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Assessment of Genetic Diversity of White Lupin (Lupinus albus L.) Accessions Based on Agro-morphological Traits

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Abstract. Large genetic diversity exists in *Lupinus albus* L. expressed by its morphological and agronomical traits. The aim of this study was to assess the genetic diversity of ten white lupin accessions regarding components of productivity and biological traits. Two years trial was carried out on the experimental field of Institute of plant genetic resources during the period 2018-2019. The traits were evaluated using the International *Lupinus albus* L. descriptor. The degree of earliness was also used. Based on agro-morphological traits the studied accessions were grouped into two clusters. The first cluster included only one accession. The second cluster was divided into two sub-clusters. The first sub-cluster included three genotypes which differed significantly from the remaining ones by its tall plants, high first formed pods and a big number of grains per plant. The second sub-cluster included six accessions possessing medium-high to short stem and medium-large to large grains. The studied traits were combined into two main clusters. The largest Euclidean distance had between vegetation period and other studied traits. According to the degree of earliness, the lupin genotypes were clustered into three groups - ultra-early, early and late. The BGR 3086 accession was selected also as an ultra-early variety with 1.00 coefficient of earliness together with two other genotypes - selected to the early group with a coefficient of earliness 1.60. Genetically distant genotypes will be involved in the breeding programs for effective combining the important features into a new genotype.

Key words: white lupin, genetic diversity, earliness, productivity.

Introduction

Lupinus is a relatively large genus and one of the most geographically widespread with a rich diversity of species. *Lupin* is an annual or perennial legume belonging to legume family, *Fabaceae*, one of the oldest crops. It is a major food legume in the Roman Empire and has a long history of cultivation in the Mediterranean basin, East Africa and the Atlantic islands of the northern hemisphere (Gladstones, 1998; Kurlovich, 2002). Among 300 *Lupinus* have been described, only five species are cultivated among which white lupin is the most important one (Hondelmann, 1984). It is probably domesticated in the Aegean region (Gladstones, 1998) and has increased in the recent years due to its high level of protein, oil and quality dietary fiber in seed's dry matter (Annicchiarico, 2008; Bhardwaj & Hamama, 2012). In our country lupin is not a traditional crop, but it has been used for a long time as a green manure source (Angelova, 2001).

The conservation and preservation of the white lupin genetic resources are of crucial importance for the breeding programs aiming the cultivar improvement (Raza & Jørnsgård, 2005; El-Sherif et al., 2014). In this respect, the success of any crop improvement programme essentially depends on the nature and magnitude of genetic variability (Hukumch & Parameshwarappa, 2019). Genetic divergence among parents is essential since the crossing programme involving genetically diverse parents is likely to produce high heterotic effects, successful combination of valuable genes and also more variability could be expected in the segregating generations (Sachan & Sharma, 1971; Kosev & Vasileva, 2020).

The aim of this study was to assess the genetic diversity of ten white lupin accessions regarding components of productivity and biological traits.

Material and Methods

The experiment was carried out on the experimental field in IPGR - Sadovo on cinnamon forest soil, after a precursor of wheat during the period 2018-2019. The area of Sadovo is characterized by a transitional continental climate with its frequent and prolonged droughts. During the period 2018-2019 mean temperature was 18.17ºC and mean precipitation was 73.84 mm. Ten white lupin genotypes were used for this study.

The field experiment was designed in Randomized Complete Block Design (RCBD) with three replications (Dimova & Marinkov, 1999). Experiment plot size was 5.0 m^2. Sowing was made by hand, in optimum sowing time, according to the technology of cultivation. At maturity, 10 plants were randomly taken from each plot to measure the following morphological traits: 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) and mass of 100 grains (g). Also several phenological traits were taken into account: beginning of flowering and plant life cycle. The phenological traits were assessment by coefficient of earliness (Kuzmova, 2002). For ultra early varieties the value of this coefficient was from 1.00 to 1.17, for the early varieties from 1.17 to 1.33, for middle-early ones from 1.34 to 1.66 and for the late varieties was greater than 1.66.

