

Breeding value of white lupin varieties

Селекционна ценност на сортове бяла лупина

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ABSTRACT

The breeding value of white lupin specimens was studied and the effect of the environment and genotype on some characteristics has been demonstrated. The role of the genotype was found the strongest for the nodulating ability of the plants. The genetic variance was within the range of 0.001 (the specific nodulating ability) to 29.16 (the number of leaves per plant), and the phenotypic variance of 0.001 (the specific nodulating ability) to 43.15 (number of leaves per plant). High genetic advance in combination with high inheritability was obtained for the number of leaves per plant (3.56, 67.58%), stem fresh weight (2.81, 68.24%) and aboveground fresh weight (1.25, 88.05%). High inheritability with low genetic advance was established for the specific nodulating ability (80.81%, 0.09) and the stem dry weight (62.60%, 0.31), indicating the involvement of no-additive gene action. The aboveground fresh weight is positively correlated with: the leaf fresh weight ($r = 0.897$), the leaf dry weight ($r = 0.881$), the plant height ($r = 0.587$) and the dry weight of the roots ($r = 0.569$). The established genetic diversity in the studied varieties allows for a targeted selection of parental forms and their inclusion in crosses on the different breeding directions.

Keywords: breeding, genetic diversity, varieties, white lupin

АБСТРАКТ

Проучена е селекционната ценност на образци бяла лупина и доказано влиянието на средата и генотипа върху проявата на изследваните признаци. Ролята на генотипа е най-силна за грудкообразуващата способност на растенията. Генетичният вариант е в границите от 0.001 (специфичната грудко образуваща способност) до 29.16 (брой листа на растение), а фенотипният вариант от 0.001 (специфичната грудкообразуваща способност) до 43.15 (брой листа на растение). За брой листа на растение (3.56; 67.58%), тегло на свежите стъбла (2.81; 68.24%) и тегло на свежата биомаса (1.25; 88.05%) е получен висок генетичен напредък съчетан с висока наследяемост. Висока наследяемост с нисък генетичен напредък е установена за специфичната грудкообразуваща способност (80.81%; 0.09) и теглото на сухите стъбла (62.60%; 0.31), което е указание за участието на неадитивни генни действия. Теглото на свежата надземна биомаса е в силна положителна корелация със: свежото тегло на листата ($r=0.897$), сухото тегло на листата ($r = 0.881$), височината на растението ($r=0.587$) и сухото тегло на корените ($r=0.569$). Установеното генетично разнообразие при изследваните сортове дава възможност за целенасочен отбор на родителски форми и включването им в кръстоски по различните селекционни направления.

Ключови думи: бяла лупина, генетично разнообразие, селекция, сортове

INTRODUCTION

White lupin (*Lupinus albus* L., Fabaceae) is one of the four economically important species of the *Lupinus* genus, which consists of over 300 annual species (Hondelmann, 1984).

White lupin ($2n=50$) is widely known, commercially important, large seeded annual lupin species in the world. It is a promising annual legume crop for human consumption, green manuring and forage (Johnson et al., 2006).

The study of the biological capabilities of the genotype, which have always been of great interest to breeders, acquire particular relevance to the shortage of natural resources. In changing the paradigms of agriculture production, the transition from intensive chemical technologies to environmentally-friendly, fully-renewable environmental resources and the biological potential of plants are increasing the requirements for the examination of genotypic, ecotypic and biotipic diversity of breeding material for the production of adaptive and highly productive varieties (Vishnyakova, 2008; Gudoshnikova et al., 2012).

The production of forages with high protein content has always been one of the most important tasks of agriculture. The leguminous crops, including white lupin, are one of the sources that make it possible to reduce the protein deficiency. According to the protein content in the seeds and the green mass, lupin significantly exceeds peas, vetches, beans and practically not inferior to soybeans. Lupin is not demanding for soil fertility and is capable of giving good yields on the soils with different mechanical composition, including poor sand soils. As an active nitrogen fixator it plays an important role in supplementing the stock of organic matter and nitrogen in the soil (Fedorova, 2001).

The advantages of lupin also refer to those that it possesses a complex of economic valuable signs and properties such as protein content and essential amino acids, surpasses peas, vetch and beans.

