



## PROSPECTS FOR BREEDING AND HETEROSIS STUDIES FOR YIELD AND YIELD COMPONENTS IN WHITE LUPINE HYBRIDS (*Lupinus. albus* L.)

Natalia Anastasova GEORGIEVA<sup>1</sup>, Valentin Ivanov KOSEV<sup>1</sup>, Vera Miloševa POPOVIĆ<sup>2\*</sup>

<sup>1</sup>Institute of Forage Crops, Pleven, Agriculture academy, Bulgaria

<sup>2</sup>Institute of Field and Vegetable Crops, Novi Sad, Serbia

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The study was conducted in the period 2019-2023 with white lupine cultivars (NORT486, BGR6305 and WAT) and their hybrids (NORT486 × BGR6305; BGR6305 × NORT486; BGR6305 × WAT; WAT × BGR6305) in F1-F3 generations. The following parameters were defined: heterosis effect in F1, inbred depression, degree of dominance in F1 and F2, transgression, dominance, epistasis, coefficient of inheritance in broad sense and narrow sense, coefficient of effectiveness of the mass of genotypes by phenotypical performance of the trait, cytoplasmic effect were determined. The highest positive hypothetical (17.76%-94.73%) and true heterosis (11.0-81.76%) was found in the crosses BGR6305 × NORT486 and BGR6305 × WAT regarding plant height, seeds number, seed weight per plant, 1000 seeds mass, and in BGR6305 × WAT – for pods number (97.09%, 90.61%). In F1 of hybrids BGR6305 × NORT486 and BGR6305 × WAT, the inheritance of plant height, seeds weight, and 1000 seeds mass was positively predominant. Negative dominance and predominance were established in WAT × BGR6305 for plant height (-7.41) and 1000 seed mass (-0.69) and in NORT486 × BGR6305 and BGR6305 × NORT486 for pods number (-1.95, -2.99). In most hybrids, epistatic gene interactions played a greater role in the inheritance of traits. The phenotypic expression of the traits of plant height, pods number and seeds number in BGR6305 × WAT, as well as seed weight per plant in BGR6305 × WAT and WAT ×

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*Corresponding author:* Vera Popović, Institute of Field and Vegetable Crops, Novi Sad, Serbia, E-mail: [drvpopovic@gmail.com](mailto:drvpopovic@gmail.com); [vera.popovic@ifvcns.ns.ac.rs](mailto:vera.popovic@ifvcns.ns.ac.rs), ORCID: [0000-0002-7701-9928](https://orcid.org/0000-0002-7701-9928); N.A.Georgieva ORCID: [0000-0002-6364-1310](https://orcid.org/0000-0002-6364-1310); V.I.Kosev ORCID: [0000-0003-3292-4200](https://orcid.org/0000-0003-3292-4200)

BGR6305 was genotypically determined. To achieve faster results in these accessions, multiple individual selection should be carried out in the early hybrid progenies (F2 - F3). Regarding 1000 seeds mass, breeding success (through mass selection) can be achieved in later hybrid generations.

*Keywords:* white lupine, parental forms, hybrids, genetic analysis

## INTRODUCTION

Genus *Lupinus* includes almost 300 species, but only four species have importance worldwide: *L. mutabilis*, *L. angustifolius*, *L. luteus* and *L. albus* (ZERICUN, 2012; YILKAL, 2015; GRESTA *et al.*, 2017). *Lupinus albus* (white lupine) is defined by many researchers as a valuable high-protein, forage, and culinary crop, slightly inferior to soybeans in terms of the biological value of protein (FILIPPOVA and MASLOVA, 2016; BURYAKOV and PROHOROV, 2017; MALYSHKINA *et al.*, 2020). Compared to soybean (ILIN *et al.*, 2025), however, it is characterized by a shorter vegetation period, better tolerance to stress conditions and considerably higher productivity (YAGOVENKO *et al.*, 2022), which is of particular importance under changing climatic conditions. The content of protein in the grain and green mass of white lupine reaches 40-45 and 20%, respectively, and of fat - 12%. Like other legumes, it can absorb atmospheric nitrogen, thus meeting 80% of its needs (ZHUCHENKO *et al.*, 2009; TSYGUTKIN *et al.*, 2011). After harvesting, lupine leaves a considerable amount of organic matter in the soil (15-20 t ha<sup>-1</sup>), which defines it as an excellent precursor in crop rotations (YILKAL, 2015). For successful production, soil fertility control analysis is important (POPOVIĆ *et al.*, 2022; 2024; STUPAR *et al.*, 2024). Lupine is undemanding in terms of soil and climatic conditions and exhibits good adaptability. Developing new white lupine varieties adapted to the relevant environmental conditions is a good alternative to soybeans (ŚWIĘCICKI *et al.*, 2015).

