UDC 575.630
https://doi.org/10.2298/GENSR2502315K
Original scientific article

GENETIC ANALYSIS OF QUANTITATIVE TRAITS IN FORAGE PEA GENOTYPES

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Kosev V., V. Vasileva, V. Popović (2025). *Genetic analysis of quantitative traits in forage pea genotypes*.- Genetika, Vol. 57, No. 2, 315-331.

The study aimed at analyze the quantitative traits of pea genotypes through the values of genetic parameters and to identify the traits that determine the productivity of F_1 and F_2 hybrid plants. Three year field experiment was conducted in the Institute of Forage Crops - Pleven, Bulgaria. The crosses (CA1P × L020140; CA1P × Wt6803 and their reciprocal) between pea varieties L020140 - *Pisum sativum ssp. arvense*, Wt6803 - *Pisum sativum var. hiemale* and CA1P - *Pisum sativum ssp. sativum* were studied. Positive true heterosis was detected at crosses L020140 × CA1P and CA1P × L020140 by fresh root weight and nodule weight; CA1P × Wt6803 by root length and nodule weight and CA1P × L020140 by plant height at both limits of the environment. It is evident that the root weight and number of nodules per plant at CA1P × Wt6803 and the weight of fresh biomass at CA1P × L020140 are inherited with a clear positive dominance or over-dominance. The dominance or over-dominance of Wt6803 × CA1P by root length and fresh root weight, number and weight of plant nodules; at CA1P × L020140 by number of nodules and at L020140 × CA1P by weight of nodules per plant were found negative. In more favorable growing conditions, epistatic gene interactions play a greater role in the inheritance of traits and the number of nodules in CA1P × Wt6803 and L020140 × CA1P, and for dense sowing at L020140 × CA1P and CA1P × L020140 by fresh aboveground biomass weight and nodule weight. Dominant gene actions were of greater importance for the number of nodules per plant at Wt6803 × CA1P. High inheritance rates in both environments are characterized by hybrids Wt6803 × CA1P and L020140 × CA1P by fresh root weight and

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number of nodules per plant, and all hybrids by number of nodules. For almost all crosses, the efficiency of the team is negative and at both limits of the environment, which implies that the mass team will be more effective if it starts early in F_4-F_5 and is based on plant height, fresh weight of aboveground biomass and fresh weight of roots.

Keywords: degree of dominance, heterosis, forage peas, inheritance, transgression

INTRODUCTION

Pea (*Pisum sativum* L.) as an important forage crop is grown almost year-round in various parts of the world. Selection of peas is based on yield and its components in hybridization programs. To increase the productive potential of peas, it is desirable to select new genotypes through gene recombination of valuable traits. Therefore, it is necessary to know their type of inheritance and genetic structure (CEYHAN, 2006; SOOD and KALIA, 2006; BURSTIN *et al*., 2007).

Hybridization is one of the main methods for combining different traits and attributes of parental genotypes. The study of heterosis manifestations is important for uncovering patterns of inheritance. The manifestations of heterosis and the inheritance of traits related to plant productivity have been the subject of numerous studies (KALAPCHIEVA, 2008; BORAH, 2009; FADEEV, 2014; KOSEV *et al*., 2023). The diversity of wintering pea forms is not great, while the genetic resources for spring peas are much more diverse. In this regard, the crossing of wintering forms with spring is of great interest. Obtaining such crosses makes it possible to increase the diversity of genetic material in the population and to transmit valuable traits and traits from spring and winter subspecies in a hybrid (BREZHNEVA and BREZHNEV, 2014; POPOVIĆ *et al.*, 2024; LAKIĆ *et al*., 2019; 2022).

The selection of peas to solve this problem is currently an exploration of the gene pool, a targeted search for sources of economically valuable traits and their involvement in the process of crops transformation. In improving the selection process, the most difficult stage is the hybridization and subsequent selection of the hybrid material (BEECK *et al.*, 2008; CEYHAN e*t al.*, 2008; ASHIEV, 2014). The contribution of selection, which is central to the creation and use of new varieties and hybrids, is an increase in yield from 30 to 70% (ZOTIKOV, 2013). Modern pea selection is based on intraspecific hybridization, using the available variety of selected varieties and collecting specimens through the use of individual - group multiple individual selection (BREZHNEVA and BREZHNEV, 2014). For a long time, the genetics and selection of peas are oriented only to the traits of the plants aboveground mass - leaves, flowers, pods, seeds, vegetation period, etc. The genetics of symbiotic traits have recently become a scientific priority (SIDOROVA *et al*., 2010). The information about the regularities of the variability and the interrelation of quantitative traits under certain conditions makes it possible to determine the value of each trait used in the selection (VYUSHKOV *et al*., 2012).

Studies of the patterns of inheritance of valuable traits and the use of methods of mathematical analysis in the genetics of quantitative trait contribute to the purposeful creation of the initial material (KOSTILEV and LISENKO, 2011). It is generally accepted that one of the parental forms at crossing should be a variety or line that is well adapted to local soil and climatic conditions. It is usually used as a maternal component. The situation when choosing the second parent component to cross is relatively more complicated. A number of approaches are used in breeding practice for this purpose. Typically, forms that contrast sharply with each other in terms of productivity determinants are used, which greatly increases the possibility of obtaining highly yielding genotypes. Generally, first- and second-generation hybrids (F1 and F2) are analyzed for some of the main features, such as plant height, height of the first pod, number of fertile units per plant, number of seeds, number of pods per plant, mass per 1000 seeds, mass of the seeds of one plant.

The purpose of the study was to analyze the quantitative traits of pea genotypes through the values of genetic parameters and to vary the group of traits that determine the productivity of F_1 and F_2 hybrid plants.