This crop is widely used as a green manure whose effect improves soil structure and enriches it with nitrogen more than other legumes (Lukashewich and Sviridenko, 2012).

Much attention is paid to the study of initial material, both in the creation of new varieties and in the improvement of existing ones. Different types of statistical analysis could be used to identify the best donors for new varieties (Kurkina and Tkachenko, 2003). In the breeding work, studying the relationships between the signs plays an important role, as they can define the direction of breeding when new varieties are created. The most interesting are the quantitative signs whose relationship can be genetically determined or result of physiological dependences (Skuridin and Koval, 2002; Zaharova et al., 2014; Vitko and Vanaga, 2015).

The purpose of the study is to assess the genetic diversity in a collection of white lupines and to identify suitable parents for the needs of combinatorial breeding.

MATERIALS AND METHODS

The study was conducted in 2014-2016 in the experimental field of the Institute of Forage Crops, Pleven, Bulgaria (43.41° N, 24.61° E), situated in the central part of the Danube hilly plain. Sowing was carried out manually in optimal time, according to the technology of cultivation of white lupin. Plant material of aboveground of the next seven white lupin varieties, i.e. PI457923 (Greece), PI368911 (Czech Republic), PI533704 (Spain), PI457938 (Morocco), KALI (Poland), Zuter (France) and Lucky801 (France) was analyzed.

The following characteristics have been assessed in the beginning of flowering stage: nodule number, nodule weight per plant (g), specific nodulating ability (SNA), root length (cm), root mass fresh weight (g), root dry mass weight (g); leaf number per plant, leaf fresh weight per plant (g), leaf dry weight per plant (g), stem fresh weight per plant (g), stem dry weight per plant (g), plant height (cm), aboveground mass fresh weight per plant (g) and aboveground mass dry weight per plant (g). Biometric

measurements were made to 10 plants of each variety.

The following statistical methods were used to process the experimental data: factor analysis by the method of principal components, 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, 2002). Genetic advance (GA) in absolute unit 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. (1955). All experimental data were processed statistically with using the computer software GENES 2009.7.0 (Cruz, 2009) and Excel for Windows XP.

RESULTS

In agro meteorological terms the conditions in the period of 2014-2016 are typical for the region of central northern Bulgaria. The main climatic parameters amount of rainfall and temperature during the period of the study can be characterized by a strong fluctuation and uneven distribution over the phenological phases of the plant development. The study period covers three consecutive

years differing in climatic terms. Table 1 presents the data on average monthly temperatures and the amount of precipitated rainfall by months during vegetation. The vegetation 2014 is the most favorable with average monthly air temperatures for April 12.3 °C, May 16.7 °C and June 20.6 °C, and rainfall 139.8 mm, 83.0 mm and 54.3 mm, respectively. As a result of the balanced combination of air temperature and optimum rainfall it has been favorable for plant development. The second year (2015) has relatively higher temperatures in May of 18.8 °C and uneven precipitation distribution, characterized by a certain drought in April (43.6 mm) and May (30.6 mm), and a larger quantity in June (95.7 mm). The third year (2016) occupies an intermediate position over the other two years with temperatures in the months of April and May, close to normal (15.3-16.4 °C) and rainfall between 73.1 and 76.5 mm.

The specificity of the meteorological conditions has enabled the assessment of the biological qualities of the white lupin specimens as well as the appearance of their potential. Based on the average values for the period, their level of variation is established.

The study of the regularities of variability of quantitative signs enables more breeding material for crossing to be considered objectively, taking into account the impact of their modification variability.

Table 1. Climatic characterization of the experimental period

Months	2014			2015			2016		
	t °C	rainfall mm	humidity %	t °C	rainfall mm	humidity %	t °C	rainfall mm	humidity %
I	0.8	41.8	82.0	1.9	12.4	80.0	-0.5	98.0	78.0
II	2.3	3.4	82.0	2.3	39.2	80.0	8.7	46.0	75.0
III	9.7	76.9	68.0	6.7	68.4	71.0	8.5	76.6	73.0
IV	12.3	139.8	76.0	12.2	43.6	54.0	15.3	73.1	66.0
V	16.7	83.0	70.0	18.8	30.6	66.0	16.4	76.5	71.0
VI	20.6	54.3	67.0	20.7	95.7	64.0	23.0	45.8	67.0
VII	23.1	71.8	67.0	25.8	21.5	54.0	24.6	7.8	57.0

Analysis of variance

Analysis of variance showed significant effect of the environment on the signs studied. They are also the factor with the highest part on the variability of the indicators, i.e. defining for the crop were the meteorological conditions. An exception is nodulating ability, where the part of genotype is almost twice as large as that of the environment (Table 2). Although significantly lower, but the effect of the genotype in the total variation of the signs has been demonstrated. These facts allowed the accuracy of the differences between the arithmetical mean of the varieties sampled to be calculated. On the individual analysed signs, genotypes are distributed in a different number of groups, statistically credible differing among themselves.

