Available online at http://bjas.bajas.edu.iq
https://doi.org/10.37077/25200860.2020.33.1.09
College of Agriculture, University of Basrah

Basrah Journal of Agricultural Sciences

ISSN 1814 – 5868 Basrah J. Agric. Sci. 33(1): 107-121, 2020 E-ISSN: 2520-0860

Genetic and Phenotypic Assessment of Garden Peas (*Pisum sativum* L.) Genotypes

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Received 17 March 2020; Accepted 29 April 2020; Available online 27 June 2020

Abstract: The field trial was conducted during the growing season 2017-2019 in the experimental fields of the Maritsa Vegetable Crop Institute, Plovdiv, Bulgaria. The study used 10 samples of garden peas (*Pisum sativum* L). for measurement. Plant tall (cm), height to first fertile node (cm), length of internode (cm), number of tillers, number of branches, number of ineffective nodes, total number of nodes, total number of pods per plant, one pod per fruiting handle, two pods per fruiting handle, pod length (cm), pod width (cm), pod weight per plant, weight of green grains per plant (g), % filled grains, % unfilled grains, average number of grains per pod were assessed. Analysis variance showed significant differences between the genotypes of garden peas in all the traits studied. A lower level of the genetic variance was found compared to the phenotypic one by the number of branches, total number of nodes and one pod per fruiting handle. The coefficient of genetic variation is higher than the phenotypic one for most of the traits and ranged from 5.51-5.82% for pod width and total number of nodes to 56.98-59.09% for number of branches and % unfilled grains. For signs of plant tall (98.32% and 129.31%), height to first fertile node (91.22% and 29.32%), weight of pods per plant (86.83%, 29.32), weight of green grains per plant (83.7%, 11.89%) and % filled grains (77.81% and 24.96%). It was found high inheritance combined with high genetic progress. This is a prerequisite for increasing the biological potential on these traits and a real opportunity to create new forms of garden peas possessing such qualities. The best genotypes were found GEN 1 (22/16-n.), GEN 6 (Marsy-n.), GEN 4 (Plovdiv-n.) and GEN 9 (1/17-n.). They may be used in new breeding programs and hybrid lines may be entered in competitive variety lists.

Key words: Garden pea, Genotypes, Breeding, inheritance, Breeding.

Introduction

Pea (*Pisum sativum* L.) is the second of the most important legume crops for grain production in the world after dry bean. Grain of pea has high level protein, amino acids, minerals and vitamins and it is used for canning or baking. Pea is also an important grain legume for crop rotation because of providing nitrogen and organic matter to the soil (Ton *et al*., 2018). For any breeding program, genetic variability plays an important role as it provides opportunity to plant breeders for selection of

high yielding genotypes (Bashir *et al*., 2017). To improve the genetic contents for any crops, genetic variability is a prerequisite for crop improvement program. For the exploitation of the desirable traits for enhancing the yield in peas, both, the nature and magnitude of genetic variability and extent to which the desirable traits were heritable are important. Genetic variability has been considered as an important factor, which is also an essential prerequisite for crop improvement program for obtaining high yielding progenies. Evaluation of genetic variability is important to know the source of genes for a particular trait within the available germplasm (Tiwari & Lavanya, 2012; Saddika *et al*., 2013; Tamene, 2017).

Estimating the parameters of variability, especially heritability and genetic gain are important indicators for improvement of traits through selection whereas the selection for highly heritable characters is more effective. Therefore, heritability along with other parameters of variability can be used in predicting the gain for a given selection intensity and expected genetic gain further gives the idea of the extent of improvement in a traits through simple selection (Yumkhaibam *et al*., 2019).

A broad choice of variability in any crop always gives the good chances of selecting desired types which could be utilized in breeding. Heritability is the segment of phenotypic variation which is transmitted from parent to progeny. The higher the heritable difference, the superior will be the opportunity of fixing the character by selection methods (Ullah *et al*., 2019). Genetic variability within tested genotypes and knowledge about it offers a basis for improvement and developing new cultivars (Milenković *et al*., 2017).

Selection aimed at improving the varietal structure of crops is determined by the variety of germplasm available. The broad genetic base makes it possible to select genotypes with desirable traits which will be used as an initial material in the selection process.

The purpose of the study was to evaluate the genetic diversity of a collection of garden pea samples for the purposes of combinational selection.

Materials & Methods

The study was conducted during the growing season 2017-2019 in the experimental fields of the Maritsa Vegetable Crop Institute, Plovdiv, Bulgaria with ten genotypes of garden peas - GEN 1 (22/16-n.), GEN 2 (22/16-af.) , GEN 3 (Casino-af.), GEN 4 (Plovdiv-n.), GEN 5 (Echo-af.), GEN 6 (Marsy-n.), GEN 7 (Shugar duarf-n.), GEN 8 (B4-34- n.), GEN 9 (1/17-n.), and GEN 10 (Vechernitza-n). The experiment was based on four replicates by RCBD design with a working plot area of 6.4 m2. The sowing was done at the end of February on a high flatbed according to the scheme high flat bed at 80 cm between the beds, on the bed itself the distances between the rows are 20 cm - 40 cm and 20 cm. Peas were grown according to the technology of growing of this crop.

