Assessment of the Genetic Diversity of a Collection of Grass Pea (*Lathyrus sativus* L.) Genotypes

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Summary

The genetic diversity of grass pea genotypes from the collection of the Institute of Forage Crops - Pleven, Bulgaria was studied. The effect of the environment and genotype on the number of leaves per plant, fresh and dry root weight and dry root weight of the plant have been demonstrated. The genotype factor had a greater effect on the number of nodules per plant, the weight of the dry stems and the number of pods per plant, while the environment affected the number of leaves per plant, the fresh weight of the leaves and the number of seeds per plant. The phenotypic variation in number and weight of nodules, fresh weight of leaves and stems, number and weight of plant seeds and fresh weight of plant was found stronger, however the genotypic variation was stronger in the number of leaves, fresh and dry root weight, weight of dry stems and weight of dry root mass. The signs of fresh plant weight, fresh leaf weight, number of branches and weight of seeds per plant had high values of coefficient of inheritance and moderate genetic progress (GA), suggesting that the selection may be successful in improving them.

Key words

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Introduction

The problem of increasing the production of vegetable protein remains relevant and cannot be solved without increasing the production of leguminous crops. The imperfection of the structure of sown areas with a low specific gravity of leguminous crops and perennial grasses has led to a decrease in gross grain production and a decrease in the protein content in the crop. There is practically no effect of leguminous crops on soil fertility (Dixit et al., 2016; Sarkar et al., 2017). In recent years, we have witnessed global and local climate change towards warming. Large areas in some parts of the world are periodically exposed to drought. In this regard, there is a need in agriculture to expand the area of cultivation of drought-resistant leguminous crops, one of which is the grass pea. It is still classified as a non-traditional crop, it is cultivated on small scale, underestimating the biological and energy potential (Vishnyakova and Burlyaeva, 2006).

Currently, there is a need to expand the area of cultivation of drought-resistant leguminous crops. Grass pea is mainly used for food in the form of seeds, hay, green food, and also as a green fertilizer. Compared to other leguminous crops, grass pea plants are more resistant to diseases and pests and are practically not damaged by bruchus (Vishnyakova and Burlyaeva, 2006; Zaytseva et al., 2014; Mihailović et al., 2019).

Grass pea plants, like other legumes, are able to enter into symbiosis with *Rhizobium* bacteria and to fix air nitrogen. It has been established that in annual legumes - soy, peas, beans, etc. the level of nitrogen fixation is from 70 to 100 kg N_2 ha^{-1} year^{-1} (Sidorova et al., 2006; 2010). The symbiogenetics of legumes as a science began to develop actively since the 1980s. Great successes have been achieved in crops such as peas and soybeans. The grass pea as an object for the study of symbiogenetics has not yet been used (Sidorova and Shumny, 2003; Hillocks and Maruthi, 2012). This plant can be successfully cultivated both in regions with an average annual rainfall of 380-650 mm, and with excess rainfall. Thanks to its strong root system, the grass pea is able to grow on various types of soils - from light to heavy clay. Such unpretentiousness and the ability to fix atmospheric nitrogen make it a crop that seems to be specially created for cultivation in adverse conditions. The cultivation of the sowing plant is cost-effective, leads to improved soil fertility and has a positive effect on the yield of crops following it. The yield of winter wheat after the grass pea is as high as after black steam, and in some cases even exceeds it (Naumkin et al., 2013).

The purpose of the study is to evaluate the genetic diversity of a collection of grass pea genotypes and to identify appropriate parental components for a future breeding program.

Material and Methods

The study was conducted in 2014-2016 in the experimental field of the Institute of Forage Crops - Pleven (43.41° N, 24.61° E), located in the central part of the Danube hilly plain of Bulgaria. The sowing was done manually at optimal times according to the technology of cultivation of the crop. The aboveground and underground biomass plant material of the following six grass pea genotypes of the collection, i.e. BGE027129, BGE025277, LAT4362, LA5108, LAT5038 and BGE015741 was analyzed. The following traits were observed: at the beginning of flowering stage - fresh plant weight (g), number of leaves, fresh leaf weight (g), fresh stem weight (g), root length (cm), fresh weight of roots (g), number of nodules, weight of nodules (g), specific nodulating ability (g nodules g^{-1} roots); in the stage of technical maturity - plant height (cm), weight of dry stems (g), number of branches, number of pods, number of seeds per plant, weight of seeds per plant (g) and weight of dry root mass (g). Biometric measurements were made for 10 plants of each variety: plant height (cm), above ground mass weight (leaves + stems) (g), pods per plant, seeds per plant, seed weight per plant (g) and nodule weight (g).