Genetic variability

As the primary criterion for the variability of quantitative signs, the average value and the coefficient of variation are used. The coefficient of variation allows to obtain information on the characteristics of the reaction rate of the different plant species and their signs, while ensuring the comparability of the results obtained (Chakraborty and Chakraborty, 2010).

Values of phenotypic (CVp) and genotypic coefficients of variation (CVg) as well as phenotypic (Vp) and genotypic variance (Vg) are given in Table 3.

For the indications relating to aboveground mass, the slightest variation in the sample of the varieties studied was observed with regard to the leaf dry weight (CVp-17.48%, CVg-4.37%) with an estimated lowest phenotypic and genotype variation coefficient. Significant variability was recorded on the other signs especially plant height (CVp-48.68%, CVg-42.84%), the stem dry weight (CVp-34.78%, CVg- 22.61%), aboveground fresh and dry weight (CVp-33.66%, CVg-42.07%; CVp- 32.62%, CVg-51.22%).

The small difference in the values of CVp and CVg by the plant height suggests that the variation observed is due to genetic factors.

The variability in the signs related to the root system (Table 3) is in smaller limits. It is the most significant with respect to the root fresh weight (CVp-25.37%, CVg-7.61%) and the specific nodulating ability (CVp-24.89%, CVg-8.71%). Less variation is recorded by the indicator nodule weight per plant (CVp-15.24%, CVg-12.50%).

Low values of genotype variation coefficient for leaf dry weight, root fresh weight and specific nodulating ability suggest some difficulty in the manipulation of these signs in the breeding process. In general, the values of CVp are higher than the values CVg as an exception is the aboveground fresh and dry weights. This shows the stronger effect of the environmental in the manifestation of most signs.

The values of genotypic variance (Vg) range from 0.001 for the specific nodulating ability to 29.16 for the leaf number, while the values of phenotypic variance (Vp) range from 0.001 for the specific nodulating ability up to 43.15 for the leaf number per plant.

The value of the genetic variance of almost all signs is less than the value of the phenotypic variance. The exception was the nodule weight and specific nodulating ability in which the genetic and phenotypic variance is leveled, indicating the significant magnitude of their genetic variability.

Higher environmental variance (Ve) for the leaf number (79.59), plant height (47.23), aboveground fresh weight (44.16) and number of nodules per plant (25.14) indicate that they are strongly influenced by the environment in which the plants grow, whereas in other signs this influence is weaker.

The genetic parameters discussed in this study are the functions of changes in environmental conditions so that varieties placed in another environment can be assessed in different ways.

Heritability and genetic advance

The obtaining of information on the nature of the inheritability of the main elements of productivity is important for the effective use of breeding material (Ashiev, 2014).

Table 2. Analysis of variation for quantitative traits in white lupin

Source	df	MS						
		NN	NW	SNA	RL	RFW	RDW	LN
Env	2	607.22**	0.48**	0.03*	364.33**	133.66**	19.59**	13.97**
REP*Y	12	42.05 ^{ns}	0.02 ^{ns}	0.01 ^{ns}	7.87*	1.75 ^{ns}	0.18 ^{ns}	14.49 ^{ns}
Var.	6	317.54**	0.20**	0.06**	22.26**	7.18**	0.77**	647.29**
Var* Years	12	159.72**	0.10**	0.01 ^{ns}	25.75**	11.59**	0.66**	209.82**
Error	72	25.13	0.02	0.01	3.91	1.89	0.20	79.58
TotalC	104							
Source	df	LFW	LDW	SFW	SDW	PH	AFW	ADW
Env	2	1.08**	26.79**	674.74**	986.62**	16.20**	6.92**	1.32**
REP*Y	12	4.52 ^{ns}	0.14 ^{ns}	16.25 ^{ns}	5.15 ^{ns}	34.02 ^{ns}	32.00 ^{ns}	4.20 ^{ns}
Var.	6	51.90**	2.28**	153.73**	26.08**	302.63**	110.38*	20.06**
Var.*Y	12	35.57**	0.93**	48.83*	9.75 ^{ns}	275.04**	184.55**	9.37 ^{ns}
Error	72	9.95	0.34	20.70	5.45	47.23	44.16	6.34
TotalC	104							

