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# Inheritance of Some Quantitative Traits in Common Bean Cross (BAT 477 X Dobroudjanski Ran)

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### Abstract

Studies were conducted in the period 2011 - 2014. Biometric analysis of the quantitative traits was performed on 50 plants from parents,  $F_1$  and  $F_2$ -generation of the cross BAT 477 X Dobroudjanski ran. Inheritance in a wide (H<sup>2</sup>) and narrow sense (h<sup>2</sup>) was established by Mahmud and Kramer (1951) and Warner (1952). The number of effective genes (n<sub>E</sub>), controling traits was determined by Wright (1968). *Overdominant inheritance* in the  $F_1$ -generation was found for the traits: height of the first pod placement, height of the plants and number of branches. *Incomplete dominance* occurs in the inheritance of traits - mass of plants with pods, number of pods per plant, number of fruit branches, mass of pods with seeds, number of seeds, seed weight and length of pods. The most strong heterosis effect was manifested in the traits - number of branches, plant height, length of the pods, number of pods per plant and a thickness of the seeds. The highest values for criteria H<sup>2</sup> and h<sup>2</sup> in F<sub>1</sub> and F<sub>2</sub>-generations were established for the traits - seed weight, number of pods and number of seeds per plant, thickness and length of the seeds. A higher value of H<sup>2</sup> and h<sup>2</sup> in F<sub>1</sub>-generation also has the trait mass of the pods with seeds, while in F<sub>2</sub>-generation - number of fruit branches and height of the first pod placement. Highest number of effective genes were reported in the control of traits: number of pods (4-5 genes); number of fruit branches and mass of the pods with seeds (2 - 3 genes), as well as the thickness of seeds (3-4 genes).

Key words: common bean, inheritance, Phaseolus vulgaris L., quantitative traits

## Introduction

A favourable combination of traits in one genotype that determine the productive potential of plants is very important for practical breeding. In this connection, one of the main methodological problems of breeding is the study of relationships between quantitative traits determining plant productivity (Dimova and Svetleva, 1992).

The term 'heritability', that has a great application in quantitative genetics and breeding, determines how much of total variation of the trait is due to genetic reasons. As lower part of the variation is due to external influences and as greater is the proportion of variation determined by genetic causes, the more secure is the success of the breeding process because its effectiveness depends on the extent to which quantitative traits are transmitted from parents to progeny, and this is determined by the genotype and genetic effect on substantiating traits. Therefore, for selection of some trait, the information of its heritability (i.e. variation caused by genetic reasons) has great importance (Genchev, 1975).

According to Robinson (1966) traits can be classified in three groups: with low (5-10%), medium (10-30%) and high heritability (30-60%).

There are two types of heritability: heritability in wide and heritability in narrow sense.

Heritability in a wide sense means a ratio between variation due to genetic causes and full phenotypic variation.

This heritability is important for the first stage of the breeding process when selecting lines and cultivars that reproduce searching trait, but that heritability is only valid for the conditions under which is observed that trait.

Heritability in a narrow sense means the ratio between variation due to the additive genes and full phenotypic variation. According to Allard (1960) under the term 'heritability' should be understood only that part of the observed variability of the trait that is due to the additive effect of genes.

Heritability in a narrow sense is important for the second stage in the breeding process, when we combined genotypes by some trait, in order to enhance its value.

The most characteristic feature of the quantitative traits is their varying, which is continuously and is due to two factors - the large number of genes that determine them and the strong influence of the environmental conditions on them.

According to Genchev et all. (1975) in the case of d/a < 1 was established incomplete dominance, while d/a = 1 was recorded complete dominance of the studied trait. When  $F_1 > P_{1, 2}$  and d/a > 1 - has overdominance. In these formulas, (d) represents the deviation of  $F_1$  to MP (the average value between that of the two parents), while (a) = (P1 - P2) / 2.

The aim of this study was to determine the mode of inheritance of some quantitative traits in common bean cross between the genotypes BAT 477 X Dobrudjanski ran. This goal was inspired by the fact, that the parental forms in this cross have some clear contrasting quality traits and BAT 477 is widely used as a standard for study of drought tolerance in common beans.

## Materials and methods

The studies were conducted during the period 2011 - 2014 year.

Biometrical analysis of the traits was conducted on 50 plants of the parental forms,  $F_{1-}$  and  $F_{2-}$ generations of the cross between the genotypes BAT 477 X Dobrudjanski ran.