MATERIALS AND METHODS

The study was conducted in 2014-2016 in the experimental field of the Institute of Forage Crops - Pleven, Bulgaria. The following crossings have been done between the pea varieties L020140 - *Pisum sativum ssp. arvense* (Czech Republic), Wt6803 - *Pisum sativum var. hiemale* (Poland), CA1P - *Pisum sativum ssp. sativum*: CA1P × L020140; CA1P × Wt6803 as well as their reciprocal combinations (Table 1). The parental forms (P1 and P2) and the first and second hybrid generations (F1 and F2) were studied. The sowing of the selection material was done manually according to the scheme P1, P2, F1, F2 at optimum terms according to the technology of cultivation of the crop at a sowing distance of 50/5 cm (dense sowing), 50/10 cm (sparse sowing) and depth of sowing 5 cm. Plant material from aboveground and root biomass of parental and hybrid forms has been analyzed. Biometric measurements were made on 10 plants of each genotype by the indicators: in the beginning of flowering stage - plant height (cm), fresh aboveground weight mass (g), root length (cm), fresh root mass weight (g)), number of nodules per plant, weight of nodules per plant (g).

Table 1. Distinctive features of the investigated genotypes

Traits/Variety	CA1P	L020140	Wt6803
Dense sowing			
Plant height, cm	37.98a	53.99b	58.29c
Fresh weight (leaves+stems), g	16.01a	18.05b	23.45c
Root length, cm	8.60a	8.47b	11.37c
Root fresh weight, g	0.58a	0.58a	1.25b
Nodule number	15.80a	24.53b	31.27c
Nodule weight, g	0.09a	0.20b	0.20b
Sparse sowing			
Plant height, cm	47.48a	67.50b	72.87c
Fresh weight (leaves+stems), g	18.41a	20.75b	26.97c
Root length, cm	9.31a	9.16b	12.30c
Root fresh weight, g	0.60a	0.59a	1.29b
Nodule number	16.74a	25.99b	33.12c
Nodule weight, g	0.10a	0.22b	0.22b

Mean followed by the same letter(s) did not differ significantly at 5 % level

For all the characteristics studied an average arithmetical (×); heterosis effect in F1 - (hypothetic and true), inbred depression by OMAROV (1975), degree of dominance in F1 (hp1) and in F2 (hp2) by ROMERO and FREY (1973), coefficient of inheritance in narrow (H2) and wide sense (h2) by KONSTANTINOV *et al.* (1979) in F2 were calculated. Using method of SOBOLEV (1976) the characteristic of transgression (Tn); number of genes, in which the parents differ (N); dominance (D); epistasis (E) and coefficient of effectiveness of the mass of genotypes by phenotypical performance of the trait (Pp) were found, cytoplasmic effect (re) according to REINHOLD (2002).

A positive value of pe (pe> 0) means that paternal inheritance factors have a greater influence on the manifestation of the trait, and a negative (pe <0) influence on maternal cytoplasmic heredity (cytoplasmic effect). The orthogonal regression method was applied to identify the phenotype by genotype described by Kramer (DRAGAVTCEV, 1993), showing the possibility of estimating pea hybrids by genetic-physiological systems at different environmental limits. The coordinate system allows identifying the genotype of an individual organism by phenotype. In this case, the relative influence of genotype and environment are quantified on a scale of actual trait measurements. All experimental data were processed statistically using the computer software SPSS 13 and Excel for Windows XP.

RESULTS

The data in Table 2 show that inheritance of plant height in compressed sowing with the participation of L020140 as a parent component, over-domination with both positive and negative sign prevails. In crosses between Wt6803 and CA1P, the effect of genes is positively dominant. Hybrid combination Wt6803 × CA1P F1 also revealed maternal cytoplasmic influence on inheritance of the trait (Figure 1), regardless of the method of plant sowing (-6.40; -3.93). All hybrid combinations showed a positive hypothetical heterosis, but only at crosses L020140 × CA1P and CA1P × L020140 a clearly pronounced true heterosis effect (42.18%; 14.84%) was observed. Only the second-generation plants of Wt6803 × CA1P were not depressed according to the study.

The data from the hybridological analysis (Table 4) show that the number of genes affecting the expression of the studied trait by which the parental forms differ varies from 68 (L020140 × CA1P) to 897 (CA1P × Wt6803). Transgression coefficient values are negative for crosses where CA1P is the paternal component. Epistatic gene interactions (except Wt6803 × CA1P) exert a significant influence on the expression of the trait, which suppress the expression of dominant genes, especially with CA1P × Wt6803 (111.46). Low values of inheritance coefficients have been found, indicating that the selection will be more effective in this generation in later generations. The values of the Pp indicator confirm the above trend.

The data in Table 2 show that the fresh aboveground biomass weight from a plant is inherited positively supra-dominantly, with the cross-parent L020140 × CA1P and its reciprocal dominating the higher fresh parental forms. The other two combinations show a similar trend, but the dominance is less pronounced (1.19; 1.21). The cytoplasmic effect is manifested at Wt6803 × CA1P but not at the reciprocal cross. When sowing was diluted, the cytoplasmic effect also shows a reciprocal cross (Figure 1).