NN, nodule number; NW, nodule weight; SNS, specific nodulating ability; RL, root length; RFW, root fresh weight; RDW, root dry weight; LN, leaf number; LFW, leaf fresh weight; LDW, leaf dry weight; SFW, stem fresh weight; SDW, stem dry weight; PH, plant height; AFW, aboveground fresh weight; ADW, aboveground dry weight

*/** significant at the 0.05/0.01 level; ns = not significant

In this study, the signs of a specific nodulating ability (H^2 - 80.81%) and aboveground fresh weight (H^2 - 88.05%) show a relatively higher values of coefficient of inheritance in broad sense (Table 3) followed by stem fresh weight (H^2 -68.24%), leaf number (H^2 -67.58%) and stem dry weight (H^2 -62.60%).

From medium to high is the inheritance of leaf dry weight, aboveground dry weight, number and weight of nodules per plant. This implies most likely that inheritability of these signs are due to the additive gene effects and when crossing appropriate parent pairs the selection of these parameters can be effective in early generations.

The coefficient of heritability used alone does not give an indication of the degree of genetic improvement that would be obtained as a result of the selection of individual genotype. Therefore, the knowledge of heritability, combined with genetic advance is more

useful and informative.

Genetic advance (GA) in the selection refers to the improvement of the signs in the future new population compared to initial. High genetic advance (GA) coupled with high heritability was obtained for the leaf number (3.56), stem fresh weight (2.81) and aboveground fresh weight (1.25), suggesting their additive type of inheritance and that they are less dependent on the environment. Therefore, these signs can be enhanced by selection and thus the executed genotypic variability can be retained next generation.

Based on the moderate level of inheritance and high genetic advance (GA) indicated by other signs, in particular the nodule number, it can be concluded that the determinants of the phenotypic effect of this attribute are mainly of additive type and breeding can be effective in improving it.

Table 3. Genetic component of variation and heritability for quantitative traits in white lupin

	Min	Max	Mean	SD	V_g	V_{ge}	V_e	V_p	CVg(%)	CVp(%)	GA	GG	H2mean (%)
NN	1.9	15.9	7.74	4.6	10.5	26.9	25.1	21.2	16.7	20.2	2.9	178.4	49.7
NW	0.1	0.4	0.3	0.1	0.0	0.0	0.0	0.0	12.5	15.2	0.2	166.3	50.1
SNA	0.1	0.2	0.2	0.0	0.0	0.01	0.0	0.0	8.7	24.9	0.1	145.6	80.8
RL	8.1	12.1	10.1	1.2	0.1	4.4	3.9	1.7	10.6	20.8	0.2	49.1	44.1
RFW	1.6	3.6	3.1	0.7	0.5	1.9	1.9	0.8	7.6	25.4	0.4	102.8	21.6
RDW	0.4	1.0	0.7	0.2	0.0	0.1	0.2	0.0	-	-	0.1	114.0	14.8
LN	25.9	44.5	34.5	6.5	29.2	26.0	79.6	43.1	20.4	30.1	3.6	54.1	67.6
LFW	6.7	12.0	8.1	1.9	1.1	5.1	9.9	3.5	17.3	27.8	0.4	72.0	31.5
LDW	0.8	2.1	1.5	0.4	0.1	0.1	0.34	0.1	4.4	17.5	0.0	51.8	59.2
SFW	7.6	17.8	11.3	3.2	6.7	5.6	20.7	10.2	20.1	31.4	2.8	99.4	68.2
SDW	4.4	8.2	6.3	1.3	1.1	0.9	5.5	1.7	22.6	34.8	0.3	89.9	62.6
PH	51.2	65.1	57.4	4.5	1.8	45.6	47.2	20.2	42.8	48.7	7.4	71.9	9.1
AFW	15.1	23.2	18.1	2.7	0.0	28.1	44.2	12.3	51.2	32.6	1.2	71.5	88.0
ADW	5.8	9.0	7.7	1.1	0.7	0.6	6.3	1.3	42.1	33.7	0.3	63.9	53.3

