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Lathyrus diversity: resources with different origin with relevance to crop improvement

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Abstract

Lathyrus sativus L. is a legume crop, possessing high protein content, tolerant to drought, waterlogging and salinity. The main aim of the study was to evaluate the phenotypic diversity of the exchanged local *Lathyrus* accessions from Mediterranean region and south eastern Europe in order to review their potential for its *ex situ* conservation and sustainable use. The subject of the study were twenty four grass pea accessions with different origin, received on a project basis. The morphological, biological and economic characteristics were assessed on 10 pre-marked, normally developed plants from each accession using the International Classification of Species *Lathyrus* sp. and list of indicators. All exchanged accessions were registered in our national database and in European Search Catalogue for Plant Genetic Resources (EURISCO). Nine *Lathyrus sativus* accessions with Bulgarian origin were reproduced at the experimental field of IPGR, Sadovo and the seeds from them was included in AEGIS (A European Genebank Integrated System). Several accessions (C000095, C0000101, C0000100, BGR43334, BGR40415 and C00000103) were selected with promising results related to grain and forage yields. Cluster analysis classified the accessions into two distinct groups as accessions from Bulgaria, Romania and part of Serbia were grouped in the first cluster and all others in the second. As the best adapted accessions to Bulgarian environment condition were two accessions from Romania (C00096 and C00095), two from Serbia (C000100 and C000101) and two from Bosnia and Herzegovina (C00093 and C00094). They demonstrated good productivity and good adaptability. All exchanged accessions were registered in our National database and in EURISCO database.

Key words: *Lathyrus* diversity; EUGrainLeg project; phenotypic diversity

INTRODUCTION

Grain legumes contribute significantly to total world food production. Legumes, together with cereals, have been fundamental to the development of modern agriculture (Upadhyaya et al., 2011). Grasspea (*Lathyrus sativus* L.) is a food and fodder crop widely cultivated (Hanbury et al., 2000). Grasspea also plays 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). The breeding work has concentrated mainly on the use grass pea with research on hay, straw and grain production (Mathur et al., 1998). Exploitation of germplasm resources for the improvement of *Lathyrus sativus* currently concentrates on landrace material (Yunus & Jackson, 1991) by conventional means. Grass pea 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*, *Lathyrus cicera* and *Lathyrus odoratus.* Although relatively few efforts were made throughout the world for the genetic improvement of these species compared with other crops, some important programmes exist that aim to improve its yield, quality and adaptability. All these breeding efforts require access to suitable genetic resources (Vaz Patto & Rubiales, 2014). 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 due to biotic or abiotic stress factors (Frankel et al., 1995; Gepts, 2006). Evaluation of phenotypic diversity among accessions could be an invaluable aid in crop improvement strategies. The crop has not attained much progress, due to the limited research on genetic and genomic grass pea resources available in the world gene banks. The knowledge that the excessive consumption of grass pea can lead to a neurological disorder in humans has further discouraged adaptive research on this orphaned crop. Therefore, conservation and sustainable use of genetic resources are of paramount importance for grass pea improvement (Singh et all., 2013).

The main purpose of this study is to evaluate the phenotypic diversity of the exchanged local *Lathyrus* accessions from Mediterranean region and south eastern Europe in order to review their potential for its *ex situ* conservation and sustainable use.

MATERIAL AND METHODS

Plant material and study traits

Two years (2019-2020) trails were carried out on the experimental field of the Institute of Plant Genetic Resources (IPGR) – Sadovo. The subject of the study were twenty four grass pea accessions with different origin. The seeds were exchanged between partners in EUGrainLeg project entitled:"*Lathyrus* diversity: available resources with relevance to crop

Table 1. List of the exchanged *Lathyrus sativus* accessions

Bulgarian catalog number	GENUS/ SPECIES	Origin_GeneBank	ACC code
C0000084	*Lathyrus sativus*	Greece	GR1
C0000085	*Lathyrus sativus*	Grecee	GR2
C0000086	*Lathyrus sativus*	Portugal	ISOP1189
C0000087	*Lathyrus sativus*	Portugal	ISOP1176
C0000088	*Lathyrus sativus*	Portugal	ISOP1177
C0000089	*Lathyrus sativus*	Portugal	ISOP1190
C0000090	*Lathyrus sativus*	BiH	GB00999
C0000091	*Lathyrus sativus*	BiH	GB01002
C0000092	*Lathyrus sativus*	BiH	GB01003
C0000093	*Lathyrus sativus*	BiH	GB00954
C0000094	*Lathyrus sativus*	BiH	GB01000
C0000095	*Lathyrus sativus*	Romania	SVGB19385
C0000096	*Lathyrus sativus*	Romania	SVGB20803
C0000097	*Lathyrus sativus*	Serbia	KL1
C0000098	*Lathyrus sativus*	Serbia	KL2
C0000099	*Lathyrus sativus*	Serbia	KL4
C0000100	*Lathyrus sativus*	Serbia	KL5
C0000101	*Lathyrus sativus*	Serbia	KL7
C0000102	*Lathyrus sativus*	Serbia	KL8
C0000103	*Lathyrus sativus*	Serbia	KL9
C0000104	*Lathyrus sativus*	Serbia	KL10
BGR40415	*Lathyrus sativus*	Bulgaria	BGR40415
BGR43334	*Lathyrus sativus*	Bulgaria	BGR43334
C0000105	*Lathyrus sativus*	Slovenia	SRGB5486

improvement – progress reviews and relationship with AEGIS". On Table 1 is presented the origin of the tested *Lathyrus sativus* accessions - from the Mediterranean region (Greece, Portugal and Slovenia), and south Eastern Europe (Serbia, Bulgaria, Romania, Bosnia and Herzegovina).