The basic morphological (biometric) characteristics of the aboveground organs were measured at the technical maturity of 10 plants per each replication: plant tall (cm), height to first fertile node (cm), length of internode (cm), number of tillers, number of branches, number of ineffective nodes, total number of nodes, total number of pods per

plant, one pod per fruiting handle, two pods per fruiting handle, pod length (cm), pod width (cm), pods weight per plant, weight of green grains per plant (g), % filled grains, % unfilled grains, average number of grains per pod.

The following statistical methods were used to process the experimental data: analysis of variance, 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 first two principal components (Yan & Rajcan, 2002). 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). MS Excel (2003) and GENES 2009.7.0 for Windows XP (Cruz, 2009) were used in the processing of experimental data.

Results

Analysis of variance

The analysis of the variance and the values obtained for the mean sum of squares of the studied parameters were presented in table (1). The presence of significant differences showed that a comparison between the average values of the parameters of these garden pea samples would be corrected (Table 2). The influence of factor year is stronger for the signs total number of pods per plant, two pods per fruiting handle, while for other indicators the factor is the genotype one. The information obtained in the study on the influence of sources of variation and on the statistically significant differences found for many of the characteristics of garden pea samples confirms the results of the studies of Ahmad *et al*. (2014), Katiyar *et al*. (2014) and Saxesena *et al*. (2014), who report significant morphological differences between their pea samples in terms of basic quantitative and qualitative indicators.

Results similar to those obtained in this study have been reported by Katoch *et al*. (2016), Kumar *et al*. (2017) found significant differences in most quantitative traits in pea samples (such as plant tall, number of node per plant, number of effective node per plant, pod bearing length, number of pod per plant, number of effective pod per plant, pod length, seed number per pod, seed number per plant, 100 seed weight, biological yield per plant).

Our findings confirm earlier findings by Lokesh *et al*. (2018) who report similar results obtained in the evaluation of genetic diversity in 60 pea samples on 23 traits.

Table (1): Analysis of variance.

	Source of variation		
Traits	Year	Genotype	Residuo
x1	396.2703	616.8167**	10.3769
x2	141.376	192.3037**	16.8804
x3	0.1563	4.6945**	0.1312
x4	0.0555	0.5002**	0.0683
x5	0.0023	0.7546*	0.2126
x6	0.0360	5.0863**	0.5854
x7	0.0090	4.6797**	1.2273
x8	13.8063	12.9671**	2.1979
x9	1.1902	1.4024**	0.3975
x10	5.1840	2.432**	0.5018
x11	0.0062	0.823**	0.0293
x12	0.0757	0.0156**	0.0035
x13	83.2496	318.3921**	41.9244
x14	17.2397	69.8152**	11.3800
x15	177.9448	484.4233**	107.5088
x16	178.0207	484.4745**	107.4926
x17	0.0360	2.3420**	0.0738

**** and * significant at 1% and 5% probability levels, respectively by F test, x1 – plant tall, x2 - height to first fertile node, x3 - length of internode, x4 - number of tillers, x5 - number of branches, x6 - number of ineffective nodes, x7 - total number of nodes, x8 - total number of pods per plant, x9 - one pod per fruiting handle, x10 - two pods per fruiting handle, x11 – pod length, x12 - pod width, x13 – pod weight per plant; x14 - weight of green grains per plant; x15 - % filled grains, x16 - % unfilled grains, x17 - average number of grains per pod.**

Genetic parameters

The assessment of genetic and phenotypic parameters was presented in table (3). The values of the genetic variance for almost all traits were higher than the corresponding phenotypic variance, such as differences in pod width, number of branches, total number of nodes and number of pods per fruiting handle is smaller than the differences in the other indicators. Genotype variance values ranged from 0.004 for pod width to 202.14 for plant tall.

The genotype variance was relatively low in number of tillers, number of branches, one pod per fruiting handle, two pods per fruiting handle, pod length, and average number of grains per pod, its numerical value not exceeding one. The highest phenotypic variance was characterized by % filled grains and % unfilled grains (107.50, 107.49), and by the weight of pods per plant (41.92). With a minimal phenotypic variance were pod width, pod length, number of tillers and average number of grains in pod, 0.003, 0.02, 0.06 and 0.07 respectively. This indicates that the % filled grains, % unfilled grains, and the weights of pods per plant were signed that were strongly influenced by the environment.