Legens as Table 2; V_g - genotypic variance; V_{ge} - genotype x environment interaction variance; V_e - environmental variance; V_p - phenotypic variance; CVg(%) - genotypic coefficient of variation; CVp(%) - phenotypic coefficient of variation; GA - genetic advance; GG - genetic gain; H2(%) - broad-sense heritability on entry-mean basis

High heritability, combined with low genetic advance is established for the specific nodulating ability and stem dry weight, which is an indication of the involvement of no-additive gene actions (dominance and epistasis). And also, that high value of the heritability is the result more of the favorable influence of the environmental as compared to the genotype. Therefore, despite the high heritability of these signs, attempts to improve them through selection may not be effective in this population.

Cluster analysis

In recombinatorial breeding of plants, the knowledge of the genetic proximity or remoteness of the genotypes used as source material is of great interest.

Transgressive disintegrations can be expected to be more likely if genetically distant genotypes are crossed. Then expect the combination of different valuable genes from both parent in the generation.

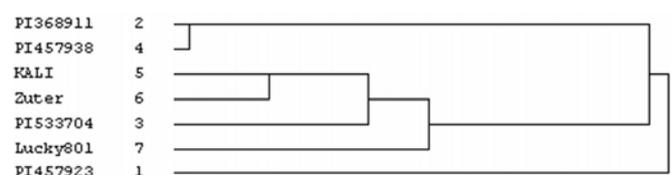


Figure 1. Dendrogram of white lupin varieties

Based on the data for the investigated signs, a cluster analysis was performed, according to which the samples are divided into two main clusters. From the dendrogram in Figure 1 it is evident that the first cluster is represented by only one variety PI457923. The second cluster is covered by the other varieties formed in two sub-clusters. The first group within the same cluster is the most numerous and included Lucky801, PI533704, KALI and Zuter, the last two varieties being the most closely related.

The second group of the same cluster is smaller and is represented by PI368911 and PI457938, which are genetically furthest from the PI457923.

Analysis of main components

The main component method is a mathematical procedure in which a baseline set of probability-correlated variables is transformed into a lower number of unrelated variables, called main components. The PCA mathematical is defined as an orthogonal linear transformation that converts the output factor space into a new coordinate system so that the greatest variation for any data projection is contained in the first coordinate, called the first main component. The amount of information not described by the first main component is contained in the second and so on.

The reduction in size (number of characteristics) of the main components method is a projection of the space of the signs in the K-dimensional factor space. This transformation is a convenient way of graphic representation and interpretation of the multifactorial data set.

A more detailed analysis of the biological capabilities of the samples examined gives the principal component analysis. Four own values (eigenvalues) are found to be larger than 1, which determines the choice of four factors responsible for the observed fluctuation. These factors determine about 89.27% of total variability. The first factor explains 42.16%, the second 20.73%, the third 19.21% and 7.17%.

Table 4 presents data on the values of the signs by main components. The first main component is related to leaf dry weight and aboveground dry weight, the leaf number and leaf fresh weight, as well as the root length. With most of the signs influencing the first major the second is in a negative or weak positive relationship. To a greater extent the second main component is influenced by the nodule number, the leaf number, the root fresh weight, the plant height the nodule weight.

Only three of the investigated signs - stem fresh weight, stem dry weight and plant height positively affect the third main component. The fourth main component is mainly related to the root length and the aboveground dry weight. The nodule number, the leaf and stem dry weights are less positively influenced.

In Figure 2 data on the sample values of the first three main components are displayed. The varieties of PI457923, Zuter and Lucky801 have positive values in all three components and the other varieties have positive values on the first and second main components. The varieties of PI457923 and PI533704 are influenced more strongly by the first main component.