The field experiment was designed in Randomized Complete Block Design (RCBD) with three replications. Experiment plot size was 5.0 m^2. The plants were grown by standard technology for field production on cinnamon-forest soils after a wheat precursor. During the vegetation, the plots were weeded and dug by hand. The morphological, biological and economic characteristics were assessed on 10 pre-marked, normally developed plants from each accession using the International Classification of Species *Lathyrus* sp. (2000) and list of indicators (Table 2).

Statistical data analysis

The obtained results were processed using the computer software SPSS for Windows Version 19.0 (IBM SPSS Statistics 19 Product Version: 19.0.0) (IBM, 2019). To investigate the genetic distance between the studied grass pea accessions a Cluster analysis was applied. The Euclidian distance was used to measure the difference/similarity between the accessions and their traits (Ward, 1963). Variability of the study traits of the experimental data were made. It was accepted that the variation is considered to be weak if the coefficient of variation does not exceed 10%, on average - when it is greater than 10% and less than 20%, strongly (significant) - when it is above 20% (Dimova & Marinkov, 1999).

RESULTS AND DISCUSSION

All exchanged accessions were recorded with full passport description in the National Register for Plant Genetic Resources and in the electronic catalogue on Plant Genetic Resources EURISCO (http://eurisco.ipk-gatersleben.de). An inventory on *Lathyrus* sp. collection was carried out at the gene bank in IPGR-Sadovo during 2019. Ten local grass pea accessions (9 *Lathyrus sativus* and 1 *Lathyrus cicera* accessions) were taken from the long-term storage for reproduction and inclusion in AEGIS (A European Genebank Integrated System). *Lathyrus cicera* accession did not germinate. Nine local grass pea accessions were successfully reproduced and evaluated (Petrova & Chipilski, 2020). Currently the seeds are available in exchange collection of the gene bank (IPGR-Sadovo) and involved in AEGIS (Table 3).

The results, concerning morphological and agronomic traits, obtained during the two years evaluations of the grass pea accessions are presented in Tables 4 and 5.

Most of the accessions had vigorous growth with predominate semi-erected plant growth habitus. The big part of accessions had lanceolate leaflet shape while the remaining genotypes had linear and ovate-lanceolate leaflet shape. The color of the parts of the flower (standard, wing and keel) was determined. The predominated flower's colors were white for standard and keel and white blue for wing. Most of the studied genotypes had oblong-elliptical pod shape. The average pod length and width of the accessions was 3.92 cm and 1.31 cm, respectively.

Table 2. List of *Lathyrus sativus* phenotypic traits and the way of their assessment

Traits	Traits	The way of assessment
Vegetative characters	**Seedling vigour (score)**	Recorded 20 days after emergence (3 Poor; 5 Intermediate; 7 Vigorous)
	Plant growth habit (score)	Recorded at the beginning of flowering period (1 Prostrate; 2 Spreading; 3 Semi-erect; 4 Erect)
Stem characters	**Plant height (cm)**	Recorded at physiological maturity measured from ground to the tip of the longest branch (1 White; 2 White blue; 3 Blue; 4 Grey; 5 Light yellow; 6 Yellow; 7 Pink; 8 Orange; 9 Red; 10 Violet–blue; 11 Violet; 99 Other)
Branch characters	**Number of primary branches**	Counted at first pod maturity (only on pod-bearing branches)
Leaf characters	**Leaflet shape (score)**	1 Linear; 2 Lanceolate; 3 Ovate-lanceolate; 4 Ovate; 99 Other