The following statistical methods were used to process the experimental data: factor analysis by the method of principal components (Vandev, 2003), hierarchical cluster analysis by the method of Ward (1963) – for grouping genotypes based on similarity as a measure of differences (the genetic distance), the Euclidean distance between them was calculated (as a measure for divergence) as the data were standardized preliminary. GGE biplot model was done, which uses singular value decomposition of the first two principal components (Yan and Rajcan, 2002).

Heritability in the broad sense (H2) was estimated according to Hanson et al. (1956). Genotypic and phenotypic variances, genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were calculated according to Burton (1952). Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller et al. (1958).

Genetic advance in absolute unit (GA) and genetic gain (GG), assuming selection of the superior 5% of the genotypes, were estimated in accordance with the methods illustrated by Johnson et al. (1995).

All experimental data were processed statistically using the computer software GENES 2009.7.0 (Cruz, 2009) and Excel for Windows XP.

Results

Meteorological report

The main climatic parameters as the amount of rainfall and temperature during the period of the study can be characterized by a strong fluctuation and uneven distribution over the phenological phases of the plant development. The study period covers three consecutive years differing in weather conditions. Fig. 1 presents the data of average monthly temperatures and the amount of precipitated rainfall by months during vegetation. The weather conditions during the vegetation season in 2014. were the most favourable with average monthly air temperatures for April 12.3 °C, May 16.7 °C and June 20.6 °C and rainfall 139.8 mm, 83.0 mm and 54.3 mm, respectively. As a result of the balanced combination of air temperature and optimum rainfall, this period was favorable for plant development. The second year (2015) had relatively higher temperatures in May of 18.8 °C and uneven precipitation distribution, characterized by a certain drought in April (43.6 mm) and May (30.6 mm), and a larger precipitation in June (95.7 mm). The third year (2016) occupied an intermediate position over the other two years with temperatures in the months of April and May, close to normal (15.3-16.4 °C) and rainfall between 73.1 and 76.5 mm.
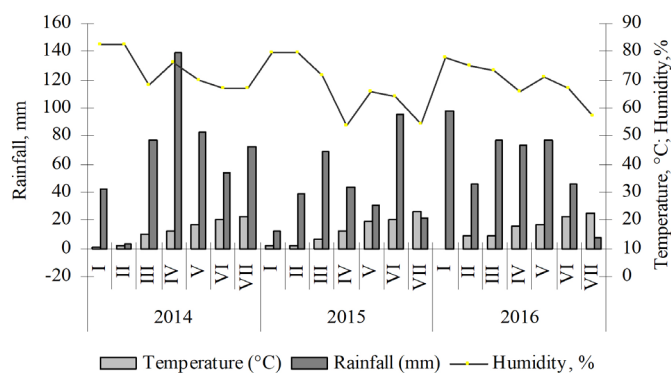
Figure 1. Climatic characterization of the experimental period (shown in Kosev et al. (2019))

Analysis of variance

The data in Table 1 show significant differences in the factors of year and genotype by the number of leaves per plant, fresh and dry root weight and dry root weight of the plant at technical maturity. Genotypic differences are insignificant for fresh weight of the plant, fresh weight of leaves and stems, root length, number and weight of nodules, specific nodulating ability, plant height, numbers of branches, number and weight of seeds per plant.

It is striking that the environment as a factor is characterized by a larger value of the variance for most of the traits studied, especially the number of plant leaves, fresh leaf weight and number of seeds per plant. This is related to the contrast periods (meteorological years) and their effect on the trait expression. On the other hand, similar effects show that the environment is the factor under the effect of which the trait is formed, i.e. invariable environmental conditions are crucial in the expression of the trait studied.

The genotype factor had the strongest effect on the values of the variance in terms of number of nodules per plant, weight of dry stems and number of pods per plant. For traits such as root length and nodule weight, relatively similar environmental and genotype effects are observed as factors. The differences observed in meteorological terms make it possible to express the individual traits within a wide range, on the one hand, and on the other, to form certain trends between the different genotypes. The data presented in Table 2 support this view. The traits are observed in which, regardless of the effect of environmental conditions, clear trends between the different genotypes can be formed. However, it should be emphasized that the behavior of the genotypes examined is not identical for the individual traits due to their different genetic basis.