The studied agro-morphological traits were processed mathematically by analysis of variance. The means were compared by the three Least Significance Difference (LSD) - 0.05%; 0.01% and 0.001%. To investigate the hierarchical structure of genetic diversity between the studied lupin accessions was used Cluster analysis (Ward, 1963). All experimental data were processed statistically with using statistical package SPSS 19.0. for Windows (IBM SPSS Statistics 19 Product Version: 19.0.0) (IBM, 2019).

Results and Discussion

The clustering of the ten evaluated lupin accessions based on their morphological traits is presenting on Fig. 1. The traits data are given on Table 1. The accessions were divided into two main groups (clusters) giving an idea about quantitative traits diversity. The main trait that distinguished the accessions was the plant hight. Only the accession BGR 3080 was included in the first cluster. This genotype had large grains (40.80 g), big mass of grains per plant (18.91 g) and big number of grains per pod (4.90).

The second cluster was divided into two sub-clusters. The first sub-cluster included three genotypes (BGR 3086, BGR 6341 and BGR 3085), with tall plants, big number of productive branches and big mass of grains per plant. The BGR 3086 genotype differed significantly (LSD=0.05%) by plant height (68.43 cm). This accession also had a high number of grains per plant (52.86) and the shortest vegetation period (90 days). The accession BGR 6341 had significant differences (LSD=0.05%) by plant height (67.43 cm), number of productive branches (4.43), number of grains per plant (64.43) and mass of grains per plant (22.20 g). This accession characterized also by high values of number of pods per plant (15.14) and number of grains per pod (5.03). The BGR 3085 accession had significant differences (LSD=0.05%) by mass of grains per plant (22.14 g). The traits related to the number of pod and grains per plant, mass of the grains per plant are from significant economic importance for the leguminous forage crops, and this defines the genotype as a potential initial material for selection.

The second sub-cluster included six accessions (BGR 3078, BGR 6337, BGR 6339, BGR 3083, BGR 3084, BGR 3079) possessing medium-high to short stem and medium-large to large grains. The data showed that within this sub-cluster significant genetic distance was observed between the genotypes. The BGR 3078 genotype differed significantly (LSD=0.001%) by the height to the first pod (38.00 cm) and had tall plants (66.43 cm). The lowest formed first pod was observed in BGR 6337 accession at LSD=0.01%.