Table 4. The Eigen values and vectors of the correlation matrix for 14 traits of white lupin genotypes

Variables	PC1	PC2	PC3	PC4
NN	-0.139	0.505	-0.035	0.300
NW	-0.272	0.092	-0.413	-0.089
SNA	-0.226	-0.229	-0.364	-0.315
RL	0.146	-0.383	-0.209	0.573
RFW	-0.093	0.280	-0.366	0.004
RDW	-0.378	-0.111	-0.175	0.026
LN	0.195	0.435	-0.255	-0.162
LFW	0.115	-0.446	-0.263	-0.072
LDW	0.226	0.138	-0.394	0.274
SFW	-0.336	-0.086	0.051	-0.383
SDW	-0.394	-0.075	0.005	0.235
PH	-0.361	0.154	0.119	0.039
AFW	0.211	-0.008	-0.405	-0.224
ADW	-0.371	-0.048	-0.129	0.338
Parameter				
Eigen value	5.900	2.900	2.680	1.004
Cumulative (%)	42.160	62.890	82.090	89.260
Variability (%)	42.160	20.730	19.210	7.170
SD	2.430	1.700	1.640	1.002

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

The second main component has higher impact on PI368911, PI457938 and Lucky801. There is no significant difference in the influence of the first two main components on KALI and Zuter.

PCA plot analysis

Multivariate methods of analysis are widely used to assess the genetic diversity of breeding materials. In Figure 2 the specimens are depicted according to their values for the first (PC1) and second factor (PC2).

PI457923 and Lucky801 specimens have negative values in PC1 and positive PC2. Their position in PC1 is determined by the indicators related to the formation of the leaf number, the leaf dry weight, the aboveground fresh weight, and PC2 from the low values of leaf fresh weight, the root length and the specific nodulating ability. In the sector with positive values of PC1 and negative PC2 are located the KALI and PI533704 specimens. Their position in relation to the first principal component is determined by the root length and the leaf fresh weight and their negative values in PC2 are related to the elements root dry weight and stem fresh and dry weights. In the plane with positive values, the varieties of PI368911 and PI457938 are located on the two principal components. Determining their position in this quadrant are the leaf number, the aboveground fresh and dry weights, the nodule number and root fresh weight. As independent of the coordinate system in the negative part of the two principal components is the Zuter variety. Its localization there is due to the signs specific nodulating ability, aboveground dry weight, root dry weight, stem fresh and dry weights.

In Figure 3 a previewed pattern of the relationship between the signs and their location in the factor space is presented.

The applied PC analysis provides information on the correlative relationships between the studied signs. Depending on the magnitude of the angle, which is formed between the vectors of each two signs, correlations between them can be determined.

Vectors of the signs root dry weight, stem fresh and dry weights and aboveground dry weight conclude sharp angles, indicating the strong positive correlation between them. The same sign is the relationship between the nodule number and the root fresh weight; the nodule weight and plant height; the root length and the leaf fresh weight.

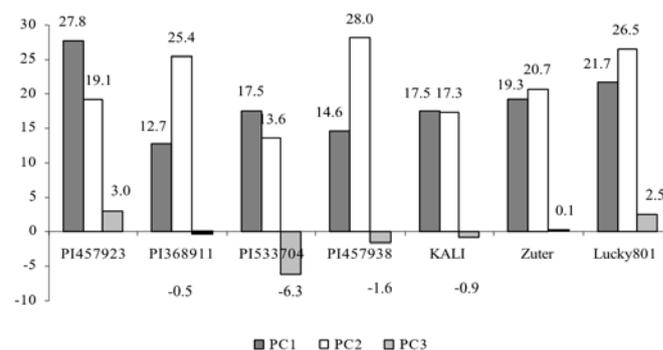


Figure 2. Values of varieties on main components (PC1, PC2, PC3 = principal component 1, 2 and 3, respectively)