Genetic variability

The results of the principal component analysis carried out (Table 2) provide an opportunity for a more detailed explanation of the variation of the characteristics of the varieties examined. GCV values ranged from 6.67% and 7.56% for number of seeds per plant and root length from 38.65% and 40.88% for nodule number and weight of dry stems. The variation in PCV values was stronger, the lowest being for the signs of root length (10.50%) and weight of dry root mass (11.10%). Strong variation was found for weight and number of nodules (47.72%; 86.82%), for fresh weight of leaves (35.13%) and for weight of seeds per plant (35.05%).

Table 1. Analysis of variance of grass pea (*Lathyrus sativus* L.) genotypes

Source of variation	DF	Traits					
		Plant fresh weight (g)	Number of leaves	Leaves fresh weight (g)	Stems fresh weight (g)	Root length (cm)	Roots fresh weight (g)
Year	2	248.9858*	2005.429**	125.8043**	43.6038*	3.7164 ns	0.2807**
Varieties	5	56.571ns	233.4036*	18.8272ns	12.0657ns	3.772ns	0.1297**
Residuo	10	20.2107	42.0142	7.9529	7.1766	1.485	0.0187
		Dry weight of the roots	Nodule number	Nodule weight	Specific nodulating ability	Plant height	Weight of dry stems
Year	2	0.0269**	257.854 ns	0.1212 ns	0.0186 ns	81.9562 ns	9.1743 ns
Varieties	5	0.0057**	433.266ns	0.0782ns	0.0469ns	41.5926ns	17.5824*
Residual	10	0.0005	145.401	0.0629	0.0662	45.065	3.2305
		Number of branches	Number of pods per plant	Number of seeds per plant	Seeds weight per plant	Weight of dry root mass	
Year	2	2.4568*	11.2307ns	114.3373ns	13.9387**	0.3516**	
Varieties	5	1.2206ns	29.8929*	65.9842ns	4.5483ns	0.0149**	
Residual	10	0.3724	8.3551	56.7175	1.4289	0.0026	

Note: ns, *, ** - nonsignificant or significant at the $P \leq 0.05$ and 0.01 level, respectively

Table 2. Genetic component of variation for quantitative traits in grass pea (*Lathyrus sativus* L.) genotypes

Trait	Min	Max	GCV (%)	PCV (%)	GA	GG	Vg	Ve	H2 mean (%)
Plant fresh weight	5.24	28.94	21.12	27.43	5.55	56.16	12.12	20.21	64.27
Number of leaves	17.40	75.40	17.22	14.00	20.28	28.78	63.80	42.01	82.00
Leaves fresh weight	1.99	20.02	23.89	35.13	2.65	72.89	3.62	7.95	57.76
Stems fresh weight	3.25	16.40	14.99	31.23	1.25	64.77	1.63	7.18	40.52
Root length	9.00	14.94	7.56	10.50	1.29	21.73	0.76	1.49	60.63
Roots fresh weight	0.26	1.21	23.87	16.93	0.56	34.78	0.04	0.02	85.56
Dry weight of the roots	0.04	0.28	24.88	12.76	0.17	27.10	0.00	0.00	91.95
Nodule number	1.00	62.00	38.65	47.72	16.39	97.99	95.96	145.40	66.44
Nodule weight	0.10	1.31	24.31	86.82	0.04	178.15	0.01	0.06	19.52
Specific nodulating ability	0.17	1.17	-	-	-0.08	218.70	-0.01	0.07	-41.14
Plant height	31.20	58.00	-	-	-0.70	58.61	-1.16	45.07	-8.35
Weight of dry stems	2.86	12.75	40.88	33.51	13.47	169.99	4.78	3.23	81.63
Number of branches	2.40	6.00	12.26	14.09	2.81	85.21	0.28	0.37	69.49
Number of pods per plant	6.40	21.4	18.75	20.16	17.54	142.81	7.18	8.36	72.05
Number of seeds per plant	5.80	36.8	6.66	28.96	3.31	229.93	3.09	56.72	14.04
Seeds weight per plant	0.60	8.81	29.79	35.05	7.88	316.67	1.04	1.43	68.58
Weight of dry root mass	0.23	0.90	13.87	11.10	0.81	111.51	0.00	0.00	82.40

Note: GCV - genotypic coefficient of variance; PCV - phenotypic coefficient of variance; GA - genetic advance; GG - genetic gain; V_g: genotypic variance; V_e: environment variance; H2 (%) - broad-sense heritability

The high values of PCV and GCV in number and weight of nodules, weight of dry stems, weight of seeds per plant and fresh weight of leaves indicate that there is considerable variability in these traits and the selection based on them can be effective.