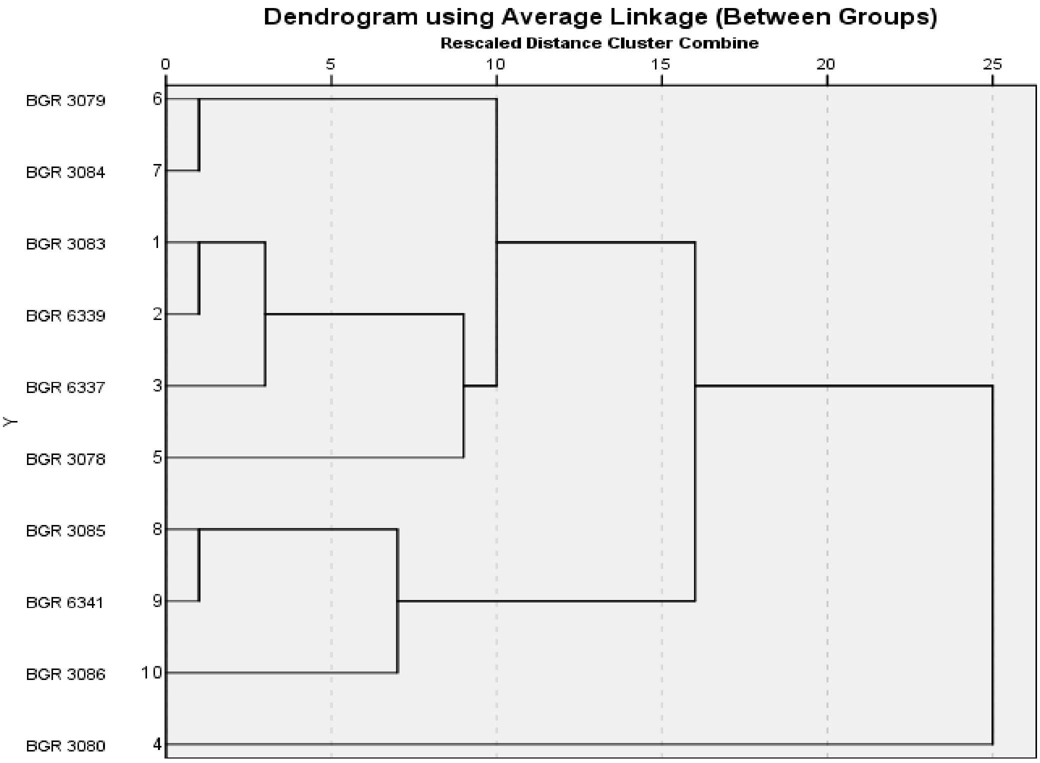

Fig. 1. Dendrogram of genotype grouping using cluster analysis during the period 2018-2019.

Table 1. Experimental data and grouping of the studied genotypes using cluster analysis during the period 2018-2019.

Accessions	Plant height, cm	Height to the first pod, cm	Number of productive branches	Number of pods per plant	Number of grains per plant	Numbe of grains per pod	Mass of grains per plant, g	100 grains mass, g
BGR 3083	53.29	28.00	2.14*	8.71	35.00	4.49	13.23	37.80
BGR 6339	51.5*	23.43*	3.14	10.14	40.29	4.77	14.84	37.05
BGR 6337	55.43	22.57**	3.57	11.57	45.43	4.80	14.43	32.45
BGR 3080	63.86	28.14	3.14	12.14	47.43	4.90	18.91	40.80
BGR 3078	66.43	38.00***	3.43	11.14	36.87	4.60	14.74	34.40
BGR 3079	56.57	30.86	2.14*	6.86	24.00*	3.91*	9.73	40.30
BGR 3084	54.71	32.57	2.71	6.14*	22.00*	3.84**	7.99*	35.30
BGR 3085	61.86	26.57	4.00	14.43	60.14	4.63	22.14*	37.75
BGR 6341	67.43*	28.14	4.43*	15.14	64.43*	5.03	22.20*	36.75
BGR 3086	68.43*	33.71	3.71	12.14	52.86	4.97	17.20	33.10
average St	59.96	29.20	3.24	10.84	42.84	4.59	15.54	36.57
min	51.57	22.57	2.14	6.14	22.00	3.84	7.99	32.45
max	68.43	38.00	4.43	15.14	64.43	5.03	22.20	40.80
LSD 0.05% *	**7.56**	**5.38**	**1.18**	**4.79**	**19.36**	**0.56**	**6.85**	**1.28**
LSD 0.01% **	**10.03**	**7.13**	**1.56**	**6.35**	**25.69**	**0.75**	**9.09**	**1.75**
LSD 0.001% ***	**12.99**	**9.24**	**2.02**	**8.23**	**33.28**	**0.97**	**11.77**	**2.35**

The clustering of the agro-morphological traits of the evaluated lupin accessions based on their similarity/differences is presented on Fig. 2. From the clustering of the traits we could concluded that they were combined into two main clusters. Only vegetation period was included in the first cluster. The second cluster was divided into two sub-clusters: the first sub-cluster included the following traits: plant height, number of grains per plant, germination-beginning of flowering, mass of 100 grains and height to the first pod united by the close value of the Euclidean distance. The remaining four traits (mass of grains per plant, number of pods per plant, number of grains per pod and number of productive branches) were combined into the second sub-cluster. The largest Euclidean distance had between traits - number of productive branches and vegetation period (281.98), vegetation period and number of grains per pod (277.76), vegetation period and number of pods per plant (257.68). Similar clustering of the traits were conducted with other grain legumes, as fababean where the traits plant height, vegetation period and mass of 100 grains were combined into one cluster, at a large distance in the factorial plane from other cluster (Velcheva & Petrova, 2020).