Methodology for determining the studied traits is described in the instruction of Genchev and Kiryakov (1994).

Significance of differences between genotypes,  $F_1$  and  $F_2$ -generations were detected by "t" criterion of Student (Shanin, 1977) at levels of significance  $P_{5\%}$ ,  $P_{1\%}$  and  $P_{0,1\%}$ .

The coefficient of inheritance in wide sense  $(H^2)$  was calculated by the method of Mahmud and Kramer (1951) and in narrow sense  $(h^2)$  – by the method of Warner (1952).

The number of effective genes controlling quantitative traits was calculated by the formula of Wright (1968) - n<sub>E</sub> = ( $\mu$ P<sub>2</sub> -  $\mu$ P<sub>1</sub>) / 8 ( $\sigma$ <sup>2</sup><sub>F2</sub> -  $\sigma$ <sup>2</sup><sub>F1</sub>), where:

 $n_{E}$  is the number of effective genes;  $\mu P_{1}$  and  $\mu P_{2}$  are average values of both parents;  $\sigma^{2}_{F1}$  and  $\sigma^{2}_{F2}$  - are variances of  $F_{1}$ - and  $F_{2}$ -generations.

#### **Results and discussion**

The results of the conducted biometrical analysis of quantitative traits, studied in parent forms and  $F_1$ -generation of the hybrid combination between genotypes BAT 477 x Dobrudjanski ran are presented in Table 1.

It was found that the plants of the F<sub>1</sub>generation significant exceed parental plants by the trait height of the plants. A clear overdominance (d/a > 1) was manifested and marked heterosis effect (118.72%). Coefficients of heritability in both wide and narrow sense, are relatively low. These results being in line with those obtained from Savova (1979) and Coyne (1965) in their studied intervarietal crosses.

According to Bliss (1971) when crossing indeterminant and determinant plants, the plant height and habitus are controlled by two epistatic genes and higher plants dominated. Other authors found that the dominance of higher plants over lower was controlled by one gene (Ram and Prasad, 1985) or by polygenic system (Petrova, 1985 a, b). Ortega (1968) considers that the high stem is determined by a dominant gene and several modifier genes.

Mitranov (1983), Nienhuis and Singh (1986 a, b) also reported significant heterosis effect on the appearance of the trait height of plants.

Coyne (1965) found that, in one of the cases, the heterosis appeared as a result of the interaction between the traits - length of the internodes and number of nodes, while in another case the heterosis appeared as a result due to the increase of only one component - the length of the internodes, or the number of nodes.

Dominance and overdominance of higher plant reported Ghaderi and Adams (1981), Radkov and Mitranov (1983), Petrova (1985 a, b), Svetleva and Dimova (1992).

The same pattern was observed for the trait - number of branches per plant. The number of branches per plant of  $F_1$ -generation exceeds those reported of both parents, although the difference in terms of maternal parent - BAT 477 is unproven. Te ratio d/a was 1.68, which is a clear indication for manifestation of overdominance (d/a > 1). It is also found high heterosis effect as plants of  $F_1$ -generation have bigger number of branches than those of the parent with the higher value. A mean of medium to low degree of heritability, in both wide and narrow sense, was established.

In the analyzing cross, where BAT 477 was a maternal parent and Dobrudjanski ran was a paternal, only for the trait - mass of the seeds per plant, hybrids of  $F_1$ -generation shown significant

lower value of the trait ( $P_{0,1\%}$ ). The ratio d/a was 0.37, indicating incomplete dominance (d/a < 1) in inheritance of the trait - mass of seeds. Heritability in wide sense was high - 33,34, and in narrow sense was medium - 25.07%. Heterosis effect was with the lowest value, compared to those of all other traits (28.99%).

The ratio d/a was (- 4.87) for the trait - height of the first pod betting, indicating that the higher first pod betting of father's parent incomplete dominated on the lower one, reported for the maternal parent.

It was found an overdominance of the parent with the lower value of the trait.

The level of heritability in wide sense was low to medium, and the heterosis effect was 52.92%.

Medium to high degree of heritability was reported for the traits - mass of the plant with pods, number of fruiting branches, number of pods per plant, weight of pods with seeds, number of seeds per plant and average length of pods. Heritability coefficients were from 21.69% to 29.31%. It was found incomplete dominance for studied traits and the ratio d/a was less than 1. The estimated heterosis effect, except for the trait number of fruiting branches and number of seeds per plant, was greater than 50%.