According to the data obtained, moderate values of PCV and GCV were reported for number of leaves (17.22%, 14.00%), number of branches (12.26%, 14.09%), number of pods per plant (18.75%, 20.16%) and weight of dry root mass (13.87%, 11.10%), but the root length had low values of both, PCV and GCV.

In this study, PCV had a relatively higher value as compared to GCV for number and weight of nodules, fresh weight of leaves and stems, number and weight of seeds per plant and fresh plant weight, but for number of leaves, fresh root weight, dry root weight, dry stem weight and weight of dry root mass, GCV values exceed those of PCV. This indicates the high proportion of genotype effect in the phenotypic manifestation of these traits.

Heritability and genetic advance

The values of the coefficient of inheritance are useful in predicting the expected genetic progress made in the breeding process. Its values ranged from 14.04% for the number of seeds per plant to 91.95% for the dry weight of the roots (Table 2). According to the interpretation of this coefficient, the inheritance of nodule weight (19.52%) and the number of seeds per plant is average, and for other signs it is high.

The traits such as fresh root weight (85.56%), dry root weight (91.95), dry stem weight (81.63%), number of leaves per plant (82.00%), number of pods per plant (72.05 %) and number of branches (69.49%) show a relatively small influence of environmental factors on the phenotype. Due to the high additive effect the selection for such traits can be relatively easy. The assessment of genetic advance (GA) is essential to predict the expected genetic benefit of a selection cycle. GA values for all traits studied are shown in Table 2. Data on the genetic advance for the trait number of leaves and number of nodules per plant, weight of dry stems and number of pods per plant indicate that when we select the best 5% high yielding genotypes as parents, plants with improved expression can be selected in the offspring of these signs, i.e. the average genotype value of the new population for these parameters will be increased. The combination of high values of genetic advance with high inheritance also implies the presence of an additive type of inheritance.

Signs that have high values of the coefficient of inheritance, combined with moderate genetic progression (GA), as a percentage of the average for the study population, i.e. the fresh weight of the plant, the fresh weight of the leaves, the number of branches and the weight of the seeds of the plant, all suggest that the selection may be successful in improving them. It also shows the greater role of non-additive gene actions in their inheritance.

Principal components analysis

The principal component analysis performed allows for a more comprehensive explanation of the variation in productivity and the related productivity elements of the varieties examined (Table 3).

Table 3. The Eigen values and vectors of the correlation matrix for 17 traits of grass pea (*Lathyrus sativus* L.) genotypes

Variable	PC1	PC2	PC3
Plant fresh weight (g)	0.302	0.059	0.173
Number of leaves	0.295	-0.052	0.261
Leaves fresh weight (g)	0.296	-0.040	0.201
Stems fresh weight (g)	0.284	0.178	0.123
Root length (cm)	0.197	0.281	-0.333
Roots fresh weight (g)	0.274	0.166	0.248
Dry weight of the roots (g)	0.299	0.168	-0.075
Nodule number	0.263	0.180	-0.255
Nodule weight (g)	0.271	-0.244	0.083
Specific nodulating ability (g nodules g^{-1} roots)	0.186	-0.382	-0.047
Plant height (cm)	0.178	0.344	-0.051
Weight of dry stems (g)	0.289	-0.181	-0.071
Number of branches	0.242	-0.112	-0.449
Number of pods per plant	0.127	-0.314	-0.437
Number of seeds per plant	0.065	-0.393	-0.190
Seeds weight per plant (g)	0.283	-0.090	0.214
Weight of dry root mass (g)	-0.016	-0.404	0.335
Parameter			
Variability (%)	56.61	26.73	10.41
Cumulative	0.5661	0.8334	0.9374
EigenValues	9.623	4.5439	1.7689

Note: PC1, PC2, and PC3 - principal component 1, 2 and 3, respectively

Three eigenvalues greater than 1 are extracted, which determines the choice of three components. They explain 93.74% of the total variation. The first component explains 56.61%, the second 26.73%, and the third 10.41% of the total variation.

Differences in varieties are also reflected by grouping them by the values of the major components (Table 4), which indicates that they respond specifically to changing environmental conditions. The lowest values of the first major component are the varieties BGE025277 and BGE015741, which are characterized by high values of fresh stem weight, weight of seeds per plant, fresh leaf weight, number of nodules and fresh root weight (Table 5). The highest values are found for LA5108 and LAT5038 varieties. For the values of the second principal component, the first position is occupied by BGE025277, followed by LAT5038, which has positive values for all three principal components.