Inflorescence characters	**Date of sowing (d)**	The date on which the seeds are sowing
	Days to flowering (d)	Number of days from beginning to end of flowering
	Days to first flowering (d)	Number of days from sowing to when the first flower opens
	Days to 50% flowering (d)	Number of days from sowing to stage when 50% of plants have begun to flower in a row
	Days to the end of flowering (d)	Number of days from sowing to stage when 80% of plants have begun to flower in a row
	Days to harvest (d)	Number of days from sowing to first mature pod separating from plant
	Days to maturity (d)	Number of days from sowing to stage when 80% of plants have mature pods
	Flower colour	Score on fresh, open flowers for score **standard**, **wing** and **keel** colours separately
	Pod-bearing position [cm]	/height to the first pod. Recorded as height to the lowest pod
Pod characters	**Number of pods per plant**	Mean number of pods; recorded from randomly selected plants at physiological maturity
	Pod shape (score)	1 Oblong-elliptical; 2 Medium oblong-elliptical; 3 Curved; 4 Beaded; 5 Broad-linear; 6 Broad-elliptical; 99 Other
	Pod length (cm)	Maximum mean length of randomly selected mature pods; recorded at physiological maturity
	Pod width (cm)	Maximum mean width of randomly selected mature pods; recorded at physiological maturity
	Number of seeds per pod	Mean number of seeds counted on randomly selected pods; recorded at physiological maturity
	Pod dehiscence (score)	Scored one week after maturity (0 No shattering; 3 Low shattering; 5 Medium shattering; 7 High shattering)
Seed characters	**Seed shape (score)**	1 Oblate or flattened; 2 Triangular; 3 Rhomboid; 4 Square; 5 Obtriangular; 6 Spherical; 99 Other
	Seed size (score)	3 Small; 5 Medium; 7 Large
	Seed length (cm)	Maximum mean length of randomly selected mature seeds; recorded at physiological maturity
	Seed width (cm)	Maximum mean width of randomly selected mature seeds; recorded at physiological maturity
	Seed coat colour (score)	1 Greyed–white; 2 Yellow–white; 3 Grey; 4 Brown; 5 Yellow–green; 6 Pink;7 Red–purple; 8 Black; 9 Grey mottled; 10 Green mottled; 99 Other
	Seed coat surface	1 Smooth; 2 Tubercular
	7.8.10 100-seed weight (g)	Weight of 100 randomly selected mature seeds at 8-10% (air-dry) seed moisture content
	Number of seeds per plant	Mean number of seeds; recorded from randomly selected plants at maturity
	Seed yield per plant (g)	Recorded as mean weight of seeds from five randomly selected plants
Yield traits	**Biological yield per plant (g)**	Yield of dried, mature plants after pulling
	Harvest index (%)	Weight of the whole plant and weight of the pods separately for 10 plants per accession
Visual assessment the susceptibility to following deseases (yes/no):		Bean aphids (*Aphis craccivora*)
		Pod borers (*Etiella zinckenella*)
		Bruchids (*Bruchus* spp.)
		Jassids
		Powdery mildew (*Erysiphe polygoni* f.sp. pisi)
		Downy mildew (*Peronospora lathyri-palustris*)
		Broomrape (*Orobanche* spp.)
		Fusarium wilt

Table 3. Local grass pea accessions involved in AEGIS

Nicode	Instcode	Genus	Accenumb	Change Timestamp	Dml Operation
BGR	BGR001	*Lathyrus*	2009-LAT-SA-1	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-10	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-3	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-11	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-12	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-13	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-9	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1955-LAT-SA-2	2021-03-16	Existing EURISCO accession labelled as part of AEGIS
BGR	BGR001	*Lathyrus*	1957-LAT-SA-11	2021-03-16	Existing EURISCO accession labelled as part of AEGIS

All materials had no shattering pods. From all studied accessions, predominated those with rhomboid seed shape, medium seed size, yellow-white, grey mottled seed coat color and tubercular seed coat surface. The predominant seed shape for all accessions was a rhomboid shape. The average seed length and width was 0.87 cm and 0.88 cm, respectively (Table 4). During the both years, the visual assessments for common diseases and pests were negative except Bruchus sp.in 2019 and Fusarium wilt during 2020, causing the death of two accessions from Bosnia and Herzegovina (GB01001 and GB01004).

The accessions from Greece, Portugal, Slovenia and most from Bosnia and Herzegovina (C0000090, C0000091, C0000093 and C0000094) had strong seedling vigour under Bulgarian environment. They also pocess semi-erect end erect plant growth habit and yellow–white seed coat colour. Four accessions from Bosnia and Herzegovina (C0000091, C0000092, C0000093 and C0000094) had the shortest days to first flowering, days to 50% flowering and days to maturity. They also characterized with large seed size (score 7), seed length and seed width between 0.90-0.98 cm and 0.90-0.97 cm, respectively. These four genotypes also had high harvest index – (40.42%, 45.05%, 42.50% and 45.59%, respectively) and the mass of 100 grains above the average (31.45 g, 24.10 g, 36.40 g and 33.70 g).

The evaluation of the main elements of productivity is an important step in establishing the best variety for the particular growing conditions. Productivity of grass pea depends largely on climatic conditions and on the individual characteristics of the variety (Tamkoc et al., 2009). The main elements of productivity were characterized by the variability above 10% (Table 5). Middle variability (10-20%) was expressed by number of the main branches, number of grains per pod and by the harves index. High genetic diversity in the collection was influenced by the significant variability of the following traits: number of pods per plant (CV = 38.98%), mass of grains per plant (CV = 35.80%), number of grains per plant (CV = 35.35%) and mass of 100 grains (CV = 29.46%). These five traits were most responsible for the high genetic diversity in the collection.

High grain yield per plant, average for the two years of the experiment, was established in four accessions: one from Romania (C000095 – 15.76 g), one from Bosnia and Herzegovina (C000092 – 11.50 g), from Serbia (C000101 -10.37 g) and one from Bulgaria (BGR40415 – 10.34 g). They had also a big number of pods per plant (C000095 –

Table 4. Morphological and phenological traits of tested *Lathyrus sativus* accessions

