Assessment of phenotypic diversity of local grass pea (*Lathyrus* sp. L.) accessions based on economically important agricultural traits

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Abstract

The success of any crop improvement program essentially depends on the nature and magnitude of genetic diversity. Although grass pea is environment-friendly grain legumes, important for food security and animal feeding, the genetic potential of this crop have been neglected for a long. The paper deals with the study of phenotypic diversity of grass pea accessions with local origin, included in IPGR's collections regarding economically important agricultural traits. The traits evaluation was performed according to *Lathyrus sativus* International Descriptors. The degree of traits variability was expressed by the coefficient of variation. Cluster and principal component analyses were applied to assemble the accessions in distinct groups. The coefficient of variation for all studied grass pea traits fluctuated between 6.29% and 16.83%. Middle variability was characteristic for six traits. Based on economically important traits the grass pea accessions were grouped in two different clusters. Two grass pea accessions (BGR4836 and BGR4831) were selected having tall plants, big number of pods and grains per plant, high yield per plant, high biological yield and harvest index. The BGR4847 accession had high biological yield, high harvest index, high 100 grains mass and big number of grains per pod. The BGR 4334 genotype was significantly different from other genotypes. The results of the conduct analyses helped to select accessions for further investigations.

Key words: cluster analysis; principal component analyses; *Lathyrus* sp.; morphological traits

INTRODUCTION

Grain legumes contribute significantly to total world food production. Legumes, together with cereals, are very important for development of modern agriculture (Upadhyaya et al., 2011). Grass pea (*Lathyrus sativus* L.) is an important crop with economic significance in some countries as Ethiopia, Bangladesh, Nepal and India. It is the fifth most important pulse crop in Ethiopia and covers about 9% of the total pulse growing area (Tsegaye et al., 2005). The most economically important *Lathyrus* species grown commercially include *Lathyrus sativus* L., *Lathyrus cicera* L and *Lathyrus odoratus* L. Grasspea is widely cultivated as food and fodder crop (Hanbury et al., 2000). It plays also an important role in many low input farming systems, and is easily cultivated and can survive under extreme environments, from drought to flooding (Vaz Patto et al., 2006). Although there are relatively few efforts being made throughout the world for the genetic improvement of these species compared with other crops, some important programs exist that aim to improve its yield, quality and adaptability. All these breeding efforts require access to suitable genetic resources (Vaz Patto & Rubiales, 2014). The breeding work on grass pea is concentrated mainly on its utilization as hay, straw and grain production. Exploitation of *Lathyrus sativus* L. germplasm resources is based currently on landrace material (Yunus

& Jackson, 1991). Diversity is a potential resource and a guarantee for improving a species of interest. It is also the source of new genes for combating threats to agricultural production caused due to biotic or abiotic factors (Gepts, 2006). Multivariate methods such as cluster analysis can be performed on morphological quantitative data as well as the mean, range and standard deviation for determining of variation of the traits could be discussed and explaining their effects in the final output of clustering (Mohammadi & Prasanna, 2003).

The aim of the current study is to assess the phenotypic diversity in grass pea accessions with local origin regarding economically important agricultural traits.

MATERIAL AND METHODS

Two years (2019-2020) trails were carried out on the experimental field at the Institute of Plant Genetic Resources – Sadovo. The subject of the study were elevant local grass pea accessions. The seeds were obtained from the *Lathyrus* sp. collections, stored in the IPGR gene-bank. The experimental plot was designed in randomized complete block design (RCBD) in three replications on 5.0 m^2 (Dimova & Marinkov, 1999). The plants were grown by standard technology for field production on cinnamon-forest soils after a wheat precursor.

The structural elements of the yield were established by biometric analysis of ten plants per accession for each crop. The traits evaluation was performed using *Lathyrus* sp. L. Descriptors of IPGRI (2000). The following quantitative characters were taken into consideration: plant height (cm), number of productive branches, height to the first pod (cm), number of pods per plant, number of grains per plant, number of grains per pods, mass of grains per plant (g), mass of 100 grains (g), biological yield (g) and harvest index (g).

The degree of variability of the studied traits was represented by the coefficient of variation (CV%): low (up to 10%), middle (10% - 20%) and strongly (significant) (over 20%) (Dimova & Marinkov, 1999). To investigate the genetic distance between the studied grass pea accessions a Cluster analysis and PC-analysis were applied. The Euclidian distance was used to measure the difference/similarity between the accessions and their traits (Ward, 1963). All experimental data were processed statistically with using the computer software SPSS for Windows Version 19.0 (IBM SPSS Statistics 19 Product Version: 19.0.0) (IBM, 2019).