Table 4. Values of grass pea (*Lathyrus sativus* L.) genotypes by major components

Genotype	Principal components - EigenValues		
	PC1	PC2	PC3
BGE027129	-0.18	-0.36	-0.18
BGE025277	-0.70	0.42	-0.70
LAT4362	-0.09	-0.17	-0.09
LA5108	0.58	-0.42	0.58
LAT5038	0.39	0.19	0.39
BGE015741	-0.49	-0.58	-0.49

Note: PC1; PC2; PC3; PC3 = principal component 1, 2 and 3 respectively

For the greater factor weight of the first component (Table 3), the fresh weight of the plant, number and fresh weight of the leaves, fresh weight of the stems, weight of the dry stems and roots, nodule weight and weight of seeds per plant are crucial. The formation of the second major component is related to the signs of root length, number of nodules and height of the plant. The signs of fresh weight of the stems and roots are involved in the formation of all three principal components and cannot be strictly related to either of them. The signs that are important for the formation of the third component are the number of leaves, the weight of the seeds of the plant and the weight of the dry root mass.

PCA plot analysis

Fig. 2 shows the arrangement of genotypes according to their values for major components PC1 and PC2. The genotypes tested are divided into four groups. In the first group with positive values for PC1 and PC2, only the variety LAT5038 is distinguished, which is characterized by tall plants, small number of leaves, low weight of fresh biomass (leaves and stems) (Table 5). The second group consists of LA5108 with a high expression of the number of pods and seeds per plant and the weight of the dry root mass, but also with lower values of the number and weight of the nodules per plant.

Table 5. Distinctive features of the grass pea (*Lathyrus sativus* L.) genotypes genotypes

	Trait/variety	BGE027129	BGE025277	LAT4362	LA5108	LAT5038	BGE015741	LSD$_{0.05}$	LSD$_{0.01}$
Beginning of flowering	Plant fresh weight (g)	18.07	17.62	19.49	9.28	13.47	21.01	8.17	11.63
	Number of leaves (g)	47.30	47.40	49.93	33.30	40.87	59.53	11.79	16.77
	Leaves fresh weight (g)	8.49	7.79	9.45	4.14	6.51	11.45	5.13	7.29
	Stems fresh weight (g)	9.58	9.83	10.04	5.14	6.96	9.56	4.87	6.93
	Root length (cm)	13.41	11.73	11.59	9.95	11.55	11.09	2.21	3.15
	Roots fresh weight (cm)	0.89	1.04	0.82	0.47	0.66	0.95	0.24	0.35
	Dry weight of the roots (cm)	0.22	0.19	0.19	0.10	0.13	0.19	0.03	0.05
	Nodule number	41.13	28.28	34.32	10.41	12.67	25.27	21.93	31.20
	Nodule weight (g)	0.35	0.23	0.27	0.17	0.15	0.59	0.45	0.64
	Specific nodule ability (g nodules g^{-1} roots)	0.40	0.22	0.32	0.36	0.23	0.62	0.46	0.66
Technological maturity	Plant height (cm)	49.21	50.67	50.73	45.6	52.53	44.13	19.23	27.36
	Weight of dry stems (g)	18.07	17.62	19.49	9.28	13.47	21.01	8.17	11.63
	Number of branches	6.00	4.92	4.60	5.53	3.73	4.87	2.52	3.58
	Number of pods per plant	15.80	10.00	12.27	15.53	9.53	14.93	5.85	8.33
	Number of seeds per plant	26.20	16.00	22.80	28.27	23.27	28.53	15.27	21.72
	Seeds weight per plant (g)	4.65	4.26	3.17	2.98	2.80	5.52	2.53	3.60
	Weight of dry root mass (g)	0.67	0.75	0.72	0.88	0.73	0.92	0.25	0.36
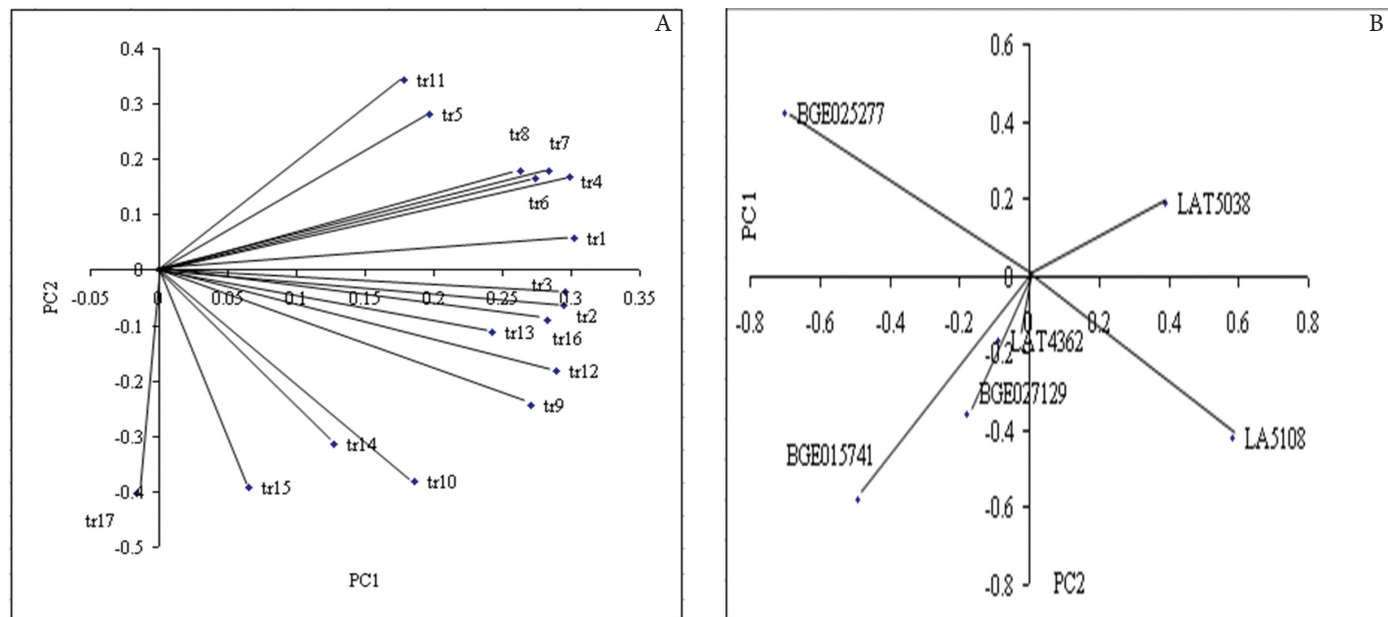
Figure 2. Projection of *Lathyrus sativus* L. genotypes and Traits on a vector plane

