



## MULTIVARIATE ANALYSIS OF SPRING FIELD PEA GENOTYPES

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**Abstract.** An analysis was carried out during 2011–2013 on eight field pea genotypes. On the basis of the obtained results, the following conclusions may be drawn and used for further research on the quantitative traits on forage pea and its application in breeding and the development of new varieties: Analysis of variance showed significant differences among genotypes for all traits. The results of coefficient of variation analysis showed that the genotypic coefficient of variation was higher than the phenotypic coefficient of variation. For all traits studied were found high heritability, indicated that these traits could be improve through selection procedure. For plant height and seeds per plant, line №115 and №9A were classified as high general adaptability to environment. The cultivars *Kerpo* and *Kristal* were classified as high general adaptability for seed weight per plant. For almost all traits line №29 was classified as having specific adaptability to unfavorable environment.

**Keyword:** breeding; genotypes, *Pisum sativum*; productivity

### Introduction

Field pea (*Pisum sativum* L.) is one of the world's oldest domesticated crops cultivated before 10<sup>th</sup> and 9<sup>th</sup> millennia BC [ZOHARY *et al.*, 2000].

*Pisum sativum* comprises both the wild species (*Pisum Fulvum* and *Pisum eratius*) and cultivated species (*Pisum abyssinicum*) origin–Nated from the Mediterranean region, primarily in the Middle East [ELLIS *et al.*, 2011].

However, the exact center of its diversity is not known yet due to significant change in the areas of origin and loss of passport data of the early accessions [PETR *et al.*, 2012; BUTNARIU *et al.*, 2012].

The crop is grown in many countries and currently ranks fourth among the pulses in the world with cultivated area of 6.33 million hectares (ha) [FAOSTAT, 2012].

It is the major food legumes with a valuable and cheap source of protein having essential amino acids (23 to 25 %) that have high nutritional values for resource poor households [NAWAB *et al.*, 2008].

The crop has important ecological and economic advantages in many countries, as it plays a significant role in soil fertility restoration and also serves as a break crop suitable for rotation to minimize the negative impact of cereal

based mono-cropping [ANGAW and ASNAKEW, 1994; BUTNARIU *et al.*, 2005].

Employing effective breeding program that can exploit the existing genetic variability in the genotypes is paramount important to fill these yield gaps and feed the ever increasing population.

To this effect, the knowledge of nature and degree of divergence in genotypes, the extent of transmissibility of the given trait and their interaction with environments are extremely valuable [NISAR *et al.*, 2008; HABTAMU and MILLION, 2013].

The research work in this study aims studying genetic variability and the heritability on different, characters of pea which may help to select suitable genotypes for future breeding programs.

### Material and methods

The experimental study was conducted during the 2011–2012 period in second experimental field of the Institute of Forage Crops, Pleven, Bulgaria.

Five spring pea (*Pisum sativum* ssp. *Sativum* L.) genotypes were included in the trial namely cultivars–*Kerpo*; and *Kristal*; hybrid lines №115; №29 and №9A from our collection.



This selection material was sown at three replications with a plot size of 2 m<sup>2</sup> and 20 cm row spacing.

The forage pea was grown by approved technology of the Institute of Forage Crops, Pleven.

Ten randomly selected plants from each genotype were marked and used to estimate yield components—plant height (cm); number seeds and pods per plant, 1000 seed weight (g); number seeds per pod; seed weight per plant (g) and vegetation period (day).

For all the traits studied an average arithmetical and coefficients of variability (VC, %) were calculated.

The next statistical methods were used to process the experimental data: factor analysis by the method of principal components [ВЪНДЕВ, 2003, BUTNARIU *et al.*, 2014], hierarchical cluster analysis by the method of Ward [WARD, 1963], for the grouping of genotypes by similarity as a measure for the difference (the genetic distance), the Euclidean distance between them was used, having previously standardization the data carried out.

Broad sense heritability (H<sub>bs</sub>) was calculated using the formula proposed by Mahmud and Kramer [MAHMUD and KRAMER 1951].

Genotypic coefficient of variation (CV<sub>g</sub>) and phenotypic coefficient of

variation (CV<sub>e</sub>) were estimated by the formula suggested by Burton [BURTON, 1952].

The analysis of adaptability was performed according to the methods proposed by Nascimento and collab. [NASCIMENTO *et al.*, 2009].