Table 2. Biometrical data of the quantitative traits of the investigated crosses, dense sowing

Hybrids	F_1	F_2	Heterosis F_1 (%)		Depression F_2 (%)	Degrees of dominance	
			hypo thetical	Real		in F_1 (h_{p1})	in F_2 (h_{p2})
Plant height							
Wt6803 × CA1P	54a	57c	12.18	-7.36	-5.56	0.58	1.75
CA1P × Wt6803	57b	50b	18.42	-2.21	12.28	0.87	0.37
L020140 × CA1P	54a	47a	17.43	42.18	12.96	-1.00	-0.25
CA1P × L020140	62c	50b	34.83	14.84	19.35	2.00	1.00
Fresh aboveground mass weight							
Wt6803 × CA1P	15.32b	13.92a	-22.35	-4.31	9.14	1.19	3.12
CA1P × Wt6803	15.22b	13.87a	-22.86	-4.93	8.87	1.21	3.15
L020140 × CA1P	12.06a	16.32b	-29.18	-24.67	-35.32	4.87	1.39
CA1P × L020140	12.03a	16.32b	-29.36	-24.86	-35.66	4.90	1.39
Root length							
Wt6803 x CA1P	8.65c	7.97c	-13.37	-23.92	7.86	-0.96	-2.91
CA1P x Wt6803	12.98d	11.88d	29.99	50.93	8.47	-2.16	-2.74
L020140 × CA1P	5.16a	4.24a	-39.54	-39.08	17.83	51.92	132.15
CA1P × L020140	7.22b	6.36b	-15.41	-14.76	11.91	20.23	66.92
Root fresh weight							
Wt6803 × CA1P	0.6a	0.53b	-34.43	-52.00	11.67	-0.94	-2.30
CA1P × Wt6803	1.17b	1.03d	27.87	-6.40	11.97	0.76	0.69
L020140 × CA1P	1.4c	0.37a	141.38	141.38	73.57	-	-
CA1P × L020140	1.64d	0.71c	182.76	182.76	56.71	-	-
Nodule number							
Wt6803 × CA1P	18a	7a	-23.52	-42.44	61.11	-0.72	-4.28
CA1P × Wt6803	30d	22d	27.47	-4.06	26.67	0.84	-0.40
L020140 × CA1P	18a	8b	-10.74	13.92	55.56	0.50	5.57
CA1P × L020140	27c	13c	33.90	70.89	51.85	-1.57	3.28
Nodule weight							
Wt6803 x CA1P	0.06a	0.03a	-58.62	-70.00	50.00	-1.55	-4.18
CA1P × Wt6803	0.13c	0.06c	-10.34	44.44	53.85	0.27	3.09
L020140 × CA1P	0.07b	0.04b	-51.72	-65.00	42.86	-1.36	-3.82
CA1P × L020140	0.16d	0.08d	10.34	-20.00	50.00	0.27	-2.36

Mean followed by the same letter(s) did not differ significantly at 5 % level

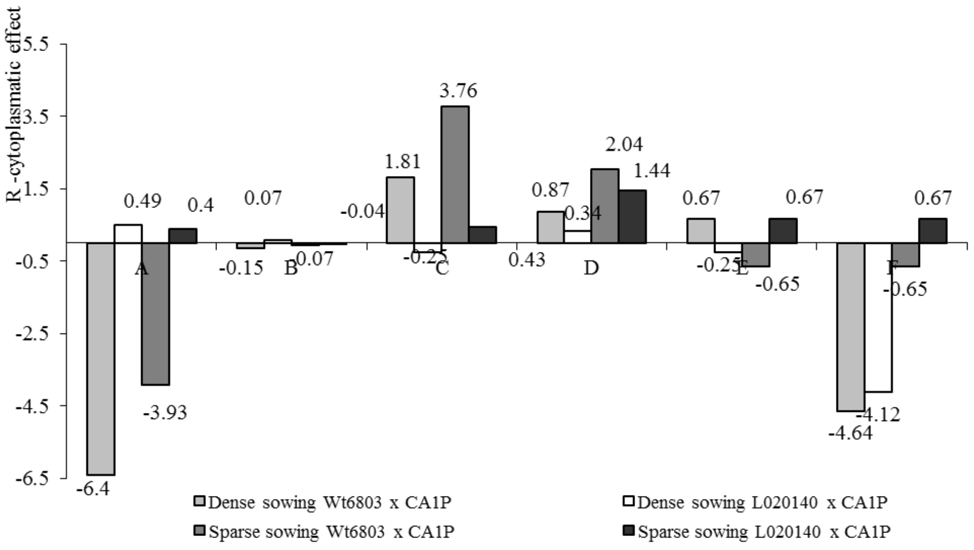

Figure 1. Cytoplasmic effect on inheritance of the traits studied

A – Plant height (cm), B – root length (cm), C - Fresh aboveground mass weight (g), D - Root fresh weight (g), E - Nodule number, F - Nodule weight (g)

In contrast to the plant height trait, the fresh biomass weight shows a marked negative hypothetical heterosis and less pronounced but with the same signs a true heterosis effect. The manifestation of the heterosis effect is probably influenced by the remoteness of the parents used for hybridization. Data on the value of genetic parameters (Table 4) indicate that the number of genes controlling the trait that different parental forms ranged from 87 to 272 (CA1P × Wt6803). At crosses L020140 × CA1P and CA1P × L020140 the dominant effect of the genes (4.94; 5.01) is more clearly expressed, and at CA1P × Wt6803 signifies severe epistasis.

The values of the transgression indicator indicate that, in the decay generations in the CA1P × Wt6803 and CA1P × L020140 hybrids, the available homozygous genotypes may be selected plants that, according to the test indicator, will outperform parents by the weight of fresh biomass. In the L020140 × CA1P crosses parental forms will predominate, and in the Wt6803 × CA1P those with lower weight. Insignificant values for inheritance have been found, indicating that environmental conditions have a strong effect on the determination of the trait. An exception is Wt6803 × CA1P, where the inheritance of this trait is high (0.79).