Accession	Vegetative characters		Leaf characters	Inflorescence characters						Pod characters			Seed characters				
							Flower colour										
	Seedling vigour	Plant growth habit	Leaflet shape	Days to first flowering (d)	Days to 50% flowering (d)	Days to maturity (d)	Standard	Wing	Keel	Pod shape	Pod length (cm)	Pod width (cm)	Seed shape	Seed size	Seed coat colour	Seed length (cm)	Seed width (cm)
C0000084	7	3	1	44	57	96	1	3	1	5	3.45	1.02	3	3	2	0.65	0.65
C0000085	7	3	1	45	57	95	3	3	1	5	3.38	1.02	3	3	2	0.57	0.60
C0000086	7	3	3	44	57	94	1	1	1	2	4.20	1.35	3	5	99	0.87	0.83
C0000087	7	3	2	47	60	94	2	3	1	1	4.08	1.32	5	5	99	0.83	0.90
C0000088	7	3	2	45	57	95	1	1	1	1	4.10	1.32	3	5	2	0.80	0.85
C0000089	7	3	3	46	56	94	3	3	1	2	4.13	1.28	3	5	99	0.87	0.90
C0000090	7	3	2	40	45	86	1	2	1	2	4.28	1.47	3	7	2	0.98	0.93
C0000091	7	4	2	42	45	85	1	2	1	1	3.92	1.38	3	7	2	0.98	0.97
C0000092	5	4	3	41	45	87	1	2	1	2	3.60	1.20	3	7	2	0.90	0.90
C0000093	7	3	3	42	45	84	1	1	1	1	3.61	1.31	3	7	2	0.90	0.97
C0000094	7	4	3	43	46	83	1	2	1	1	3.30	1.40	3	7	99	0.90	0.90
C0000095	5	3	2	49	57	98	1	1	1	2	4.15	1.43	3	5	2	0.88	0.92
C0000096	7	3	2	49	57	98	1	2	1	1	3.63	1.23	3	5	2	0.80	0.78
C0000097	5	3	1	49	52	98	1	2	1	1	3.93	1.38	3	5	2	0.78	0.87
C0000098	7	3	1	50	52	98	1	2	1	1	4.25	1.33	3	7	99	1.03	0.87
C0000099	7	3	1	48	54	96	1	2	1	1	4.25	1.40	3	7	2	0.97	0.93
C0000100	7	3	1	48	51	97	1	2	1	1	4.13	1.60	3	7	2	1.05	1.02
C0000101	5	3	1	47	53	98	1	2	1	1	3.57	1.20	3	5	99	0.92	0.80
C0000102	5	3	1	48	53	96	1	2	1	1	3.98	1.32	3	5	2	0.88	0.90
C0000103	5	3	2	49	52	97	1	2	1	1	3.92	1.27	3	5	2	0.88	0.83
C0000104	5	3	2	49	51	97	1	2	1	2	4.12	1.42	3	5	99	0.83	0.90
BGR40415	5	4	2	62	65	114	1	2	1	2	3.93	1.23	3	5	2	0.83	0.95
BGR43334	5	4	3	61	66	103	1	1	1	2	4.15	1.37	3	5	2	0.79	0.96
C0000105	7	3	2	46	52	94	1	1	1	5	4.05	1.23	3	5	2	0.93	0.87

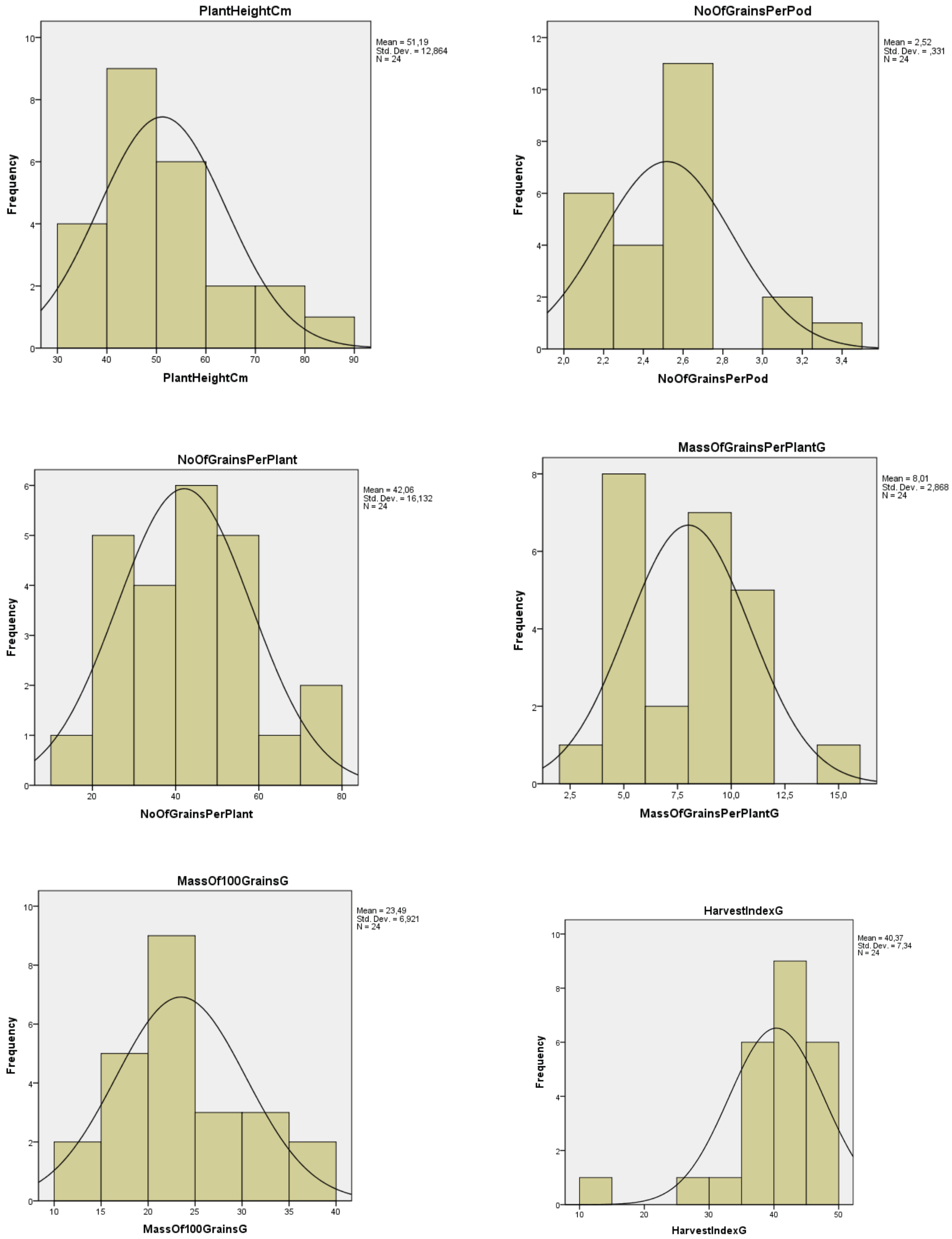
38.92; C000092 – 28.25; C0000101 – 24.95 and BGR40415 – 26.46), tall plants (C000095 – 63.57 cm and BGR40415 – 75.38 cm) and high harves index (C0000101 – 49.52 % and C000095 – 48.28 %). Two genotypes from Bulgaria (BGR43334 – 80.58 cm and BGR40415 – 75.38 cm) and one from Serbia (C00098 – 71.33 cm) had the tallest plants. These accessions distinguished also by high first pod formation, over the average grain yield per plant and the number of the main branches.