Table (2): Morphological characteristics of garden pea genotypes.

	x1	x2	x3	x4	x5	x6	x7	x8	x9
GEN 1	64.30	31.50	5.13	0.60	1.55	12.05	18.25	11.80	2.80
GEN 2	60.65	40.25	4.10	0.26	0.95	14.00	19.85	10.55	3.45
GEN 3	58.85	38.50	4.48	0.40	0.40	14.00	19.60	10.00	2.80
GEN 4	62.95	30.80	5.15	1.15	0.30	10.65	18.45	12.70	4.50
GEN 5	59.45	29.90	4.90	0.55	0.85	12.20	18.55	12.65	3.15
GEN 6	76.30	46.40	4.95	0.90	0.50	12.70	19.95	15.60	3.50
GEN 7	48.20	27.05	3.45	1.10	0.56	10.00	15.75	14.20	4.50
GEN 8	101.20	49.55	7.95	0.80	0.65	11.80	18.20	14.20	3.40
GEN 9	60.10	44.60	4.48	0.85	0.11	12.90	17.40	9.10	2.50
GEN 10	61.15	44.75	3.63	1.65	1.60	13.10	18.40	10.95	2.95
$LSD_{0.05}$	5.52	7.04	0.62	0.44	0.79	1.31	1.90	2.54	1.08
$LSD_{0.01}$	7.57	9.65	0.85	0.61	1.08	1.79	2.60	3.48	1.48
$LSD_{0.001}$	10.31	13.15	1.16	0.83	1.47	2.45	3.54	4.74	2.01
	x10	x11	x12	x13	x14	x15	x16	x17	
GEN 1	4.50	7.53	1.26	39.95	16.45	77.55	22.45	5.05	
GEN 2	3.55	7.05	1.12	26.21	10.67	80.94	19.06	4.85	
GEN 3	3.60	7.25	1.18	27.50	11.45	80.40	19.60	5.20	
GEN 4	4.10	6.28	1.12	38.36	19.01	91.99	8.00	5.50	
GEN 5	4.75	6.73	1.07	25.60	11.81	85.82	14.18	4.55	
GEN 6	6.05	8.20	1.15	59.30	26.54	48.16	51.84	6.70	
GEN 7	5.10	6.90	1.26	32.00	13.83	86.35	13.65	6.20	
GEN 8	5.35	7.45	1.22	37.40	13.42	81.48	18.52	6.55	
GEN 9	3.20	7.53	1.15	28.45	14.72	94.63	5.37	6.90	
GEN 10	4.00	7.20	1.06	27.58	11.44	82.94	17.06	6.70	
$LSD_{0.05}$	1.21	0.29	0.10	11.10	5.78	17.78	17.79	0.46	
$LSD_{0.01}$	1.66	0.40	0.13	15.21	7.92	24.36	24.36	0.63	
$LSD_{0.001}$	2.26	0.54	0.18	20.73	10.80	33.20	33.19	0.86	

x1 – plant tall, x2 - height to first fertile node, x3 - length of internode, x4 - number of tillers, x5 - number of branches, x6 - number of ineffective nodes, x7 - total number of nodes, x8 - total number of pods per plant, x9 - One pod per fruiting handle, x10 - Two pods per fruiting handle, x11 – pod length, x12 - pod width, x13 – pod weight per plant; x14 - weight of green grains per plant; x15 - % filled grains, x16 - % unfilled grains, x17 - average number of grains per pod GEN 1 (22/16-n.), GEN 2 (22/16-af.) , GEN 3 (Casino-af.), GEN 4 (Plovdiv-n.), GEN 5 (Echo-af.), GEN 6 (Marsy-n.), GEN 7 (Shugar duarf-n.), GEN 8 (B4-34- n.), GEN 9 (1/17-n.), GEN 10 (Vechernitza-n).

Phenotypic and genotypic coefficient of variation

The genotypic coefficient of variation (GCV) is an indicator of experimental precision and also it is part of the assessment of genetic variability. The calculated genotypic coefficients of variation for the different traits studied were shown in table (3). GCV ranged from 5.51-5.82% for pods width and total number of nodes to 56.98-59.09%, respectively for number of branches and % unfilled grains. The relative GCV values for pod length and the

number of ineffective nodes indicated that their variation was also very low (7.13%, 9.93%). On the other hand, the genotypic variation coefficient (GCV,%) was higher for a significant part of the traits studied (excepting number of branches, total number of nodes, one pod per fruiting handle). The genotypic coefficient of variation was greater than the phenotypic coefficient of variation. The ratio of GCV to CVP in these was greater than 1. Among the studied indicators, there was a relatively small difference between GCV and CVP for total number of nodes, one pod per fruiting handle, two pods per fruiting handle, pod width and % filled grains. This indicates that the variation observed was mainly due to genetic factors.

High values of the genotype coefficient of variation have also been reported by Jaiswal *et al*. (2015). They observed for high genotypic and phenotypic coefficient of variation for plant tall, seed yield per plant and pods per plant in field pea. The authors also report approximately similar magnitude for the same traits and phenotypic coefficient of variation, which is out of sync with our studies.