Biometric data for hybrids grown in dense crops (Table 2) show that a pronounced hypothetical heterosis effect with respect to root length was observed at all crosses, but only at CA1P × Wt6803 was found positive (29.99%). The same cross also exhibits a strong positive true heterosis with respect to this trait. Inheritance of plant root lengths had positive (at L020140

× CA1P and reciprocal) and negative (at CA1P × Wt6803) over-domination, and negative dominance (at Wt6803 × CA1P), as with the parent with lower values, as well as the one with higher values depending on the cross. In hybrids L020140 × CA1P and CA1P × L020140, epistasis has a greater effect on inheritance of the trait.

The results of the hybridological analysis show that the number of genes affecting the manifestation of root lengths by which parental forms differ is very different and ranges from 24 (CA1P × Wt6803) to 1115 (L020140 × CA1P). It is noteworthy that the number of genes is many times higher when CA1P is the paternal form. In cross CA1P × Wt6803, which found action of a large number of dominant genes (23.55), negative epistasis (-8.17) was found, while in all other hybrids it was very strong pronounced. Low values for inheritance coefficients have been found, indicating that the phenotypic manifestation of this trait is strongly influenced by environmental conditions.

The values for the transgression coefficient show differences at the individual crosses with respect to the studied indicator. A positive value was observed at two of the CA1P × Wt6803 (1.85) and L020140 × CA1P (0.10) crosses, but this is negligible, especially for the second hybrid. For other crosses, the coefficients are negative, indicating that plants with shorter root lengths will prevail in decaying generations, which is undesirable. The effectiveness of the selection judging by the negative values of the coefficient "Pp" in the early hybrid generations will not produce the desired result. The results in Table 2 show that, with respect to fresh root weight, positive hypothetical and true heterosis was found in two of the crosses (L020140 × CA1P and reciprocal), with higher values (CA1P × L020140) (182.76). In the second hybrid generation, depression was observed in all plants. Inheritance of root weight was negative (-0.94) at Wt6803 × CA1P and positive dominance at CA1P × Wt6803 (0.76).

The values of the transgression coefficient (Table 4) show that in decaying generations, it is possible (without Wt6803 × CA1P) to select plants with a higher fresh root weight, with a greater probability at CA1P × Wt6803 (0.46). Variation in the number of genes determining the trait was observed - from 1 (CA1P × Wt6803) to 828 (L020140 × CA1P). Epistasis is strongly expressed in all hybrids, which is likely to result in less expression of the sign in future generations. Significant differences in values of inheritance coefficients have been found, indicating that environmental conditions play a large role in determining this trait. The team (Pp) on this basis will be effective in later generations.

The inheritance of the trait number of nodules per plant ranged from negative dominant (CA1P × L020140) and super-dominant (Wt6803 × CA1P) to positive incomplete dominant (CA1P × Wt6803) and dominant (CA1P × Wt6803) with lower parental values. At cross CA1P × L020140, the positive heterosis manifestations are well expressed. A negative true heterosis effect (-42.44%; -4.06%) was observed at the crosses between Wt6803 and CA1P. The values of the transgression coefficient in the indicator of the number of nodules of the plants are different at the individual crosses. For CA1P × Wt6803 (8.22) and CA1P × L020140 (4.58), the coefficients indicate that plants with a greater number of nodules can be selected in decaying generations than the parent varieties. The values for "D" and "E" indicate that at all crosses the phenotypic expression of the trait will be influenced by strongly expressed epistatic interactions.

The number of genes determining the trait was from 203 (CA1P × Wt6803) to 1329 (Wt6803 × CA1P). Both in terms of plant height and number of nodules per plant, low inheritance rates have been established. We can assume that the team on this basis will be effective in later generations. Positive true heterosis with respect to the weight of the nodules per plant (Table 2) was found at CA1P × Wt6803 (44.44%). It turns out that despite the value of the heterosis effect in all crosses, depression is high and approximately similar in magnitude.

The inheritance of nodule weights is negatively over-dominant at Wt6803 × CA1P and L020140 × CA1P, or incompletely dominant in the direction of the parent with lower values, i.e. inheritance of this trait is varied depending on the direction of crossing.

The values for the transgression coefficient are low and show differences at the individual crosses with respect to the weight of nodules per plant. No significant differences were found in the number of genes that differentiated parents by the weight of nodules. Epithelial gene interactions play a major role in expression of the trait. The inheritance coefficient values for this trait are very high for all hybrids (0.76% to 0.94%), but due to the low “Pp” values the selection by weight of nodules is not recommended in early hybrid combinations.

Changes in the environment limit (sparse sowing, Table 3) also show some differences in the response of hybrid plants to the growing medium. In terms of fresh root weight and number of nodules per plant, true heterosis has a negative sign similar to that of the environment limit for dense sowing. In CA1P × Wt6803 plants, depression is negative in both (Table 3) and epistatic gene actions are prevalent in the second generation. The number of nodules at CA1P × Wt6803 was found to be negative, and at the cross CA1P × Wt6803 by the same trait in the second generation, dominant gene actions play a greater role in the manifestation of the trait (0.86).

In terms of plant height, L020140 × CA1P exhibits weak true (2.63%) and negative hypothetical (-12.59%) heterosis, with plants of all hybrids characterized by good vitality in the next generation, judging by the negative values of depression. All hybrids were found to exhibit intermediate inheritance in F1. The value of the degree of dominance in F2 at L020140 × CA1P indicates that the inheritance of the plant height sign is similar to that of restrictive plants.