RESULTS AND DISCUSSION

The average value of investigated quantitative traits, as well as their variation coefficients are presented on Table 1. The variability of all studied traits varied between 6.29% and 16.83%. Middle variability was recorded for the following traits: height to the first pod (13.93%), number of productive branches (10.38 %), number of pods per plant (11.66 %), number of grains per plant (13.42 %), mass of grains per plant (16.83 %) and biogical yield (13.74 %). Similar phenotypic investigation on grass pea has been conducted by many researchers (Talukdar & Biswas, 2008; Rahman et al., 2010; Hobdari et al., 2012; Parihar et al., 2015). Most of them established high genetic variation among the studied genotypes. According to Rahman et al. (2010) the coefficient of variation ranged from 3.44-12.65%. The author established higher coefficient of variation in pods per plant, plant height, seeds per plant, seed yield per plant and branches per plant compared to other traits.

A cluster analysis was carried out in order to group the evaluated grass pea accessions based on their morphological traits (Figure 1). The accessions were divided into two main groups (clusters) giving an idea about quantitative traits diversity. The main traits that distinguished the accessions were number of pods and grains per plant. The first cluster was divided into two sub-clusters.

The first sub-cluster was of great interest with two accessions (BGR4836 and BGR4831) possessing tall plants (91.33 cm and 80.33 cm), big number of pods (33.42 and 34.08) and grains (80.42 and 83.18) per plant, high yield per plant (14.13 g and 15.46 g), high biological yield (38.32 g and 37.97 g) and harvest index (39.44% and 40.68%).

The second sub-cluster included eight genotypes (BGR 4833, BGR 4847, BGR 4830, BGR BGR 4834, BGR 4832, BGR 33111, BGR 4835 and BGR 40415) with medium-high to short stem, with more grains per pod, with big number of grains and pods per plant and harvest index.

Table 1. Phenotypic assessment of grass pea accessions by quantitative traits

Accessions	Plant height, cm	Height to the first pod, cm	Number of productive branches	Number of pods per plant	Number of grains per plant	Number of grains per pod	Mass of grains per plant, g	100 grains mass, g	Biological yield, g	Harvest index, g
BGR40415	75.38	22.17	2.75	26.46	63.88	3.00	10.34	16.88	26.20	39.06
BGR4830	83.58	22.08	2.75	29.42	73.25	3.07	13.03	19.48	37.05	36.44
BGR4831	80.33	23.83	3.33	34.08	83.17	2.70	15.46	21.45	37.97	40.68
BGR4832	80.17	25.42	3.50	33.17	73.75	2.97	13.53	19.13	33.93	39.83
BGR4833	89.42	22.50	2.92	27.08	60.75	2.73	12.33	22.00	27.07	45.57
BGR4834	79.33	25.92	2.50	29.75	69.75	2.77	12.23	19.95	31.13	39.44
BGR4835	74.08	23.58	2.67	26.33	64.83	2.97	9.95	20.65	27.72	37.18
BGR4836	91.33	25.67	2.92	33.42 c	80.42	2.92	14.13 b	20.23	38.32	39.44
BGR4847	82.08	31.17	2.58	29.33	66.75	3.18	13.67	21.35	31.80	41.85
BGR 33111	72.42	19.83	3.00	25.58	72.17	2.97	10.49	16.85	33.27	35.35
BGR43334	80.58	30.25	2.83	24.33	50.08	2.57	8.82	20.03	28.63	31.73
Average St	**80.79**	**24.77**	**2.89**	**29.00**	**68.98**	**2.89**	**12.18**	**19.82**	**32.10**	**38.78**
Min	**72.42**	**19.83**	**2.50**	**24.33**	**50.08**	**2.57**	**8.82**	**16.85**	**26.20**	**31.73**
Max	**91.33**	**31.17**	**3.50**	**34.08**	**83.17**	**3.18**	**15.46**	**22.00**	**38.32**	**45.57**
Std. Deviation	**5.85**	**3.45**	**0.30**	**3.38**	**9.26**	**0.18**	**2.05**	**1.70**	**4.41**	**3.62**
CV (%)	**7.24**	**13.93**	**10.38**	**11.66**	**13.42**	**6.29**	**16.83**	**8.58**	**13.74**	**9.33**