As regards to the traits characterizing the particle size of the seeds (Table 2) was shown that the plants from the  $F_1$ -generation formed seeds with significant greater length than those of the maternal parent – BAT 477.

The coefficient of heritability was medium - 28.82%, and the reported heterosis effect was 78.14%. Plants of the hybrid generation formed seeds with width of the level of BAT 477. Although paternal parent has wider seeds, but the difference was insignificant. The ratio d/a was (- 1.00), which indicates that lesser width characteristic of the maternal parent (BAT 477) completely dominates over that exhibited by the paternal parent.

It was found a moderate level of heritability in wide sense - 24.20% and low - in narrow sense. Heterosis effect was 76.9%.

The trait - thickness of the seeds was characterized by incomplete dominance, a relatively high coefficient of heritability in wide sense and higher heterosis effect, in comparison to the traits - length and width of seeds.

In table 3 are shown the mean values and their errors, variation coefficients and coefficients of heritability of both parental forms - BAT 477 and Dobrudjanski ran, as well as the hybrid populations in  $F_2$ -generation, divided into two groups - like the maternal and paternal parent.

Maternal parent - BAT 477 was characterized by a lower variability of almost all analyzed traits,

compared to the paternal parent - Dobrudjanski ran. The same pattern applies to the choicest plants from  $F_2$ -generation resembling to the maternal and paternal parent.

Plants from F<sub>2</sub>-generation were with a greater height, a greater number of branches and larger mass of seeds, in comparison to the both parental pairs. With intermediate expression were the traits - mass of plants with pods, height of the first pod placement, number of fruiting branches, number of pods, mass of pods with seeds, seed number and average length of pods. Variability of traits in F<sub>2</sub>-generation was in the range - from 17.5 % to 28.5 %. As more variable were the traits - number of fruit branches, number of pods, seed weight and height of the first pod placement. Higher values of the heritability coefficients were also reported for them.

This means that the majority of their variation was determined by genetic causes and the selection on the basis of these traits would be a good perspective.

For traits length, width and thickness of the seeds (Table 4) with the highest coefficient of heritability in wide sense was the trait - length of the seeds.

The find coefficient of heritability in narrow sense (h<sup>2</sup>), has higher value for the trait - thickness of the seeds.

The coefficient of heritability in narrow sense (h<sup>2</sup>), has importace to the second stage in the breeding process, when combined genotypes determined the trait in order to its improvement.

It was found that quantitative traits have complex genetic control. They have polygenic control and difficult can be determine the exact number of genes controlling them. By statistical methods we can determine the number of effective genes that have the greatest impact on the formation and manifestation of quantitative traits (Wright, 1968).

It was established, from our studies, that the largest number of effective genes were reported in the control of the traits: number of pods (4-5 genes); number of fruiting branches and mass of pods with seeds (2-3 genes), as well as the thickness of the seeds (3-4 genes).

Genetic control of the traits – mass of plants with pods, number of branches, number of seeds, average length of the pods and length of the seeds were controlled by one effective gene (Tables 3 and 4).