Based on the weight of fresh plant biomass, it appears that hybrid plants derived from the crossing of the Wt6803 variety with CA1P show a small positive true heterosis effect (8.96%; 2.17%), but they are not depressed. The inheritance type of fresh aboveground biomass weight at L020140 × CA1P is similar at both environment limits, whereas for plants resulting from Wt6803 × CA1P crosses, the gene actions in F1 are negative-over-dominant and in F2 are of non-allelic gene interactions. Along the root length and the nodule weight of the plant, in both environments hybrid plants Wt6803 × CA1P exhibit negative true and hypothetical heterosis. The behavior of its reciprocal cross is similar, exhibiting positive true heterosis on both traits. For these two traits, in general, all plants are less depressed, with the CA1P × Wt6803 rate of depression even negative (-3.42%; -14.29%).

The transgression coefficients (Tn) for the traits of the plants grown under sparse sowing (Table 5) are very similar to those under limiting environmental conditions, at CA1P × Wt6803. CA1P × L020140 plant height and fresh aboveground biomass weight values are slightly better expressed. It is noteworthy that their reciprocal crosses in both environments have a negative transgression rate. This may suggest that the selection of genotypes suitable for forage should be performed on hybrids with CA1P as the maternal component.

Table 3. Values of the gene parameters for the quantitative traits of the investigated crosses in F_2 generation, sparse sowing

Hybrids	F_1	F_2	Heterosis F_1 (%)		Depression F_2 (%)	Degrees of dominance	
			Hypo thetical	real		in F_1 (h_{p1})	in F_2 (h_{p2})
Plant height							
Wt6803 × CA1P	55a	57a	-8.60	-24.52	-3.64	-0.41	-0.50
CA1P × Wt6803	58b	78d	-3.61	-20.41	-34.48	-0.17	2.81
L020140 × CA1P	59c	64b	2.63	-12.59	-8.47	0.15	1.30
CA1P × L020140	63d	68c	9.58	32.69	-7.94	-0.55	-2.10
Fresh aboveground mass weight							
Wt6803 × CA1P	17.62a	21.89b	-22.34	-34.67	-24.23	-1.18	-0.37
CA1P × Wt6803	17.62a	19.45a	-22.34	-34.67	-10.39	-1.18	-1.51
L020140 × CA1P	20.06c	27.09c	2.45	8.96	-35.04	-0.41	-12.84
CA1P × L020140	18.81b	27.09c	-3.93	2.17	-44.02	0.66	-12.84
Root length							
Wt6803 × CA1P	9.36a	10.67b	-13.37	-23.90	-14.00	-0.97	-0.18
CA1P × Wt6803	14.05c	14.53d	30.03	50.91	-3.42	-2.17	-4.98
L020140 × CA1P	11.71b	8.09a	26.80	27.84	30.91	-33.00	30.53
CA1P × L020140	14.93d	12.14c	61.67	62.99	18.69	-75.93	-77.47
Root fresh weight							
Wt6803 × CA1P	0.62a	0.18a	-34.39	-51.94	70.97	-0.94	-4.43
CA1P × Wt6803	1.21b	1.35d	28.04	-6.20	-11.57	0.77	2.35
L020140 × CA1P	1.41c	0.36b	135.00	135.00	74.47	-163.00	94.00
CA1P × L020140	2.75d	0.70c	358.33	358.33	74.55	431.00	42.00
Nodule number							
Wt6803 × CA1P	19a	17b	-23.79	-42.63	10.53	-0.72	-1.94
CA1P × Wt6803	32c	37d	28.36	-3.38	-15.63	0.86	2.95
L020140 × CA1P	24b	14a	12.33	43.37	41.67	-0.57	3.18
CA1P × L020140	42d	24c	96.58	150.90	42.86	-4.46	-1.14
Nodule weight							
Wt6803 × CA1P	0.06	0.05a	-62.50	-72.73	16.67	-1.67	-3.67
CA1P × Wt6803	0.14	0.16d	-12.50	40.00	-14.29	0.33	0.01
L020140 × CA1P	0.08	0.05a	-50.00	-63.64	37.50	-1.33	-3.67
CA1P × L020140	0.21	0.11c	31.25	-4.55	47.62	0.83	-1.67

Mean followed by the same letter(s) did not differ significantly at 5 % level

Table 4. Values of the gene parameters for the quantitative traits of the investigated crosses in F_2 generation, dense sowing

Crosses/ Indicators	T_n	N	D	E	H^2	Pp
Plant height						
Wt6803 × CA1P	-9.31	115	35.04	-28.09	0.20	-8.84
CA1P × Wt6803	10.25	897	-15.25	111.46	0.01	-17.72
L020140 × CA1P	-7.01	68	-3.99	12.08	0.10	-0.02
CA1P × L020140	9.23	99	0.04	13.06	0.09	-2.12
Fresh aboveground mass weight						
Wt6803 × CA1P	-3.06	87	-28.38	21.74	0.79	-7.35
CA1P × Wt6803	3.94	272	-86.51	65.90	0.17	-22.62
L020140 × CA1P	-0.59	99	4.94	-16.48	0.09	-0.58
CA1P × L020140	1.45	100	5.01	-16.60	0.09	-0.58
Root length						
Wt6803 × CA1P	-1.33	394	-116.34	93.24	0.46	-32.69
CA1P × Wt6803	1.58	24	23.55	-8.17	0.32	-8.35
L020140 × CA1P	0.10	1115	-353.41	267.01	0.22	-103.46
CA1P × L020140	-0.02	568	-161.10	132.42	0.63	-45.11
Root fresh weight						
Wt6803 × CA1P	-0.32	212	-70.06	52.04	0.68	-19.58
CA1P × Wt6803	0.46	1	1.58	0.39	0.12	0.10
L020140 × CA1P	0.02	828	-103.42	154.51	0.54	-10.21
CA1P × L020140	0.03	370	-19.25	57.04	0.22	-3.49
Nodule number						
Wt6803 × CA1P	-7.55	1329	-326.52	296.70	0.95	-74.01
CA1P × Wt6803	8.22	203	-25.83	39.08	0.83	-2.09
L020140 × CA1P	-4.20	1212	-278.88	265.89	0.51	-63.50
CA1P × L020140	4.58	952	-161.43	192.52	0.92	-29.53
Nodule weight						
Wt6803 × CA1P	-0.05	397	-122.94	95.07	0.81	-25.90
CA1P × Wt6803	0.06	362	-84.18	80.30	0.76	-17.06
L020140 × CA1P	-0.05	348	-106.33	83.21	0.94	-23.83
CA1P × L020140	0.06	324	-66.01	69.61	0.84	-12.71