A - for quantitative Traits: Tr 1- Plant fresh weight (g); Tr 2- Number of leaves; Tr 3 - Leaves fresh weight (g); Tr 4- Stems fresh weight (g); Tr 5- Root length (cm); Tr 6 - Roots fresh weight (g); Tr 7 - Dry weight of the roots (g); Tr 8 - Nodule number; Tr 9 - Nodule weight (g); Tr 10- Specific nodule ability (g nodules g^{-1} roots); Tr 11- Plant height (cm); Tr 12 - Weight of dry stems (g); Tr 13 - Number of branches; Tr 14 - Number of pods per plant; Tr 15 - Number of seeds per plant; Tr 16- Seeds weight per plant (g); Tr 17- Weight of dry root mass (g); **B** – *Lathyrus sativus* L. genotypes

The third group combines the varieties BGE015741, LAT4362, BGE027129, located in the quadrant with negative PC1 and PC2 and having high values for number of leaves, fresh weight of leaves and stems, root length, number and weight of nodules and number of seeds per plant. In the quadrant bounded by negative PC1 and positive PC2, only the variety BGE025277 is located.

Information about the correlative relationships between the signs is also given by the PC analysis applied, by the magnitude of the angle that the vectors of two signs conclude. The vectors of the signs are fresh stem weight, fresh root weight, dry root weight and number of nodules forming sharp angles, indicating a positive relationship between them. The relationship between the number of leaves and the fresh weight of the leaves is similar. Positive correlative relationships were also found between specific nodulation ability and number of pods per plant, number of branches, weight of dry stems and root length. There are blunt angles between the vectors of the signs of dry root weight and root length, fresh root weight, dry root weight, number of nodules and the plant height, indicating the presence of negative correlative relationships between them.

Correlations

The results of Table 6 show that there is a strong positive correlation between fresh plant weight and number of leaves per plant (r = 0.818), fresh leaf weight (r = 0.830), fresh stem weight (r = 0.837). A strong positive correlation was found of dry root weight with fresh plant weight (r = 0.716), number of leaves per plant (r = 0.843), fresh leaf weight (r = 0.786), fresh root weight (r = 0.892), and number of nodules (r = 0.709), clearly emphasizing their relationship in these genotypes. There is a high positive correlation between the nodule weight and specific nodulating ability (r = 0.899) and the dry stem weight (r = 0.760).