As a result of their research, Meena *et al.* (2017) make findings that do not correspond with the present results. They revealed that the relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for the characters such as plant height, pod bearing

length, pods per plant and seed yield per plant indicating environmental influence on these traits.

Different from our results are obtained by Lokesh *et al.* (2018) who report that the phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits.

Coefficient of inheritance and Genetic advance

Inheritance coefficient in a broad sense (H2,%), based on the sample of garden peas shows high values especially for the signs plant tall (98.32%), internode length (97.20%), average number of grains in pods (96.85) %), pod length (96.44%), height to first fertile node (91.22%), number of ineffective nodes (88.49%) and weight of plant pods (86.83%), which was an indication that most of the observed differences are due rather the effect of genetic rather than environmental factors (Table 3).

From the lower inheritance coefficient for the one pod per fruiting handle (71.66%), the number of branches (71.82%) and the total number of nodes (73.77%) it can be assumed that the environment has a greater impact on the phenotypic manifestation of these signs. Similar are the results of the study of Tyagi & Srivastava (2002). They reported high estimate of genetic advance for characters viz. plant height, pods per plant and biological yield per plant, and also results of Salam *et al.* (2007). They reported high genetic advance for plant height and pods per plant in field pea.

The experimental data obtained do not confirm the results of some other researchers such as Singh *et al.* (2011). They reported moderate to high heritability coupled with moderate genetic advance for the characters viz. plant height, pod length and 100 seed weight suggesting the role of additive gene action in the expression of these traits.

Table (3): Genetic component of variation for quantitative traits in garden pea genotypes.

Parameters	x1	x2	x3	x4	x5	x6	x7	x8	x9
Min	41.20	20.80	3.10	0.01	0.01	9.50	14.90	7.70	1.70
Max	108.90	56.10	7.95	2.10	2.70	14.40	21.30	16.90	5.30
Mean	75.05	38.45	5.52	1.05	1.35	11.95	18.10	12.30	3.50
StDev	14.34	8.01	1.25	0.41	0.50	1.30	1.25	2.08	0.68
GCV (%)	21.77	19.95	25.59	45.96	56.98	9.93	5.82	15.56	17.25
CVP (%)	4.94	10.73	7.53	31.70	61.93	6.21	6.00	12.16	18.75
V_g	202.14	58.47	1.52	0.14	0.18	1.50	1.15	3.58	0.33
Vp	10.37	16.88	0.13	0.06	0.21	0.58	1.22	2.19	0.39
GA	129.31	29.32	8.68	1.18	0.81	4.06	2.14	4.98	1.09
GG	8.84	22.01	13.44	47.83	69.67	13.13	12.57	24.78	36.76
Herdability (%)	98.32	91.22	97.20	86.35	71.82	88.49	73.77	83.05	71.66
	x10	x11	x12	x13	x14	x15	x16	x17	
Min	2.20	6.25	0.97	22.60	9.52	14.84	5.20	4.40	
Max	6.90	8.45	1.43	64.19	28.98	94.80	85.16	7.20	
Mean	4.55	7.35	1.20	43.39	19.25	54.82	45.18	5.80	
StDev	0.90	0.52	0.07	10.30	4.82	12.71	12.71	0.88	
GCV (%)	18.15	7.13	5.51	28.04	29.56	13.83	59.09	14.94	
CVP (%)	16.06	2.38	5.10	18.95	22.56	12.81	54.71	4.67	
V_g	0.64	0.26	0.004	92.15	19.47	125.63	125.66	0.75	
Vp	0.50	0.02	0.003	41.92	11.38	107.50	107.49	0.07	
GA	1.86	3.79	0.15	29.32	11.89	24.96	24.97	5.84	
GG	32.01	3.96	9.40	30.74	36.10	38.96	47.27	9.40	
Heritability (%)	79.37	96.44	77.80	86.83	83.70	77.81	77.81	96.85	

x1 – plant tall, x2 - height to first fertile node, x3 - length of internode, x4 - number of tillers, x5 - number of branches, x6 - number of ineffective nodes, x7 - total number of nodes, x8 - total number of pods per plant, x9 - One pod per fruiting handle, x10 - Two pods per fruiting handle, x11 – pod length, x12 - pod width, x13 – pod weight per plant; x14 - weight of green grains per plant; x15 - % filled grains, x16 - % unfilled grains, x17 - average number of grains per pod; GCV (%), genotypic coefficient of variation; CVP (%), phenotypic coefficient of variation V_g, genotypic variance; Vp, phenotypic variance; GA, Genetic Advance; GG, Genetic Gain; H^2 (%), broad-sense heritability

The heritability can be enhanced with combined genetic advance. The heritability estimate could be best-utilized in combination with the selection differential in predicting genetic gain following selection process. The value of genetic progress obtained by different selection methods can be used to estimate the expected progress in the selection process (Table 3). The signs of plant tall (129.31), height to first fertile node, weight of plant pods (29.32), % filled grains (24.96), % unfilled grains (24.97) and weight of green grains per plant (11.89) show the best and preferred presentation, the others, especially pod width (0.15), number of branches (0.81) and one pod per fruiting handle (1.09) occupy the last positions. The high GG values for traits with higher genetic progression suggest that there is a higher genetic benefit than for indicators with lower such parameters.