The variability of the six most important yield traits is presented by histograms visualizing the frequency of appearance on the basis of Standard Deviation (Figures 1-6). The graphs gave an indication of presence of genetic diversity in the studied quantitative characteristics.

Cluster analysis classified the accessions into two distinct groups using the Euclidean intergroup distance as a similarity measure. The most responsible trait of the grouping was the plant high. Cluster I and II consisted of 7 and 17 accessions, respectively (Figure 7). The threshold value of the coefficient for similarity was 80 %. The clustering pattern revealed that accessions from Bulgaria, Romania and part of Serbia were grouped in the first cluster but all others in the second. The high-

Table 5. Characterization of the grass pea accessions by the main elements of productivity and their variation

№	Accession	Plant height (cm)	Height to first pod (cm)	No. of main branches	Number of pods per plant	Number of grains per pod	Number of grains per plant	Grain yield per plant (g)	Mass of 100 grains (g)	Harvest index (g)
1	C000096	67.75	25.75	2.67	26.58	2.67	53.50	8.26	17.95	41.21
2	C000095	63.58	23.83	3.00	38.92	2.57	71.67	15.76	26.15	48.28
3	C000097	57.75	22.92	2.67	23.92	2.62	56.17	10.10	19.60	14.37
4	C000098	71.33	25.58	2.50	20.08	2.57	35.67	7.63	25.00	40.40
5	C000099	49.30	20.18	2.83	21.12	2.59	49.27	9.37	22.08	38.70
6	C0000100	49.67	18.83	3.08	18.50	2.33	32.08	9.83	38.93	42.92
7	C0000101	39.98	19.20	2.33	24.95	2.51	52.53	10.37	22.15	49.52
8	C0000102	50.37	19.92	2.67	24.58	2.72	45.60	8.96	25.50	43.52
9	C0000103	54.83	16.83	2.83	39.75	2.70	72.92	10.83	16.73	41.34
10	C0000104	48.50	16.83	2.67	22.00	2.50	42.92	9.25	21.90	46.04
11	C0000105	53.50	18.33	2.75	24.50	2.47	45.75	5.97	18.55	34.37
12	C0000087	36.17	14.83	2.08	13.50	2.30	29.58	5.23	23.15	26.60
13	C0000088	42.33	15,61	1.96	15.23	2.08	33.33	5.72	20.25	39.95
14	C0000086	51.55	19.87	2.73	13.65	2.06	22.53	4.57	20.5	38.06
15	C0000089	45.45	17.60	2.35	17.57	2.39	30.42	5.91	22.83	37.86
16	C0000084	47.75	13.83	2.33	17.17	3.08	41.42	5.15	14.05	37.94
17	C0000085	51.25	15.67	2.17	15.92	3.40	46.25	5.69	12.50	44.47
18	C0000094	30.25	17.00	2.50	5.75	2.15	11.00	2.63	33.75	43.93
19	C0000091	40,75	20.76	2.42	12.07	2.23	20.92	5.55	31.45	40.42
20	C0000092	34.00	12.00	4.25	28.25	2.70	53.00	11.50	24.10	45.05
21	C0000093	45.10	21.12	2.74	10.17	2.11	20.01	6.26	36.40	42.50
22	C0000090	41.50	18.42	2.83	14.92	2.12	28.92	8.57	33.70	45.59
23	BGR43334	80.58	30.25	2.83	24.33	2.57	50.08	8.82	20.03	46.42
24	BGR40415	75.38	22.17	2.75	26.46	3.00	63.88	10.34	16.88	39.45
	Mean	**51.19**	**19.47**	**2.66**	**20.83**	**2.52**	**42.06**	**8.01**	**23.49**	**40.37**
	Min	**30.25**	**12.00**	**1.96**	**5.75**	**2.06**	**11.00**	**2.63**	**12.50**	**14.37**
	Max	**80.58**	**30.25**	**4.25**	**39.75**	**3.40**	**72.92**	**15.75**	**38.93**	**49.52**
	VC, %	**25.13**	**21.45**	**16.51**	**38.98**	**13.17**	**35.35**	**35.80**	**29.46**	**18.18**