Genetic variability within a plant population plays an important role in the breeding process. The level of diversity in accessions collection determines the limit of breeding of the culture, which, with trait variability, is a prerequisite for success in a given direction (HEFNY, 2013).

In conventional breeding programs, various strategies were applied to achieve combinative variability in hybrid plants. The correct choice of suitable starting parental forms ensures, to a large extent, breeding success (POLIGNANO *et al.*, 2009; KURENSKAYA, 2016). The main selection method in white lupine is inter-varietal artificial hybridization. Hybridization programs use multiple, reciprocal, recurrent, or diallel schemes of crossing. Due to genomic barriers, interspecific crossing between different lupine species cannot result in fertile hybrids under natural conditions (GLOMBIK *et al.*, 2020).

New varieties of white lupine should combine characteristics such as early maturity, productivity and disease resistance. Yield increase is possible by obtaining transgressive forms, for which it is necessary to establish the value of the resulting hybrid combinations. In this sense, it is advisable to study the manifestations of transgression in the second and subsequent hybrid generations according to the importance of the traits (MALYSHKINA *et al.*, 2021).

The present investigation aimed to study the inheritance of main quantitative traits in white lupine hybrids seeking opportunities for targeted selection of promising genotypes concerning productivity.

#### MATERIAL AND METHODS

The experimental activity was conducted at the Institute of Forage Crops (Pleven) during the period 2019-2023. The varieties BGR6305 (originating in Poland), WAT (Poland) and NORT486 (Spain) were used as parental components. The following crosses were performed, as well as their reciprocal combinations: *NORT486* × *BGR6305*, *BGR6305* × *NORT486*, *BGR6305* × WAT, WAT × *BGR6305*. The cultivars used as parental components are characterized by alternative traits related to grain productivity and phenological features. Artificial sexual hybridization (2019) was performed by castration and pollination of the best lower flowers FIEN *et al.* (2021), the parental forms (P1 and P2) and the first, second, and third hybrid generations (F1, F2, and F3) were studied. The selection material was sown manually, according to the schemes P1, F1, F2, P2 (2022), and P1, F3, P2 (2023), at an optimal sowing time (the end of March) and an inter-row/intra-row distance of 50/10 cm. An average of 10-15 flowers of each hybrid combination were pollinated, and about 20-25 hybrid seeds were obtained. Artificial sexual hybridization was performed by castration and pollination of the best lower flowers. The parental forms (P1 and P2) and the first, second, and third hybrid generations (F1, F2, and F3) were studied. The selection material was sown manually, according to the schemes P1, F1, F2, P2, and P1, F3, P2, at an optimal sowing time (the end of March) and an inter-row/intra-row distance of 50/10 cm. Biometric measurements included plant height (cm), number of pods and seeds per plant, seed weight per plant (g) and 1000 seeds mass (g).

To calculate the heritability coefficient in a narrow sense, an one-way analysis of variance is used in F2 for the studied traits. Seeds from selected F2 hybrids were sown in 2022. Trait broad-sense heritability was computed from these components of variance by the equation (ANNICCHIARICO *et al.*, 2023):

$$H^2 = s^2_g / (s^2_g + s^2_e/n) \quad (2)$$

where n is the number of experiment replicates.

The parent component values are presented in Figure 1. In Table 2, the obtained negative values of the depression parameter show that in the second generation of the corresponding cross, the expression of the trait is better expressed compared to the parental form. The ratio of trait level in F1 and F2 was determined. As an indicator of change in the level of the studied traits, the genetic parameter inbred depression (in F2) is calculated according to the following formula:

$$\text{“Inbred depression” (\%)} = \frac{F_1 - F_2}{F_1} 100$$

From the first hybrid generation, the selection process was conducted using the pedigree procedure (multiple individual pedigree).

Later generations is the latest generation is the F3 (2023). The manifestations of transgression in the hybrids of the third generation are presented in figure 3. The values of these parameters are the result of comparing the magnitude of the trait between the parental forms and

the corresponding hybrid. The figure shows the final result - norm and frequency of transgression. For this reason, in order not to overload the article with redundant data, we have provided Figure 3.

The following parameters were defined: heterosis effect in F1 (hypothetic and true), inbred depression degree of dominance in F1 (hp1) and F2 (hp2) (according to LI *et al.*, 2008; KACHIGUMA *et al.*, 2022). Using method of SCHNEEMANN *et al.*, (2022) were calculated as follows: transgression (Tn); number of genes, in which the parents differ (N); dominance (D); epistasis (E), coefficient of inheritance in broad sense (H2) and narrow sense (h2), and coefficient of effectiveness of the mass of genotypes by phenotypical performance of the trait (Pp). In addition, the norm and frequency of transgression in third-generation hybrids and cytoplasmic effect (re) (LI *et al.*, 2008) were determined. The positive value of re ( $re > 0$ ) means that paternal hereditary factors have a greater influence on the manifestation of a given trait, and the negative value ( $re < 0$ ) indicates influence of maternal cytoplasmic heredity (cytoplasmic effect). All experimental data were processed statistically using the computer software SPSS 13 and Excel for Windows XP.