The computer software GENES 2009.7.0 for Windows XP [CRUZ, 2009, BUTNARIU and BOSTAN, 2012] and Excel for Windows XP were used for all analysis.

## Results and discussion

### 4.1. ANOVA of quantitative traits

Genetic diversity of germplasm determinates the limit of selection in crop improvement.

Furthermore knowledge of genetic associations among agronomic traits is regarded to support considerable help to maintain genetic improved to breeding programme.

Crop improvement with heritable characters, estimation of genetic parameters and their association is prime importance in breeding [ESIYOK *et al.*, 2011].

The analysis of variance (Table 1) indicated the existence of significant variability for the all characters plant height; number seeds and pods per plant, 1000 seed weight; number seeds per pod; seed weight per plant and vegetation period.

**Table 1.**

Analysis of variation for quantitative traits in pea (*Pisum sativum*)

SV	DF	Mean square						
		Plant height	Pods per plant	Seeds per pod	Seeds per plant	1000 seed weight	Seed weight per plant	Vegetation period
Years	2	1063.467	25.8667	0.2803	183.2	2844.536	9.2241	54.4667
Varieties	4	3696.7667**	15.7667**	1.2237*	407.2667**	8168.3193**	1.0742**	42.6**
Residue	8	131.7167	1.1167	0.2522	48.3667	134.3343	0.0415	4.3
CV(%)		12.14	12.48	14.37	23.34	5.42	4.75	2.16

\*\* and \* significant at 1 and 5% probability levels

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### 4.2. Cluster analysis

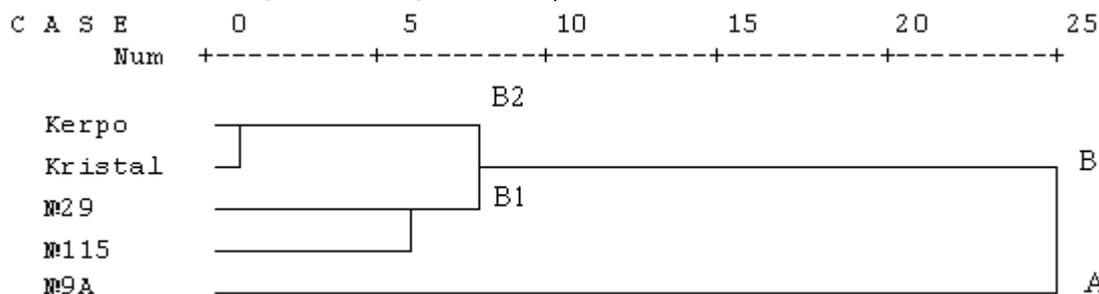
Hierarchical cluster analysis of the varieties was done on the basis of the values of the quantitative traits studied.

The Euclidean distance was used for as a measure for genetic distance.

Results shown as a dendrogram (Figure 1) indicated the different grouping



of the varieties by similarity and difference.



**Figure 1.** Dendrogram of spring pea varieties (2012–2014)

Samples were clustered into two main groups (A and B).

Data showed that there was observed significant genetic distance between line №9A and all other genotypes.

The plants from this hybrid were characterized by high values of the traits plant height, pod per plant and seeds per plant and are separated into group “A”.

In the subgroup of “B1” based on the main group “B” fall genotypes №29 and №115. *Kerpo* and *Kristal* forming the second branch in the same group (subgroup “B2”).

These cultivars are genetically closed by plant height, seeds per plant and 1000 seed weight. To obtain more pronounced transgressive forms in hybrid combinations should be genotypes from different groups included to expect better combination of the favourable genes in one genotype.

The hierarchical cluster analysis can be used in the selections to plan the initial parent combinations [DRAGAVTSEV and AVERYANOVA, 1983, BUTNARIU et al., 2006, CAUNII et al.,

2015, BOSTAN et al., 2013; FERENCZ et al., 2012].

**4.3. Principal component analysis**

Principal component analysis was done to assess the pattern of variations by considering all the 7 variables simultaneously.

There are two eigenvalues greater than 1 which determined the choice of the two main components.