CV (%)-coefficient of variation

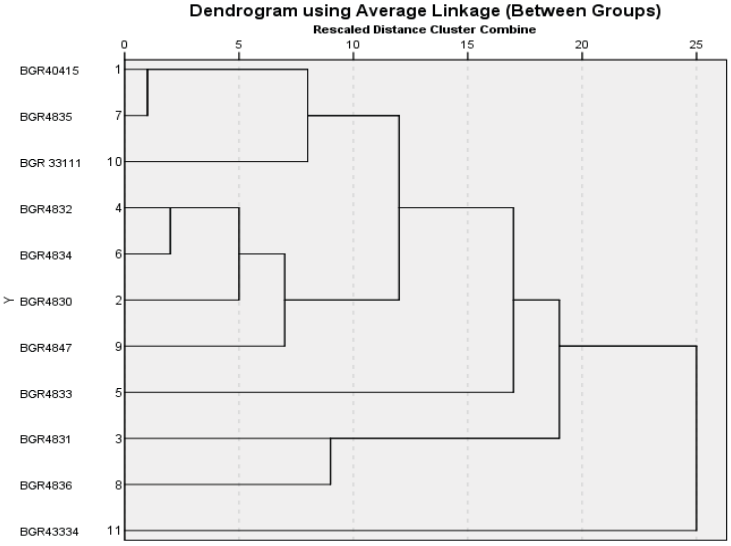

Figure 1. Dendogram of grasspea genotype grouping on their morphological traits using cluster analysis

Only one accessions was included in the second cluster (BGR 43334). The BGR 4334 genotype characterized by medium tall plants (80.58 cm), high first formed pods (30.25 cm), large grains (20.03 g) and with no big number of grains and pods per plant. The data showed that this accession had significant genetic distance between him and other genotypes. The traits related to the number of pod and grains per plant, mass of the grains per plant, biological yield, harvest index were from significant economic importance for the leguminous forage crops, and this defines the genotype as a potential initial material for selection. Similar grouping of grass pea accessions by cluster analysis was obtained by Kosev & Vasileva (2019).

The clustering of the economical important traits of the evaluated grass pea accessions based on their similarity/differences is presented on Figure 2. As a result, two main clusters were observed. The first one was divided into two sub-clusters. The first one included number of main branches, number of grains per pod and mass of grains per plant. The second sub-cluster included number of pods per plant, biological yield, height to the first pod, mass of 100 grains and harvest index. The remaining two traits (plant height and number of grains per plant) were combined into the second sub-cluster, at a large distance in the factorial plane from another cluster.

Similar clustering of the traits was conducted with other grain legumes, as faba bean (Velcheva & Petrova, 2020). The authors reported one cluster combining plant height, vegetation period and mass of 100 grains, at a large distance in the factorial plane from another cluster.

The analysis of the main components completed the cluster analysis. The results of the PC analysis (Table 2) shown, that the four main components PC 1, PC 2, PC 3 and PC 4 are 87.0% of the total variation of all traits by genotype, which is large enough.

The data in Table 3 show that four traits are in the first component: number of pods per plant

Table 2. Component analysis of the variance in the studied traits

Component	Total	% of variance	Cumulative %
1	**4.25**	42.5	42.5
2	**2.16**	21.6	64.2
3	**1.25**	12.5	76.6
4	**1.04**	10.4	87.0
5	0.57	5.6	92.7
6	0.40	4.0	96.7
7	0.23	2.3	99.1
8	0.07	0.7	99.7
9	0.03	0.2	100.0
10	0.00	0.0	100.0