### RESULTS AND DISCUSSION

It is known that the genotypes effect is greater when the parents differ considerably in certain traits. Using accessions with alternative characters in hybridization schemes implies obtaining hybrids with wider form-generating process and a greater probability for effective breeding. Quantitative characterization in terms of principal traits is an appropriate tool for the objective assessment of differences in productivity of a group of genotypes. That estimation allows the comparison of selected materials of different origins, but according to the same criteria (TSENOV *et al.*, 2014; KOSEV *et al.*, 2024). Characteristics of the parental components and obtained hybrids regarding main quantitative traits are presented in Figure 1 and Table 1.

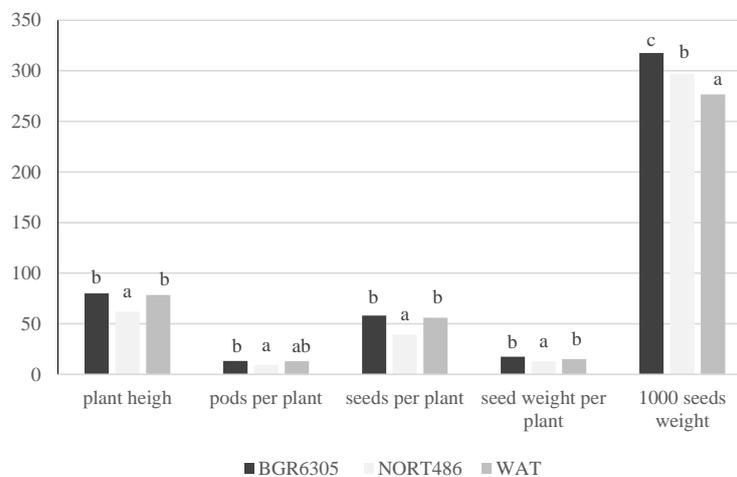


Figure 1. Biometric characteristic of parent components

Table 1. Biometric data of quantitative traits in white lupine hybrids

Hybrids	F1	F2	Heterosis F1		Depression F2 (%)	Degrees of dominance	
			hypothetical (%)	true (%)		In F1 (hp1)	In F2 (hp2)
plant height							
<i>NORT486</i> × <i>BGR6305</i>	85.7	45.9	20.65	7.17	46.44	1.64	-5.63
<i>BGR6305</i> × <i>NORT486</i>	105.9	54.8	49.08	32.43	48.25	3.90	-3.63
<i>BGR6305</i> × WAT	99.5	58.4	29.64	27.24	41.31	15.69	-25.31
WAT × <i>BGR6305</i>	66	36.5	-14.01	-15.60	44.70	-7.41	-55.52
pods number per plant							
<i>NORT486</i> × <i>BGR6305</i>	7.6	18.9	-33.27	-42.98	-148.68	-1.95	7.75
<i>BGR6305</i> × <i>NORT486</i>	5.6	19.4	-50.83	-40.74	-246.43	-2.99	8.26
<i>BGR6305</i> × WAT	20.3	5.7	97.09	90.61	71.92	27.57	-28.29
WAT × <i>BGR6305</i>	18.1	6.1	69.95	75.73	66.30	21.29	-26.00
seeds number per plant							
<i>NORT486</i> × <i>BGR6305</i>	72.1	33.2	48.10	23.99	53.95	2.47	-3.27
<i>BGR6305</i> × <i>NORT486</i>	94.8	29.7	94.73	63.03	68.67	4.87	-4.01
<i>BGR6305</i> × WAT	88.6	28.1	72.37	57.93	68.28	7.91	-9.91
WAT × <i>BGR6305</i>	78.9	27.1	53.50	40.64	65.65	5.85	-10.34
seed weight per plant							
<i>NORT486</i> × <i>BGR6305</i>	17.97	9.89	19.91	3.49	44.96	1.26	-4.29
<i>BGR6305</i> × <i>NORT486</i>	28.31	10.15	88.90	63.04	64.15	5.60	-4.07
<i>BGR6305</i> × WAT	26.01	9.95	91.53	81.76	61.75	17.03	-9.95
WAT × <i>BGR6305</i>	13.99	8.9	3.02	-2.24	36.38	0.56	-12.82
1000 seeds mass							
<i>NORT486</i> × <i>BGR6305</i>	316.35	254.87	2.94	-0.40	19.43	0.88	-10.17
<i>BGR6305</i> × <i>NORT486</i>	355.88	289.51	15.81	12.05	18.65	4.71	-3.45
<i>BGR6305</i> × WAT	349.7	282.3	17.76	11.0	19.30	2.89	-1.6
WAT × <i>BGR6305</i>	284.4	315.25	-4.23	-9.77	-23.51	-0.69	5.96