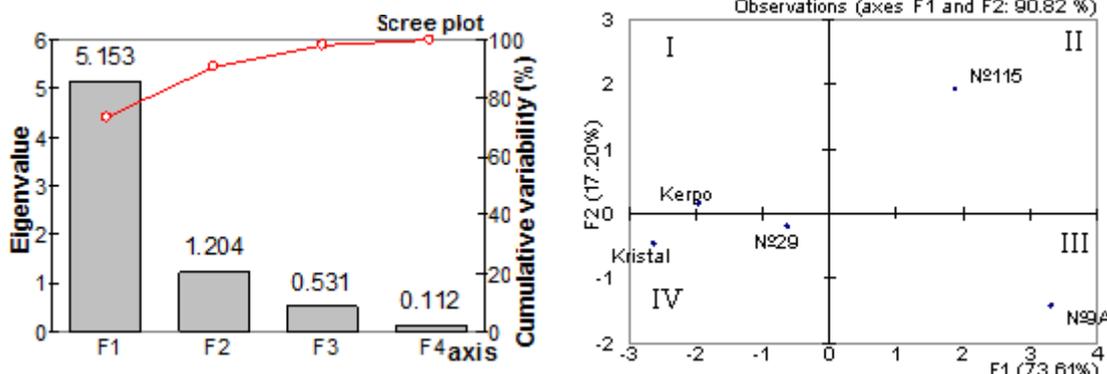
The first component explained 73.61 % and the second–17.20 % of the total variance.

The main principal components (F1 and F2) accounted more than 90% of the total variation in the field pea varieties (Table 2).

The first component was mainly related to the characteristics plant height; seeds per plant, 1000 seed weight; number seeds per pod and seed weight per plant.

In the formation of the second component characteristics pod per plant and vegetation period have participated.

Genotypes were phenotypically very different between them (Figure 2).



**Figure 2.** Principal component analysis of quantitative traits of spring pea genotypes

Samples were clustered into two main groups (A and B). Data showed that

there was observed significant genetic distance between line №9A and all other



genotypes.

The plants from this hybrid were characterized by high values of the traits plant height, pod per plant and seeds per plant and are separated into group "A".

In the subgroup of "B1" based on the main group "B" fall genotypes №29 and №115. *Kerpo* and *Kristal* forming the second branch in the same group (subgroup "B2") *Kerpo* and *Kristal*.

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**Table 2.**

The Eigenvalues and vectors for 7 traits of pea genotypes

Parameters	F1	F2	F3	F4
Plant height	0.862	0.056	0.065	0.017
Pods per plant	0.852	0.055	0.084	0.008
Seeds per pod	0.454	0.258	0.277	0.011
Seeds per plant	0.998	0.000	0.000	0.001
1000 seed weight	0.703	0.285	0.012	0.000
Seed weight per plant	0.741	0.177	0.057	0.026
Vegetation period	0.541	0.372	0.037	0.049
Eigenvalue	5.153	1.204	0.531	0.112
Variability (%)	73.612	17.204	7.586	1.598
Cumulative %	73.612	90.816	98.402	100.000

F1; F2; F3; F4 = principal component 1, 2, 3 and 4 respectively

The first component was mainly related to the characteristics plant height; seeds per plant, 1000 seed weight; number seeds per pod and seed weight per plant.

In the formation of the second component characteristics pod per plant and vegetation period have participated.

Genotypes were phenotypically very different between them (Figure 2).

Line №115 characterized by positive values of the both components (F1 and F2).

*Kerpo* which was arranged in the first quadrant has positive values only for component F2.

*Kristal* and №29 are situated in fourth quadrant showing negative values of both components.

Apart position of the genotypes in the quadrants showed that together they are phenotypically similar in a small number of characteristics.

### 4.4. Estimation of genotypic (GCV) and phenotypic coefficient of variation (PCV)

The comparison of characters as regards to the extent of genetic variation could be better judged by the estimation of genotypic coefficient of variation (CVg) in relation to their respective phenotypic coefficient of variation (CVe).



Amongst the investigated characters very small difference between CVg and CVe was observed for the trait like seed

per pod, seed per plant and vegetation period (Table 3).

**Table 3.**

Genetic component of variation for quantitative traits in pea (*Pisum sativum*)

Traits Parameters	Plant height	Pods per plant	Seeds per pod	Seeds per plant	1000 seed weight	Seed weight per plant	Vegetation period
Min	53.00	4.00	2.11	12.00	112.00	1.86	91.00
Max	154.00	15.00	4.63	59.00	283.70	6.46	109.00
CVg (%)	36.47	26.10	16.29	36.70	24.19	13.69	3.73
CVg/CVe	3.00	2.09	1.13	1.57	4.46	2.88	1.72
$\sigma^2_g$	1188.35	4.88	0.32	119.63	2677.99	0.34	12.77
$\sigma^2_p$	131.72	1.117	0.25	48.37	134.33	0.042	4.30
H <sup>2</sup> (%)	96	92	79	88	98	96	89

CVg–genotypic coefficient of variation;  
 CVe–phenotypic coefficient of variation;  
 $\sigma^2_g$ –genotypic variances;  
 $\sigma^2_p$ –phenotypic variances;  
 H<sup>2</sup>–broad sense heritability (%)

It indicates that the observed variations for the trait were mostly due to genetic factors.