Figures 1-6. Histograms of the variability of some studied traits

est genetic diversity was observed in accessions from Portugal.

The genotypes from the first cluster characterized by a high plants and high first pod formation. The accessions C000095 and C00000103 distinguished by the highest values of the following traits: number of pods per plant and number of grains per plant. BGR43334 and BGR40415 characterized by tall plants and high first pod formation. In the second cluster two accessions from Serbia were involved. The first one had the highest harves index (C0000101 - 49.52 %) and the second - the highest mass of 100 grains (C0000100 - 38.93 g).

Similar grouping of grass pea accessions by cluster analysis was obtained by Kosev & Vasileva, (2019), Petrova, (2022) and Petrova et al., 2022.

From the clustering of the traits we can conclude that they are conditionally combined into two main factors responsible for the grouping of the genotypes, part of the collection (Figure 2). The first

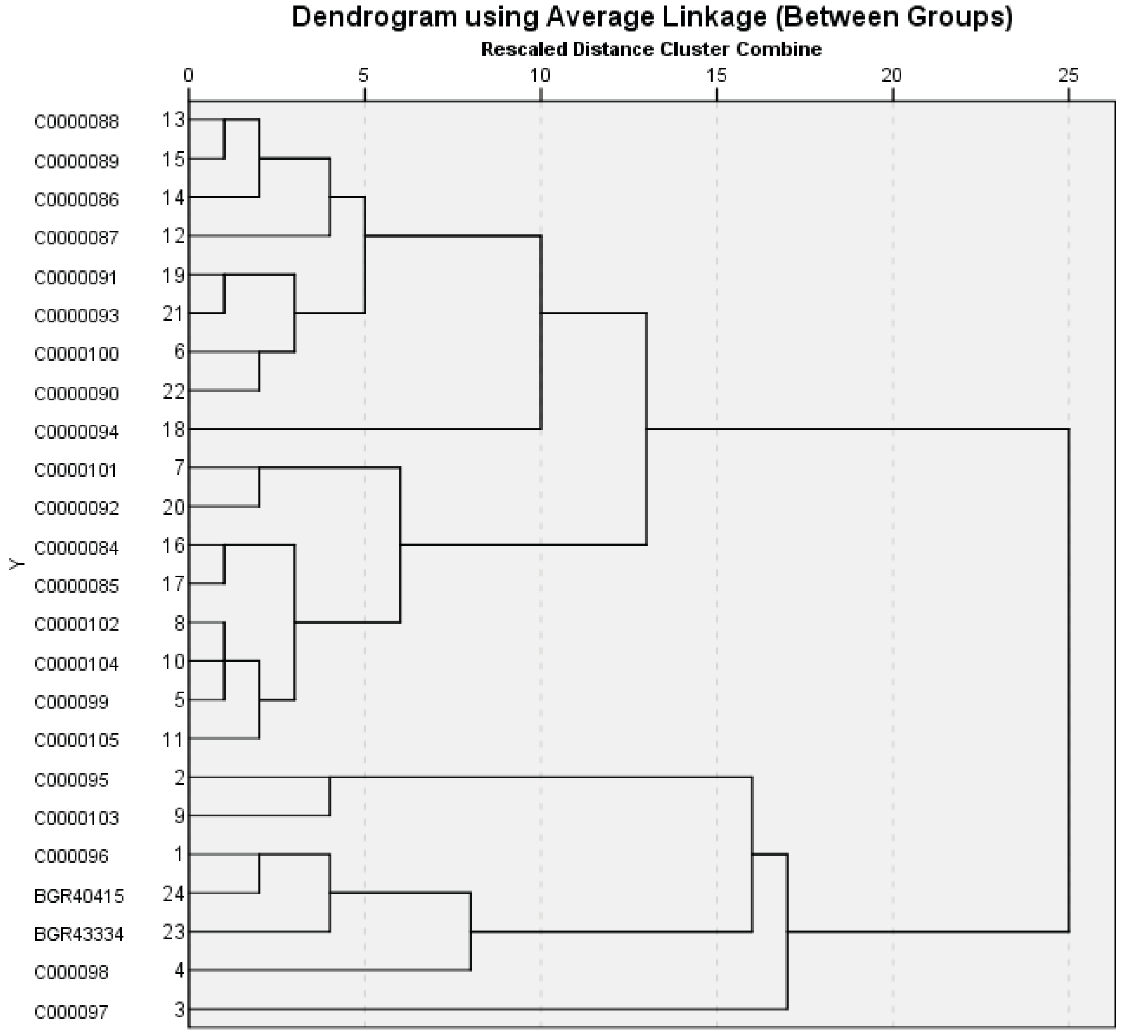


Figure 7. Dendogram of grouping of studied accessins using cluster analysis

cluster sequentially includes traits: plant height, harvest index and number of grains per plant combined at a close Euclidean distance. The number of branches, number of grains per pod, number of pods per plant, mass of 100 grains and grains per plant are into a second cluster at a large distance in the factorial plane.