From the results obtained, it is clear that a high coefficient of inheritance, combined with

medium to high genetic progress, was established for plant tall, height to first fertile node, weight of pods per plant, weight of green grains per plant and % filled grains. This is a prerequisite for enhancing the biological potential of these traits and a real opportunity to create new genotypes possessing such traits. In the case of combining breeding approaches (such as the application of recurrent reciprocal selection) the expected genetic progress (profit) would be higher than when applying a single method alone. The estimated genetic progression based on the relative values of genetic variability and heredity indicates the breeding progress and efficiency of the method used to identify the promising samples.

Principal component analysis

If we have more than two factors (PC1, PC2, PC3, etc.) which variation can be distributed, the impact of a given recognition remains non-linear. With a similar survey of the views we can present, the samples analyzed so that we cannot see them, that we can remain part of those who respond positively or change stable opportunities to recognize you in the opposite direction. This has certainly created some difficulties in assessing the value of genotype release against the background of the group of samples tested.

Table (4) presents data for the applied principal component analysis. Four major components with a unit weight exceeding 80.45% of the total variation were extracted. The first component was related to the signs of weight of pods per plant, % of unfilled grains, weight of green grains per plant, two pods per fruiting handle and total number of pods per plant.

The second component determines the variation due to the number of ineffective nodes, the total number of nodes, the height to the first fertile node, and the length of the pods. Genotypes GEN 1 and GEN 6 are characterized by positive values of the first two principal components (Figure 1) (first quadrant). Samples GEN 2, GEN 3, GEN 9 and GEN 10 refer to the quadrant bounded by the negative values of PC1 and the positives of PC2. Their close location within the quadrant gives reason to believe that they are phenotypically very close in some of the studied traits. GEN 8 was located independently in the lower right quadrant of the coordinate system with positive values only on component PC1. Its projection in the plane shows that by phenotype it was quite different from other samples in many characteristics, but in morphology it was partially similar to GEN 1 and GEN 6. In the lower left quadrant are located GEN 5, GEN 4 and GEN 7. The figure shows that the last two genotypes are relatively close to the negative part of the ordinate axis (PC2), and GEN 5 was located immediately adjacent to the negative part of the abscissa (PC1) near GEN 10 from the adjacent quadrant. This proximity suggests that, despite being located in different quadrants, these specimens have similarities in some traits.

Table (4): The Eigen values and vectors of the correlation matrix for 17 traits in garden pea genotypes.

Variables	PC1	PC2	PC3	PC4
Plant tall	0.2665	0.0891	0.2805	0.4020
Height to first fertile node	0.1876	0.3135	0.4083	-0.0111
Length of internode	0.1854	0.0107	0.2232	0.5795
Number of tillers	0.0385	-0.2170	0.3531	-0.4580
Number of branches	-0.0257	0.1036	-0.1259	-0.1446
Number of ineffective nodes	-0.0345	0.4999	-0.0549	-0.0622
Total number of nodes	0.1228	0.3720	-0.2811	0.0507
Total number of pods per plant	0.3094	-0.2842	-0.1067	0.0671
One pod per fruiting handle	0.0456	-0.4200	-0.1431	-0.0026
Two pods per fruiting handle	0.3371	-0.2048	-0.0913	0.0609
Pod length	0.2899	0.2471	0.1178	-0.1048
Pod width	0.0949	-0.1859	0.0049	0.2834
Pod weight per plant	0.3811	-0.0781	-0.0865	-0.0743
Weight of green grains per plant	0.3259	-0.1051	-0.0962	-0.1758
% filled grains	-0.3562	-0.1296	0.2428	0.1513
% unfilled grains	0.3561	0.1297	-0.2428	-0.1513
Average number of grains per pod	0.1773	-0.0460	0.5417	-0.2892
Parameter				
Variability (%)	34.79	22.51	12.41	10.74
Cumulative	0.3479	0.573	0.697	0.8044
EigenValues	5.9130	3.826	2.109	1.825

PC1; PC2; PC3, PC4 = principal component 1, 2, 3 and 4, respectively

The location of the traits in the bipolar plane (Fig. 1) shows that the quantitative indicators studied determine the number of ineffective nodes, % filled grains, the total number of pods per plant, the one pod per fruiting handle, the weight of pods per plant and two pods per fruiting handle. They are also the longest vectors determining the level of diversity.