However, the environment played a little role on the expression of this trait.

On the other hand, large difference between CVg and CVe was observed for the characters 1000 seed weight, plant height and seed weight per plant.

This indicated the role of environmental influence over these characters. The high CVg for these traits indicated further selection could improve the genotypes.

#### 4.5. Estimation of heritability

The heritable variation with heritability (broad sense) estimates would give reliable indication of the expected improvement through selection.

High estimates of broad sense heritability (Table 3) were recorded for all traits 1000 seed weight (98 %), plant height (96 %), and seed weight per plant (96 %), pod per plant (92 %), vegetation period (89 %), seeds per plant (88 %) and seeds per pod (79 %). Heritability estimate provides guide for the selection procedure to be followed by the breeder for improvement of these traits under a given environment. Nawab and collab. also reported for high heritability for 1000 seed weight [NAWAB *et al.*, 2008, BUTNARIU and BOSTAN, 2011].

#### 4.6. Estimation of phenotypic and genetic variances

Estimates of phenotypic variances of the quantitative traits were smaller than their respective genetic variances for all traits. Genotypic variances ranged from 0.34 for seed weight per plant to 2679.99 for 1000 seed weight. The genotypic variance was the highest for thousand seed weight and plant height indicating the greater magnitude of genetic variability for these traits. Phenotypic variance values ranged from 0.042 to 134.33. The highest phenotypic variance was that of 1000 seed weight.

Minimum phenotypic variance was observed for seed weight per plant.

Higher environmental variance was observed in plant height and seeds per plant. This indicates that both traits are highly influenced by environment.

#### 4.7. Analysis of adaptability

For the centroid method (Table 4), it was found that cultivar *Kristal* was grouped in class IV for all traits with the exception of 1000 seed weight and seed weight per plant, i.e. behaving as poorly adapted cultivars.

The №29 line had a mean overall adaptability for almost traits except of seed weight per plant; being grouped in Class V. *Kerpo* and №29 presents the group VII for seed weight per plant that



represents specific adaptability to | unfavorable environment.

**Table 4.**

Estimation of parameters of adaptability of seven pea cultivars for yield, based on the methodologies of centroid [NASCIMENTO *et al.*, 2009]

Genotype	Traits	Plant height	Pods per plant	Seeds per pod	Seeds per plant	1000 seed weight	Seed weight per plant	Vegetation period
Rank								
Kerpo		IV	IV	V	IV	I	VII	IV
Kristal		IV	IV	IV	IV	I	I	IV
№115		I	V	I	I	V	V	I
№29		V	V	V	V	V	VII	IV
№9A		I	I	VII	I	IV	IV	V

Class I: high general adaptability;  
 Class II: specific adaptability to favorable environments;  
 Class III: Specific adaptability to adverse environments;  
 Class IV: Partially adapted;  
 Class V: Adaptability overall average;  
 Class VI: specific adaptability to favorable environments;  
 Class VII: Adaptability specific to unfavorable environments.

Line №9A is grouped in Class I for plant height; seeds and pod per plant, that represents high general adaptability. Line №115 is characterized with high general adaptability (Class I) for plant height, seeds per plant and seed per pod.

### Conclusions

On the basis of the obtained results, the following conclusions may be drawn and used for further research on the quantitative traits on forage pea and its application in breeding and the development of new varieties: Analysis of variance showed significant differences among genotypes for all traits. The results of coefficient of variation analysis showed that the genotypic coefficient of variation was higher than the phenotypic coefficient of variation. For all traits studied were found high heritability, indicated that these traits could be improve through selection procedure. For plant height and seeds per plant, line №115 and №9. A were classified as high general adaptability to environment. The cultivars *Kerpo* and *Kristal* were classified as high general adaptability for seed weight per plant. For almost all traits line №29 was classified as having specific adaptability to unfavorable environment.

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