*Plant height*

In annual legumes breeding, plant height is one of the most important traits related to lodging resistance and thus indirectly influencing yield. Higher genotypes are prone to lodging, especially under intensive farming conditions. Under the experimental conditions, plant height was inherited predominantly positively, with a weaker influence of epistatic gene actions (Table 1). The hybrid combination WAT × BGR6305 was characterized by negative predominance of

the trait. A negative true (-15.60%) and hypothetical (-14.01%) heterosis was found for the hybrid combination WAT × BGR6305. In the reciprocal combination BGR6305 × WAT, the heterosis was positive and reached 29.64%. In F2 generation, depression was found in all hybrids, regardless of the crossing direction, with relatively less depressed plants in BGR6305 × WAT and WAT × BGR6305. In a similar study with peas, KATYUK and MAISTRENKO (2018) observed both positive predominance and intermediate inheritance of the plant height trait. It confirms partially in the present study.

#### *Pods number per plant*

Positive hypothetical and true heterosis was found in BGR6305 × WAT and its reciprocal cross for this parameter. It should be noted that when BGR6305 is used as the maternal form, the true and especially hypothetical heterosis had considerably higher values (near 100%). The F1 hybrids of cultivars NORT486 and BGR6305 formed a smaller pod number compared to the parents, and therefore their heterosis was negative. In the second hybrid combination, no depressed plants were found. Epistatic gene effects predominated in this hybrid combination. The obtained results confirm the studies of VITKO and TARANUHO (2010) in yellow lupine. The authors reported a high positive heterosis effect in the F1 hybrids for pods number, seeds number, seed weight per plant and 1000 seeds mass.

#### *Seeds number per plant*

Regarding number of seeds per plant, the true and hypothetical heterosis, and the degree of dominance in F1 hybrids, were different but with a positive value. The maximum value of heterosis was found in BGR6305 × NORT486 (94.73%-63.03%). In the reverse combination, heterosis was significantly lower. A similar dependence, but to a lesser extent, was observed in the other hybrid combination. The effect of lower true heterosis (23.99%) in NORT486 × BGR6305, generally, did not affect the degree of depression, which was significant in all hybrids. Inheritance of the seeds number trait was of the type of positive predominance. In F2 hybrids, dominant gene effects were predominant. Similar were the conclusions of TYURIN and ZOLOTARYOV (2013) when studying the offspring of selected vetch plants. The authors have obtained results according to which the material presented in their experiment is a dynamically heterozygous population, and new hybrid forms are constantly formed in them. The researchers propose an individual selection of genotypes. That would restore the average trait level in the population and would guarantee selection success.

#### *Seed weight per plant.*

The data show that for the combination WAT × BGR6305, the hypothetical heterosis effect was below 5%, and the true one had a negative sign (-2.24%). Strong heterosis is observed in the reciprocal combination (BGR6305 × WAT). The cultivar BGR6305, as a maternal form, affected the heterosis value under crossing with NORT486. The reported heterosis effect for BGR6305 × NORT486 reached 63.04- 88.90%. The plants of WAT × BGR6305 (36.38) were the least depressed, although, in all hybrid combinations, the depression had a positive sign. The trait of seed weight per plant in F1 was inherited positively predominantly in all crosses except WAT × BGR6305. No differences were found regarding the influence of gene effects in trait

inheritance in F<sub>2</sub>. In a study of yellow lupine hybrids, KAVCEVICH (2000) observed different types of inheritance, from negative to positive predominance, concerning seed productivity per plant. Heterosis in peas can be manifested only in some of the quantitative traits, depending on the hybrid combination. Most often, hybrids outperform the parental forms in terms of dry weight and seed weight per plant. The author has obtained values analogous to the present ones concerning the magnitude of the investigated traits. Analyzing the results of experimental work with soybean hybrids, MINKACH and SELIKHOVA (2012) indicated that hybrid combinations with predominance present the greatest selection interest. The authors reported that in F<sub>2</sub> generation (where breeding decomposition is the strongest), plants with positive transgressions were selected. An analogous breeding approach was carried out in the present experiment.

Regarding the trait of 1000 seeds mass, BGR 6305 × NORT486 is of interest because it demonstrated high values of parameters in both hybrid generations. Only the hybrid WAT × BGR6305 did not exceed the values of the better parent or the parent average, as demonstrated by the negative heterosis values. In accordance with these manifestations, WAT × BGR6305 could be determined as the least depressed (-23.51).