Similar grouping of economicaly important traits by cluster analysis was observed by us in grass pea (Petrova, 2022). The first cluster combining plant height and number of grains per plant and the second - number of main branches, number of grains per pod and mass of grains per plant, number of pods per plant, biological yield, height to the first pod, mass of 100 grains and harvest index.

CONCLUSIONS

All project exchanged accessions were registered in our National database and also in EURISCO database.

During the years nine local *Lathyrus sativus* accessions with Bulgarian origin were reproduced and their seeds were involved in AEGIS.

The variations of the most important morphological and agronomic traits were established based on the two years experiment results: the plant height varied from 30.25 cm to 80.58 cm; height to the first productive pod from 12.00 cm to 30.25 cm; number of pods per plant from 5.75 to 39.75; the average seed length and width was 0.87 cm and 0.88 cm,

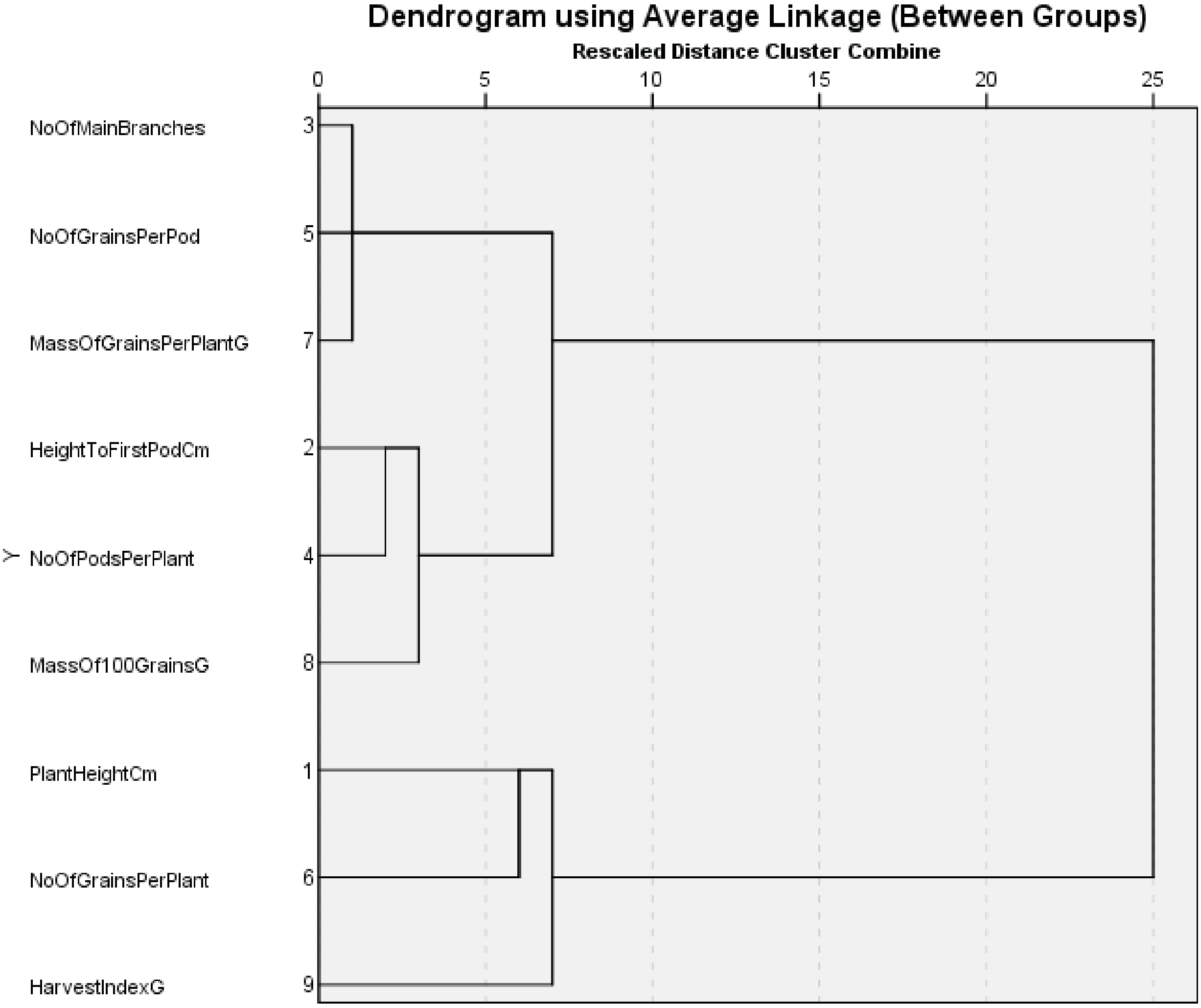


Figure 8. Dendogram of grouping of studied traits using cluster analysis

respectively. The big part of accessions had plant growth habitus semi-erect, lanceolate leaflet shape, oblong-elliptical pod shape, rhomboid seed shape, medium seed size, yellow-white, grey mottled seed coat color and tubercular seed coat surface. The predominated flower's colors were white for standard and keel and white blue for wing. Some accessions from Romania, Bulgaria and Serbia (C000095, C0000101, C0000100, BGR43334, BGR40415 and C00000103) were selected with promising results related to grain and forage yields and will be used as initial materials in breeding for productivity. Four accessions from Bosnia and Herzegovina characterized with the shortest days to first flowering, days to 50% flowering and days to maturity, large seed size and high harvest index and mass of 100 grains. They will be used as parent components in breeding for earliness and productivity. As the best adapted accessions to Bulgarian environment were two accessions from Romania (C00096 and C00095), two from Serbia (C000100 and C000101) and two from Bosnia and Herzegovina (C00093 and C00094). They demonstrated good productivity and good adaptability.

Agro-morphological assessment and multiplication of the exchanged local *Lathyrus* accessions derived from Mediterranean region and south Eastern Europe contributed for sustainable use of the *Lathyrus* germplasm and it conservation in the National Genebank of Bulgaria.

REFERENSES

Dimova, D & Marinkov, E. (1999). Experiment and Biometrics. Academic Publishing House of Agricultural University, Plovdiv, 194 p. (Bg).

Hanbury, C. D., White, C.L., Mullan, B. P. & Siddique, H. M. (2000). A review of the potential of *Lathyrus sativus* L. and *L. cicero* L. grain for use as animal feed. *Anim Feed Sci Technol*, 87(1), 23.