The vectors of the signs pods weight the average number of grains in pod and the weight of the green grains from the plant form sharp angles with each other, indicating a strong positive relationship between them. Similar dependencies with the same sign are found between the one pod per fruiting handle and the number of tillers, plant tall and % unfilled grains, and between the number of branches and the number of unfilled nodes.

When comparing the figures (Fig.1A and Fig. 1B), the similarity of the samples in groups can be judged by certain traits. The closer the projections of the patterns in Figure 1A are to the vectors of the corresponding features in Figure 1B, the more specific the indicator is decisive in grouping them.

As can be seen from the figures, a certain selection value by weight of green grains per plant was the GEN 5; in terms of length of internodes and average number of grains in pod GEN 8 and in number of branches GEN 10.

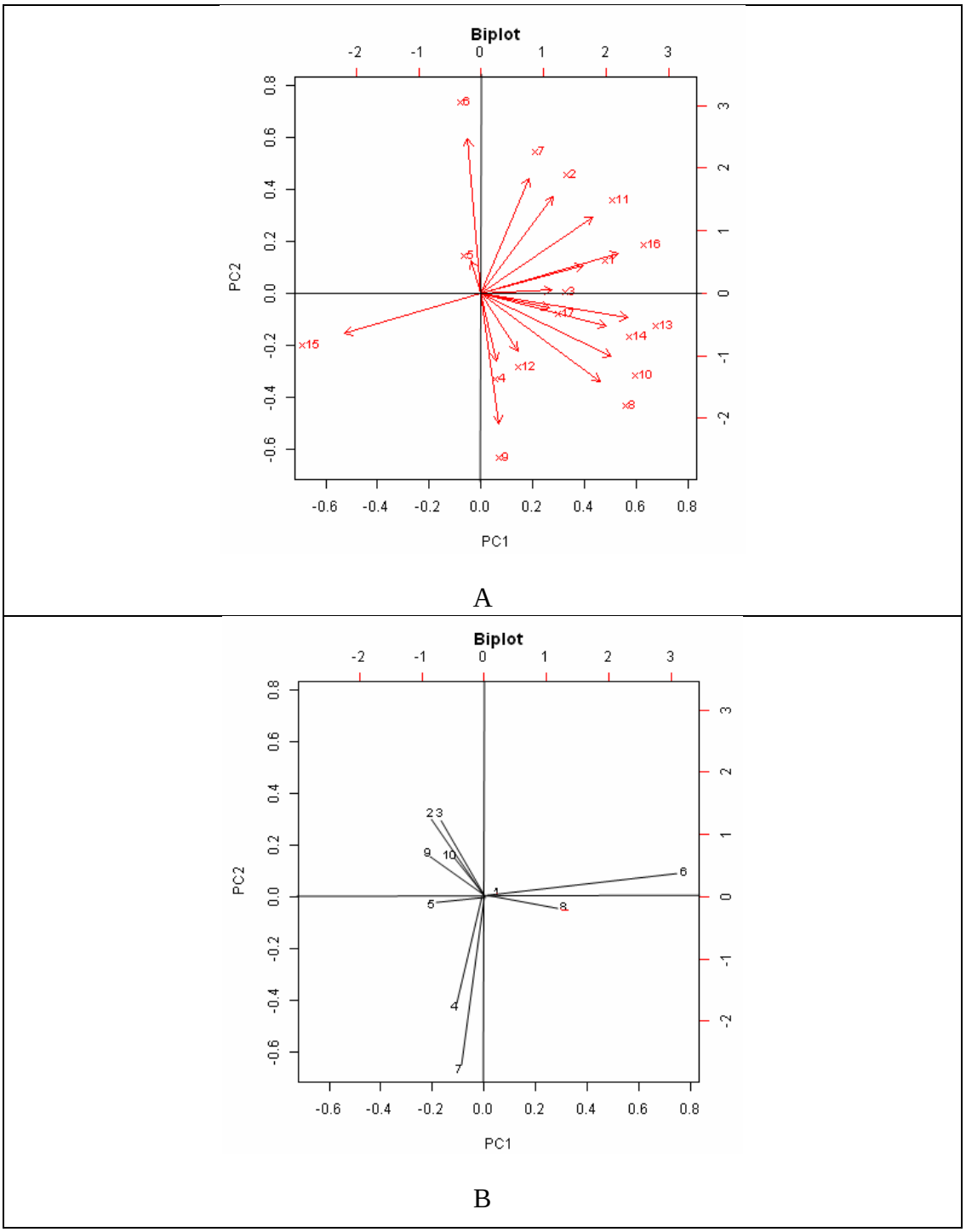

Fig. (1): Projection of the characteristics and varieties of garden peas on a vector plane.