For NORT486 and BGR6305 hybrid combination, genes determining the formation of smaller mass seeds are expressed. According to this trait, gene interactions almost analogous to the plant height were established in the F<sub>1</sub> hybrid generation – from positive dominance and predominance to negative dominance. In the F<sub>2</sub> generation of WAT × BGR6305, the 1000-seed mass was determined by predominant epistatic effects, which provide a lower trait expression. The research done is in support of previous studies. TARANUHO (2010) reported that intervarietal hybridization is an effective method for creating start material in lupine breeding by selecting parental forms with contrasting trait manifestations. Using the method of sexual hybridization, VITKO and TARANUHO (2011) have obtained valuable hybrids of yellow and narrow-leaved lupine, exceeding the parental forms in terms of seed weight per plant and other characteristics.

#### *Genetic parameters*

Table 2 presents the values of genetic parameters for the investigated traits in the hybrid crosses. The data show positive manifestations of transgression in all traits. The highest transgressions were found in WAT × BGR6305 (21.67) and its reciprocal (21.37) concerning 1000 seeds mass. In this trait, the transgression was considerably weaker in NORT486 × BGR6305 and BGR6305 × NORT486 compared to the previous hybrids. In the generations of crosses between NORT486 and BGR6305 in terms of pods number (2.78-3.15), productivity (3.97-4.64), plant height (9.13-9.25) and seeds number (15.25-14.30), homozygous genotypes can be expected with gene recombinations leading to a quantitative increase in these traits. The results support those of MINKACH and OBORSKAYA (2022), who found evidence for transgression in some F<sub>2</sub> generation of soybean hybrids in terms of seed productivity. The excess (compared to the parent forms) has reached 57%. The authors reported that in F<sub>3</sub>, a minority of hybrids exhibited positive transgression but at an increased frequency compared to F<sub>2</sub>.

The number of genes on which the parents differed was essential concerning plant height. When variety BGR 6305 is used as the paternal component, the differences were more considerable. Parent cultivars BGR6305 and WAT differed more in pod number (254). The situation was similar in seed weight (144) and 1000 seeds mass (1046). The reciprocal cross

WAT × BGR6305 had a slight advantage in seeds number. The number of genes controlling the trait seed weight per plant (by which the parental forms WAT and BGR6305 differ) was relatively fewer (from 35 to 74).

Table 2. Values of gene parameters of quantitative traits in white lupine hybrids in F2 generation

Hybrids	T <sub>n</sub>	N	D	E	H <sup>2</sup> (%)	h <sup>2</sup> (%)	Pp
plant height							
<i>NORT486</i> × <i>BGR6305</i>	9.13	3268	-595	671	94	15	-123.18
<i>BGR6305</i> × <i>NORT486</i>	9.25	2255	-321	433	62	34	-49.43
<i>BGR6305</i> × WAT	0.97	2819	-473	566	12	34	-90.97
WAT × <i>BGR6305</i>	0.93	3627	-878	805	71	38	-224.11
pods number per plant							
<i>NORT486</i> × <i>BGR6305</i>	2.78	212	41	-45	52	39	-7.10
<i>BGR6305</i> × <i>NORT486</i>	3.15	171	31	-36	58	40	-4.88
<i>BGR6305</i> × WAT	1.03	254	-44	52	83	27	-5.58
WAT × <i>BGR6305</i>	1.94	100	-19	22	44	33	-2.01
seeds number per plant							
<i>NORT486</i> × <i>BGR6305</i>	15.25	89	-15	19	61	19	-1.29
<i>BGR6305</i> × <i>NORT486</i>	14.30	175	-25	35	26	36	-2.16
<i>BGR6305</i> × WAT	5.29	203	-35	42	24	34	-4.21
WAT × <i>BGR6305</i>	4.15	251	-45	52	62	31	-6.46
seed weight per plant							
<i>NORT486</i> × <i>BGR6305</i>	3.97	74	-15	16	29	14	-1.72
<i>BGR6305</i> × <i>NORT486</i>	4.64	100	-14	20	19	12	-0.83
<i>BGR6305</i> × WAT	2.59	144	-23	30	46	38	-2.41
WAT × <i>BGR6305</i>	3.89	35	-10	9	55	35	-1.16
1000 seeds mass							
<i>NORT486</i> × <i>BGR6305</i>	12.48	490	-101	105	96	6	-22.95
<i>BGR6305</i> × <i>NORT486</i>	11.33	869	-118	165	43	9	-16.16
<i>BGR6305</i> × WAT	21.37	1046	-133	196	55	13	-16.36
WAT × <i>BGR6305</i>	21.67	1009	202	-213	93	21	-46.48

transgression (T<sub>n</sub>); number of genes, in which the parents differ (N); dominance (D); epistasis (E), coefficient of inheritance in broad sense (H<sup>2</sup>); h<sup>2</sup> - coefficient of effectiveness of the mass of genotypes by phenotypical performance of the trait (Pp)