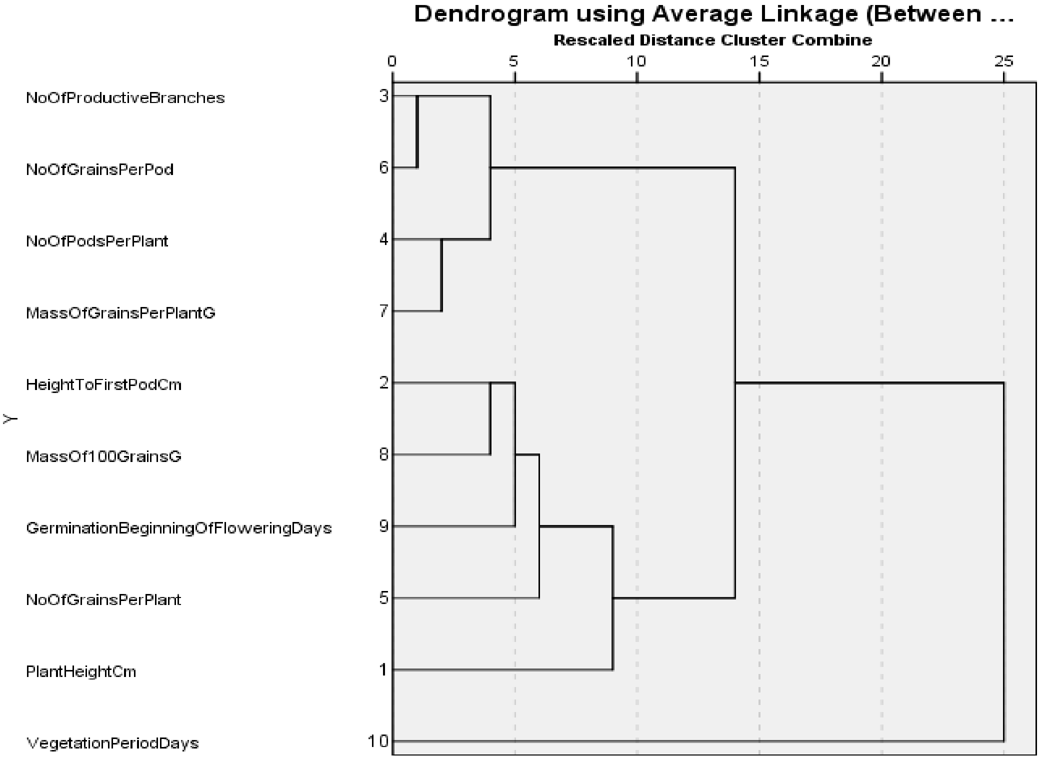

Fig. 2. Dendogram of studied traits grouping using cluster analysis during the period 2018-2019.

The phenological observations were performed in order to evaluate the earliness of the white lupin accessions (Table 2). The duration of the vegetation period for all genotypes varied between 90-99 days. The earliest blossom was observed in BGR 3086 accession (49 days), classified as ultra-early variety with a coefficient of earliness 1.00. Two accessions BGR 3084 and BGR 6341 with 52 days from sowing to beginning of flowering, were included in the group of early varieties with a coefficient of earliness 1.60. This period was slightly longer for the accession with BGR 3083 (53 days). All other accessions possessed coefficient of earliness greater than 1.66. The established phenological differences were preserved during the whole vegetation period. Similar grouping by the degree of earliness was done by Kosev & Vasileva (2019) in grass pea accessions.