Frankel, O. H., Brown, A. H. D. & Burdon, J. J. (1995). The conservation of plant biodiversity. Cambridge University Press, Cambridge, 10–15.

Gepts, P. (2006). Plant genetic resources conservation and utilization: The accomplishments and future of a societal insurance policy. *Crop Sci*, 46, 2278–2292.

IBM. (2019). SPSS Statistics 19 (Statistical Product and Service Solutions), Vers. 19.0.0 Retrieved from https://www.ibm.com/support/pages/spss-statistics-190-fix-pack-1

IPGRI. (2000). Descriptors for *Lathyrus* spp. International Plant Genetic Resources Institute, Rome, Italy.

Kosev, V. I. & Vasileva, M. V. (2019). Morphological characterization of Grass pea (*Lathyrus sativus* L.) varieties. *The Journal of Agricultural Sciences - Sri Lanka* 14, (2), 67-76.

Mathur, P. N., V. Ramanatha Rao & Arora, R. K. (1998). Lathyrus Genetic Resources Network: Proceeding of a IPGRI-ICARDA-ICAR Regional Working Group Meeting, 8-10 December 1997, National Bureau of Plant, New Delhi. IPGRI Office for South Asia, New Delhi, India.

Petrova, S. (2022). Assessment of phenotypic diversity of local grass pea (*Lathyrus* sp. L.) accessions based on economically important agricultural traits. *Bulgarian Journal of Crop Science*, 59(6), 48-53.

Petrova, M., Petrova, S., & Velcheva, N. (2022). Genetic diversity of local accession from forage crops, stored in the National genebank. *Bulgarian Journal of Crop Science*, 59(6), 84-91 (Bg).

Petrova S. & Chipilski, R. (2020). Agrobiological and physiological evaluation of the accessions of the Lathyrus sp. collection from the Genebank in Sadovo. *Phytologia Balcanica,* 26(3), 457–460.

Tamkoc, A., Ustun, A. , Altİnok, S. & Acİkgoz, E. (2009). Biomass and seed yield stability of pea genotypes. *Journal of Food, Agriculture & Environment*, 7(1), 140-146.

Tsegaye, D., Tadesse W. & Bayable, M. (2005). Performance of grass pea (*Lathyrus sativus* L.) somaclones at Adet, northwest Ethiopia. *Lathyrus Lathyrism Newsl,* 4, 5–6.

Singh, K. A., Bharati, C. R., Manibhushan, C. N. & Pedpati, A. (2013). An assessment of faba bean (*Vicia faba* L.) current status and future prospec. *African Journal of Agricultural Researc*, 8(50), 6634-6641.

Upadhyaya, H. D. S. L., Dwivedi, M., Ambrose, N. Ellis, J., Berger, P., Smy´kal, D., Debouck, G., Duc, D., Dumet, A., Flavell, S. K., Sharma, N., Mallikarjuna, C. L., Gowda, L. (2011). Legume genetic resources: management, diversity assessment, and utilization in crop improvement. *Euphytica*. 180, 27–47.

Vaz Patto, M. C. & Rubiales, D. (2014). *Lathyrus* diversity: available resources with relevance to crop improvement – *L. sativus* and *L. cicera* as case studies. *Ann Bot.* 113(6), 895–908.

Ward, J. H. (1963). Herarchical grouping to optimize an objective function. *Journal of the American statistical Association, 58*, 236.

Yunus, A. G. & Jackson, M. T. (1991). The gene pools of the grasspea (*Lathyrus sativus* L.) *Plant Breeding*, 106, 319–328.

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