A – traits: x1 – Plant tall, x2 - Height to first fertile node, x3 - Length of internode, x4 - Number of tillers, x5 - Number of branches, x6 - Number of ineffective nodes, x7 - Total number of nodes, x8 - Total number of pods per plant, x9 - One pod per fruiting handle, x10 - Two pods per fruiting handle, x11 – pod length, x12 - pod width, x13 – pod weight per plant; x14 - weight of green grains per plant; x15 - % filled grains, x16 - % unfilled grains, x17 - average number of grains per pod B – genotypes garden pea: 1- GEN 1 (22/16-n.), 2- GEN 2 (22/16-af.) , 3 - GEN 3 (Casino-af.), 4 - GEN 4 (Plovdiv-n.), 5 - GEN 5 (Echo-af.), 6 - GEN 6 (Marsy-n.), 7 - GEN 7 (Shugar duarf-n.), 8 - GEN 8 (B4-34- n.), 9 - GEN 9 (1/17-n.), 10 - GEN 10 (Vechernitza-n).

Cluster analysis

A hierarchical cluster analysis was applied to identify the similarity and proximity of the garden pea samples, and the results of the clustering were presented graphically via a dendrogram (Fig. 2).

The pea genotypes studied differ in the quantitative indicators analyzed and are grouped into two main clusters. The first cluster was the smallest and only GEN 6 was involved in it. It has higher values of the traits as total number of pods per plant, Two pods per fruiting handle, pod length, weight of the pods of the plant, and % of unfilled grains and with the lowest level of % filled grains (almost twice compared to other samples). The second cluster includes the other 9 pea genotypes in the collection. This cluster, as a separate subgroup, occupies an individual place GEN 8. The dendrogram shows that this genotype was at a very high level from the first division and, by morphological characteristics, stands very close to GEN 6 and was characterized by higher values for plant tall, height to the first fertile node, two pods per fruiting handle, length and width of pods. In terms of the value of many of the other indicators, it was similar to the other samples and this determines its intermediate position on the dendrogram.

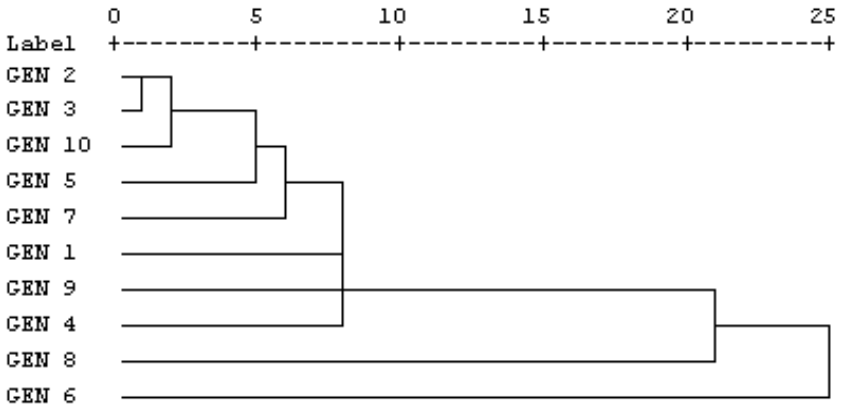

Fig. (2): Dendrogram of genotypes of garden peas (2018-2019).

GEN 1 (22/16-n.), GEN 2 (22/16-af.) , GEN 3 (Casino-af.), GEN 4 (Plovdiv-n.), GEN 5 (Echo-af.), GEN 6 (Marsy-n.), GEN 7 (Shugar duarf-n.), GEN 8 (B4-34- n.), GEN 9 (1/17-n.), GEN 10 (Vechernitza-n).

The second subgroup of the arrangement of the samples shows that GEN 1, GEN 10 and GEN 4 are the second subgroup of the arrangement of the samples shows that GEN 1, GEN 9 and GEN 4 are separated at the mid-level of the original division. They can be considered relatively close in only some traits, such as the number of ineffective nodes, the one pod per fruiting handle, two pods per fruiting handle, % filled grains, and the average number of grains per pod. Genetically closer are especially the plant tall, length of internodes, total number of nodes, length and width of the pods. Genotypes GEN 5 and GEN

7 exhibit some similarity due to the manifestation of the traits height to first fertile node, total number of pods per plant, length and width of pods, filled and unfilled grains. When arranging samples GEN 2, GEN 3 and GEN 10 occupy the uppermost part of the dendrogram. Their position indicates that they are very similar in genotype with similar genetic formulas, which determine the plant tall, the total number of pods per plant, the two pods per fruiting handle, the weight of the pods per plant and weight of green grains per plant, and with satisfactory representation of the number of unproductive nodes, the total number of nodes, and the length of the pods.

A number of studies (Tahernezhad *et al*., 2010) showed that cluster analysis suggests very well the presence of genetic similarity or distance between genotypes, which is also confirmed by the data obtained in this study. The same authors believe that to obtain a more objective assessment, it is advisable to use different methods to determine the polymorphism of the available genetic plasma.