Table 2. Phenological development of white lupin accessions during the period 2018-2019.

Accessions	**BGR 3080**	**BGR 3085**	**BGR 3083**	**BGR 3079**	**BGR 3086**	**BGR 3078**	**BGR 6337**	**BGR 6339**	**BGR 3084**	**BGR 6341**
Sowing-beginning of flowering, days	54	54	53	54	49	54	54	54	52	52
Sowing-maturity, days	97	98	99	93	90	97	97	99	95	95
Earliness coefficient	2.00	2.00	1.80	2.00	1.00	2.00	2.00	2.00	1.60	1.60

The established diversity in agro-morphological traits within the evaluated lupin accessions during the 2-years trial is an important initial step for every one breeding program aiming to select appropriate parents. Similar evaluations were performed by Julier et al. (1995), Raza & Jørnsgård (2005) and Lara-Rivera et al. (2017). Using cluster analysis the white lupin genotypes were grouped according to their yield potential, an important criteria for selection. It was used by some other researchers in evaluating lupin genotypes for yield and yield components (Berger et al., 2008; Abo-Hegazy et al., 2020). It will be useful to identify promising genotypes with high yield potential and quality trails direct as new cultivars. The main task of modern white lupin selection is the creation of varieties combining high grain yield with optimum duration of vegetation period (Naumkin et al., 2012).

Conclusions

Ten *Lupinus albus* L. accessions were characterized by their agro-morphological traits. The variability of the studied traits proved the genetic diversity within the accessions. The accessions were clustered in two groups by the economical important quantitative traits. On the other hand, the traits were combined into two main clusters that would facilitate the crop breeding programs. According to the coefficient of earliness, the white lupin accessions are grouped in three groups: ultra-early, early and late. BGR 3086, BGR 3084 and BGR 6341 were selected as early accessions and will be used as gene sources for improvement of vegetation period. The carried out assessment gave valuable data about important economical traits in tested accessions. This will increase opportunities for their use in different fields: indirectly in breeding programs, reproduction, recovery in the gene bank, international exchange, technology assessment and direct implementation open pollinated varieties.

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References

Angelova, A. (2001). Maintenance, Enrichment and Preservation of Grain Legume Collection in Bulgaria. *Report of a Working Group on Grain Legumes*, pp. 57-60.

Abo-Hegazy, S. R. E., Ashrei, A. A. M., & Abeer, A. A. (2020). Evaluation of Some Lupin Genotypes Using Different Agro-morphological, Statistical and Chemical Methods. *Asian J. Crop Sci*., *12*(2), 72-83. doi: 10.3923/ajcs.2020.72.83.

Annicchiarico, P. (2008). Adaptation of cool-season grain legume species across climatically contrasting environments of southern Europe. *Agron. J., 100*, 1647-1654. doi: 10.2134/agronj2008.0085.

Berger, J. D., Adhikari, K. N., Wilkinson, Buirchell, D. B. J. & Sweetingham, M. W. (2008). Ecogeography of the oldworld lupins. 1. Ecotypic variation in yellow lupin (*Lupinus luteus* L.). *Aust. J. Agric. Res., 59*, 691-701. doi: 10.1071/AR07384.

Bhardwaj, H. L. & Hamama, A. A. (2012). Yield and Nutritional Quality Traits of White Lupin Sprouts. *Journal of Agricultural Science, 4,* 58-61. doi:10.5539/jas.v4n1p58.

Dimova, D. & Marinkov, E. (1999). Experimental Work and Biometrics. Academic Publishing House of the Agricultural University, Plovdiv, пп. 193-205.