Regarding plant height, seeds number and seed weight per plant was observed unidirectionality in the action of the dominant gene alleles. Their negative value suggests that their action will determine a decrease in the phenotypic manifestation of the trait. That was most pronounced in the crosses *NORT486* × *BGR6305* (-595) and WAT × *BGR6305* (-878) in plant height. The combinations between *NORT486* and *BGR6305* were characterized by positive allelic dominance of the genes for pods number, as well as the hybrid WAT × *BGR6305* for 1000 seeds mass, which determines the formation of more pods and heavier seeds, respectively. The interallelic interaction index values showed that in the F<sub>2</sub> generation of WAT × *BGR6305*, epistatic interactions is negative (-213) prevailed in 1000 seeds mass. Interallelic interactions in *NORT486* × *BGR6305* had the same sign regarding pods number. It can be assumed that in these hybrids, this will reduce the degree of phenotypic expression of the trait compared to full

additive inheritance. Positive epistatic gene interactions were observed in all other hybrids – from 9.00 (at WAT × BGR6305 for seed weight per plant) to 805 (at WAT × BGR6305 for plant height). Stronger inter-allelic interactions were reported for plant height and 1000-seed weight.

#### *Coefficient of heritability in broad and narrow sense*

Statistical methods for assessing the character of heredity of traits are a prerequisite for the selection of parental forms for hybridization. Calculating the heritability coefficient is important to achieve this breeding purpose. Heritability is the proportion of phenotypic variation (VP) due to variation in genetic values (VG) and is based on the alleles that are inherited. The effect of alleles depends on their frequency in the population. Broad-sense heritability of a trait is defined as the proportion of trait variation that is due to genetic effects, and thus includes all potential sources of genetic variation (additive, maternal, paternal, dominance and epistasis effects). Narrow-sense heritability is the proportion of genetic variation due to additive genetic effects only and describes the degree of resemblance between relatives (HOFFMANN and MERILÄ, 1999). Heritability is a good indicator of transmission of characters from parents to its progeny. Heritability is classified as low (below 30%), medium (30%–60%) and high above 60%), (TERFA and GURMU, 2020). In breeding, heritability is usually used in narrow sense, as it allows predicting the results of research work. The heritability coefficient characterizes the degree of transmission of a trait from the paternal form to the hybrid. To calculate the heritability coefficient in a narrow sense, an one-way analysis of variance is used in F<sub>2</sub> for the studied traits. The minimum heritability coefficient value in which successful breeding can take place is 30%. If the heritability coefficient is below the minimum value, it is recommended to start a selection of suitable hybrids in later generations. Our results indicated a higher genetic share ( $H^2$ ) to the overall phenotypic expression as follows: in NORT486 × BGR6305 regarding plant height (94%) and 1000 seeds mass (96%), in BGR6305 × WAT for pods number (83%), in WAT × BGR6305 for seeds number (62%) and seed weight (55%) (Table 2). With respect to seed productivity, NORT486 and BGR6305 hybrids had lower inheritance coefficients in narrow sense, regardless of the direction of crossing. A similar analogy can be made in the inheritance of pod number, as the inheritance coefficient for NORT486 × BGR6305 and BGR6305 × NORT486 was 52-58%.

It is evident that the direction of crossing matters in most of the hybrids for the traits studied. A higher broad-sense heritability coefficient is obtained when cultivar BGR6305 was the paternal parent form. The obtained heritability coefficients in a broad sense ( $H^2$ ) were higher than those in a narrow sense ( $h^2$ ). Relatively high  $h^2$  (39-40%) was found in NORT486 × BGR6305 and BGR6305 × NORT486 for pods number, in WAT × BGR6305 for plant height (38%), in BGR6305 × NORT486 for seeds number and in BGR6305 × WAT for seed weight (38). Similar conclusions were made by BEYER *et al.* (2015) in *Lupinus angustifolius*. According to the authors, the heritability of almost all traits was high ( $H^2 > 50\%$ ), especially in seed productivity per plant and 1000 seeds mass. The authors concluded that the investigated traits are under relatively strong genetic control which indicates a potential for genetic progress in improving the quantitative elements of yield. Our results confirm those of GUILENGUE *et al.* (2019), who found high values of heritability for seeds number in *Lupinus mutabilis*. According to PROVOROV and TIKHONOVICH (2003), in various legume crops (alfalfa, soybean, clover), the

coefficient of inheritance in a broad sense for some traits was high and reached 80-90%, and the inheritance coefficient in a narrow sense was lower (0.60-0.80).

According to the values for the effectiveness of the mass selection ( $P_p$ ), the hybrids of F2 demonstrated negative differences compared to the parent forms in all characters. Considering the heritability coefficients, it can be assumed that in the combinations NORT486 × BGR6305 and its reciprocal, mass selection for seeds number and seeds weight per plant would be effective in the later hybrid generations. Faster breeding success in the created hybrids regarding seed productivity direction can be achieved if strict multiple individual selection is applied in F2-F3 generations.