The number of genes influencing the manifestation of the sign that parents differ is different. At Wt6803 × CA1P along root lengths and at L020140 × CA1P, the fresh root weight and nodule weight of the genes by which the parents differ in the two environmental limits is relatively constant. At Wt6803 × CA1P crosses at plant height and fresh root weight, as well as at L020140 × CA1P along root length, the difference in the number of genes between parents is much larger.

Negative values of epistatic gene interactions at part of crosses, such as Wt6803 × CA1P for plant height and for almost all crosses (excluding CA1P × Wt6803), fresh root weight, when changing environmental conditions indicate that there is a suppression of dominant expression alleles leading to a lower phenotypic expression of the trait.

Table 5. Values of the gene parameters for the quantitative traits of the investigated crosses in F_2 generation, sparse sowing

Crosses/ Indicators	T_n	N	D	E	H^2	Pp
			Plant height			
Wt6803 × CA1P	-11.35	4	-5.58	1.74	0.09	-1.25
CA1P × Wt6803	13.88	296	62.26	-64.10	0.40	-13.25
L020140 × CA1P	-9.05	103	25.49	-23.92	0.16	-5.36
CA1P × L020140	11.06	124	34.93	-29.66	0.22	-8.43
			Fresh aboveground mass weight			
Wt6803 × CA1P	-3.89	111	4.78	-17.73	0.04	-0.93
CA1P × Wt6803	5.14	9	-9.21	3.29	0.21	-2.51
L020140 × CA1P	-0.28	146	33.33	-32.79	0.47	-6.86
CA1P × L020140	2.05	162	34.97	-35.85	0.49	-6.92
			Root length			
Wt6803 × CA1P	-1.45	316	19.55	-50.77	0.05	-1.83
CA1P × Wt6803	1.57	440	149.64	-107.98	0.31	-45.01
L020140 × CA1P	0.13	838	-120.04	162.15	0.57	-17.91
CA1P × L020140	-0.03	9	118.70	-4.61	0.11	-54.69
			Root fresh weight			
Wt6803 × CA1P	-0.33	862	-221.49	195.17	0.78	-43.81
CA1P × Wt6803	0.37	212	62.82	-50.54	0.36	-16.59
L020140 × CA1P	0.02	855	-109.76	160.73	0.96	-11.46
CA1P × L020140	0.03	617	-45.19	101.31	0.63	-1.49
			Nodule number			
Wt6803 × CA1P	-7.91	294	-91.84	70.73	0.90	-27.12
CA1P × Wt6803	8.53	433	121.78	-100.89	0.42	-32.99
L020140 × CA1P	-4.40	748	-145.10	157.01	0.60	-30.72
CA1P × L020140	5.07	460	-22.94	69.82	0.57	-4.78
			Nodule weight			
Wt6803 × CA1P	-0.06	252	-89.09	62.89	0.72	-21.95
CA1P × Wt6803	0.06	244	21.33	-42.65	0.02	0.90
L020140 × CA1P	-0.06	316	-97.34	75.71	0.76	-22.55
CA1P × L020140	0.07	276	-47.36	56.83	0.82	-7.70