El-Sherif, N. A., Mohamed, A. A., Saad, M. E., Barakat, H. & Aly, S. (2014). Genetic variation in egyptian white lupin (*Lupinus albus* L.) genotypes based on combined data of ISSR and fluorescence-based AFLP markers. *Egyptian Journal of Genetics and Cytology, 43*(1), 1-23. doi: 10.21608/ejgc.2014.9930.

Gladstones, J. S. (1998). Distribution, Origin, Taxonomy, History and Importance. In Gladstones, J. S., Atkins, C. A., & Hamblin, J. (Eds.), *Lupin as Crop Plants.* (Biology, Production and Utilization, pp. 1-39). Oxon, UK: CAB International. Retrieved from https://catalogue.nla.gov.au/Record/221739

Hondelmann, W. (1984). The lupin: Ancient and modern crop plant. *Theor. Appl. Genet., 68*, 1-9. doi: 10.1007/BF00252301.

Hukumchand, P. S. G. (2019). Genetic diversity analysis for quantitative traits in advanced breeding lines of sesame (*Sesamum indicum* L.). *International Journal of Current Microbiology and Applied Sciences. 8*(12), 2970-2979. doi: 10.20546/ijcmas.2019.812.345.

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

Julier, B., Huyghe C., Papineau, J. Billot, C. & Deroo, C. (1995). Genetic and environmental variation in architecture and yield components in determinate white lupin (*Lupinus albus* L.). *Euphytica, 81,* 171-179. doi: 10.1007/BF00025430.

Kosev, V. & Vasileva, V. (2019). Morphological characterization of Grass pea (*Lathyrus sativus* L.) Varieties. *The Journal of Agricultural Sciences - Sri Lanka. 14*(2), 67-76. doi: 10.4038/jas.v14i2.8509.

Kosev, V. & Vasileva, V. (2020). Breeding value of white lupin varieties. *Journal of Central European Agriculture, 21*(2), 409-419. doi: 10.5513/JCEA01/21.2.2536.

Kurlovich, B. S. (2002). *Lupins: Geography, Classification, Genetic Resources and Breeding*. St. Petersburg, Russia, Publiching house "Intan". Retrieved from https://www.academia.edu/5907968/LUPINS_Geography_Classification_Genetic_Resources_and_Breeding_

Kuzmova, K. (2002). Quantitative assessment of wintering and spring varieties of peas in terms of earliness. Jubilee Scientific Session-120 years of agricultural science in Sadovo, Bulgaria, pp. 109-112.

Lara-Rivera, A. H., Ruiz-Lopez, M. A., Rodriguez-Macias, R., Soto-Velasco, C., Garcia-Lopez P. M., Barrientos-Ramirez, L. & Zamora-Natera, J. F. (2017). Grain yield and chemical andprotein composition of *Lupinus angustifolius* varieties grown in Mexico. *Myton, 86*, 89-96. Retrieved from http://www.revistaphyton.fund-romuloraggio.org.ar/vol86/Lara-Rivera.pdf

Naumkin, V. N., Naumkina, L. A. & Meshteryakov, O. D. (2012). Perspectives of lupine cultivation in the Central Black Earth region. *Agriculture, 1*, 27-29.

Raza, S., & Jørnsgård, B. (2005). Screening of white lupin accessions for morphological and yield traits. *Afr. Crop Sci. J., 13*, 135-141. doi: 10.4314/acsj.v13i2.27906.

Sachan, K. S. & Sharma, J. R. (1971). Multivariate analysis of genetic divergence in tomato. *Indian Journal of Genetics and Plant Breeding, 31*, 86-93.

Velcheva, N. & Petrova, S. (2020). Statistical analysis of genetic diversity using faba bean landraces database. *Agricultural science and technology, 12*(3), 210-215. doi: 10.15547/ast.2020.03.033.

Ward, J. H. (1963). Herarchical grouping to optimize an objective function. *Journal of the American statistical Association, 58*, 236. doi: 10.1080/01621459.1963.10500845.