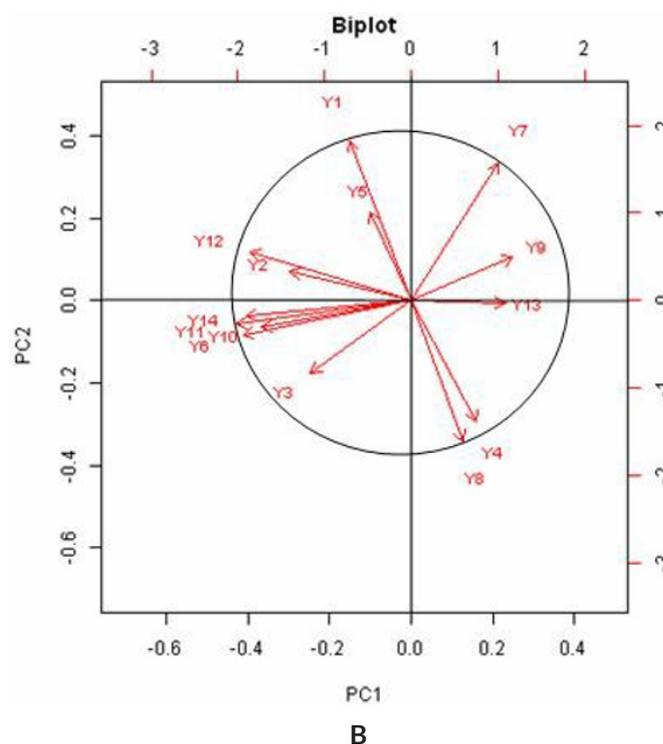


Figure 3. Projection of varieties and signs on the vector plane (A - for quantitative traits: Y1 - nodule number, Y2 - nodule weight, Y3 - specific nodulating ability, Y4 - Root length, Y5 - Root fresh weight, Y6 - Root dry weight, Y7 - Leaf number, Y8 - Leaf fresh weight, Y9 - Leaf dry weight, Y10 - Stem fresh weight, Y11 - Stem dry weight, Y12 - Plant height, Y13 - Aboveground fresh weight, Y14 - Aboveground dry weight; B - for lupin genotypes)

In the comparison of the two figures (Figure 2A and Figure 2B), the binding of genotypes in groups of certain signs may be assessed. The genotypes points of the Figure 2B are positioned closer to the vectors of the corresponding Figure 2B, so this attribute is decisive in their grouping.

Correlation analysis

Correlation coefficients appear to be very appropriate indicators to study dependencies between signs. Correlation studies are of interest to create adaptive genotypes and to obtain information about the characteristics of the signs.

Correlation coefficients have been identified between the investigated signs (Table 5). The positive correlations between the nodule weight and all the other signs are found significant without the leaf number. The nodule number correlates positively with the nodule weight ($r = 0.310$), root mass fresh weight ($r = 0.275$) and leaf

number ($r = 0.270$), and negative with the greater part of the remaining signs. The strongest significant positive correlations has shown the aboveground dry weight with stem dry weight ($r = 0.989$) and with the plant height ($r = 0.936$).

The aboveground fresh weight is in a negative and statistically significant correlation only with the nodule number of nodules ($r = -0.330$), from which it follows that the varieties with heavier aboveground fresh biomass form a smaller number of nodules but with higher weight. With other signs the dependencies are positive. They are particularly strong with the leaf fresh and dry weights ($r = 0.881$ and $r = 0.897$) with the plant height ($r = 0.963$) as well as the plant height ($r = 0.587$) and the root dry weight ($r = 0.569$).

Given the importance of the signs related to the productivity of fresh biomass, the selection of parental pairs in hybridization schemes should be directed to genotypes with high values of these indicators.

Table 5. Correlation coefficients (r) among the quantitative traits of white lupin varieties

	NN	NW	SNA	RL	RFW	RDW	LN	LFW	LDW	SFW	SDW	PH	AFW
NW	0.31**												
SNA	0.04	0.38**											
RL	-0.30**	0.27**	0.04										
RFW	0.27**	0.26**	-0.14	-0.03									
RDW	-0.27**	0.40**	0.13	0.58**	0.27**								
LN	0.27**	0.16	-0.32**	-0.27**	0.75**	0.04							
LFN	-0.38**	0.32**	0.04	0.54	-0.07	0.53**	-0.05						
LDW	-0.20*	0.39**	-0.13	0.40**	0.15	0.54**	0.33**	0.75**					
SFW	-0.11	0.24*	-0.04	0.19*	0.31**	0.58**	0.22*	0.40**	0.34**				
SDW	-0.18	0.34**	-0.04	0.32**	0.38**	0.77**	0.33**	0.53**	0.53**	0.83**			
PH	-0.14	0.39**	-0.11	0.33**	0.37**	0.72**	0.40**	0.53**	0.64**	0.77**	0.92**		
AFW	-0.33**	0.37**	-0.08	0.54**	0.09	0.57**	-0.00	0.89**	0.88**	0.36**	0.51**	0.59**	
ADW	-0.19*	0.37**	-0.06	0.36**	0.36**	0.78**	0.35**	0.61**	0.65**	0.80*	0.99**	0.94**	0.61**