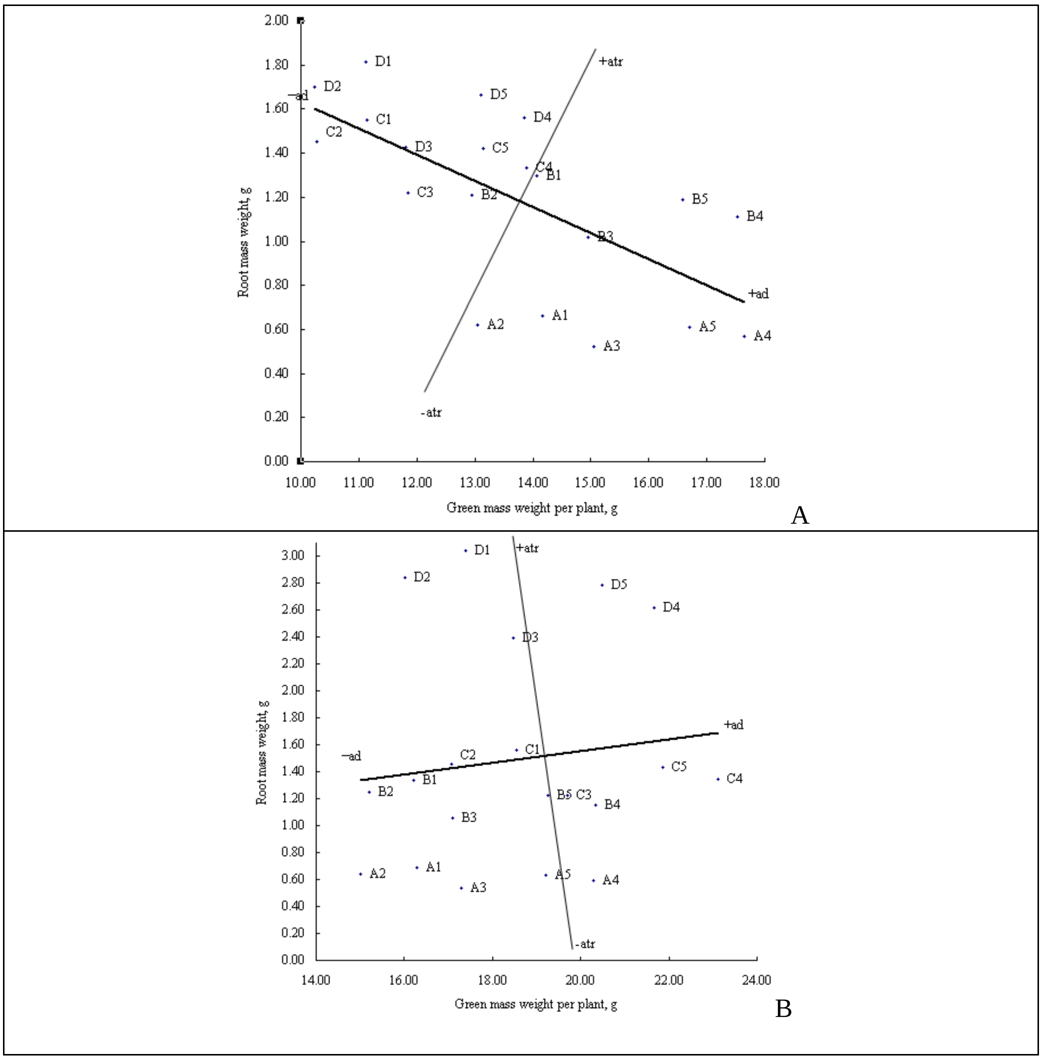

Figure 2. Distribution of mean values of fodder pea hybrids in a two-dimensional trait coordinate system
A - Wt6803 × CA1P, B - CA1P × Wt6803, C- L020140 × CA1P, D - CA1P × L020140, 1, 2, 3, 4 – individual plant from the respective hybrid, A - hybrids F1 dense sowing, B - hybrids F1 sparse sowing

The values of inheritance coefficients in the broad sense (H2) L020140 × CA1P and its reciprocal are higher for the signs of fresh weight of aboveground biomass and fresh weight of roots placed under favorable cultivation conditions, whereas at Wt6803 × CA1P01 and CA1P01 and CA1P01 along the roots, CA1P × Wt6803 and CA1P × L020140 by number of nodules, and in all hybrids by nodule weights, a reverse trend was observed. The values of the coefficient of effectiveness of the team (Pp), as well as under restrictive growing conditions indicate that in the general phenotypic manifestation of the traits studied, the genotype has a relatively small part. In almost all hybrids (excluding CA1P × Wt6803) with sparse sowing, the parameter (Pp) for selection efficiency is negative, indicating that, despite the high inheritance rate, for some of the traits the team may be effective in later hybrid generation (F5 - F6).

Figure 2 (A and B) shows the results of a test of 16 F1 hybrid forage peas at an environment limit, expressed by two different sowing rates (dense sowing and sparse) for the root weight and fresh aboveground biomass weight of a plant. In case of worsening of the cenotic environment (dense sowing - Figure 2A), the additive most valuable hybrid is CA1P × Wt6803 (4), followed by CA1P × Wt6803 (5). These hybrids exhibit a good combination of adaptability and attractiveness genes (rapid displacement of plastics) in case of worsening environment. Under sparse sowing (Figure 2B), such combinations have CA1P × L020140 (4) and CA1P × L020140 (5) hybrids with positive attractiveness and adaptability values.

The CA1P × Wt6803 (2) hybrid, at both limits of the environment retains its place in the same quadrant, bounded by the negative part, both in attraction and in adaptability. Favorable growing conditions (less competition) do not improve its adaptability. The CA1P × L020140 (1), CA1P × L020140 (2) and L020140 × CA1P (1) hybrids also do not change their quadrants, although they do change their exact location. Under favorable cultivation conditions (sparse sowing) CA1P × L020140 (1), CA1P × L020140 (2) exhibit a maximum positive attraction rate, suggesting that it bears strong attraction genes (productivity genes according to the traits studied). The other hybrid L020140 × CA1P (1) retains its attractiveness permanently but does not have the ability to adapt to adverse conditions. Most of the hybrids derived from the parental components of Wt6803 with CA1P, regardless of the direction of crossover under adverse conditions, fall into quadrants determined by negative adaptability and attraction, indicating that genetic control of adaptability is adversely affected by higher sowing densities for these hybrids.

By changing the attraction of hybrids, forage peas can be judged to have a strong polymorphism. The genetic diversity obtained is a good prerequisite for improving this crop on the traits studied. Selection work in self-pollinated crops is based on the manifestations of transgression in the second and later generations of hybrid genotypes, in which the level and magnitude of trait exceeds the maximum degree of their manifestation in parental forms.

DISCUSSIONS

When studying the genetic control of the trait height of the plant TSUKANOVA *et al.* (2012) note the complex type of inheritance. The authors found that the genes controlling this trait were located on all seven chromosomes of the chromosome set. The strong shortening of the internodes is due to both recessive and dominant genes. According to their studies, the manifestation of this trait is determined by two major gene systems that determine the number and length of nodes.