Traits		$\overline{X} \pm \mathbf{S} \overline{X}$	D	t	Significance	d/a	H <sup>2</sup>	h²	Heterosis effect, %
Height of plants,	P <sub>1</sub>	48,33 ± 2,32	9,56	3,03	++				
in cm	P <sub>2</sub>	48,76 ± 1,19	9,13	3,75	+++				
	F <sub>1</sub>	57,89 ± 2,13				1,5	13,61	0,85	118,72
Mass of plants with	P <sub>1</sub>	70,65 ± 2,79	- 34,28	8,93					
pods, in g	P <sub>2</sub>	18,01 ± 1,13	18,36	6,37	+++				
	F <sub>1</sub>	36,37 ± 2,65				0,3	21,76	2,06	51,49
Number of branches	P <sub>1</sub>	3,89 ± 0,15	0,74	1,48	n.s				
per plant	P <sub>2</sub>	1,74 ± 0,15	2,89	11,11	+++				
	F <sub>1</sub>	4,63 ± 0,22				1,68	12,29	2,16	119,02
Height of first pod	P <sub>1</sub>	10,56 ± 0,20	- 1,57	4,14					
placement, in cm	P <sub>2</sub>	16,97 ± 0,73	- 7,98	9,97					
	F <sub>1</sub>	8,99 ± 0,33				- 4,87	15,44	4,14	52,92
Number of fruit	P <sub>1</sub>	5,26 ± 0,06	0,52	5,78					
brunches	P <sub>2</sub>	2,37 ± 0,08	2,37	21,54	+++				
	F <sub>1</sub>	4,74 ± 0,07				0,63	29,31	10,29	29,92
Number of pods per	P <sub>1</sub>	9,37 ± 0,33	- 2,00	4,54					
plant	P <sub>2</sub>	3,74 ± 0,34	3,63	4,90	+++				
	F <sub>1</sub>	7,37 ± 0,31				0,92	22,80	16,28	78,55
Mass of pods with	P <sub>1</sub>	13,36 ± 0,20	- 6,13	15,71					
seeds, in g	P <sub>2</sub>	3,12 ± 0,06	4,11	15,20	+++				
	F <sub>1</sub>	7,23 ± 0,37				0,60	21,69	17,35	54,04
Number of seeds per	P <sub>1</sub>	37,16 ± 0,91	-19,06	17,02					
plant	P <sub>2</sub>	7,23 ± 0,07	10,87	16,22	+++				
	F <sub>1</sub>	18,10 ± 0,67				0,24	28,60	19,47	48,71
Mass of seeds per	P <sub>1</sub>	9,04 ± 0,17	-5,37	29,80					
plant, in g	P <sub>2</sub>	12,66 ± 0,11	-8,99	11,09					
	F <sub>1</sub>	3,67 ± 0,06				0,37	- 33,34	25,07	28,99
Average length of	P <sub>1</sub>	9,53 ± 0,35	-1,99	3,90					
pods, in cm	P <sub>2</sub>	7,50 ± 0,360	0,01	1,90	n.s				
	F <sub>1</sub>	7,54 ± 0,370				0,28	22,34	8,86	79,11
			t P <sub>5%</sub> =	2,021; t P <sub>1</sub>	<sub>%</sub> = 2,704; t P <sub>0,1%</sub> = 3,	551			

Table 1. Character of trait dominance in F<sub>1</sub>-generation of common beans in the cross between the genotypes BAT 477 x Dobrudjanski ran

Traits		$\overline{X} \pm S\overline{X}$	D	t	Significance	d/a	H²	h²	Heterosis effect,		
									%		
Length of seeds, in	P1	1,053 ± 0,012	0,131	5,69	+++						
cm	P <sub>2</sub>	1,510 ± 0,007	- 0,326	16,30							
	F <sub>1</sub>	1,184 ± 0,021				0,39	28,82	3,54	78,14		
Width of seeds,	P1	0,700 ± 0,300	0		n.s						
in cm	P <sub>2</sub>	0,910 ± 0,007	- 0,210	0,56	n.s						
	F <sub>1</sub>	0,700 ± 0,100				-1,00	2,20	3,32	76,9		
Thickness of seeds,	P1	0,426 ± 0,011	0,026	1,85	n.s						
in cm	P <sub>2</sub>	0,558 ± 0,012	- 0,106	7,57							
	F <sub>1</sub>	0,452 ± 0,012				0,61	27,27	4,14	80,64		
t $P_{5\%}$ = 2,021; t $P_{1\%}$ = 2,704; t $P_{0,1\%}$ = 3,551											