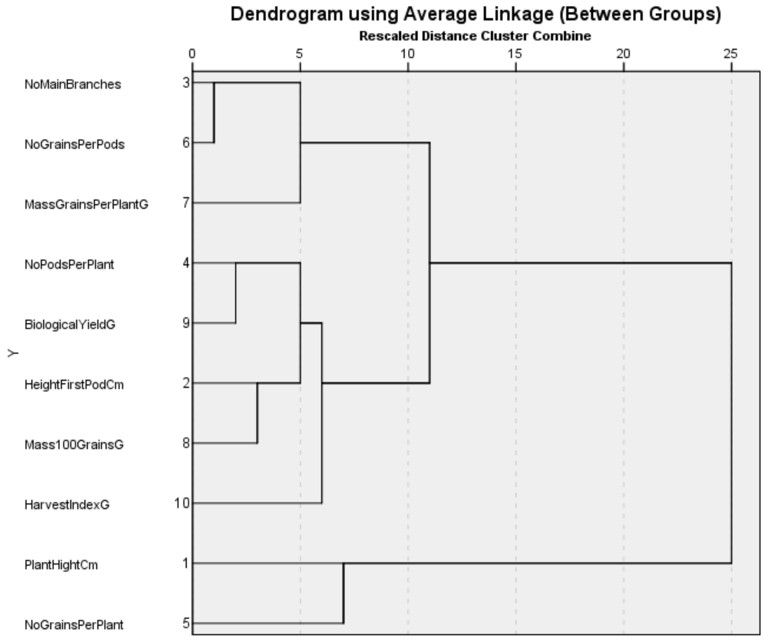

Figure 2. Dendogram of grouping of grass pea studied traits using cluster analysis

(0.951), number of grains per plant (0.841), mass of grains per plant (0.976) and biological yield (0.801) and they are relate positively to it. There were three traits in the second component: plant height (0.594), height to the first pod (0.670) and 100 grains mass (0.806) and they were also relate positively to it.

The third component included the trait number of grains per pod (0.808), which refers positively and number of productive branches (-0.570), which refers negatively to PC3. The fourth component included only the harvest index (-0.572) which negatively refers to PC4.

According to Biabani & Pakniyat (2008) and Stamatov & Deshev (2012), the traits found in the individual components are determined by nearby genes in the genome.

The studied grass pea accessions were related differently to the four main components (Table 4). Five genotypes belong to the first main component, three of which are positive with PC 1 (BGR4831, BGR4832 and BGR4836) and the other two negative (BGR 4833 and BGR4835). To the negative value of the second main component referred only one accession - BGR 33111. In the positive values of PC 3 include the accession BGR4834, and in the negative values of PC 3 contains the genotype BGR40415. In the positive values of PC 4 were included two accessions (BGR4830 and BGR4847).

The genotypes BGR4847, BGR4831 and BGR4836, located in the farthest parts of the factorial plane, can be mentioned as sources of variation in order to create a diverse starting material and enrich the gene pool in grass pea. These three accessions can be used as parental pairs in the breeding and improvement work of grass pea.

Table 3. Explained significant components by traits in grasspea

№	Indicators	Components			
		1	**2**	**3**	**4**
1	Plant height, cm	0.564	**0.594**	0.000	-0.045
2	Height to the first pod, cm	-0.010	**0.670**	-0.060	0.628
3	Number of productive branches	0.502	-0.318	**-0.570**	-0.286
4	Number of pods per plant	**0.951**	-0.057	-0.062	0.108
5	Number of grains per plant	**0.841**	-0.473	0.060	0.046
6	Number of grains per pod	0.120	-0.399	**0.808**	0.261
7	Mass of grains per plant, g	**0.976**	0.057	0.116	0.017
8	100 grains mass, g	0.413	**0.806**	-0.025	-0.039
9	Biological yield, g	**0.801**	-0.310	-0.190	0.389
10	Harvest index, g	0.541	0.353	0.456	**-0.572**

Table 4. Explained significant components by grasspea accessions

№	**Accessions**	Components			
		1	**2**	**3**	**4**
1	BGR40415	-0.964	-0.373	**-1.191**	0.739
2	BGR4830	0.659	-0.412	0.050	**0.844**
3	BGR4831	**1.521**	0.415	-0.323	-1.246
4	BGR4832	**1.016**	-0.104	-0.484	-0.457
5	BGR4833	**-1.189**	2.235	-0.748	-0.882
6	BGR4834	-0.243	0.141	**0.429**	0.168
7	BGR4835	**-0.921**	-0.245	-0.176	0.456
8	BGR4836	**1.304**	0.366	0.660	0.112
9	BGR4847	-0.069	0.722	1.503	**1.745**
10	BGR 33111	0.010	**-1.464**	-1.399	0.213

CONCLUSIONS

A number of local *Lathyrus sativus* L. accessions were characterized by their economically important quantitative traits. **The genetic diversity within the accessions of grass pea were proved through the variability of the studied traits.** Based on quantitative traits the grass pea accessions were clustered in two groups. On the other hand, the traits were combined into two main clusters that would facilitate the crop breeding programs. **The results of the cluster analysis and the analysis of the main components will help to select accessions with maximum genetic distance to** assemble the broad-based panel of genetic resources of these legume crops for future research and use. Four grass pea accessions with numbers - BGR4836, BGR4831, BGR4847 and BGR 43334 may to be used in further breeding programs.

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