#### *Cytoplasmic effect*

In the F1 of cultivars NORT486 and BGR6305 (Figure 2) was found an influence of the factors of maternal cytoplasm in the inheritance of pods number per plant. Regarding this trait, a relatively stronger cytoplasmic effect (-5.95) occurred when crossing BGR6305 and WAT. In the same cross, maternal cytoplasm affected the inheritance of seeds number per plant (-4.75). It was not established influence of the maternal cytoplasm in the inheritance of plant height, seed weight, and 1000 seeds mass. The source material evaluation allows with high probability to guide the selection of valuable genotypes according to the studied characteristics and to speed up the creation process of new varieties of white lupine.

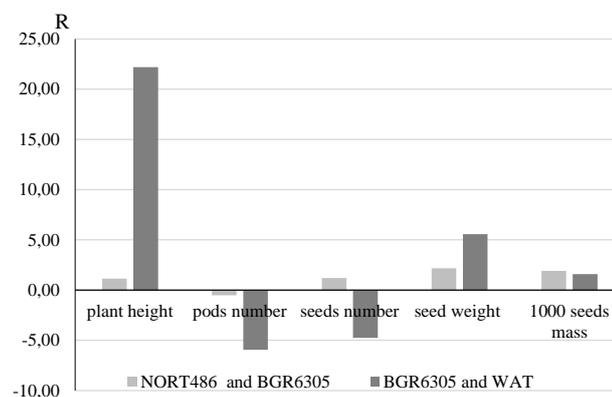


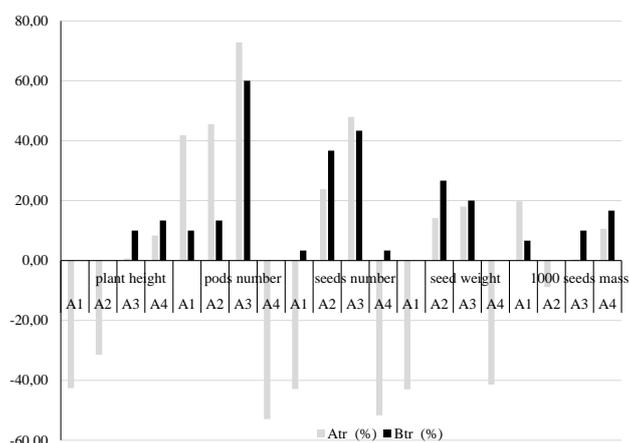
Figure 2. Cytoplasmic effect (R) in white lupine hybrids

#### *Transgressive hybrid forms in F3*

Seeds from selected F2 hybrids were sown in 2022. The hybrids were analyzed for valuable traits for subsequent breeding work. Data analysis showed that the positive norm of transgression was not retained in all hybrid combinations and not for all characteristics (Figure 3). In terms of plant height, negative values of the transgression norm were found in F3 hybrids of NORT486 × BGR6305 (-42.60%) and BGR6305 × NORT486 (-31.47%). Therefore, it is possible to select homozygous genotypes with lower stems in the decomposing progeny compared to the parents' stems. In BGR6305 × WAT, a small but positive transgression rate

(6.6) was recorded, while in the reciprocal hybrid WAT × BGR6305, the transgression norm and frequency were higher.

Depending on the pods number per plant, a positive norm of transgression was found in most of the hybrid combinations (except WAT × BGR6305). There is a high probability in the progeny of BGR6305 × WAT to be selected transgressive individuals with an increased number of pods (72.84%, 60.00%). The transgression norm and frequency in the hybrids of NORT486 and BGR6305 were slightly lower and positive. In these cultivars, the choice of maternal and paternal component was not decisive for obtaining positive transgressive forms.



Atr – norm (%); Btr - frequency (%);  
A1 - NORT486 × BGR6305; A2 -BGR6305 × NORT486; A3 - BGR6305×WAT; A4 - WAT × BGR6305

Figure 3. Manifestations of transgression in F3 hybrids of white lupine

Regarding seeds number per plant, a positive norm of transgression was observed in the progeny of the parental pairs in which BGR6305 was maternal form. Maximum values for transgression norm and frequency were reported for BGR6305 × WAT (47.92%, 43.33%), followed by BGR6305 × NORT486 (23.82%, 36.67%). In terms of seed weight per plant, positive manifestations of transgression were established in the same hybrid populations as in the previous trait.

Data related to 1000 seeds mass data showed positive rate and frequency of transgression in BGR6305 × WAT (0.36%, 10.10%) and WAT × BGR6305 (10.59%, 16.67%). Manifestations of transgression were most pronounced in NORT486 × BGR6305 (19.75%, 6.67%).

In the resulting transgressive combinations, the best plants were selected according to pods number, seeds number and seed productivity per plant. In the course of the experimental work, promising hybrids with positive transgression were identified and selected, and they were superior to the parental forms in terms of the main quantitative characteristics. The obtained data confirm the results of previous studies (MINKACH, 2018), which indicate that in breeding work

with self-pollinated crops, special attention should be paid to transgressive hybrid forms. The identification of the manifestations of transgression in the early stages of breeding allows to reduce the volume of the studied material and to shorten the breeding process.