A statistically significant correlation with the same sign also exists between the number of pods per plant with specific nodulating ability (r = 0.567), the number of branches (r = 0.559) and the number of seeds per plant (r = 0.658). This suggests that in the group studied, it is relatively easy to combine in one genotype high productivity and specific nodulating ability. These dependencies in the selection of the grass pea are favorable, since the increase in productivity is associated with an increase in the nodulating ability.

The sign seed weight per plant was positively correlated with fresh root weight (r = 0.499) and specific nodulating ability (r = 0.520) and strong with nodule weight (r = 0.712) and dry stems weight (r = 0.853). The relationship between grain productivity and weight of dry root mass (r = - 0.590) was negatively demonstrated.

The lack of a statistically significant relationship between seed weight per plant with fresh plant weight (r = 0.16), plant height (r = 0.124), and number of branches (r = 0.164) indicates that there are opportunities to achieve high productivity at lower genotypes with fewer basal branches.

Cluster analysis

The presented cluster analysis was done on the basis of the data obtained from the traits studied. From Fig. 3 it can be seen that the dendrograms have samples in two main clusters.
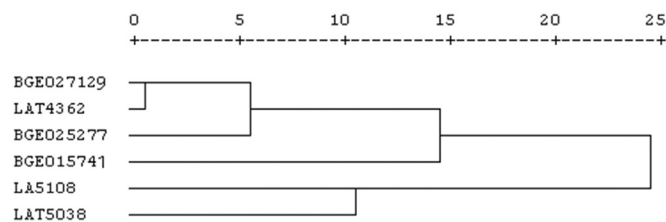

Figure 3. Dendrogram of *Lathyrus sativus* L. genotypes

The first cluster located at the bottom of the dendrogram is represented by two varieties - LA5108 and LAT 5038. The second cluster comprises the other varieties formed into two subclusters. BGE01574 takes the stand alone. Within this subcluster, the most closely related, with the least distance units are the LAT4362 and BGE02712 varieties. BGE02527 may also be assigned to their group. Genetically the most distant are BGE02712 and LAT4362 from the second cluster relative to LAT 5038 from the first.

Discussion

Facts have been reported in the literature partially contrary to the results of the present study. Conducted by Lokesh et al. (2018), analysis of variance for multiple quantitative traits and qualitative traits showed that the average sum of squares due to genotypes is strongly expressed for the duration of the sowing - beginning of the flowering period, vegetation period, number of basal branches, number of fertile nodes per plant, number of seeds per pod and plant, weight of 1000 seeds aSnd protein and ash content. These results are supported by Katoch et al. (2016) and Kumar et al. (2017), while Patel (2017) reported a greater influence of the environment on the appearance of the signs number of seeds per pod, length of pods and number of days from sowing to full flowering.

Tadesse and Bekele (2003) reported that when working with Ethiopian genotypes of grass pea, a statistically insignificant difference in plant height was observed. The authors believe that these results may be due to differences in the biological characteristics of the individual genotypes and to their cultivation under other environmental conditions.

Lokesh et al. (2018) in another annual legume crop - peas, provide information on the presence of significant genetic variability and high magnetization of the genotype coefficient of variation for most of the quantitative traits they have studied. In their view, this is indicative of the smaller environmental impact on the quantitative expression of the relevant parameter.

Saxesena et al. (2014) also report similar results, especially for the duration of the growing season. But in terms of the number of seeds in the pods and the protein content of the grain, they establish a low, both genotypic and phenotypic coefficient of variation.

Sidorova et al. (2012) report significant genetic diversity in different representatives of the grass pea species with respect to specific symbiotic traits such as number of nodules per plant and nitrogen-fixing activity. The authors found differences in types and varieties in terms of nodule formation - number and size of nodules, their location in the root system and nitrogen fixing capacity.

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Table 6. Correlation coefficients (r) among the quantitative traits of grass pea (*Lathyrus sativus* L.) genotypes