## **Table 2**. Inheritance in F<sub>1</sub>-generation of the traits, characterizing the common bean size of the seeds

 Table 3. Inheritance in F2-generation of common bean quantitative traits

	Cultivars and hybrid combinations												
	P1 BAT 4	77	P <sub>2</sub> Dobrudjanski		F <sub>2</sub> BAT (plants	F <sub>2</sub> BAT 4 (plants are lik	ne						
Indicators Traits	$\overline{X} \pm \mathbf{S}\overline{X}$	S%	$\overline{X} \pm \mathbf{S}\overline{X}$	S%	$\overline{X} \pm \mathbf{S} \overline{X}$	S%	H <sup>2</sup>	h²	$\overline{X} \pm S\overline{X}$	S%	H <sup>2</sup>	h²	
Height of plants, in cm	48,33 ± 2,32	16,2	48,76 ± 1,19	24,5	54,75 ± 1,85	18,3	23,5	10,1	56,45 ± 2,00	20,4	22,5	8,6	0,001
Mass of plants with pods, in g Number of branches per plant	70,65±2,79 3,89±0,15	20,3 20,9	18,01±1,13 1,74±0,15	21,0 28,6	45,25±2,05 4,55±0,25	19,5 22,0	24,5 25,2	14,5 16,5	48,30±1,95 4,75±0,28	20,0 21,7	26,5 28,4	15,0 8,7	- 0,30 - 0,45
Height of first pod placement, in cm Number of fruit	10,56±0,20 5,26±0,06	10,9 19,7	16,97±0,73 2,37±0,08	18,1 19,1	15,25±0,75 4,5±0,05	20,0 18,5	25,4 25,0	19,5 18,5	15,95±0,80 5,05±0,07	28,5 26,5	27,3 32,5	20,1 24,5	0,07 - 2,89
brunches Number of pods per plant	9,37±0,33	16,2	3,74±0,34	21,1	7,5±0,25	19,5	37,0	29,0	8,2±0,35	20,5	34,5	27,9	4,16
Mass of pods with seeds, in g	13,36±0,20	17,1	3,12±0,06	21,7	10,5±0,35	17,5	11,5	5,8	9,9±0,40	19,5	9,5	6,1	2,59
Number of seeds per plant	37,16±0,91	20,0	7,23±0,07	19,3	25,5 ± 0,35	21,5	25,0	14,5	24,5 ± 0,40	20,5	23,0	10,5	0,66
Mass of seeds per plant, in g	9,04 ± 0,17	15,1	12,66±0,81	21,4	12,9±0,09	18,5	33,5	27,0	9,3 ± 1,50	20,5	38,6	25,0	0,01
Average length of pods, in cm	9,53±0,35	14,2	7,5±0,36	18,6	9,5 ± 0,35	17,5	2,7	20,4	8,8 ± 0,45	19,5	39,4	27,5	- 0,19

	Cultivars and hybrid combinations												
	P1 BAT	477	P2 Dobrudja	<b>F</b> <sub>2</sub> <b>BAT 477 x Dobrudjanski ran</b> <b>Dobrudjanski ran</b> (plants are like parent BAT 477)					F <sub>2</sub> BAT	ne			
Indicators	$\overline{X} \pm \mathbf{S}\overline{X}$	S%	$\overline{X} \pm \mathbf{S} \overline{X}$	S%	$\overline{X} \pm \mathbf{S}\overline{X}$	S%	H²	h²	$\overline{X} \pm \mathbf{S} \overline{X}$	S%	H²	h²	
Length of seeds, in cm	1,05 ± 0,012	10,5	1,51±0,07	10,2	1,55±0,09	11,3	23,5	4,6	1,55 ± 0,10	12,4	27,0	3,8	0,30
Width of seeds, in cm	0,70 ± 0,03	8,5	0,91±0,02	10,2	0,75±0,04	10,5	11,7	6,0	0,67±0,02	15,0	9,8	5,2	0,14
Thickness of seeds, in cm	0,43±0,01	11,5	0,56±0,01	11,9	0,50±0,01	12,7	12,6	10,0	0,47±0,02	13,0	15,0	10,3	3,30

Table 4. Inheritance in F<sub>2</sub>-generation of the traits, characterizing the common bean size of the seeds

For the other traits - plant height, height of the first pod placement, mass and width of seeds per plant can be supposed that responsible for their formation is also one gene but  $n_E$  values are very low.

## Conclusion

Based on the obtained results from our study, can be drawn the following conclusions:

**1.** Overdominant inheritance in  $F_{1-}$  generation of the cross between common bean genotypes BAT 477 x Dobrudjanski ran, was found for the traits - height of the first pod placement, plant height and number of branches.

2. Incomplete dominance occurs in inheritance of quantitative traits - mass of plants with pods, number of pods per plant, number of fruit branches, mass of pods with seeds, number of seeds, mass of seeds and average length of pods.

**3.** The highest values for criteria  $H^2$  and  $h^2$  in F<sub>1</sub> and F<sub>2</sub>-generations were found for the traits – mass of seeds, number of pods and number of seeds per plant, thickness and length of the seeds. A higher value of  $H^2$  and  $h^2$  in F<sub>1</sub>-generation also has the trait mass of pods with seeds, while in F<sub>2</sub>-generation – number of fruit branches and height of the first pod logging.

**4.** The strongest heterosis effect in  $F_{1-}$  generation occurs for the traits - number of branches, plant height, average length of pods, number of pods per plant, and thickness of seeds.

**5.** The largest number of effective genes were reported in the control of quantitative traits: number of pods (4-5 genes); number of fruit branches and mass of the pods with seeds (2-3 genes), as well as the thickness of seeds (3-4 genes).

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