The results of our study are in agreement with the opinion of other researchers such as Bhandari *et al*. (2017) who recommend multivariate statistical methods for genetic diversity assessment be applied when analyzing different samples (varieties, lines). According to the authors, these techniques have a very good theoretical basis for providing reliable information about the actual genetic similarity between the different genotypes and can thus be used to determine the extent of genetic diversity.

Conclusions

The calculating genetic and phenotypic parameters referred to different genetic material of experimental material that responded in a specific way to environmental conditions. Information on the overall phenotypic variation resulting from the joint action of genetic and environmental factors is very important for the breeder to make the right decision using the available genetic resources and to predict future breeding success.

Analysis of variance shows significant differences between the genotypes of garden peas in all the traits studied. A lower level of the genetic variance was found compared to the phenotypic one by number of branches, total number of nodes and one pod per fruiting handle traits. The coefficient of genetic variation is higher than the phenotypic one for most of the traits and ranges from 5.51-5.82% (for pod width and total number of nodes) to 56.98-59.09% (for number of branches and % unfilled grains). The analysis of the variance shows significant differences between the genotypes of garden peas in all the traits studied. For signs of plant height (98.32% and 129.31), height to first fertile node (91.22% and 29.32), weight of pods per plant (86.83%, 29.32), weight of green grains per plant (83.7% and 11.89) and % filled grains (77.81% and 24.96) high inheritance combined with high genetic progress. This is a prerequisite for increasing the biological potential on these traits and a real opportunity to create new forms of garden peas possessing such qualities. The applied hierarchical cluster analysis groups the studied pea genotypes according to the analyzed characteristics into two main clusters. Only the GEN 6 is present in the first cluster, with higher trait values as the traits as total number of pods per plant, two pods per fruiting

handle, length of pods, weight of pods per plant and % unfilled grains. The second cluster includes the other 9 pea genotypes in the collection. GEN 1 (22/16-n.), GEN 6 (Marsy-n.), GEN 4 (Plovdiv-n.) and GEN 9 (1/17-n.) were found the best genotype for the future breeding programs.

Conflict of interest

The authors declare that they have no conflict of interest.

Acknowledgements

The research leading to these results has received funding from the National Science Fund, Bulgaria [Grant КП-06-Н26/12].

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التقييم الوراثي والمظهري للتراكيب الوراثية للبازلاء الخضراء .*Pisum sativum* L

المستخلص: أجريت هذه التجربة خلال موسم الزراعة 2017- 2019 في حقول التجارب في معهد ماريستا لبحوث محاصيل الخضر، بلوفديف، بلغاريا. أختيرت في الدراسة 10 نباتات من البازلاء (*Pisum sativum* L) لقياس طول النبات(سم)، ارتفاع أول عقدة خصبة (سم) ، طول السلامية (سم)، عدد الأفرع، عدد التفرعات، عدد العقد غير الفعالة، عدد العقد الكلية في النبات، عدد القرنات في النبات، قرنة لكل حامل ثمري، قرنتين لكل حامل ثمري، طول القرنة(سم)، عرض القرنة(سم)، وزن القرنة (غم)، وزن الحبوب الخضراء في النبات(غم)، البذور الممتلئة%، البذورغير الممتلئة %، متوسط عدد الحبوب في القرنة. بيَن تحليل التباين وجود اختلافات عالية المعنوية بين مختلف التراكيب الوراثية للبازلاء في جميع صفات الدراسة. أظهرت النتائج أن التباين الوراثي كان أقل من التباين المظهري في عدد الأفرع، العدد الكلي للعقد في النبات وقرنة لكل حامل ثمري. كان التباين الوراثي اعلى من التباين المظهري في معظم الصفات وتراوحت قيمته 5.51-5.82 ٪ (لعرض القرنة وعدد العقد الكلية) 56.98-59.09 ٪ (عدد التفرعات والبذور غير الممتلئة %) .لقيم طول النبات (98.32 و129.31%)، الأرتفاع الى أول عقدة خصبة (91.22 و29.32%)، وزن القرنات بالنبات (86.83 و29.32%)، وزن البذور الخضراء بالنبات (83.7 و11.89%) والبذور الممتلئة % (77.81% و24.96%).ووجد ان هناك درجة توريث عالية مرتبطة مع التطور الجيني .وهذا هو الشرط الأساس من اجل تحسين الامكانيات البيولوجية لهذه الصفات، فضلاً عن انها فرصة حقيقية لإنتاج أشكال جديدة من البزاليا تمتلك هذه الصفات. ان أفضل التراكيب الوراثية وجدت في ,GEN 1 (22/16-n.)، GEN 6 (Marsy-n.)، GEN 4 (Plovdiv-n.) و GEN 9 (1/17-n.) . ويمكن أن تستخدم في برامج تربية جديدة في خطوط للتهجين وربما ستدرج في قائمة الأصناف المنافسة.

الكلمات المفتاحية: البازلاء الخضراء، تراكيب وراثية، تربية ، توريث.