	Tr1	Tr2	Tr3	Tr4	Tr5	Tr6	Tr7	Tr8	Tr9	Tr10	Tr11	Tr12	Tr13	Tr14	Tr15	Tr16
Tr2	0.818**															
Tr3	0.830**	0.601**														
Tr4	0.837**	0.534*	0.510*													
Tr5	0.184	0.031	0.302	0.107												
Tr6	0.09	-0.307	0.513*	0.079	0.3											
Tr7	0.716**	0.843**	0.786**	0.422	0.377	0.892**										
Tr8	0.49*	0.512*	0.502*	0.34	0.409	0.633**	0.709**									
Tr9	0.517*	0.534*	0.711**	0.105	0.317	0.436	0.491*	0.37								
Tr10	0.259	0.236	0.465	-0.101	0.168	0.039	0.15	0.169	0.899**							
Tr11	-0.076	-0.235	-0.127	0.015	0.221	-0.25	-0.218	0.044	0.043	0.112						
Tr12	0.284	0.321	0.383	0.068	0.43	0.448	0.428	0.411	0.760**	0.631**	0.188					
Tr13	0.033	-0.231	-0.08	0.182	0.351	-0.168	-0.187	0.253	0.181	0.266	0.358	0.391				
Tr14	0.421	0.27	0.405	0.327	0.014	0.027	0.147	0.264	0.513*	0.567*	-0.057	0.46	0.559*			
Tr15	0.386	0.197	0.269	0.444	-0.185	-0.146	-0.1	-0.094	0.129	0.126	-0.129	0.005	0.405	0.658**		
Tr16	0.16	0.245	0.322	-0.111	0.457	0.499*	0.425	0.238	0.712**	0.520*	0.124	0.853**	0.164	0.131	-0.205	
Tr17	0.208	0.021	0.018	0.416	-0.548*	-0.307	-0.358	-0.168	-0.155	0.014	0.151	-0.281	0.142	0.271	0.423	-0.590**

Note: *, ** - significant at the *P* ≤ 0.05 and 0.01 level, respectively

Tr 1- Plant fresh weight (g); Tr 2- Number of leaves; Tr 3 - Leaves fresh weight (g); Tr 4- Stems fresh weight (g); Tr 5- Root length (cm); Tr 6 - Roots fresh weight (g); Tr 7 - Dry weight of the roots (g); Tr 8 - Nodule number; Tr 9 - Nodule weight; Tr 10- Specific nodule ability (g nodules g^{-1} roots); Tr 11- Plant height (cm); Tr 12 - Weight of dry stems (g); Tr 13 - Number of branches; Tr 14 - Number of pods per plant; Tr 15- Number of seeds per plant (g); Tr 16- Seeds weight per plant (g); Tr 17- Weight of dry root mass (g)

Zhuzhukin et al. (2017) report significant differences in the morphological characteristics of grass pea genotypes of their collection, and find an average variation in signs of height of the first pod, number of seeds and pods per plant, but by height of plant, mass of 1000 seeds and weight of plant - low variation. Ahmad et al. (2012) report that in *Vigna radiate* L., plant height at technical maturity, number of branches and number of pods are strongly negatively correlated with the weight of seeds per plant, while the mass of 1000 seeds is positively correlated with grain productivity.

Singh et al. (2017) found that plant height, weight of fresh biomass and length of pods were negatively correlated with the weight of seeds per plant, but the primary and secondary branches, number of pods, number of seeds per plant, and mass per 1000 seeds, due to their positive correlation was evaluated as important productivity components contributing to increasing grain yield.

Conclusions

The effect of the environment and genotype on the number of leaves per plant, fresh and dry root weight and dry root weight of the plant have been demonstrated. The genotype factor had a greater effect on the number of nodules per plant, the weight of the dry stems and the number of pods per plant, and the environment influenced the number of leaves per plant, the fresh weight of the leaves and the number of seeds per plant. The phenotypic variation in number and weight of nodules, fresh weight of leaves and stems, number and weight of plant seeds and fresh weight of plant was found stronger, however the genotypic variation was stronger in the number of leaves, fresh and dry root weight, weight of dry stems and weight of dry root mass. The traits of fresh root weight (85.56%), dry root weight (91.95), dry stem weight (81.63%), number of leaves per plant (82.00%), number of pods per plant (72.05%) and the number of branches (69.49%) are characterized by high inheritance coefficient. The signs of fresh plant weight, fresh leaf weight, number of branches and weight of seeds per plant have high values of coefficient of inheritance and moderate genetic progress (GA), suggesting that the selection may be successful in improving them. A strong positive correlation was determined between the fresh plant weight and number of leaves per plant (r = 0.818), fresh leaf weight (r = 0.830) and fresh stem weight (r = 0.837); of dry root weight with fresh plant weight (r = 0.716), number of leaves per plant (r = 0.843), fresh leaf weight (r = 0.786), fresh root weight (r = 0.892) and number of nodules

(r = 0.709). The weight of plant seeds correlated positively with fresh root weight (r = 0.499), specific nodulating ability (r = 0.520), nodule weight (r = 0.712), and dry stem weight (r = 0.853). The grouping of varieties based on PC analysis facilitates their evaluation by a set of traits related to grain productivity and helps to identify the genotypes with the best combination between them for future use in the combinatorial selection. The results obtained could be of use for the breeding process in grass pea.

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