The complexity and diversity of genetic control of symbiosis in legumes is reported by SIDOROVA (2010), according to which research data indicate that few genes controlling this process have been identified. The author finds that macro-symbiotic genes determine the ability to form nodules, their number, their intracellular organization, nitrogen fixation and its duration, the amount of root mass, ect. According to ZYKIN (2007), transgressive decay is observed in cases where the parental forms used in hybridization do not have the ultimate degree of expression of the corresponding trait. POSTMA *et al*. (1988) report that the stimulation of nodule formation in mutant pea plants is due to the nod3 gene, which is associated with changes in root morphology and has a pleiotropic effect. Similar gene effects have also been found in soybean mutants.

SIDOROVA *et al.* (2006) report that the so-called super lump mutants, which are characterized by high nodule formation and active nitrogen fixation, have a serious disadvantage - they are significantly inferior in productivity to high yielding varieties. However, in field experiments as precursors to cereals, they have shown good results.

ASHIEV (2014) identifies in F4 hybrid generation transgressive recombinant pea forms with a complex of economically valuable qualities. The morpho-biological transformations of pea plants of ordinary leaf type obtained from him are related to the inclusion in their genome of recessive mutant genes def, le, af, controlling pod breakage, low stalking, leaf mustache leaves, resistance to lodging and increasing of seed productivity.

Analyzing hybrid vetch populations in terms of seed productivity and fresh biomass, TIURIN (2014) found different manifestations of these traits under different conditions. When crossing forms with different levels of productivity in third-generation hybrid generations, he noted an intermediate value of a trait or approaching one parent.

CONCLUSIONS

Positive true heterosis was detected at crosses L020140 × CA1P and CA1P × L020140 by fresh root weight and nodule weight; CA1P × Wt6803 by root length and nodule weight and CA1P × L020140 by plant height at both limits of the environment. Both root weight and number of nodules per plant at CA1P × Wt6803 and the weight of fresh biomass at CA1P × L020140 are inherited with a clear positive dominance or over-dominance. Negative was the dominance or over-dominance of Wt6803 × CA1P by root length and fresh root weight, number and weight of plant nodules; at CA1P × L020140 by number of nodules and at L020140 × CA1P by weight of nodules per plant. In more favorable growing conditions, epithelial gene interactions play a greater role in the inheritance of traits and the number of nodules in CA1P × Wt6803 and L020140 × CA1P, and for dense sowing at L020140 × CA1P and CA1P × L020140 by fresh aboveground biomass weight and nodule weight and at Wt6803 × CA1P, dominant gene actions are more important for the number of nodules per plant. High inheritance rates in both environments are characterized by hybrids Wt6803 × CA1P and L020140 × CA1P by fresh root weight and number of nodules per plant, and all hybrids by number of nodules. For almost all crosses, the efficiency of the team is negative and at both limits of the environment, which implies that the mass team will be more effective if it starts early in F4-F5 and is based on plant height, fresh weight of aboveground biomass and fresh weight of roots. The results obtained will complement the selection evaluation of the materials studied and will allow their targeted inclusion in the selection process.

Received, April 08h, 2025
Accepted September 30h, 2025

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GENETIČKA ANALIZA KVANTITATIVNIH OSOBINA GENOTIPA GRAŠKA

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Izvod

Studija je imala za cilj da analizira kvantitativne osobine genotipova graška kroz vrednosti genetskih parametara i da se odrede osobine od kojih varira produktivnost F1 i F2 hibridnih biljaka. Trogodišnji terenski ogled je sproveden u Institutu za krmno bilje – Pleven, Bugarska. Sledeća ukrštanja su proučavana, (CA1P × L020140; CA1P × Vt6803 i njihova uzajamnost) između sorti graška L020140 - *Pisum sativum* ssp. arvense, Vt6803 - *Pisum sativum* var. hiemale i CA1P - *Pisum sativum* ssp. sativum. Pozitivna prava heterozisa su otkrivena na ukrštanjima L020140 × CA1P i CA1P × L020140 prema težini svežeg korena i težine nodula; CA1P × Vt6803 po dužini korena i težini nodula i CA1P × L020140 po visini biljke na obe granice sredine. Znaci težine korena i broja kvržica po biljci na CA1P × Vt6803 i težina sveže biomase na CA1P k L020140 nasleđuju se sa jasnom pozitivnom dominacijom ili prekomernom dominacijom. Negativna je bila dominacija ili prekomerna dominacija Vt6803 × CA1P po dužini korena i težini svežeg korena, broju i težini biljnih nodula; kod CA1P × L020140 po broju nodula i kod L020140 × CA1P po težini nodula po biljci. U povoljnijim uslovima rasta, interakcije epitelnih gena igraju veću ulogu u nasleđivanju osobina i broja nodula kod CA1P × Vt6803 i L020140 × CA1P, a za gustu setvu kod L020140 × CA1P i CA1P × L020140 po težini svežeg nadzemnog bilja. Dominantna dejstva gena su bila od većeg značaja za broj nodula po biljci na Vt6803 × CA1P. Visoke stope nasleđivanja u obe sredine karakterišu hibridi Vt6803 × CA1P i L020140 × CA1P po težini svežeg korena i broju nodula po biljci, a svi hibridi po broju nodula. Za skoro sva ukrštanja, efikasnost tima je negativna i to na obe granice sredine, što implicira da će masovni tim biti efikasniji ako počne rano u F4-F5 i zasniva se na visini biljke, svežoj težini nadzemne biomase i svežem korenu.

Primljeno 08.IV.2025.
Odobreno 30.IX. 2025.

How to cite this article: Kosev V., V. Vasileva, V. Popović (2025). *Genetic analysis of quantitative traits in forage pea genotypes*.- Genetika, Vol. 57, No. 2, 315-331.