*/** significant at the 0.05/0.01 level

DISCUSSION

According to Vitko (2016) varieties of *Lupinus angustifolius* are complex populations with diverse genetic material, especially in the quantitative indications, which in turn are subject to a strong modificational variability major obstacle to increasing the reeding of the desired genotypes. The same author establishes that signs such as the number of seeds per plant, the mass of plant seeds and others are characterised by a high level of modificational variability, and therefore the identification of valuable genotypes of these signs is difficult. Relatively stable in terms of the indicator modificational variability is the sign of the plant height. In the opinion of a number of researchers in most cases, the quantitative signs are formed and amended over a period of time in the process of ontogenesis, depending on the time and severity of the action of limiting factors. According to some researchers, the quantitative signs determining the productivity of the plant are not so much a product of the action of genes or chromosomes, as result from the interaction of limiting factors in the external environment with the systems of gene complexes.

Each genotype is characterized by an inherently defined amount of individual variability. The various signs of a genotype vary under the influence of environmental factors inconsistent in a different way. Each attribute is characterized by the limit of its variability (Taranuho, 2001; Angelova et al., 2011; Atnaf et al., 2017).

In research related to peas Singh and Singh (2006) reported high heritability of plant height, number of plant beans and a mass of 1000 seeds combined with high genetic advance. Sharma and Bora (2013) also reported high genotypic variability of the yield of grain and its components. Panse (1957) stated that high heritability coupled with high genetic advance indicates the additive gene effects while high heritability coupled with low genetic advance indicates the non-additive gene effects for the control of a particular character. Accordingly, the presence of high estimates of GCV, heritability and genetic advance as percent of mean for grain yield in this study indicate the preponderance of additive gene action

in governing the expression of the trait and consequently high expected genetic gain through selection. High estimates of heritability and low genetic advance observed for some of the traits suggest the presence of non-additive gene action and/or significant genotype by environment interaction in the expression of the traits that will make selection difficult for the improvement of these traits. Several researchers reported similar results to the present finding on different legume and other crop species, such as soybean (Malek et al., 2014) and mungbean (Payasi, 2015).

The relative contributions of different traits of the identification of desirable genotype found in this study by the traits comparing biplot procedure of the GT biplot are similar to those found in other crop studies soybean (Yan and Rajcan, 2002) and white lupin (Rubio et al., 2004).

Tsenov et al. (2014) expressed the view that correlations between the main signs should be established in order to be able to make a quantitative assessment of the varieties studied. The authors consider that this is necessary for the following reasons: in order to establish any weighting factors that may be attributed to another and in order to be able to adjust the character values according to real relationships between them in particular experiment.

CONCLUSIONS

The effect of environment and genotype on the occurrence of the signs studied has been demonstrated. The role of the genotype is the strongest for the nodulating ability of the plants.

The variability of the signs associated with the root system is in smaller limits than that of aboveground biomass. The phenotypic coefficient of variation is higher than the genotype coefficient of variation for all signs with the exception of the aboveground fresh and dry weights (CVp - 32.62%, CVg - 51.22%; CVp - 33.66%, CVg - 42.07%).

The genetic variance is within the range of 0.001 (the specific nodulating ability) to 29.16 (the number of leaves per plant), and the phenotypic variance of 0.001 (the specific nodulating ability) to 43.15 (number of leaves per

plant). For the number of leaves per plant (3.56, 67.58%), stem fresh weight (2.81, 68.24%) and aboveground fresh weight (1.25, 88.05%) high genetic advance (GA) was obtained in combination with high heritability.

High heritability with low genetic advance was established for the specific nodulating ability (80.81%, 0.09) and the stem dry weight (62.60%, 0.31), which is an indication of the involvement of no- additive gene action.

The aboveground fresh weight is positively correlated with: the leaf fresh weight ($r = 0.897$), the leaf dry weight ($r = 0.881$), the plant height ($r = 0.587$) and the dry weight of the roots ($r = 0.569$).

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