### CONCLUSIONS

The carried out experiment and evaluation provide insight into the genetic properties of hybrid populations of three cultivars of white lupine BGR6305, WAT, and NORT486. The highest positive hypothetical (17.76%-94.73%) and true heterosis (11.0-81.76%) was found in the crosses BGR6305 × NORT486 and BGR6305 × WAT regarding plant height, seeds number, seed weight per plant, 1000 seeds mass, and in BGR6305 × WAT – for pods number (97.09%, 90.61%).

In F1 of hybrids BGR6305 × NORT486 and BGR6305 × WAT, the inheritance of plant height, seeds weight, and 1000 seeds mass was positively predominant. Negative dominance and predominance were established in WAT × BGR6305 for plant height (-7.41) and 1000 seed mass (-0.69) and in NORT486 × BGR6305 and BGR6305 × NORT486 for pods number (-1.95, -2.99).

In most hybrids, epistatic gene interactions played a greater role in the inheritance of traits. High coefficients of heritability in a broad sense were found as follows: in NORT486 × BGR6305 and WAT × BGR6305 for plant height (94%, 71%), seeds number (61%, 62%) and 1000 seeds mass (96%, 93%); in BGR6305 × WAT for pods number (83%) and in WAT × BGR6305 for seed weight per plant (55%).

The phenotypic expression of the traits of plant height, pods number and seeds number in BGR6305 × WAT, as well as seed weight per plant in BGR6305 × WAT and WAT × BGR6305 was genotypically determined. To achieve faster results in these accessions, multiple individual selection should be carried out in the early hybrid progenies (F2 - F3). Regarding 1000 seeds mass, breeding success (through mass selection) can be achieved in later hybrid generations.

Transgressions with high norm and frequency were established in hybrids WAT × BGR6305 – for plant height and 1000 seeds mass, in BGR6305 × NORT486 and BGR6305 × WAT – for pods number, seeds number and seed weight. The resulting material will be used to create highly productive cultivars of white lupine.

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## IZGLEDI ZA OPLEMENJIVANJE I PROUČAVANJE HETEROZISA ZA PRINOS I KOMPONENTE PRINOSA HIBRIDA BELE LUPINE (*Lupinus albus* L.)

Natalija Anastasova GEORGIEVA<sup>1</sup>, Valentin Ivanov KOSEV<sup>1</sup>, Vera Miloševa POPOVIĆ<sup>2\*</sup>

<sup>1</sup>Institut za krmno bilje, Pleven, Poljoprivredna akademija, Bugarska

<sup>2</sup>Institut za ratarstvo i povrtarstvo, Novi Sad, Srbija

### Izvod

Studija je sprovedena u periodu 2019-2023 godine sa sortama bele lupine (NORT486, BGR6305 i VAT) i njihovim hibridima (NORT486 × BGR6305; BGR6305 × NORT486; BGR6305 × VAT; VAT) × BGR6305 u generaciji. Definisani su sledeći parametri: efekat heterozisa u F1, inbred depresija, stepen dominacije u F1 i F2, transgresija, dominacija, epistaza, koeficijent nasleđivanja u širem i užem smislu, koeficijent efektivnosti mase genotipova po fenotipskom ponašanju utvrđeno je svojstvo, citoplazmatski efekat. Najveći pozitivni hipotetički (17,76%-94,73%) i pravi heterozis (11,0-81,76%) pronađen je kod ukrštanja BGR6305 × NORT486 i BGR6305 × VAT u pogledu visine biljke, broja semena, težine semena po biljci, mase 1000 semena i BGR6305 × VAT – za broj mahuna (97,09%, 90,61%). U F1 hibrida BGR6305 × NORT486 i BGR6305 × VAT pozitivno je dominiralo nasleđivanje visine biljke, težine semena i mase 1000 semena. Negativna dominacija i prevlast utvrđena je u VAT × BGR6305 za visinu biljke (-7,41) i masu 1000 semena (-0,69) i u NORT486 × BGR6305 i BGR6305 × NORT486 za broj mahuna (-1,95, -2,99). Kod većine hibrida, epistatičke interakcije gena su igrale veću ulogu u nasleđivanju osobina. Genotipski je određena fenotipska ekspresija osobina visine biljke, broja mahuna i broja semena u BGR6305 × VAT, kao i težine semena po biljci u BGR6305 × VAT i VAT × BGR6305. Da bi se postigli brži rezultati u ovim akcesijama, potrebno je izvršiti višestruku individualnu selekciju u ranim hibridnim potomstvima (F2 - F3). Što se tiče mase 1000 semena, uspeh oplemenjivanja (kroz masovnu selekciju) se može postići u kasnijim hibridnim generacijama.

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