Ilin<sup>2</sup> i Maja V. Ignjatov<sup>1</sup>

<sup>1</sup>Institut za ratarstvo i povrtarstvo, Novi Sad, Srbija

<sup>2</sup>Poljoprivredni fakultet, Univerzitet u Novom Sadu, Novi Sad, Srbija

## R e z i m e

U toku ovog istraživanja izvršena je fenotipska karakterizacija 12 genotipova povrtarskog graška, različite dužine vegetacije, koji pripadaju kolekciji Instituta za ratarstvo i povrtarstvo u Novom Sadu. Biljni materijal obuhvatao je 10 perspektivnih selekcionih linija i dve priznate sorte *tamiš* i *dunav*. Ogled je izveden tokom 2022. godine, postavljen je po slučajnom blok sistemu, u pet ponavljanja na lokalitetu Rimski Šančevi. Analizirano je 14 agronomskih osobina. Dobijeni rezultati istraživanja ukazuju na postojanje divergentnosti u ispitivanom biljnom materijalu. Analizom varijanse ispitivanih agronomskih osobina utvrđena je statistička značajnost svih izvora varijacije. Kao najvarijabilnija osobina istakla se visina prvog rodnog nodusa sa koeficijentom varijacije od 40,54%. Ispitivani genotipovi su primenom klaster analize grupisani u dve grupe sa dve podgrupe u okviru druge grupe. Korelacionom analizom ispitivanih kvantitativnih svojstava utvrđeno je postojanje nekoliko statistički značajnih pozitivnih i negativnih međuzavisnosti. Neke od najznačajnijih pozitivnih korelacija utvrđene su između osobina: masa zrna po biljci i prinos tehnološki zrelog zrna, kao i broja zrna po biljci i prinosa tehnološki zrelog zrna, dok svojstva širina mahune i suma rodnih nodusa po biljci imaju najviše negativnih korelacija sa ostalim ispitivanim osobinama.

**Ključne reči:** povrtarski grašak, fenotipizacija, genotip, korelacije, divergentnost.

Primljeno: 27. aprila 2023.  
Odobreno: 29. januara 2024.

---

\* Autor za kontakt: e-mail: srdjan.zec@ifvcns.ns.ac.rs